	1511 TOT	1511 TOT	Descriptions
AFFX-MurI	196.4	A	M16762 Mouse interleukin 2 (IL-2) gene, exon 4
AFFX-MurI	74.5	A	M37897 Mouse interleukin 10 mRNA, complete cds
AFFX-MurI	61.1	A	M25892 Mus musculus interleukin 4 (Il-4) mRNA, complete cds
AFFX-MurF	36	A	M83649 Mus musculus Fas antigen mRNA, complete cds
AFFX-BioB	6125.8	P	J04423 E coli bioB gene biotin synthetase (-5, -M, -3 represent trans
AFFX-BioB	6436.7	P	J04423 E coli bioB gene biotin synthetase (-5, -M, -3 represent trans
AFFX-BioB	5937.7	P	J04423 E coli bioB gene biotin synthetase (-5, -M, -3 represent trans
AFFX-BioC	11733.2	P	J04423 E coli bioC protein (-5 and -3 represent transcript regions 5
AFFX-BioC	13516.3	P	J04423 E coli bioC protein (-5 and -3 represent transcript regions 5
AFFX-BioD	3877.2	P	J04423 E coli bioD gene dethiobiotin synthetase (-5 and -3 represen
AFFX-BioD	20490.3	P	J04423 E coli bioD gene dethiobiotin synthetase (-5 and -3 represen
AFFX-CreX	5837.6	P	X03453 Bacteriophage P1 cre recombinase protein (-5 and -3 repres
AFFX-CreX	10423.9	P	X03453 Bacteriophage P1 cre recombinase protein (-5 and -3 repres
AFFX-BioB	91.5	A	J04423 E coli bioB gene biotin synthetase (-5, -M, -3 represent trans
AFFX-BioB	405.7	A	J04423 E coli bioB gene biotin synthetase (-5, -M, -3 represent trans
AFFX-BioB	199.9	A	J04423 E coli bioB gene biotin synthetase (-5, -M, -3 represent trans
AFFX-BioC	208.4	A	J04423 E coli bioC protein (-5 and -3 represent transcript regions 5
AFFX-BioC	80.5	A	J04423 E coli bioC protein (-5 and -3 represent transcript regions 5
AFFX-BioD	340.5	A	J04423 E coli bioD gene dethiobiotin synthetase (-5 and -3 represen
AFFX-BioD	777.6	A	J04423 E coli bioD gene dethiobiotin synthetase (-5 and -3 represen
AFFX-CreX	69.5	A	X03453 Bacteriophage P1 cre recombinase protein (-5 and -3 repres
AFFX-CreX	69	A	X03453 Bacteriophage P1 cre recombinase protein (-5 and -3 repres
AFFX-DapX	78.3	A	L38424 B subtilis dapB, jojF, jojG genes corresponding to nucleotide
AFFX-DapX	209.6	A	L38424 B subtilis dapB, jojF, jojG genes corresponding to nucleotide
AFFX-DapX	32.5	A	L38424 B subtilis dapB, jojF, jojG genes corresponding to nucleotide
AFFX-LysX	22.4	A	X17013 B subtilis lys gene for diaminopimelate decarboxylase corres
AFFX-LysX	80.3	A	X17013 B subtilis lys gene for diaminopimelate decarboxylase corres
AFFX-LysX	181.1	A	X17013 B subtilis lys gene for diaminopimelate decarboxylase corres
AFFX-PheX	55	A	M24537B subtilis pheB, pheA genes corresponding to nucleotides 20
AFFX-PheX	46.9	A	M24537B subtilis pheB, pheA genes corresponding to nucleotides 20
AFFX-PheX	713.6	A	M24537B subtilis pheB, pheA genes corresponding to nucleotides 20
AFFX-ThrX	74.4	A	X04603 B subtilis thrC, thrB genes corresponding to nucleotides 248
AFFX-ThrX	273.8	A	X04603 B subtilis thrC, thrB genes corresponding to nucleotides 248
AFFX-ThrX	76.4	A	X04603 B subtilis thrC, thrB genes corresponding to nucleotides 248
AFFX-Trpn	83.6	A	K01391 B subtilis TrpE protein, TrpD protein, TrpC protein correspon
AFFX-Trpn	32.8	A	K01391 B subtilis TrpE protein, TrpD protein, TrpC protein correspon
AFFX-Trpn	43.9	A	K01391 B subtilis TrpE protein, TrpD protein, TrpC protein correspon
AFFX-YFL	33174.7	P	V01288 SGD:YFL039C Yeast S. cerevisiae gene for actin (5, M, 3 re
AFFX-YFL	26408.8	P	V01288 SGD:YFL039C Yeast S. cerevisiae gene for actin (5, M, 3 re
AFFX-YFL	31711.4	P	V01288 SGD:YFL039C Yeast S. cerevisiae gene for actin (5, M, 3 re
AFFX-YER	7549.8	P	X16860 SGD:YER148W Yeast S. cervisiae TATA-binding protein (tfI
AFFX-YER	14017.3	P	X16860 SGD:YER148W Yeast S. cervisiae TATA-binding protein (tfI
AFFX-YER	22629.7	P	X16860 SGD:YER148W Yeast S. cervisiae TATA-binding protein (tfI
AFFX-YER	938.9	P	L12026 SGD:YER022W Yeast S. cerevisiae subunit of RNA polymer
AFFX-YER	1250.5	P	L12026 SGD:YER022W Yeast S. cerevisiae subunit of RNA polymer
AFFX-YER	1304.9	P	L12026 SGD:YER022W Yeast S. cerevisiae subunit of RNA polymer
AFFX-18sr	3884.3	P	Z75578 SGD:YLR154C Yeast S. cerevisiae 18S ribosomal RNA corr
AFFX-18sr	4048	P	Z75578 SGD:YLR154C Yeast S. cerevisiae 18S ribosomal RNA corr
AFFX-18sr	1318.4	P	Z75578 SGD:YLR154C Yeast S. cerevisiae 18S ribosomal RNA corr
AFFX-18sr	2137.8	P	Z75578 SGD:YLR154C Yeast S. cerevisiae 18S ribosomal RNA corr
AFFX-18sr	2200.6	P	Z75578 SGD:YLR154C Yeast S. cerevisiae 18S ribosomal RNA corr

AFFX-25sr	4669.6	P	Z73326 SGD:YLR154C Yeast S.cerevisiae 25S ribosomal RNA corre
AFFX-25sr	2857.7	P	Z73326 SGD:YLR154C Yeast S.cerevisiae 25S ribosomal RNA corre
AFFX-25sr	723.9	P	Z73326 SGD:YLR154C Yeast S.cerevisiae 25S ribosomal RNA corre
AFFX-25sr	2116.6	P	Z73326 SGD:YLR154C Yeast S.cerevisiae 25S ribosomal RNA corre
AFFX-25sr	23564.1	P	Z73326 SGD:YLR154C Yeast S.cerevisiae 25S ribosomal RNA corre
AFFX-YEL	12659.4	P	X61388 SGD: YEL002C Yeast S.cerevisiae WBP1 Oligosaccharyltra
AFFX-YEL	4916.5	P	U18530 SGD:YEL018W Yeast S. cerevisiae Protein of unknown func
AFFX-YEL	10071.7	P	M23316 SGD:YEL024C Yeast S.cerevisiae RIP1 Rieske iron-sulfur
AFFX-YEL	1178.8	P	K02207 SGD:YEL021W Yeast S.cerevisiae URA3 gene coding for O
11378_at	52	A	Aldehyde dehydrogenase 1, mitochondrial
11379_at	2036.2	P	Suppressor of Sulfoxyde Ethionine resistance
11380_at	505.5	P	hypothetical protein
11381_at	460.1	A	putative pseudogene
11382_at	403.6	A	putative pseudogene
11383_at	9.4	A	putative pseudogene
11384_at	124.3	A	hypothetical protein
11385_s_a	1559.1	M	putative Flo1p homolog
11386_at	1155.3	A	NADP-linked glutamate dehydrogenase
11387_at	736.4	A	similarity to alcohol/sorbitol dehydrogenase
11388_at	5314.4	P	similarity to alcohol/sorbitol dehydrogenase
11389_at	9341.6	P	ExtraCellular Mutant
11390_at	3214.2	P	Calnexin and calreticulin homolog
11391_at	620.1	A	questionable ORF
11392_at	1215.6	P	similarity to hypothetical protein YOR371c
11393_at	4375.3	P	hypothetical protein
11356_at	3115.3	P	inducible acetyl-coenzyme A synthetase
11357_at	6191.3	P	strong similarity to hypothetical proteins YOR365c,YGL139w,YPL22
11358_at	1987.8	P	peroxisome proliferating transcription factor
11359_at	14592	P	weak similarity to Legionella small basic protein sbpA
11360_at	733.5	P	weak similarity to GTP-binding proteins
11361_at	454.9	P	Spc72p interacts with Stu2p in the two-hybrid assay\; Spc72p localize
11362_at	4076.8	P	hypothetical protein
11363_at	1153.2	P	hypothetical protein
11364_at	15080	P	H-protein subunit of the glycine cleavage system
11365_at	4694	P	pre-tRNA processing
11366_at	49	A	questionable ORF
11367_at	25561.4	P	Function unknown now
11368_at	3309.1	P	Guanine nucleotide exchange factor (a.k.a. GDP-release factor) for
11369_at	9769.4	P	G(sub)1 cyclin
11370_at	17866.4	P	cytochrome c heme lyase (CCHL)
11371_at	13604.1	P	Pyruvate kinase
11372_at	1611.1	M	strong similarity to GTP-binding proteins
11373_at	18479.6	P	Function unknown now
11374_at	23014.5	P	97 kDa protein
11375_at	121.7	A	questionable ORF
11376_at	1035.9	M	hypothetical protein
11377_at	3960.9	P	Function unknown now
11333_at	5857.1	P	An integral subunit of RNase P and apparent subunit of RNase MRP
11334_at	754.7	A	Function unknown now
11335_at	2458.4	A	FUN21
11336_at	3881.1	P	homolog of Snc2p, vesicle-associated membrane protein (synaptob
11337_at	16072.2	P	homolog of Snc2p, vesicle-associated membrane protein (synaptob

11338_at	6287.5	P	myosin
11339_at	347.5	A	similarity to hypothetical protein YOR324c
11340_at	1061	P	hypothetical protein
11341_at	1701.2	P	Membrane-spanning Ca-ATPase (P-type),member of the cation tran
11342_at	1732.6	P	putative nuclear protein
11343_at	1680.8	P	putative GTP-exchange protein
11344_at	24483.5	P	dolichyl phosphate-D-mannose:protein O-D-mannosyltransferase
11345_at	6368.9	P	predicted membrane protein
11346_at	12962	P	95 kDa containg leucine rich tandem repeats
11347_at	4379.4	P	Protein with similarity to human RCC1 protein
11348_at	3753.4	P	Shows homology to SNF2 transcriptional regulator
11349_at	1080.2	P	3 transmembrane domains
11350_at	5999.3	P	Serine\/threonine kinase
11351_at	18662.7	P	protein phosphatase 2A regulatory subunit A
11352_at	1525.1	P	DNA glycosylase
11353_at	3864.9	P	protein of unknown function
11354_at	6599.2	P	regulation of phospholipid metabolism
11355_at	35569.7	P	cystathionine gamma-lyase
11310_at	1187.2	P	possible mitochondrial transit peptide
11311_at	710	P	Mitochondrial outer membrane protein involved in mitochondrial mor
11312_at	2709	P	sporulation protein
11313_at	3946	P	protein of unknown function
11314_at	11598.1	P	p24 protein involved in membrane trafficking
11315_i_at	15543.1	A	Heat shock protein of HSP70 family, cytoplasmic
11316_r_a	0.5	A	Heat shock protein of HSP70 family, cytoplasmic
11317_s_a	35212.1	P	Heat shock protein of HSP70 family, cytoplasmic
11318_at	991.3	P	strong similarity to A.klebsiana glutamate dehydrogenase
11319_at	16067	P	Translation elongation factor EF-1beta, GDP\/GTP exchange factor
11320_at	26830.8	P	Translation elongation factor EF-1beta, GDP\/GTP exchange factor
11321_at	597.6	A	Vps8p is a membrane-associated hydrophilic protein which contains
11322_at	3329.9	P	transcription factor tau (TFIIIC) subunit 138
11323_at	1812.9	P	transcription factor tau (TFIIIC) subunit 138
11324_at	5265.7	P	protein of unknown function
11325_at	23447.4	P	p24 protein involved in membrane trafficking
11326_at	2663.7	P	beta transducin domain
11327_at	16034.6	P	69 kDa subunit of the heterotrimeric RPA (RF-A) single-stranded DN
11328_at	2160.6	P	34kDa subunit of the tetrameric tRNA splicing endonuclease
11329_at	4249.1	P	maximal growth
11330_at	10502.2	P	phosphoribosyl amino imidazolesuccinocarbozamide synthetase
11331_at	891.9	P	protein kinase
11332_at	577.1	P	protein kinase domain
11287_f_at	1842.8	P	strong similarity to members of the srp1p/Tip1p family
11288_at	512.3	P	membrane protein
11289_at	909.3	P	membrane protein
11290_at	2346.8	P	membrane protein
11291_at	361	P	membrane protein
11292_at	55.3	A	hypothetical protein
11293_at	1086.1	P	membrane protein
11294_g_a	3125.7	P	membrane protein
11295_r_a	2603.6	P	membrane protein
11296_s_a	1404.5	P	membrane protein
11297_at	2448.5	P	Outer carnitine acetyltransferase, mitochondrial

11298_at	5134.4	P	ankyrin repeat
11299_at	1997.9	P	Shows homology to the human oxysterol binding protein (OSBP)
11300_at	143	A	predicted nuclear targeting signal
11301_i_at	34	A	FLO1 putative cell wall glycoprotein
11302_at	1114.8	P	predicted membrane protein
11303_s_a	678.6	P	strong similarity to hypothetical protein YHR212c
11304_at	752.2	A	putative pseudogene
11305_s_a	142.9	A	putative pseudogene
11306_at	764.2	M	Potential membrane protein
11307_s_a	1781.9	P	identical to YHR214w hypothetical protein, similarity to Sta1p
11308_s_a	1337.7	A	Potential membrane protein
11309_at	547.6	A	Potential membrane protein
11261_at	214.6	A	potential mitochondrial transit peptide
11262_s_a	38690.6	P	Acid phosphatase, secreted
11263_f_at	9582	P	strong similarity to IMP dehydrogenases
11264_f_at	15127.5	P	strong similarity to IMP dehydrogenases
11265_i_at	3051.6	A	hypothetical protein
11266_f_at	12557.1	A	hypothetical protein
11267_at	357.5	P	identified by SAGE
11268_at	346.9	A	hypothetical protein
11269_at	821.3	A	non-annotated SAGE orf Found forward in NC_001133 between 101
11270_at	111.2	A	non-annotated SAGE orf Found forward in NC_001133 between 237
11271_at	79.6	A	non-annotated SAGE orf Found reverse in NC_001133 between 312
11272_at	689.9	P	non-annotated SAGE orf Found reverse in NC_001133 between 222
11273_at	1010.1	P	non-annotated SAGE orf Found forward in NC_001133 between 734
11274_at	920.3	P	non-annotated SAGE orf Found reverse in NC_001133 between 139
11275_at	1549.8	P	non-annotated SAGE orf Found reverse in NC_001133 between 166
11276_at	53.1	A	non-annotated SAGE orf Found reverse in NC_001133 between 317
11277_at	10.3	A	non-annotated SAGE orf Found forward in NC_001133 between 197
11278_f_at	1714.3	P	non-annotated SAGE orf Found reverse in NC_001133 between 199
11279_s_a	571.5	A	non-annotated SAGE orf Found reverse in NC_001133 between 223
11280_at	135.8	A	non-annotated SAGE orf Found reverse in NC_001133 between 290
11281_at	276.6	A	non-annotated SAGE orf Found forward in NC_001133 between 299
11282_i_at	0.4	A	non-annotated SAGE orf Found reverse in NC_001133 between 182
11283_r_a	253.7	P	non-annotated SAGE orf Found reverse in NC_001133 between 182
11284_f_at	13253	A	non-annotated SAGE orf Found reverse in NC_001133 between 182
11285_at	13.9	A	non-annotated SAGE orf Found forward in NC_001133 between 198
11286_at	111.6	A	non-annotated SAGE orf Found reverse in NC_001133 between 199
11238_at	33.9	A	non-annotated SAGE orf Found forward in NC_001133 between 200
11239_at	139.5	A	non-annotated SAGE orf Found reverse in NC_001133 between 203
11240_s_a	315.3	M	non-annotated SAGE orf Found reverse in NC_001133 between 219
11241_at	519.8	P	non-annotated SAGE orf Found reverse in NC_001133 between 138
11242_f_at	125.8	A	non-annotated SAGE orf Found forward in NC_001133 between 223
11243_s_a	440.2	P	non-annotated SAGE orf Found forward in NC_001133 between 223
11244_s_a	537.5	P	non-annotated SAGE orf Found forward in NC_001133 between 223
11245_i_at	9.3	A	Centromere
11246_r_a	34.4	A	Centromere
11247_s_a	19471.8	P	strong similarity to members of the Sir1p/Tip1p family
11248_s_a	980.4	P	strong similarity to members of the Sir1p/Tip1p family
11249_f_at	5614.4	P	strong similarity to members of the Srp1p/Tip1p family
11250_s_a	1669.4	M	strong similarity to Pep1p
11251_s_a	845	P	homology to maltase(alpha-D-glucosidase)

11252_s_a	31.9	A	questionable ORF
11253_s_a	250.1	A	High-affinity hexose transporter
11254_at	449	P	strong similarity to E.coli galactoside O-acetyltransferase
11255_at	356.3	A	hypothetical protein
11256_at	31.7	A	strong similarity to Mal62p
11257_at	297.5	A	hypothetical protein
11258_at	218	A	High-affinity hexose transporter
11259_at	2630.3	P	similarity to Methanobacterium aryldialkylphosphatase related proteir
11260_at	4878.9	P	strong similarity to S.pombe isp4 protein
11215_at	192.8	A	questionable ORF
11216_at	12308.2	P	CH3HC4 zinc-binding integral peroxisomal membrane protein
11217_at	1792.4	P	Protein required for COB mRNA stability or 5 processing
11218_at	2772.5	P	mitochondrial nuclease
11219_at	2607.3	P	weak similarity to rat omega-conotoxin-sensitive calcium channel alp
11220_at	1191.9	P	similarity to YIL130p and Put3p
11221_at	17427.7	P	involved in secretion of proteins that lack classical secretory signal se
11222_at	4105.6	P	weak similarity to Tor2p
11223_at	1513.1	P	RNA splicing factor
11224_at	201.2	A	questionable ORF
11225_at	1148.4	P	ExtraCellular Mutant
11226_at	18250.6	P	strong similarity to aconitate hydratase
11227_at	3808.4	P	hypothetical protein
11228_at	25416.5	P	strong similarity to Pho87p
11229_at	1887.4	P	ubiquitin carboxyl-terminal hydrolase
11230_at	30383.6	P	Elongation enzyme 1, required for the elongation of the saturated fat
11231_at	57.9	A	questionable ORF
11232_at	1849.3	P	Protein involved in initiation of DNA replication
11233_at	6446	P	similarity to Sly41p
11234_at	6870.8	P	hypothetical protein
11235_at	15148	P	Ribosomal protein S14B (rp59B)
11236_at	8233	P	Ribosomal protein S22A (S24A) (rp50) (YS22)
11237_at	24948.4	P	Ribosomal protein L39 (L46) (YL40)
11192_at	777	P	questionable ORF
11193_at	3231.1	P	protein kinase homolog
11194_at	2601.9	P	putative mannosyltransferase
11195_at	775.9	P	hypothetical protein
11196_at	3260.4	P	hypothetical protein
11197_at	7580.8	P	A new gene encoding a protein that is related to Mnn10p, and that is
11198_at	198.3	A	questionable ORF
11199_at	3626.5	P	similarity to hypothetical protein YJR030c
11200_at	1073	P	essential for assembly of a functional F1-ATPase
11201_at	1323.7	P	Putative homolog of subunit 1 of bovine prefoldin, a chaperone com
11202_at	11608.3	P	hypothetical protein
11203_i_at	26647.1	P	Ribosomal protein L17B (L20B) (YL17)
11204_s_a	20575.9	P	Ribosomal protein L17B (L20B) (YL17)
11205_i_at	1088.6	P	Ribosomal protein L17B (L20B) (YL17)
11206_f_at	25170.8	P	Ribosomal protein L17B (L20B) (YL17)
11207_at	937.3	P	transcription factor
11208_at	726.2	A	questionable ORF
11209_at	15857.2	P	Cell wall beta-glucan assembly
11210_at	17966.2	P	subunit 3 of replication factor-A
11211_at	2911.7	P	carboxypeptidase yscS

11212_at	13093.3	P	similarity to YBR162c
11213_at	45	A	An a-specific gene that is induced to a higher expression level by alp
11214_at	50.3	A	questionable ORF
11170_at	361.5	A	transcription factor containing a SET domain
11171_at	17289.1	P	Farnesyl diphosphate synthetase (FPP synthetase)
11172_at	14978	P	Ubiquinol cytochrome-c reductase subunit 8 (11 kDa protein)
11173_at	6831.2	P	Protein kinase homolog, mutant is salt and pH sensitive
11174_at	4068	P	putative catalytic subunit of cAMP-dependent protein kinase
11175_at	1313.1	P	hypothetical protein
11176_at	260.2	A	weak similarity to dnaJ proteins
11177_at	118.9	A	hypothetical protein
11178_at	1365.5	P	member of the Pir1p/Hsp150p/Pir3p family
11179_at	12008	P	Heat shock protein, secretory glycoprotein
11180_at	24698.2	P	Protein with homology to Hsp150p and Pir1p, Pir2p, and Pir3p
11181_at	16060.1	P	Factor arrest protein
11182_at	2292.5	P	sensitive to sulfonylurea herbicides on complex media (YPD)
11183_at	2139.5	P	Fructose-2,6-bisphosphatase
11184_at	2488	P	Protein involved in vacuolar sorting
11185_at	938.1	A	L-myo-inositol-1-phosphate synthase
11186_at	1923.3	P	questionable ORF
11187_at	21171.5	P	similarity to hypothetical protein YDL123w
11188_at	473.7	P	questionable ORF
11189_at	1951.6	P	similarity to hypothetical protein YDR131c
11190_at	17161.9	P	RNA polymerase I subunit, not shared (A34.5)
11191_at	1370.2	P	weak similarity to C.elegans hypothetical protein C43G2.4
11147_at	1643.6	P	IME2-Dependent Signalling
11148_at	5541.9	P	weak similarity to T.pacificus retinal-binding protein
11149_at	255.2	A	hypothetical protein
11150_at	20118	P	16.5 kDa inner membrane protein required for import of mitochondria
11151_at	1143.4	P	questionable ORF
11152_g_a	2446.2	P	questionable ORF
11153_at	2326.7	P	Serine-threonine protein kinase
11154_at	4027.2	P	fourth-largest subunit of RNA polymerase II
11155_at	5718.8	P	Probable glycosyltransferase of KRE2\/KTR1\/YUR1 family\; located
11156_s_a	32237.3	P	translation initiation factor eIF4A
11157_at	1037.1	P	self-glucosylating initiator of glycogen synthesis\; similar to mammalia
11158_i_at	0.1	P	Ribosomal protein S21B (S26B) (YS25)
11159_s_a	22002.6	P	Ribosomal protein S21B (S26B) (YS25)
11160_at	415.8	P	questionable ORF
11161_at	7509.2	P	putative plasma membrane transporter capable of transporting sphin
11162_at	3022.3	P	mitochondrial carrier protein
11163_at	404.5	P	weak similarity to human phospholipase D
11164_at	1650.3	P	weak similarity to nonepidermal Xenopus keratin, type I
11165_at	24697.7	P	carbamoyl-phophate synthetase, aspartate transcarbamylase, and g
11166_at	2393.8	P	180 kDa high affinity potassium transporter
11167_at	3210.3	P	MAP kinase kinase (MEK), may act as a scaffolding protein for Sho1
11168_at	362.4	P	negative transcriptional regulator
11169_at	2732.3	P	Nit2 nitrilase
11124_at	4647	P	translational repressor of GCN4
11125_at	4688	P	Like Sm-B protein\; contains the Sm consensus motifs and most clo
11126_at	12609.9	P	weak similarity to D.melanogaster troponin T and human nucleolin
11127_at	13789.1	P	weak similarity to dog-fish transition protein S2

11128_at	25095	P	D-ribulose-5-Phosphate 3-epimerase
11129_at	658.5	P	questionable ORF
11130_at	603.5	A	questionable ORF
11131_at	6874	P	hypothetical protein
11132_at	13297.2	P	Putative inorganic phosphate transporter
11133_at	4391.5	P	With NCA2, regulates proper expression of subunits 6 (Atp6p) and
11134_at	8082	P	Anti-silencing protein that causes depression of silent loci when over
11135_at	2781.3	P	similarity to Met30p and N.crassa sulfur controller-2
11136_at	7547.5	P	Component of Chaperonin Containing T-complex subunit seven
11137_at	2660.7	P	GATA zinc finger protein 3 homologous to Dal80 in structure and fun
11138_at	8791.1	P	weak similarity to ATPase Drs2p
11139_at	7756	P	strong similarity to hypothetical S. pombe protein
11140_at	531.5	P	similarity to hypothetical S. pombe protein
11141_at	384.2	P	Serine\/Threonine protein kinase, positively regulated by IME1
11142_at	139.7	A	similarity to hypothetical protein YKR029c
11143_at	2239.7	P	weak similarity to C.elegans hypothetical protein F45G2.c
11144_at	294.8	A	putative regulatory protein
11145_at	3034	P	mitochondrial elongation factor G-like protein
11146_at	2989.3	P	gamma-glutamylcysteine synthetase
11102_at	3806.3	P	similarity to hypothetical C. elegans protein C56A3.8
11103_at	1925.6	P	Involved in chitin biosynthesis and\/or its regulation
11104_at	3272.4	P	SIT4 associated protein, MW of 185 kDa
11105_at	17465.5	P	similarity to hypothetical C. elegans protein T15B7.2
11106_at	8255.9	P	ribosomal protein YmL49, mitochondrial
11107_at	2485	P	putative 163 kDa protein kinase
11108_at	3767.6	P	similarity to E.hirae NaH-antiporter NapA
11109_at	1365.4	P	outward-rectifier potassium channel
11110_at	2989.7	P	DNA helicase
11111_at	8621.6	P	weak similarity to human G protein-coupled receptor
11112_at	1359.6	P	Part of the DNA polymerase II complex, acts in a checkpoiint pathw
11113_at	210.9	A	shows homology to DNA binding domain of Gal4p, has a leucine zip
11114_at	1822.4	P	Ornithine carbamoyltransferase
11115_at	1281.1	P	tRNA ligase
11116_at	28.8	A	questionable ORF
11117_at	509.2	P	70 kD component of the Exocyst complex\; required for exocytosis
11118_at	1842	P	similarity to hypothetical protein YKR021w
11119_at	1688.3	P	similarity to hypothetical protein YKR019c
11120_at	3004.5	P	strong similarity to hypothetical protein YKR018c
11121_at	6023.9	P	54.8 kDa actin-related protein
11122_at	23493.4	P	May be required during cell division for faithful partitioning of the ER
11123_at	9783.5	P	Similar to plant PR-1 class of pathogen related proteins
11079_at	9495.3	P	Similar to plant PR-1 class of pathogen related proteins
11080_at	366.9	A	hypothetical protein
11081_at	10595.3	P	Establishes Silent omatin\; homolog of TOF2
11082_at	1010.7	A	questionable ORF
11083_at	3270.9	P	required for structural maintenance of chromosomes
11084_at	1659.8	P	DnaJ-like protein of the endoplasmic reticulum membrane
11085_at	1760.6	P	hypothetical protein
11086_at	3315.2	P	Acetylglutamate Synthase
11087_at	732.6	P	similarity to AMP deaminases
11088_at	8425.6	P	similarity to C.elegans hypothetical protein
11089_at	8334.1	P	strong similarity to human esterase D

11090_at	948.9	M	questionable ORF
11091_at	1679.7	P	hypothetical protein
11092_at	12558.3	P	weak similarity to DNA-directed DNA polymerase II chain C
11093_at	342.1	A	hypothetical protein
11094_at	10971.9	P	Mitochondrial ribosomal protein MRPL8 (YmL8) (E. coli L17)
11095_at	6133.6	P	similarity to S.pombe SPAC13G6.3 protein
11096_at	1310.6	P	82-kDa protein, with putative coiled-coil domain, has carboxy-termin
11097_at	2025.7	P	similarity to kynurenine aminotransferase and glutamine-phenylpyruv
11098_at	919.9	P	Homolog of human CLN3
11099_at	39.8	A	strong similarity to hypothetical protein YBR270c
11100_at	743.9	P	probable serine\/threonine kinase
11101_at	2090.6	P	Metalloregulatory protein involved in zinc-responsive transcriptional r
11057_at	16602.1	P	similarity to R.fascians hypothetical protein 6
11058_at	4372.6	P	Translocase for the insertion of proteins into the mitochondrial inner
11059_at	1970.5	P	Vacuolar protein similar to mouse gene H<beta>58
11060_at	12362.4	P	Glyceraldehyde-3-phosphate dehydrogenase 1
11061_g_a	11511.9	P	Glyceraldehyde-3-phosphate dehydrogenase 1
11062_at	1020	P	hypothetical protein
11063_at	3795.8	P	DEAD-box family helicase required for mRNA export from nucleus
11064_at	2248.1	P	hypothetical protein
11065_at	6903.3	P	similarity to hypothetical protein YBR273c
11066_at	1027	P	Regulator of Ty1 Transposition
11067_at	1019.4	P	similarity to E.coli lipoate-protein ligase A
11068_at	435.4	A	strong similarity to succinate dehydrogenase flavoprotein
11069_at	1374.5	P	GTPase-activating protein for Ypt6
11070_at	153.8	A	similarity to hypothetical protein YKR015c
11071_at	9319.6	P	Putative microtubule-associated protein (MAP)
11072_at	8584.6	P	Nucleoskeletal protein found in nuclear pores and spindle pole body
11073_at	2439.6	P	similarity to human protein interacting with human nuclearpore protei
11074_at	48.3	A	strong similarity to hypothetical protein YJL037w
11075_at	1728.1	P	strong similarity to hypothetical protein YJL038c
11076_at	490.2	P	weak similarity to Mvp1p
11077_at	1980.8	P	weak similarity to P.gingivalis PgaA and B.japonicum nitrogen fixatio
11078_at	21583	P	Homologue of mammalian BiP (GPR78) protein\; member of the HS
11034_at	4055.1	P	putative RNA helicase
11035_at	2070.4	P	questionable ORF
11036_at	779.2	P	Geranylgeranyltransferase Type II alpha subunit (PGGTase-II, alpha
11037_at	3227.9	P	spindle-assembly checkpoint protein
11038_at	2722.5	P	similarity to C.elegans hypothetical protein T05G5.8
11039_at	130	A	hypothetical protein
11040_at	2316.3	P	hypothetical protein
11041_at	25217.3	P	small subunit of ribonucleotide reductase
11042_at	1240.8	P	member of yeast Pol I core factor (CF) also composed of Rrn11p, R
11043_at	1789.7	P	similar to Aps1p and mammalian small subunit (sigma-2 adaptin) of
11044_at	704.1	P	Nuclear gene encoding mitochondrial protein
11045_at	59.5	A	questionable ORF
11046_at	3497.8	P	weak similarity to S.pombe hypothetical protein SPAC23A1.16
11047_at	6464.4	P	similarity to P.falciparum glutamic acid-rich protein
11048_at	471	P	hypothetical protein
11049_g_a	996.8	P	hypothetical protein
11050_at	2067.6	P	questionable ORF
11051_at	1371.7	P	hypothetical protein

11052_at	4291.3	P	weak similarity to hypothetical protein YNL278w and YLR187w
11053_at	215.5	P	questionable ORF
11054_at	8441.4	P	Cytoplasmic chaperonin subunit gamma
11055_at	599.4	P	Checkpoint protein required for cell cycle arrest in response to loss o
11056_at	26779.5	P	weak similarity to regulatory protein PHO81
11010_at	3383.9	P	weak similarity to chicken hypothetical protein
11011_at	4795.4	P	weak similarity to C.elegans hypothetical protei ZK792.5
11012_at	1743.3	P	questionable ORF
11013_at	21270.7	P	Component of Chaperonin Containing T-complex subunit eight
11014_at	237	A	hypothetical protein
11015_at	1806.5	P	cyclin-related subunit of the kinase complex that phosphorylates the
11016_at	1999.6	P	adenylate cyclase
11017_at	3996.9	P	Multicopy suppressor of ypt6 null mutation
11018_at	1917.4	P	hypothetical protein
11019_at	28331.5	P	64-kDa, alpha subunit of oligosaccharyltransferase complex\; homol
11020_i_a	5395.2	P	Subunit of 20S proteasome
11021_f_a	9383	A	Subunit of 20S proteasome
11022_at	20694.7	P	Subunit of 20S proteasome
11023_at	15027	P	weak similarity to A.thaliana aminoacid permease AAP4
11024_at	4072.6	P	Protein component of the U3 small nucleolar ribonucleoprotein (sno
11025_at	2954.6	P	hypothetical protein
11026_at	27046.5	P	alpha-agglutinin
11027_at	2341.4	P	beta-adaptin, large subunit of the clathrin-associated protein comple
11028_at	2031.4	P	DNA-directed DNA polymerase delta, 55 KD subunit
11029_at	6198.4	P	Translation initiation factor eIF-2 alpha subunit
11030_at	220.1	A	similarity to S.pombe hypothetical protein
11031_s_a	35482.7	P	glyceraldehyde 3-phosphate dehydrogenase
11032_at	1690.8	P	ATP sulfurylase
11033_at	1876.5	P	Homologue of the SPC12 subunit of mammalian signal peptidase co
10988_at	744.4	P	hypothetical protein
10989_at	975.3	P	hypothetical protein
10990_at	6241.1	P	similarity to C.elegans B0491.1 protein
10991_at	8366.6	P	strong similarity to S.pombe hypothetical protein SPBC16C6.05
10992_at	5142.6	P	strong similarity to Sng1p
10993_at	34073.8	P	dihydroxyacid dehydratase
10994_at	21208.6	P	Peptidyl-prolyl cis\/trans isomerase (PPIase)
10995_at	2292.2	P	questionable ORF
10996_at	3810.2	P	peroxisomal acyl-CoA thioesterase
10997_at	476.1	P	questionable ORF
10998_at	1199	A	meiotic recombination protein
10999_at	178.1	A	meiotic recombination protein
11000_at	2180.8	P	Sm-like protein
11001_at	342.7	A	hypothetical protein
11002_at	9573	P	weak similarity to C.elegans Z49131_E ZC373.5 protein
11003_at	20098.1	P	3-hydroxyanthranilic acid dioxygenase
11004_at	1035.9	P	similarity to hypothetical protein YJL181w
11005_at	3410.4	P	Component of a complex guanine nucleotide exchange activity for th
11006_at	1457.6	P	a cyclophilin related to the mammalian CyP-40\; physically interacts
11007_at	2054.6	P	similarity to Drosophila DmX gene
11008_at	2174.2	P	Required for assembly of active cytochrome c oxidase
11009_at	627.5	P	DNA-dependent ATPase, homologous to human Cockayne syndrom
10965_at	1139.1	P	similarity to human E6-associated protein

10966_at	419.3	A	questionable ORF
10967_at	1074.1	A	questionable ORF
10968_at	1054.9	P	hypothetical protein
10969_at	1491.5	P	putative transport protein involved in intracellular iron metabolism
10970_at	2947.8	P	hypothetical protein
10971_at	10029	P	Protein in nuclear pore complex\; may function in nuclear envelope ir
10972_at	115	A	third (55 kDa) subunit of DNA polymerase delta
10973_at	19934.6	P	weak similarity to putative transport protein YKR103w
10974_at	8116.3	P	Mitochondrial matrix protein involved in protein import\; subunit of Sc
10975_at	3816.6	P	weak similarity to Xenopus vimentin 4
10976_at	4424.4	P	anaerobically expressed form of translation initiation factor eIF-5A
10977_at	32623.6	P	iso-1-cytochrome c
10978_at	2236.2	P	Associated with ferric reductase
10979_at	740.6	P	Interacts with Syf1p: Isy1p was identified through a two-hybrid scree
10980_at	3028.5	P	osmotic growth protein
10981_at	4691.3	P	Nucleotide excision repair protein involved in G(sub)2 repair of inacti
10982_at	568.6	P	hypothetical protein
10983_at	2996.3	P	similarity to hypothetical protein YML047c
10984_at	1076.6	P	Protein required for growth at high temperature
10985_at	1518.1	P	hypothetical protein
10986_at	2428	P	thymidylate kinase
10987_at	6048.6	P	Clathrin-associated protein, small subunit
10943_at	5191.7	P	Putative serine\/threonine protein kinase that enhances spermine upt
10944_at	680	M	basic helix-loop-helix protein
10945_at	130.5	A	similarity to Mnn4p
10946_at	904.3	P	52-kDa amidase specific for N-terminal asparagine and glutamine
10947_at	9086.4	P	A12.2 subunit of RNA polymerase I
10948_at	26262.2	P	subunit of chaperonin subunit epsilon
10949_at	9980.1	P	actin-related gene
10950_at	3021.3	P	phosphatidylinositol kinase homolog
10951_at	2314.6	P	Essential protein of unknown function
10952_at	4206.6	P	Subunit 2 of Replication Factor C\; homologous to human RFC 37 kD
10953_at	8764.3	P	controls 6-N-hydroxylaminopurine sensitivity and mutagenesis
10954_at	29579.6	P	similarity to C.elegans hypothetical protein C14A4.1
10955_at	70.3	A	questionable ORF
10956_at	6889.6	P	strong similarity to C.elegans hypothetical protein and similarity to YL
10957_at	16433.3	P	Methylene-fatty-acyl-phospholipid synthase (unsaturated phospholipi
10958_at	4260.8	P	Protein interacts with Gsp1p
10959_at	3290.8	P	putative mannosyltransferase
10960_at	8318.3	P	Component of 10 nm filaments of mother-bud neck
10961_at	22318.6	P	Mir1p has been purified as a mitochondrial import receptor (p32) wh
10962_at	4162	P	similarity to mammalian indoleamine 2,3-dioxygenase
10963_at	4535.3	P	questionable ORF
10964_at	9367.3	P	hypothetical protein
10920_at	377.8	A	questionable ORF
10921_at	822.3	P	hypothetical protein
10922_at	1078.4	P	hypothetical protein
10923_at	2764	P	weak similarity to S.pombe hypothetical protein SPAC1B3.08
10924_at	27020.9	P	hypothetical protein
10925_at	2139.6	P	gamma subunit of G protein coupled to mating factor receptors
10926_at	911.5	P	questionable ORF
10927_at	2846.7	P	weak similarity to S.pombe hypothetical protein SPBC14C8.18c

10928_at	1205.7	P	hypothetical protein
10929_at	2555	P	F box protein with several leucine rich repeats
10930_at	2920.5	P	Benomyl dependent tubulin mutant
10931_at	2445.1	P	Component of a pre-mRNA polyadenylation factor that interacts with
10932_at	1118.3	P	meiotic gene expression\; meiosis inducing protein
10933_at	11361.2	P	Ribosomal protein L43B
10934_at	562.1	A	protein related to mitochondrial carriers
10935_at	1512.8	P	similarity to Corynebacterium 2,5-diketo-D-gluconic acid reductase
10936_at	915.2	P	weak similarity to Caj1p
10937_at	1759.6	P	weak similarity to Bacillus licheniformis esterase
10938_at	1008.9	P	ubiquitin hydrolase
10939_at	2962	P	weak similarity to Bud3p
10940_at	2588.1	P	weak similarity to superoxide dismutases
10941_at	2491.4	P	hypothetical protein
10942_at	11229.1	P	CTP synthase
10897_at	24161.2	P	Cu, Zn superoxide dismutase
10898_at	26673.6	P	strong similarity to human adenosine kinase
10899_at	572.9	A	ExtraCellular Mutant
10900_at	3119.1	P	weak similarity to acylglycerol lipase
10901_at	460.4	A	similarity to hypothetical protein YIL014c-a
10902_at	8150.3	P	carbamyl phosphate synthetase
10903_at	1741.8	P	similarity to human myotubularin
10904_at	3880.4	P	weak similarity to E.coli colanic acid biosynthesis positive regulator R
10905_at	3533.3	P	involved in nuclear function
10906_at	9020.4	P	similarity to bacterial, chloroplast and mitochondrial ribosomal protei
10907_at	672.5	A	questionable ORF
10908_at	2577.9	A	similarity to hypothetical protein YBL043w
10909_at	9447.9	P	similarity to hypothetical protein YPR114w
10910_at	9419	P	zinc metallo-protease that catalyzes the first step of N-terminal proce
10911_at	6769.5	P	weak similarity to Helicobacter pylori UreD protein
10912_at	219.9	P	similarity to human retinoblastoma binding protein 2
10913_at	121.1	A	hypothetical protein
10914_at	22983.1	P	F(1)F(0)-ATPase complex beta subunit, mitochondrial
10915_at	1257.3	P	CCR4 associated factor
10916_at	31193.9	P	Ribosomal protein S5 (S2) (rp14) (YS8)
10917_at	3544.4	P	weak similarity to Staphylococcus multidrug resistance protein
10918_at	4355.3	P	similarity to human KIAA0171 protein
10919_at	4195.1	P	similarity to human prostate-specific membrane antigen and transfe
10875_at	4339.9	P	similarity to regulatory protein Ard1p
10876_at	88.4	A	questionable ORF
10877_at	2031	P	weak similarity to hypothetical protein YNL024c
10878_at	1938	P	similarity to O-succinylhomoserine (thiol)-lyase
10879_at	1693.5	P	specific alpha-mannosidase
10880_at	2647	P	Putative Upf1p interacting protein
10881_at	29400	P	strong similarity to hypothetical protein YDR399w
10882_at	514.7	P	similarity to paramyosin, myosin
10883_at	221.6	P	Required for maintenance of chromosomes and minichromosomes
10884_at	980.6	P	weak similarity to human 3 ,5 -cyclic-GMP phosphodiesterase
10885_at	10554	P	ExtraCellular Mutant
10886_at	1087.3	P	similarity to C.elegans hypothetical protein T08A11.1
10887_at	33452.7	P	Homoserine dehydrogenase (L-homoserine:NADP oxidoreductase)
10888_at	2787.2	P	involved in cell-cycle regulation of histone transcription

10889_at	1757.3	P	hypothetical protein
10890_at	2093.6	P	similarity to thiamin pyrophosphokinase
10891_at	15932.7	P	dolichyl phosphate-D-mannose:protein O-D-mannosyltransferase
10892_at	3176.5	P	involved in mitochondrial genome maintenance
10893_s_a	31788.7	P	Ribosomal protein S4A (YS6) (rp5) (S7A)
10894_at	991.2	P	questionable ORF
10895_at	6482.9	P	heat shock transcription factor homolog
10896_at	24868.9	P	Branched-Chain Amino Acid Transaminase
10851_at	1074.3	P	similarity to 2-nitropropane dioxygenase
10852_at	1177.9	A	Protein induced during anaerobic growth
10853_at	3000.5	P	similarity to mucin proteins, YKL224c, Sta1p
10854_at	1683.8	P	allantoate permease
10855_at	903.5	A	Endo-polygalacturonase
10856_at	708.9	P	hypothetical protein
10857_at	2016.5	P	Hypothetical aryl-alcohol dehydrogenase (AAD)
10858_s_a	2093.2	P	Thiamine biosynthetic enzyme
10859_at	106.4	A	hypothetical protein
10860_s_a	929.1	P	hexose transporter
10861_s_a	1739.7	P	sorbitol-induced sorbitol dehydrogenase
10862_s_a	356	A	strong similarity to Mal31p
10863_i_at	2728.9	P	identified by SAGE
10864_r_a	2436.9	M	identified by SAGE
10865_at	2463.5	P	C-terminal part of YJR030c
10866_at	6373.9	P	similarity to human DDP gene, hypothetical protein of S.pombe (YA
10867_s_a	2967.6	P	Co-assembles with Bud3p at bud sites
10868_at	10774.5	P	non-annotated SAGE orf Found reverse in NC_001142 between 159
10869_at	5737.2	P	non-annotated SAGE orf Found reverse in NC_001142 between 181
10870_i_at	180.7	P	non-annotated SAGE orf Found reverse in NC_001142 between 227
10871_s_a	2958.9	P	non-annotated SAGE orf Found reverse in NC_001142 between 227
10872_at	8805	P	non-annotated SAGE orf Found reverse in NC_001142 between 227
10873_at	243.6	A	non-annotated SAGE orf Found reverse in NC_001142 between 471
10874_at	12371.6	P	non-annotated SAGE orf Found forward in NC_001142 between 316
10828_at	442.4	A	non-annotated SAGE orf Found forward in NC_001142 between 444
10829_at	1073	P	non-annotated SAGE orf Found forward in NC_001142 between 445
10830_at	229.2	A	non-annotated SAGE orf Found reverse in NC_001142 between 451
10831_s_a	2370.9	P	non-annotated SAGE orf Found reverse in NC_001142 between 731
10832_s_a	377.2	P	non-annotated SAGE orf Found reverse in NC_001142 between 740
10833_at	1202	P	non-annotated SAGE orf Found forward in NC_001142 between 106
10834_at	532.1	A	non-annotated SAGE orf Found reverse in NC_001142 between 121
10835_at	1156.1	A	non-annotated SAGE orf Found reverse in NC_001142 between 187
10836_at	7075.7	P	non-annotated SAGE orf Found reverse in NC_001142 between 289
10837_at	455.5	P	non-annotated SAGE orf Found reverse in NC_001142 between 312
10838_at	29211.6	P	non-annotated SAGE orf Found reverse in NC_001142 between 410
10839_at	780.9	P	non-annotated SAGE orf Found reverse in NC_001142 between 518
10840_at	765.2	A	non-annotated SAGE orf Found forward in NC_001142 between 548
10841_at	1141.6	P	non-annotated SAGE orf Found forward in NC_001142 between 622
10842_at	5777.4	P	non-annotated SAGE orf Found forward in NC_001142 between 637
10843_at	60.2	A	non-annotated SAGE orf Found reverse in NC_001142 between 136
10844_at	389.9	P	non-annotated SAGE orf Found forward in NC_001142 between 900
10845_at	549.2	A	non-annotated SAGE orf Found reverse in NC_001142 between 116
10846_at	736.1	P	non-annotated SAGE orf Found forward in NC_001142 between 142
10847_at	2292.7	P	non-annotated SAGE orf Found forward in NC_001142 between 180

10848_at	2558.7	P	non-annotated SAGE orf Found forward in NC_001142 between 236
10849_at	1183.5	A	non-annotated SAGE orf Found forward in NC_001142 between 337
10850_at	249.1	A	non-annotated SAGE orf Found reverse in NC_001142 between 416
10806_at	10.2	A	non-annotated SAGE orf Found reverse in NC_001142 between 424
10807_at	1315.8	A	non-annotated SAGE orf Found reverse in NC_001142 between 448
10808_at	33.1	A	non-annotated SAGE orf Found forward in NC_001142 between 471
10809_g_a	429.8	P	non-annotated SAGE orf Found forward in NC_001142 between 471
10810_i_at	208.6	A	non-annotated SAGE orf Found forward in NC_001142 between 471
10811_at	621.7	P	non-annotated SAGE orf Found reverse in NC_001142 between 626
10812_s_a	326.6	P	non-annotated SAGE orf Found reverse in NC_001142 between 731
10813_s_a	1154	A	non-annotated SAGE orf Found reverse in NC_001142 between 734
10814_s_a	5895.5	P	non-annotated SAGE orf Found forward in NC_001142 between 741
10815_at	1139.9	P	non-annotated SAGE orf Found reverse in NC_001142 between 104
10816_at	15.1	A	non-annotated SAGE orf Found reverse in NC_001142 between 172
10817_at	2172.9	P	non-annotated SAGE orf Found forward in NC_001142 between 283
10818_at	1590.5	P	non-annotated SAGE orf Found forward in NC_001142 between 322
10819_at	2073.4	P	non-annotated SAGE orf Found reverse in NC_001142 between 396
10820_at	4336.1	P	non-annotated SAGE orf Found forward in NC_001142 between 447
10821_g_a	364.8	M	non-annotated SAGE orf Found forward in NC_001142 between 447
10822_at	179.6	A	non-annotated SAGE orf Found forward in NC_001142 between 447
10823_at	1434.8	P	non-annotated SAGE orf Found forward in NC_001142 between 549
10824_at	699.4	A	non-annotated SAGE orf Found forward in NC_001142 between 578
10825_at	972.6	P	non-annotated SAGE orf Found reverse in NC_001142 between 637
10826_at	7.9	A	non-annotated SAGE orf Found reverse in NC_001142 between 727
10827_s_a	517.1	P	non-annotated SAGE orf Found reverse in NC_001142 between 737
10782_at	10101.7	P	small nuclear RNA128
10783_at	283.6	A	small nuclear RNA190
10784_at	2470.4	P	small nuclear RNA37
10785_at	1000.3	P	snRNA
10786_i_at	3.1	A	Centromere
10787_at	3596.8	P	small nuclear RNA3
10788_at	134.9	A	ARS121 Found forward in NC_001142 between 683650 and 683699
10789_f_at	2681.5	P	strong similarity to members of the Srp1p/Tip1p family
10790_at	834.1	P	weak similarity to transcription factors, similarity to finger proteins YC
10791_at	40	A	weak similarity to human X-linked PEST-containing transporter
10792_at	597.3	A	Ferric reductase, similar to Fre1p
10793_at	2386	P	Protein with similarity to subtelomerically-encoded proteins such as
10794_at	2415.3	P	threonine dehydratase
10795_at	124.6	A	carboxylic acid transporter protein homolog
10796_at	28972	P	dihydroorotate dehydrogenase
10797_at	4120.9	P	similarity to P. aeruginosa hyuA and hyuB
10798_at	5157.1	P	weak similarity to mouse transcriptional coactivator ALY
10799_at	7351.1	P	phospholipase A2-activating protein
10800_at	18815.2	P	integral membrane protein localizing to the ER and Golgi
10801_at	5282.4	P	anthranilate synthase Component II and indole-3-phosphate (multifur
10802_at	12826.9	P	ubiquitin activating enzyme, similar to Uba2p
10803_at	474.5	P	ABC transporter, glycoprotein, component of a-factor secretory path
10804_at	1771.9	P	Subunit of complex involved in processing of the 3 end of cytochrom
10805_at	5160.1	P	hypothetical protein
10760_at	3360.2	P	hypothetical protein
10761_at	4210.6	P	nuclear protein LOS1
10762_at	9471.3	P	probable purine nucleotide-binding protein

10763_at	3579.1	P	phosphatidylinositol kinase homolg
10764_at	460.7	A	questionable ORF
10765_at	3332.1	P	member of the AAA-protein family
10766_at	16669.6	P	v-SNARE
10767_at	5166.9	P	similarity to rabbit histidine-rich calcium-binding protein
10768_at	1648.2	P	mitochondrial threonine-tRNA synthetase
10769_at	2372.9	P	Interacts with and may be a positive regulator of GLC7 which encode
10770_at	17464.2	P	acyl carrier protein
10771_at	12491.1	P	diphthamide synthesis protein
10772_at	1795.4	P	Type 2B protein phosphatase\; regulatory B subunit of calcineurin
10773_at	6961.6	P	Type 2B protein phosphatase\; regulatory B subunit of calcineurin
10774_at	1571.7	P	The homologue in Aspergillus nidulans, hymA, is involved in develop
10775_at	345.1	P	peroxisomal ABC transporter 2
10776_at	759	P	strong similarity to hypothetical protein YLR413w
10777_at	2810	P	mRNA transport regulator
10778_at	2184	P	probable purine nucleotide-binding protein
10779_at	5855.7	P	Ornithine decarboxylase
10780_at	2362.3	P	hypothetical protein
10781_at	14947	P	pentafunctional enzyme consisting of the following domains : acetyl
10737_at	26329	P	ribose-phosphate pyrophosphokinase
10738_i_at	924.9	A	Ribosomal protein L17A (L20A) (YL17)
10739_f_at	26728.7	P	Ribosomal protein L17A (L20A) (YL17)
10740_at	6805	P	kinesin-like protein
10741_at	16777.1	P	a factor recptor
10742_at	854.5	A	questionable ORF
10743_at	2588.9	P	hypothetical protein
10744_at	10106.5	P	weak similarity to E.coli hypothetical protein
10745_at	1921.3	P	probable transport protein
10746_at	5302.1	P	U5 snRNP-specific protein related to EF-2
10747_at	9023.5	P	Nucleolar protein
10748_at	1643.8	M	probable serine\/threonine-specific protein kinase (EC 2.7.1.-)
10749_at	4343.1	P	mitochondrial ribosomal protein L14
10750_at	1089.7	P	questionable ORF
10751_at	1281.5	P	probable serine\/threonine-specific protein kinase (EC 2.7.1.-)
10752_at	6408.8	P	16 kDa mitochondrial ribosomal large subunit protein
10753_at	2370	P	cAMP-dependent protein kinase catalytic subunit
10754_at	12881.7	P	Morphogenesis Checkpoint Dependent
10755_at	26053.9	P	Protein containing tandem internal repeats
10756_at	1703.6	P	Protein containing tandem internal repeats
10757_at	498.1	P	hypothetical protein
10758_at	682.7	P	probable serine\/threonine-specific protein kinase (EC 2.7.1.-)
10759_at	12515.3	P	similarity to hypothetical S. pombe protein
10714_at	1279.8	P	hypothetical protein
10715_at	5136.8	P	hypothetical protein
10716_at	9546.8	P	aminopeptidase yscII
10717_at	27170.9	P	40S ribosomal protein S27A (rp61) (YS20)
10718_at	1266	P	hypothetical protein
10719_at	2801.2	P	signal recognition particle receptor, beta chain
10720_at	363.7	P	questionable ORF
10721_at	32040	P	Phosphoglycerate mutase
10722_at	3142.9	P	similarity to C.elegans hypothetical protein R107.2
10723_at	7698.6	P	NADH-cytochrome b5 reductase

10724_at	1932.4	P	debranching enzyme
10725_at	5569	P	flavoprotein subunit of succinate dehydrogenase
10726_at	1148.5	M	questionable ORF
10727_at	16736	P	strong similarity to S.pombe hypothetical protein C3H1.09C
10728_at	27190.3	P	putative ATPase, 26S protease subunit component
10729_at	4205.8	P	Subunit of RNA polymerase III
10730_at	4228.6	P	low temperature viability protein
10731_at	7923.7	P	mitochondrial ribosomal protein
10732_at	12628.2	P	succinate dehydrogenase cytochrome b
10733_at	2597.5	P	triglyceride lipase-cholesterol esterase
10734_at	1377	P	alpha subunit of the kinase which phosphorylates the RNA polymera
10735_at	4499	P	15.5 kDa mitochondrial ribosomal protein YmL31
10736_at	882.7	P	hypothetical protein
10692_at	1486.4	P	questionable ORF
10693_at	4141.5	P	Beta-adaptin, large subunit of the clathrin-associated protein (AP-1)
10694_at	737.5	P	probable neutral zinc metalloproteinase
10695_at	414.8	P	probable purine nucleotide-binding protein
10696_at	1896.8	P	probable folyl-polyglutamate synthetase
10697_at	398.7	A	questionable ORF
10698_at	4281.2	P	Required for mother cell-specific HO expression
10699_at	1487.1	P	myosin I
10700_at	10161.7	P	Phospo-mutase homolog
10701_at	5701.9	P	phosphoglucomutase, minor isoform
10702_at	7403.2	P	76.5 kDa Serine\/threonine protein kinase with similarity to protein ki
10703_at	3421.6	P	DNA-independent RNA Polymerase I transcription factor
10704_at	371.7	A	suppressor of SHR3\; confers leflunomide resistance when overexpr
10705_g_a	54	A	suppressor of SHR3\; confers leflunomide resistance when overexpr
10706_at	785.2	P	questionable ORF
10707_at	8115.9	P	component of signal recognition particle
10708_at	1655.6	P	strong similarity to YMR102c
10709_at	20472.4	P	similarity to mitochondrial uncoupling proteins (MCF)
10710_at	2297.4	P	25.2 kDa protein involved in assembly of vacuolar H(+) ATPase
10711_at	389.9	P	questionable ORF
10712_at	23687.9	P	Hsp90 (Ninety) Associated Co-chaperone
10713_at	3468.9	P	probable serine\/threonine-specific protein kinase (EC 2.7.1.-)
10669_at	152.8	A	questionable ORF
10670_at	6015.3	P	major apurinic\/apyrimidinic endonuclease\/3 -repair diesterase
10671_at	4893.2	P	42 kDa 5 to 3 exonuclease required for Okazaki fragment processir
10672_at	2662.4	P	transcriptional activator and ARS1 binding protein
10673_at	1072.7	P	questionable ORF
10674_at	12998.6	P	Protein involved in resistance to K. lactis killer toxin
10675_at	5784	P	transcriptional activator protein of CYC1 (component of HAP2\/HAP3
10676_at	138.2	A	DNA replication and checkpoint protein 1
10677_at	8.7	A	weak similarity to S.antibioticus probable oxidoreductase
10678_at	4218.7	P	aspartate aminotransferase, mitochondrial
10679_at	745.7	P	similarity to YMR086w
10680_at	11677.5	P	Glutamine_fructose-6-phosphate amidotransferase (glucoseamine-6
10681_at	3982	P	vacuolar aminopeptidase ysc1
10682_at	40.6	A	hypothetical protein
10683_at	361.5	P	Putative protein kinase homologous to S. pombe cdr1\/nim1
10684_at	9314.3	P	similarity to C.elegans hypothetical protein
10685_at	1140.8	P	similarity to C.elegans hypothetical proteins C18G6.06 and C16C10.

10686_at	4107.1	P	hypothetical protein
10687_at	426	A	hypothetical protein
10688_at	19327.4	P	cell wall mannoprotein
10689_at	13644.5	P	cell wall mannoprotein
10690_at	561.8	P	similarity to C.elegans hypothetical proteins
10691_at	8301.9	P	weak similarity to E.coli hypothetical protein
10646_at	432.7	A	MBR1 protein precursor
10647_at	757.8	P	GTPase-activating protein (GAP) for Rsr1p\/Bud1p
10648_at	1789	P	strong similarity to Sec14p
10649_at	506.1	M	hypothetical protein
10650_at	955.7	P	Centromere protein required for normal chromosome segregation an
10651_at	2002.6	P	similarity to C.tropicalis hal3 protein, to C-term. of Sis2p and to hypo
10652_at	5358.4	P	cytochrome c1 heme lyase
10653_at	1263.7	M	hypothetical protein
10654_at	19415.4	P	mitochondrial malate dehydrogenase
10655_at	8796.5	P	strong similarity to S.pombe hypothetical protein SPAC29B12
10656_at	5951.7	P	weak similarity to C.elegans hypothetical protein
10657_at	1588.5	A	questionable ORF
10658_at	16551.6	P	Translation elongation factor EF-1gamma
10659_at	29573.5	P	Translation elongation factor EF-1gamma
10660_at	12669	P	Vacuolar H-ATPas hydrophilic subunit C of V1 sector
10661_at	2029.4	P	kinesin heavy chain homolog, but is not believed to act as a kinesin,
10662_at	5623.6	P	probable ATP-dependent RNA helicase
10663_at	15681.2	P	hypothetical protein
10664_at	1516.8	P	questionable ORF
10665_g_a	1360	P	questionable ORF
10666_at	1783.5	P	hypothetical protein
10667_at	2776.5	P	involved in early pre-mRNA splicing
10668_at	2660.1	P	novel member of the Hsp70 family of molecular chaperones that loca
10624_at	782.1	P	Binds Sin3p in two-hybrid assay
10625_at	390.8	A	weak similarity to A.parasiticus nor-1 protein
10626_at	306.5	P	similarity to B.subtilis transcriptional regulatory protein
10627_at	9857.9	P	strong similarity to hypothetical E.coli protein b1832
10628_at	7105.4	P	Nuclear pore complex protein homologous to Nup116p
10629_at	10860.8	P	Nucleoside diphosphate kinase
10630_at	3168.9	P	hypothetical protein
10631_at	11477	P	Yeast endoplasmic reticulum 25 kDa transmembrane protein
10632_at	6548.8	P	overexpression overcomes manganese toxicity
10633_at	5237.6	P	weak similarity to mammalian microtubule-associated protein MAP 1
10634_at	3481.4	P	zinc finger protein
10635_at	592.8	P	hypothetical protein
10636_at	23824.8	P	aldolase
10637_at	8453.7	P	similarity to C.elegans hypothetical protein
10638_at	7318.3	P	Transcription factor IIA, small chain
10639_at	2923.5	P	100-kDa protein (predicted molecular weight is 120 kDa) with two le
10640_at	27550.6	P	strong similarity to human IgE-dependent histamine-releasing factor
10641_at	742.4	P	probable acetoacetyl-CoA reductase
10642_at	23554.1	P	similarity to glutenin, high molecular weight chain proteins and Snf5
10643_at	21444.9	P	similarity to C.elegans hypothetical protein T09A5.7 (12.5 kD)
10644_at	2674.2	A	questionable ORF
10645_at	3855.9	P	hypothetical protein
10601_at	3030.8	P	hypothetical protein

10602_at	304.6	P	similarity to YMR031c
10603_at	1321.5	P	high similarity to histone H3 and to human centromere protein CENP
10604_at	1355.7	P	protein kinase
10605_at	1805.8	P	hypothetical protein
10606_at	9051.7	P	strong similarity to YMR238w
10607_at	2329.6	P	p58 polypeptide of DNA primase
10608_at	6903.1	P	hypothetical protein
10609_at	9723	P	putative transcription factor
10610_at	1703.4	P	component of the spindle pole body
10611_at	2843.7	P	endosomal Vps protein complex subunit
10612_at	3466.5	P	NifU-like protein B
10613_at	8429.6	P	Putative membrane protein
10614_at	4502	P	transcriptional repressor and activator
10615_at	1258.4	A	weak similarity to C.elegans ubc-2 protein
10616_at	20	A	questionable ORF
10617_at	24481.9	P	Uridinephosphoglucose pyrophosphorylase
10618_at	3936.5	P	weak similarity to YOL013c
10619_at	1510.7	P	hypothetical protein
10620_at	10558.4	P	intrastrand crosslink recognition protein
10621_at	1835.2	M	hypothetical protein
10622_at	130.9	A	questionable ORF
10623_at	21401.3	P	mitochondrial malic enzyme
10579_at	3683.5	P	Large subunit of transcription factor tfIIE
10580_at	3535.7	P	similarity to E.coli molybdopterin-converting factor chlN
10581_at	1178.1	P	strong similarity to glutathione peroxidase
10582_at	5321.9	P	76-kDa subunit of Pab1p-dependent poly(A) ribonuclease (PAN)
10583_at	19227.2	P	uridine-monophosphate kinase (uridylate kinase)
10584_at	963.2	P	weak similarity to human cylicin II
10585_at	1307.9	P	putative metal-binding nucleic acid-binding protein, interacts with Cd
10586_at	4501.3	P	contains four beta-transducin repeats
10587_at	3211.6	P	suppressor protein
10588_at	6886.6	P	CAAX farnesyltransferase alpha subunit
10589_at	4619.4	P	similarity to C.elegans hypothetical protein
10590_at	2232	P	DNA helicase A
10591_at	6341.5	P	ATP synthase d subunit
10592_at	1887.8	P	zinc-finger transcription factor of the Zn(2)-Cys(6) binuclear cluster d
10593_at	7292.1	P	hypothetical protein
10594_at	6224	P	Arp Complex Subunit
10595_at	2235.4	P	Splicing component that associates with the yeast U1 small nuclear r
10596_at	1121	P	cruciform cutting endonuclease
10597_at	3810	P	Ubiquitin Fusion Degradation
10598_at	17462.2	P	mRNA turnover 4
10599_at	4895.3	P	strong similarity to Lag1p
10600_at	7278.4	P	alpha subunit of capping protein
10555_at	2789.1	P	required for transport of proteins between an early and a later golgi c
10556_i_at	39785.6	P	Ribosomal protein L14A
10557_f_at	18629.1	P	Ribosomal protein L14A
10558_s_a	31423.2	P	Ribosomal protein L14A
10559_at	2726.9	P	weak similarity to YKR029c and D.melanogaster transcription elonga
10560_at	25034.2	P	aureobasidin-resistance protein
10561_at	11551.4	P	Mitochondrial ribosomal protein MRP17
10562_at	6044.2	P	similarity to hypothetical protein YKL041w

10563_at	2870.7	P	adenylylsulfate kinase
10564_at	5147.5	P	putative GTP-binding protein\; similar to mammalian Mx proteins
10565_at	3944.2	P	poly(A) polymerase
10566_at	2056.3	P	similarity to Kes1p, Hes1p and Osh1p
10567_at	2007.7	P	ExtraCellular Mutant
10568_at	1087	P	hypothetical protein
10569_at	6691.6	P	mitochondrial ribosomal protein YmL13
10570_at	3581.7	P	weak similarity to Streptococcus protein M5 precursor
10571_at	1793.8	P	Member of RSC complex.
10572_at	1105.6	P	peroxisomal multifunctional beta-oxidation protein
10573_at	2069.3	A	topoisomerase I interacting factor 2
10574_at	1947.8	P	hypothetical protein
10575_at	39.1	A	questionable ORF
10576_at	31454.6	P	Similar to plant PR-1 class of pathogen related proteins
10577_at	5439.8	P	probable purine nucleotide-binding protein
10578_at	20.9	A	similarity to hypothetical protein YJL043w
10533_at	2090.8	P	weak similarity to mysoin heavy chain proteins
10534_at	341	A	similarity to human hypothetical KIAA0161 protein
10535_at	4244.1	P	strong similarity to hypothetical protein YJL082w
10536_at	685.5	P	Increased rDNA silencing
10537_at	244.2	A	hypothetical protein
10538_at	1143.3	P	strong similarity to hypothetical protein YJL084c
10539_at	745.6	P	hypothetical protein
10540_at	647.7	P	similarity to S.pombe hypothetical protein SPAC23C4
10541_at	4809.4	P	putative RNA helicase
10542_at	2772.4	P	hypothetical protein
10543_at	10602.4	P	translation initiation factor eIF2B, 34 KD, alpha subunit\; negative reg
10544_at	3041.3	P	strong similarity to Chs6p
10545_at	9983.8	P	Type 2A-related protein phosphatase
10546_at	1257.4	P	similarity to YJL105w and Lentinula MFBA protein
10547_at	6107.9	P	weak similarity to NADH dehydrogenases
10548_at	2898.3	P	Phospholipase D
10549_at	83.4	A	hypothetical protein
10550_at	259.8	A	questionable ORF
10551_at	128.7	A	negative regulator of multiple nitrogen catabolic genes
10552_at	2156.2	P	RAD52 Inhibitor (Fifty Two Inhibitor)
10553_at	2337.2	P	CCR4 associated factor
10554_at	1542.7	P	component of spindle pole
10510_at	4754.3	P	probable calcium-binding protein
10511_at	1116.5	A	general amino acid permease
10512_at	1452.8	P	questionable ORF
10513_at	119.1	A	hypothetical protein
10514_at	32890.7	P	YOUTH, involved in determining yeast longevity
10515_at	18782.4	P	weak similarity to phosphoglycerate mutase
10516_at	1336.8	P	hypothetical protein
10517_at	2080.9	P	hypothetical protein
10518_at	26695.3	P	hypothetical protein
10519_at	3599.7	P	questionable ORF
10520_at	16532.8	P	nucleosome assembly protein I
10521_at	3641.4	P	hypothetical protein
10522_at	3206.9	P	membrane protein\; low affinity potassium transport
10523_at	865.4	P	similarity to C.elegans hypothetical protein

10524_at	1770.7	P	mitochondrial carrier protein, highly homologous to Mrs3p
10525_at	1267.5	P	DHS-1-P phosphatase
10526_at	5633.7	P	heavy chain of cytoplasmic dynein
10527_at	2404.7	P	ras homolog--GTP binding protein
10528_at	6733.4	P	endo-exonuclease yNucR
10529_i_at	2461.3	P	Ribosomal protein S21A (S26A) (YS25)
10530_at	388.7	P	self-glucosylating initiator of glycogen synthesis\; similar to mammalia
10531_at	2865.1	P	hypothetical protein
10532_at	2164.2	P	putative mannosyltransferase\; type 2 membrane protein
10487_at	1001.2	P	Small subunit of TFIIE transcription factor
10488_at	1897.4	P	May regulate expression of genes involved in bud formation and mor
10489_at	1795.8	P	weak similarity to transcription factors
10490_at	14795.8	P	hypothetical protein
10491_at	7653.6	P	Cytochrome-c peroxidase
10492_at	4460.7	P	strong similarity to Sct1p
10493_at	12550.2	P	Hydrophilic protein that acts in conjunction with SNARE proteins in ta
10494_at	4417.9	P	siroheme synthase
10495_at	1880.9	P	strong similarity to S. pombe phosphatidyl synthase
10496_at	3826.1	P	weak similarity to C.elegans hypothetical protein
10497_at	6762	P	sit4 suppressor
10498_at	1495.9	P	hypothetical protein
10499_at	6576.7	P	strong similarity to hypothetical S. pombe protein
10500_at	7289.4	P	weak similarity to negative regulator Reg1p
10501_at	1283.6	P	ExtraCellular Mutant
10502_at	1479.6	P	hypothetical protein
10503_at	540.9	P	similarity to Vps5p
10504_at	2217.5	P	similarity to S.pombe hypothetical protein SPAC1D4.10
10505_at	7482.4	P	NAD-dependent 5,10-methylenetetrahydrafolate dehydrogenase
10506_at	29678.4	P	hypothetical protein
10507_at	4905.4	P	Nuclear pore complex protein involved in poly(A)+ RNA transport, nu
10508_at	1094.2	M	weak similarity to S.japonicum paramyosin
10509_at	3840.1	P	Protein related to translation elongation factor EF-1alpha and to Suf1
10464_at	4695.1	P	22.3 kDa mitochondrial ribosomal large subunit protein YmL20\; hom
10465_at	2107.9	P	putative ATP-binding protein
10466_at	5881.8	P	similarity to hypothetical Myxococcus xanthus protein
10467_at	6242.5	P	weak similarity to b.subtilis spore germination protein II
10468_at	2682.2	P	strong similarity to YOR081c
10469_at	2073.3	P	similarity to chicken Lim protein kinase and Islet proteins
10470_at	3122.2	P	Suppressor of rad53 lethality
10471_at	27119.5	P	nucleolar protein that is immunologically and structurally related to ra
10472_at	18049.1	P	Peptide transporter
10473_i_at	36631.1	P	Ribosomal protein L40B
10474_s_a	36183.8	P	Ribosomal protein L40B
10475_at	3494.1	P	myosin-like protein
10476_at	3697.2	P	similarity to mitochondrial aldehyde dehydrogenase Ald1p
10477_g_a	772.4	P	similarity to mitochondrial aldehyde dehydrogenase Ald1p
10478_at	846.5	P	phosphoenolpyruvate carboxylkinase
10479_at	1768.8	P	Ubiquitin-specific protease
10480_at	1091.8	P	Transcription factor regulating basal and induced activity of histidine
10481_at	4761.7	P	cause growth inhibition when overexpressed
10482_at	600	P	repressor of silent mating loci
10483_at	1127.4	P	Protein with similarity to flocculation protein Flo1p

10484_at	655.3	P	similarity to multidrug resistance proteins
10485_at	941.5	P	similarity to multidrug resistance proteins
10486_s_a	330.4	A	strong similarity to Sge1p and hypothetical protein YCL069w
10442_s_a	1259.6	P	regulates the mannosylphosphorylation
10443_at	228.6	A	hypothetical protein identified by SAGE
10444_at	1861.3	P	hypothetical protein
10445_s_a	5134.3	P	regulates the mannosylphosphorylation
10446_s_a	2411.1	P	Protein of unknown function
10447_s_a	5137	P	probable serine\/threonine-specific protein kinase (EC 2.7.1.-)
10448_s_a	3783.8	P	strong similarity to holacid-halidohydrolase
10449_at	18.9	A	non-annotated SAGE orf Found forward in NC_001143 between 916
10450_at	178.8	A	non-annotated SAGE orf Found forward in NC_001143 between 940
10451_at	270.7	A	non-annotated SAGE orf Found forward in NC_001143 between 146
10452_at	987.2	P	non-annotated SAGE orf Found reverse in NC_001143 between 403
10453_at	101.7	M	non-annotated SAGE orf Found forward in NC_001143 between 618
10454_at	767.1	A	non-annotated SAGE orf Found forward in NC_001143 between 618
10455_at	259	A	non-annotated SAGE orf Found reverse in NC_001143 between 168
10456_at	6596.9	P	non-annotated SAGE orf Found forward in NC_001143 between 982
10457_at	132.4	A	non-annotated SAGE orf Found forward in NC_001143 between 145
10458_at	1077.1	P	non-annotated SAGE orf Found reverse in NC_001143 between 145
10459_at	1145.4	A	non-annotated SAGE orf Found reverse in NC_001143 between 164
10460_at	898.3	P	non-annotated SAGE orf Found forward in NC_001143 between 178
10461_at	683.8	P	non-annotated SAGE orf Found reverse in NC_001143 between 195
10462_at	15200.3	P	non-annotated SAGE orf Found forward in NC_001143 between 233
10463_at	374.9	A	non-annotated SAGE orf Found reverse in NC_001143 between 261
10419_at	2033.9	P	non-annotated SAGE orf Found forward in NC_001143 between 320
10420_at	2663.5	P	non-annotated SAGE orf Found forward in NC_001143 between 612
10421_at	2768.9	P	non-annotated SAGE orf Found reverse in NC_001143 between 638
10422_at	1154.4	P	non-annotated SAGE orf Found forward in NC_001143 between 219
10423_at	397.4	A	non-annotated SAGE orf Found forward in NC_001143 between 298
10424_at	117.7	A	non-annotated SAGE orf Found reverse in NC_001143 between 379
10425_at	4275.4	P	non-annotated SAGE orf Found reverse in NC_001143 between 464
10426_at	88.5	A	non-annotated SAGE orf Found reverse in NC_001143 between 189
10427_at	462.2	P	non-annotated SAGE orf Found reverse in NC_001143 between 389
10428_at	5.9	A	non-annotated SAGE orf Found forward in NC_001143 between 465
10429_at	109.8	A	non-annotated SAGE orf Found reverse in NC_001143 between 939
10430_at	451	P	non-annotated SAGE orf Found reverse in NC_001143 between 983
10431_at	118.5	A	non-annotated SAGE orf Found reverse in NC_001143 between 108
10432_at	1499	P	non-annotated SAGE orf Found reverse in NC_001143 between 136
10433_at	420.2	A	non-annotated SAGE orf Found reverse in NC_001143 between 136
10434_at	1296.6	P	non-annotated SAGE orf Found reverse in NC_001143 between 142
10435_at	758	P	non-annotated SAGE orf Found reverse in NC_001143 between 184
10436_at	126.4	A	non-annotated SAGE orf Found reverse in NC_001143 between 219
10437_at	1497.4	P	non-annotated SAGE orf Found reverse in NC_001143 between 264
10438_at	56.8	A	non-annotated SAGE orf Found reverse in NC_001143 between 308
10439_at	1600.4	P	non-annotated SAGE orf Found forward in NC_001143 between 308
10440_at	640.3	P	non-annotated SAGE orf Found reverse in NC_001143 between 340
10441_at	93.3	A	non-annotated SAGE orf Found reverse in NC_001143 between 468
10396_at	534.4	A	non-annotated SAGE orf Found reverse in NC_001143 between 468
10397_at	418.3	A	non-annotated SAGE orf Found reverse in NC_001143 between 527
10398_at	83.2	A	non-annotated SAGE orf Found forward in NC_001143 between 533
10399_at	141.9	A	non-annotated SAGE orf Found reverse in NC_001143 between 137

10400_at	24.7	A	non-annotated SAGE orf Found forward in NC_001143 between 173
10401_at	727.9	P	non-annotated SAGE orf Found reverse in NC_001143 between 185
10402_at	117.5	A	non-annotated SAGE orf Found forward in NC_001143 between 219
10403_at	102.3	A	non-annotated SAGE orf Found reverse in NC_001143 between 442
10404_at	1179.4	P	non-annotated SAGE orf Found reverse in NC_001143 between 447
10405_at	849.2	P	non-annotated SAGE orf Found forward in NC_001143 between 456
10406_at	1903.8	P	non-annotated SAGE orf Found forward in NC_001143 between 619
10407_at	506.8	P	snRNA
10408_at	3978.5	P	snRNA
10409_at	6851.6	P	snRNA
10410_at	635.9	A	snRNA
10411_f_a	1175.7	P	Growth INhibitory protein
10412_f_a	3379	P	strong similarity to members of the Srp1/Tip1p family
10413_at	1523.9	A	transacetylase
10414_at	371.2	M	weak similarity to M.leprae metH2 protein
10415_at	455.1	A	strong similarity to amino acid transport protein Gap1p
10416_at	838.5	P	Glutathione transferase
10417_at	141.5	A	hypothetical protein
10418_at	1343.6	P	similarity to N.crassa O-succinylhomoserine (thiol)-lyase
10373_at	22.8	A	similarity to E.coli dioxygenase
10374_at	2160.6	P	weak similarity to Y.pseudotuberculosis CDP-3,6-dideoxy-D-glycero-
10375_at	1050.6	P	similarity to Dal5p
10376_at	1550.9	P	similarity to transcription factor Pip2p
10377_at	6824.4	P	similarity to water channel proteins
10378_at	2768.9	P	member of mip family transmembrane channels
10379_at	599.3	P	similar to FRE2
10380_at	26688.9	P	Cofilin, actin binding and severing protein
10381_at	1245.3	P	hypothetical protein
10382_at	20684.9	P	yeast bile transporter, similar to mammalian bile transporter
10383_at	279.8	M	questionable ORF
10384_at	614.7	A	ribonucleoprotein 1
10385_i_at	40780.7	P	Ribosomal protein L8B (L4B) (rp6) (YL5)
10386_s_a	33895	P	Ribosomal protein L8B (L4B) (rp6) (YL5)
10387_at	772.5	P	questionable ORF
10388_at	7766.3	P	Suppressor of tps1\/fdp1 and member of the MIP family of transmem
10389_at	754.8	P	hypothetical protein
10390_at	9434.6	P	Succinate dehydrogenase (ubiquinone) iron-sulfur protein subunit
10391_at	6150.3	P	involved in regulating membrane traffic
10392_at	2081.8	P	ubiquitin
10393_at	1285	P	weak similarity to YJR125c and YDL161w
10394_at	209.9	A	weak similarity to human platelet-activating factor receptor
10395_at	5200.2	P	RNA splicing factor
10351_at	1254.4	P	hypothetical protein
10352_at	8327.3	P	similarity to mammalian valosin
10353_at	410.4	P	hypothetical protein
10354_at	1240	P	hypothetical protein
10355_at	5757.5	P	similarity to hypothetical protein YJL062w
10356_at	124.1	A	hypothetical protein
10357_at	5039.1	P	similarity to M.jannaschii X-Pro dipeptidase and S.pombe hypothetica
10358_at	14648.2	P	similarity to multidrug resistance proteins
10359_at	6258.8	P	similarity to H.influenzae and E.coli hypothetical proteins
10360_at	3718.8	P	heat shock protein 104

10361_f_a	1463	A	strong similarity to members of the Srp1p/Tip1p family
10362_at	16487.7	P	member of 70 kDa heat shock protein family
10363_at	11710.1	P	similarity to hypothetical protein YLR064w
10364_at	9191.1	P	Hat1 Interacting Factor 1
10365_at	3351.2	P	spindle pole antigen
10366_i_a	2037.4	P	questionable ORF
10367_r_a	1105	P	questionable ORF
10368_s_a	5585.3	P	questionable ORF
10369_at	675.2	P	protein kinase homolog
10370_at	27063.4	P	Aspartyl-tRNA synthetase, cytosolic
10371_at	72.6	A	maybe part of SCD25
10372_at	216.9	P	homologous to cdc25
10328_at	1824.1	P	similarity to metal resistance proteins
10329_at	8253.1	P	hypothetical protein
10330_at	1746.7	P	similarity to Drosophila pumilio protein
10331_at	7163.1	P	similarity to triacylglycerol lipases
10332_at	9570.8	P	56 kDa nucleolar snRNP protein that shows homology to beta subuni
10333_at	3610.8	P	strong similarity to hypothetical protein YLR019w
10334_at	7148.6	P	cysteine-rich cytoplasmic protein
10335_at	5229.8	P	putative ATP dependent RNA helicase
10336_at	332.6	P	hypothetical protein
10337_at	2730.1	P	mitochondrial outer membrane protein
10338_at	18.5	A	similarity to A.thaliana hyp1 protein
10339_at	2648.9	P	Third subunit of the origin recognition complex
10340_at	1942.7	P	protein of unknown function
10341_at	2095.5	P	Killed in Mutagen, sensitive to diepoxybutane and\/or mitomycin C
10342_at	2106.9	P	Dynamin-related protein
10343_at	2439.4	P	hypothetical protein
10344_at	2822.1	P	similarity to hypothetical C. elegans protein
10345_at	3580.7	P	hypothetical protein
10346_at	724.6	A	similarity to allantoate transport protein
10347_at	8941.3	P	Component of RNA polymerase transcription factor TFIIH
10348_at	1401.3	P	Two-component signal transducer that with Sln1p regulates osmoser
10349_at	1459.6	P	hypothetical protein
10350_at	13618.9	P	similarity to hypothetical protein YNL328c
10305_at	10495.8	P	similarity to ribosomal protein L24.e.B
10306_at	465.5	A	weak similarity to Aquifex aeolicus adenylosuccinate synthetase
10307_at	1010.4	P	weak similarity to E.coli hypothetical 20.4 kDa protein
10308_at	14.5	A	hypothetical protein
10309_at	20.8	A	weak similarity to nitrogen regulatory proteins
10310_at	1671.3	P	zinc-finger transcription factor of the Zn(2)-Cys(6) binuclear cluster d
10311_at	821.9	P	weak similarity to S.pombe hypothetical protein SPBC13G1
10312_at	1022.1	P	hypothetical protein
10313_at	4961.3	P	Protein that regulates ADH2 gene expression
10314_at	1378.3	P	hypothetical protein
10315_at	2532.3	P	strong similarity to YLL010c
10316_at	1499.9	P	similarity to triacylglycerol lipase
10317_at	3178.1	P	hypothetical protein
10318_at	3654.1	P	similarity to C.elegans and M.jannaschii hypothetical proteins
10319_at	9038.6	P	similarity to S.pombe hypothetical protein SPAC30D11.11
10320_at	1413.6	P	similarity to ubiquitin--protein ligase Ubr1p
10321_at	3044	P	involved in derepression of SUC2 in response to glucose limitation

10322_at	1330.2	P	Sed5p is a t-SNARE (soluble NSF attachment protein receptor) requi
10323_at	32324	P	aspartate aminotransferase, cytosolic
10324_at	10285.8	P	5-aminoimidazole-4-carboxamide ribonucleotide (AICAR) transformy
10325_at	33710.7	P	Ribosomal protein L15A (YL10) (rp15R) (L13A)
10326_g_a	29427.8	P	Ribosomal protein L15A (YL10) (rp15R) (L13A)
10327_at	21.6	A	hypothetical protein
10283_at	163.1	A	similarity to hypothetical protein YMR124w
10284_at	1813.7	P	putative ATPase\/DNA helicase
10285_at	2466.2	P	hypothetical protein
10286_at	13015.8	P	strong similarity to SMF2 protein
10287_at	1699.1	P	similarity to human mutL protein homolog
10288_at	4043.4	P	similarity to YIL089w
10289_f_a	3855.4	P	strong similarity to members of the Srp1p/Tip1p family
10290_at	25228.3	P	subunit VIb of cytochrome c oxidase
10291_at	1435.2	P	involved in transcription of ribosomal proteins and ribosomal RNA
10292_at	18233.3	P	weak similartity to hypothetical protein YIL011w
10293_at	228.8	P	questionable ORF
10294_at	2356.8	P	hypothetical protein
10295_at	12973.1	P	thioredoxin
10296_at	26560.8	P	pyruvate decarboxylase
10297_at	3448.4	P	May play a role in attachment, organization, and\/or dynamics of mic
10298_at	841.9	P	strong similarity to Rta1p and Rtm1p protein
10299_at	515.1	P	similarity to hypothetical protein YGL160w
10300_f_a	32714.6	P	Ribosomal protein S0B
10301_at	2728.4	P	Ribosomal protein S0B
10302_g_a	18132.9	P	Ribosomal protein S0B
10303_at	3363.2	P	hypothetical protein
10304_at	15688.7	P	weak similarity to human MAC30 C-terminus
10260_at	5214.4	P	similarity to human acidic 82 kDa protein
10261_at	2534.2	P	hypothetical protein
10262_at	117.2	A	hypothetical protein
10263_at	1015.5	P	hypothetical protein
10264_at	6496.6	P	transcription factor, probable member of histone acetyltransferase S
10265_at	30473.3	P	C-5 sterol desaturase
10266_at	1605.5	P	weak similarity to mouse alpha-mannosidase
10267_at	21957.8	P	serine hydroxymethyltransferase
10268_at	5679.4	P	suppressor of rna12/yme2
10269_at	31663.9	P	Phenylalanyl-tRNA synthetase, alpha subunit, cytoplasmic
10270_at	8345.2	P	Ribosomal protein L22A (L1c) (rp4) (YL31)
10271_at	1150.1	P	questionable ORF
10272_at	2373.4	P	ser/thr protein kinase
10273_at	12848.7	P	weak similarity to Anopheles NADH-ubiquinone oxidoreductase, cha
10274_at	21898.5	P	hypothetical protein
10275_at	9773.6	P	signal peptidase subunit
10276_at	907	P	Involved in expression of mitochondrial COX1 by regulating translatic
10277_at	1731.4	A	hypothetical protein
10278_at	7155.2	P	mitochondrial elongation factor G-like protein
10279_at	948	P	strong similarity to sugar dehydrogenases
10280_at	5304.6	P	component of RNA polymerase II holoenzyme\/mediator complex, in
10281_at	1166.2	P	similarity to YFL042c, YFL043c, YDR326c and YHR080c
10282_at	3888.1	P	hypothetical protein
10238_at	7738.2	P	weak similarity to human zinc finger protein

10239_at	20597.2	P	Ribosomal protein L10\; Ubiquinol-cytochrome C reductase complex
10240_at	798.7	P	questionable ORF
10241_at	2619.7	P	weak similarity to Xenopus RCC1 protein
10242_at	2733.5	P	necessary for vesicular transport from the ER to the Golgi complex
10243_at	2533.3	P	P40 inhibitor of Cdc28p-Clb5 protein kinase complex
10244_at	402.2	P	strong similarity to Emp47p
10245_at	501.5	A	galactose permease
10246_at	945.6	P	Suppressor of rad53 lethality
10247_at	20296.2	P	integral membrane protein\; p24a protein
10248_at	8899.7	P	weak similarity to S.pombe hypothetical protein SPAC6F6
10249_at	3171	P	Actin-related protein
10250_at	862.6	P	Smc4 protein, member of SMC family
10251_at	1786.2	P	hypothetical protein
10252_at	7178.1	P	Possible component of GPI:protein transamidase
10253_at	23173.3	P	strong similarity to alanine transaminases
10254_at	3597.2	P	Homolog of E. coli DnaJ, closely related to Ydj1p
10255_at	1005.6	A	hypothetical protein
10256_at	1525.4	P	high affinity sulfate permease
10257_at	1336.3	P	vacuolar v-SNARE
10258_at	1224.3	P	hypothetical protein
10259_at	6396.3	P	hypothetical protein
10215_at	4993.9	P	Serine\/threonine protein kinase
10216_at	1219	P	hypothetical protein
10217_at	1440.4	P	DNA-binding transcriptional activator or CHA1
10218_at	4149.6	P	similarity to YDR125c
10219_at	24957.3	P	similarity to rat ovarian specific protein
10220_at	903.8	A	questionable ORF
10221_at	748.9	P	subunit of the anaphase promoting complex (APC)
10222_at	1865.3	P	omosomal DNA replication initiation protein
10223_at	3310.1	P	hypothetical protein
10224_at	5843.8	P	tRNA splicing endonuclease subunit
10225_at	3198.1	P	similarity to Kaposi s sarcoma-associated herpes-like virus ORF73 h
10226_at	1790.3	P	similarity to Pan troglodytes prot GOR
10227_at	1304.8	P	strong similarity to YDR132c
10228_at	26431.4	P	similarity to C.boidinii peroxisomal membrane protein 20K A
10229_at	0	P	strong similarity to Flo1p
10230_at	988.3	A	hypothetical protein
10231_at	4439.4	P	hypothetical protein
10232_at	18001.7	P	mitogen-activated protein kinase (MAP kinase)
10233_at	1123.8	P	similarity to C.elegans hypothetical protein and YOR054c
10234_at	1376.2	P	Component of cleavage factor II (CF II)\; 105-kDa protein associated
10235_at	5132.8	P	Branchpoint bridging protein -- component of the splicing commitmer
10236_at	424.3	P	SYnthetic lethal with cdc40 (Forty)
10237_at	4282.5	P	similarity to several esterases
10192_at	1163.5	P	suppressor of rna1-1 mutation
10193_at	10526.4	P	GPI-anchored aspartic protease
10194_at	4576.1	P	GPI-anchored aspartic protease
10195_at	19.2	A	hypothetical protein
10196_g_a	1130.7	M	hypothetical protein
10197_at	368.9	P	questionable ORF
10198_at	663.7	P	hypothetical protein
10199_at	17.8	A	hypothetical protein

10200_at	458.4	A	weak similarity to P.aeruginosa anthranilate synthase component II
10201_at	505.1	P	subunit of the anaphase promoting complex (APC)
10202_at	977.3	P	similarity to S.pombe hypothetical protein SPBC24E9
10203_at	7642.1	P	DOM34 Interacting Protein
10204_at	7843.7	P	Low-affinity zinc transport protein
10205_at	2477	P	zinc finger transcription factor
10206_at	1519.7	P	hypothetical protein
10207_at	5621.4	P	choline kinase
10208_at	5038.8	P	pyruvate decarboxylase
10209_at	528.2	A	hypothetical protein
10210_at	233.1	A	zinc finger containing homolog of mammalian TIS11, glucose repres
10211_at	1862.1	P	hypothetical protein
10212_at	1946.9	P	Putative Na+\/H+ antiporter
10213_at	1083.2	P	73 kDa mitochondrial integral membrane protein
10214_at	712.9	A	questionable ORF
10170_g_a	10179	P	questionable ORF
10171_at	1642.9	P	transcription factor, member of UAF (upstream activation factor) alo
10172_at	546.5	A	proline oxidase
10173_at	1808.5	P	weak similarity to Pyrococcus horikoshii hypothetical protein PHBJ01
10174_at	3312.6	P	Identified as an activity necessary for actin polymerization in permea
10175_at	840	P	hypothetical protein
10176_at	3180	P	Spermine Synthase
10177_at	3147.6	P	encodes a core snRNP protein
10178_at	188.6	A	vacuolar membrane protein
10179_at	258.7	A	hypothetical protein
10180_at	32214.6	P	specific affinity for guanine-rich quadruplex nucleic acids
10181_at	868.3	P	weak similarity to A.thaliana hypothetical protein ATU78721
10182_at	2219.9	P	similarity to YOR3165w and YNL095c
10183_at	19034	P	acetyl-coenzyme A synthetase
10184_at	5610.5	P	hypothetical protein
10185_s_a	13485.1	P	nitrogen catabolite-regulated cell-wall L-asparaginase II
10186_s_a	251	A	identical to hypothetical proteins YLR161w and YLR159w
10187_at	4064.7	P	hypothetical protein
10188_at	4810.7	P	mitochondrial processing protease subunit
10189_at	589.7	A	strong similarity to Sdh4p
10190_at	885.6	P	weak similarity to H.influenzae hypothetical protein HI0176
10191_at	2458	P	100 kD component of the Exocyst complex\; required for exocytosis.
10147_at	32183.7	P	Ribosomal protein S31 (S37) (YS24)
10148_at	2405.5	P	probably involved in intramitochondrial protein sorting
10149_at	644.3	A	questionable ORF
10150_at	4625.7	P	clathrin-associated protein complex, small subunit
10151_at	905.7	P	questionable ORF
10152_at	17372	P	S-adenosylmethionine (AdoMet)-dependent methyltransferase of dip
10153_at	398.8	A	hypothetical protein
10154_at	284.3	A	Cytosolic form of NADP-dependent isocitrate dehydrogenase
10155_at	21014.5	P	major low affinity 55 kDa Centromere\/microtubule binding protein
10156_at	1348.6	P	DNA binding protein, homologous to a family of mammalian RFX1-4
10157_at	3572.3	P	similarity to suppressor protein Psp5p
10158_at	2736.4	P	suppressor of cdc25
10159_at	32106.7	P	similarity to Tfs1p
10160_at	14368.5	P	S-adenosylmethionine synthetase
10161_g_a	2397.9	P	S-adenosylmethionine synthetase

10162_at	2023.4	P	hypothetical protein
10163_at	2244.6	P	regulatory protein
10164_at	2486.6	P	similarity to YDR501w
10165_at	463.6	P	weak similarity to ribulose-bisphosphate carboxylase
10166_at	2668	P	60S ribosomal protein L37A (L43) (YL35)
10167_at	15187.9	P	strong similarity to S.pombe hypothetical protein C18G6.07C
10168_at	1563.9	P	similarity to hypothetical protein YNL278w
10169_at	10939.9	P	ATP-binding cassette (ABC) transporter family member
10124_at	3190.8	P	similarity to P.aeruginosa rhamnosyltransferase 1 chain B
10125_at	4390.1	P	hypothetical protein
10126_at	1013	P	Peroxisomal membrane protein that contains Src homology 3 (SH3)
10127_at	20559.9	P	weak similarity to fruit fly transcription factor 5 large chain
10128_at	2899	P	similarity to G.gallus px19 and Msf1p
10129_at	9415.1	P	hypothetical protein
10130_at	6600.7	P	N-myristoyl transferase
10131_at	19325.5	P	Protein with periodic trytophan residues that resembles members of
10132_at	14330.6	P	homology to microtubule binding proteins and to X90565_5.cds
10133_at	2300.8	P	questionable ORF
10134_at	5082.1	P	hypothetical protein
10135_at	2875.1	P	Polypeptide 6 of a Yeast Non-native Actin Binding Complex, homolo
10136_at	5273.8	P	similarity to hypothetical S. pombe protein
10137_at	258.9	A	questionable ORF
10138_g_a	1843.7	P	questionable ORF
10139_i_at	27765.2	A	questionable ORF
10140_r_a	12852.9	P	questionable ORF
10141_at	8030.6	P	Protein involved in maturation of COX1 and COB mRNA
10142_at	6146.1	P	protein of unknown function
10143_at	9014	P	hypothetical protein
10144_at	4884.1	P	similarity to human tricohyalin and protein KIAA0171
10145_at	1323.8	P	HMG-CoA Reductase Degradation
10146_at	25634.7	P	cytoplasmic protein involved in release of transport vesicles from the
10101_at	6195.5	P	strong similarity to purine-nucleoside phosphorylases
10102_at	2091.2	P	G(sub)2-specific B-type cyclin
10103_at	802.7	P	hypothetical protein
10104_at	2529	P	gamma tubulin-like protein, interacts with Spc98p and Spc97p, the T
10105_at	799.4	P	similarity to UTR2 protein
10106_at	13814.9	P	Ferric (and cupric) reductase
10107_at	2502.9	P	strong similarity to rat cell cycle progression related D123 protein
10108_at	25312.3	P	a cyclophilin related to the mammalian CyP-40\; physically interacts
10109_at	258.5	A	questionable ORF
10110_at	1426.5	P	hypothetical protein
10111_at	2608.1	P	hypothetical protein
10112_at	3024.9	P	Possible transmembrane Ca2+ transporter
10113_at	5617.2	P	hypothetical protein
10114_at	6831.1	P	similarity to Dip2p
10115_at	2501.4	P	has a weak RNA-dependent ATPase activity which is not specific for
10116_at	1934.2	P	hypothetical protein
10117_at	3069.6	P	strong similarity to YDR222w
10118_at	3723.6	P	hypothetical protein
10119_at	42.4	A	hypothetical protein
10120_at	3460.9	P	strong similarity to YDR213w, weak similarity to Lys14p
10121_at	29307	P	member of the Rho subfamily of Ras-like proteins

10122_at	400.2	A	questionable ORF
10123_at	4691.5	P	strong similarity to rat kynureninase
10079_at	446.2	A	questionable ORF
10080_at	579.1	A	Telomere elongation protein (ever shorter telomeres)
10081_at	1003.6	P	DNA Topoisomerase III
10082_at	935.8	A	questionable ORF
10083_g_a	775.6	A	questionable ORF
10084_at	1660.7	A	hypothetical protein
10085_at	7182.3	P	thiamine transporter
10086_at	1680.3	P	similarity to YDR200c
10087_at	1664.2	P	weak similarity to H.influenzae lipoate biosynthesis protein B
10088_at	2155.5	P	phosphatidylinositol 3-kinase
10089_at	2576.8	P	similarity to hypothetical S.pombe protein SPAC2G11.09
10090_at	967.8	P	weak similarity to C.elegans R05H5.5 protein and Nup120p
10091_at	9685.5	P	strong similarity to YOR262w
10092_at	6698	P	methionine aminopeptidase
10093_at	1794.8	P	strong similarity to B.subtilis cytidine deaminase
10094_at	2934.6	P	similarity to human DHHC-domain-containing cysteine-rich protein
10095_at	2436.5	P	similarity to S.pombe rad8 protein and Rdh54p
10096_at	9845.9	P	Serine\/threonine protein kinase
10097_at	27193.9	P	EF-3 (translational elongation factor 3)
10098_at	3098.7	P	secretory protein
10099_at	1188.4	A	similarity to peroxisomal rat membrane protein PMP22
10100_at	745.6	P	questionable ORF
10055_at	1033.8	P	weak similarity to bacterial aminoglycoside acetyltransferase regulat
10056_at	1599	P	hypothetical protein
10057_at	1249.2	P	hypothetical protein
10058_at	2433.3	P	zinc-finger transcription factor of the Zn(2)-Cys(6) binuclear cluster d
10059_at	5779	P	hypothetical protein
10060_at	1516.2	P	Glycogen synthase (UDP-gluocse--starch glucosyltransferase)
10061_at	27131.1	P	heat shock protein 60\; chaperonin protein
10062_at	3365.6	P	sphingoid long chain base (LCB) kinase
10063_i_at	1098.8	P	questionable ORF
10064_s_a	2244.6	P	questionable ORF
10065_at	780	P	highly homologous to the human GTPase, Rab6
10066_s_a	7471.9	P	strong similarity to F49C12.11 (Z68227_K) from C. elegans
10067_at	637.5	A	Meiosis-specific protein involved in homologous chromosome synaps
10068_i_at	35684.3	P	Ribosomal protein S28B (S33B) (YS27)
10069_f_at	16550.2	P	Ribosomal protein S28B (S33B) (YS27)
10070_at	330.1	A	hypothetical protein
10071_at	802.5	P	weak similarity to transcription factors
10072_at	316.2	A	Bypass of PAM1
10073_at	3183.4	P	Synaptobrevin (v-SNARE) homolog present on ER to Golgi vesicles
10074_at	67.9	A	questionable ORF
10075_at	4140.3	P	strong similarity to YOR173w
10076_at	781.4	A	hypothetical protein
10077_at	1337	P	similarity to human hypothetical ORF
10078_at	475.1	A	Protein similar to Gac1p, a putative type 1 protein phosphatase targe
10032_at	716.4	P	Member of complex that acts at ARS s to initiate replication
10033_at	1438.1	P	U1 snRNP protein of the Sm class
10034_at	9794.5	P	DEAD-Box Protein 9
10035_at	5320.8	P	subunit of Polyadenylation factor I (PF I)

10036_at	1089.3	P	weak similarity to regulatory proteins
10037_at	1980.7	A	questionable ORF
10038_i_at	8166.8	A	questionable ORF
10039_s_a	601.8	A	questionable ORF
10040_at	486	M	similarity to polypeptide chain release factors
10041_at	287.9	A	questionable ORF
10042_at	570.4	P	weak similarity to Smc2p
10043_at	80.5	A	Peroxisomal enoyl-CoA hydratase
10044_at	6440.9	P	hypothetical protein
10045_at	34688	P	Endochitinase
10046_at	834.2	P	weak similarity to S.pombe hypothetical protein SPAC22E12
10047_f_at	35854.5	P	Ribosomal protein S30A
10048_at	1316.7	P	involved in checkpoint control and DNA repair
10049_at	770.5	P	GTPase
10050_at	3577.9	P	hypothetical protein
10051_at	14457	P	translation initiation factor eIF2b, 43 kDa subunit\; negative regulato
10052_at	4346	P	protein involved in membrane protein insertion into the ER
10053_at	35949.8	P	GTP-binding protein
10054_at	15964.9	P	questionable ORF
10010_at	12444	P	ATP synthase subunit h
10011_at	336.1	A	hypothetical protein
10012_at	1013.1	P	weak similarity to Vibrio vulnificus VvpC protein
10013_at	1020.4	P	U1 snRNP protein required for pre-mRNA splicing
10014_at	3443.5	P	gamma-glutamyltransferase homolog
10015_at	26261.7	P	Exo-1,3-beta-glucanase
10016_at	12198.8	P	hypothetical protein
10017_at	92.8	A	questionable ORF
10018_at	27127	P	O-Acetylhomoserine-O-Acetylserine Sulfhydralase
10019_at	23191.9	P	Aconitase, mitochondrial
10020_at	4347.2	P	encodes a phosphatidylinositol-4-kinase, homologous to VPC34
10021_at	1204	P	Ubiquitin-conjugating enzyme
10022_at	23.5	A	Chitin Deacetylase
10023_at	93.5	A	Chitin Deacetylase
10024_at	2694.5	P	similarity to human centromere protein E
10025_at	1082.1	P	regulatory protein of adenylate cyclase
10026_at	32.4	A	weak similarity to S.tarentolae cryptogene protein G4
10027_at	122.6	A	hypothetical protein
10028_at	1316.5	A	homologous to Spa2p, localizes to sites of polarized growth
10029_at	3294.9	P	Component of 10 nm filaments of mother-bud neck
10030_at	685.7	A	weak similarity to rat apolipoprotein A-IV
10031_at	5301.1	P	weak similarity to H.influenzae hypothetical protein HI0906
9986_at	2591.5	P	questionable ORF
9987_at	375.8	P	103 kD basic protein, catalytic subunit of telomerase
9988_at	2482.4	P	Actin Interacting Protein
9989_at	1337.4	P	hypothetical protein
9990_at	4648.8	P	homolog of Snf5p, member of the chromatin remodeling complex, R
9991_at	11.1	A	questionable ORF
9992_at	1548	P	weak similarity to N.crassa uvs2 protein
9993_at	473.3	A	strong similarity to YGR004w
9994_at	26947.9	P	Ribosomal protein L38
9995_at	2852.8	P	hypothetical protein
9996_at	596.8	P	strong similarity to Stf2p

9997_at	7084	P	strong similarity to YGR010w
9998_at	38.9	A	23 kDa protein containing a putative leucine zipper\; meiosis specific
9999_at	4702.9	P	Involved in chitin synthase III activity, also required for homozygosis
10000_at	134.8	A	questionable ORF
10001_at	5455.5	P	Protein required for mating
10002_i_at	29303.2	A	Ribosomal protein S25B (S31B) (rp45) (YS23)
10003_f_at	35209.3	P	Ribosomal protein S25B (S31B) (rp45) (YS23)
10004_at	257.2	A	questionable ORF
10005_at	5681	P	nuclear pore complex protein with central repetitive domain similar to
10006_at	2663.7	P	Suppressor of Glycerol Defect
10007_at	4488.3	P	Proline-rich protein verprolin
10008_at	63.9	A	questionable ORF
10009_at	110.1	A	questionable ORF
9964_at	925.6	P	60S ribosomal protein P0 (A0) (L10E)
9965_at	141.9	A	hypothetical protein
9966_at	29606.7	P	1,3-beta-D-glucan synthase
9967_at	652.3	P	strong similarity to Gas1p and C.albicans pH responsive protein
9968_s_at	11740.2	P	Ribosomal protein L26A (L33A) (YL33)
9969_at	3630.9	P	similarity to Pfk26p and other 6-phosphofructo-2-kinases
9970_at	1914.6	P	weak similarity to YGR035c
9971_at	6298.1	P	95 kDa structural and functional homolog of vertebrate karyopherin b
9972_at	25028.9	P	mitochondrial dicarboxylate transport protein
9973_at	2763.9	P	questionable ORF
9974_at	23068.8	P	strong similarity to YGR038w
9975_at	20888.5	P	Nit3 nitrilase
9976_at	1755.2	P	hypothetical protein
9977_at	2865	P	budding protein
9978_at	21313.2	P	Transaldolase, enzyme in the pentose phosphate pathway
9979_at	21589.8	P	acetohydroxyacid reductoisomerase
9980_at	2699.2	P	similarity to SCM4 protein
9981_at	1330.3	P	questionable ORF
9982_at	7632.6	P	Member of RSC complex.
9983_at	17698.2	P	Adenylosuccinate Lyase
9984_at	358.8	A	protein involved in vacuolar sorting
9985_at	3346.9	P	similarity to YOR3329c
9941_at	2322.5	P	Ser\/Thr protein kinase\; MEKK homolog
9942_at	578.5	P	putative Upf1p-interacting protein
9943_at	1232.5	P	hypothetical protein
9944_at	263.5	A	weak similarity to Udf2p
9945_at	194.7	A	hypothetical protein
9946_at	14456.8	P	Ribosomal protein S22B (S24B) (rp50) (YS22)
9947_i_at	38022.2	P	Ribosomal protein S22B (S24B) (rp50) (YS22)
9948_f_at	24186.1	P	Ribosomal protein S22B (S24B) (rp50) (YS22)
9949_at	1552.2	P	hypothetical protein
9950_at	465.2	P	Hsp70 protein
9951_at	4583.8	P	Arp2\/3 Complex Subunit
9952_at	3868.9	P	GDP-GTP Exchange Protein (GEP) for the Rho1p Small GTP-bindin
9953_at	28120.7	P	required for conversion of 24-carbon fatty acids to 26-carbon species
9954_at	3058.9	P	similarity to hypothetical protein YGR071c
9955_at	269.3	A	questionable ORF
9956_at	9113.3	P	Involved in pre-tRNA splicing and in uptake of branched-chain amino
9957_at	870.5	P	hypothetical protein

9958_at	329.4	A	fructose-1,6-bisphosphatase
9959_at	24004.9	P	membrane component of ER protein translocation apparatus
9960_at	29.3	A	questionable ORF
9961_at	10709.7	P	weak similarity to SEC14 protein
9962_at	928.3	P	hypothetical protein
9963_at	2087.9	P	mitochondrial leucyl tRNA synthetase
9918_at	2338.4	P	Protein involved in recombination repair, homologous to S. pombe ra
9919_at	7113.4	P	confers sensitivity to killer toxin
9920_at	478.2	P	hypothetical protein
9921_at	4143.8	P	similarity to hypothetical S. pombe protein
9922_at	7116.5	P	similarity to YBR267w
9923_f_at	30807.8	P	Ribosomal protein S29A (S36A) (YS29)
9924_at	3396.6	P	protease involved in a-factor processing
9925_at	5417.8	P	ExtraCellular Mutant
9926_at	28681.2	P	Secretory Stress Response protein 1
9927_at	545.1	A	hypothetical protein
9928_at	943.5	P	essential for assembly of a functional mitochondrial ATPase comple
9929_at	739.6	P	weak similarity to chicken RING zinc finger protein
9930_at	18392	P	Cytochrome-c oxidase chain VIII
9931_at	1721.4	P	Vacuolar sorting protein essential for vacuolar morphogenesis and fu
9932_at	4988.9	P	homology to the CDC48 gene product
9933_at	7501.3	P	antiviral protein, putative helicase
9934_at	5739.5	P	Bdf1p contains two bromodomains, localizes to the nucleus and to c
9935_at	555.8	A	hypothetical protein
9936_at	1721.7	P	similarity to A.brasilense nifR3 protein
9937_at	1980.7	P	hypothetical protein
9938_at	1368.9	P	split zinc finger protein
9939_at	2250.1	A	hypothetical protein
9940_at	2608.5	P	similarity to A.brasilense nifR3 protein
9895_i_at	15101.3	P	Ribosomal protein L31B (L34B) (YL28)
9896_f_at	19745.7	P	Ribosomal protein L31B (L34B) (YL28)
9897_f_at	37277.3	P	Ribosomal protein L31B (L34B) (YL28)
9898_at	1926	P	hypothetical protein
9899_at	943.7	P	hypothetical protein
9900_at	5669.1	P	strong similarity to S. pombe beta-transducin
9901_at	10773.4	P	Homologous to S. pombe asp1+
9902_at	14340.7	P	Copper Transporter
9903_at	4055	P	weak similarity to Candida maltosa cytochrome P450
9904_at	5535	P	strong similarity to YKL187c
9905_at	15164.9	P	weak similarity to YLR413w
9906_at	113.8	A	questionable ORF
9907_at	264	P	hypothetical protein
9908_at	1031.7	P	defective in vacuolar protein sorting
9909_at	12490.1	P	Accessory factor associated with RNA polymerase II by affinity chron
9910_at	4685.1	P	similarity to helicases
9911_at	24005.6	P	dihydroorotase
9912_at	15104.1	P	weak similarity to human 42K membrane glycoprotein
9913_at	7195	P	similarity to human DOCK180 protein
9914_at	422.9	P	hypothetical protein
9915_at	570	P	weak similarity to Stu1p
9916_at	1621.9	P	hypothetical protein
9917_at	9464	P	weak similarity to 3-oxoacyl-[acyl-carrier-protein] reductase from E. c

9873_at	1389.3	P	weak similarity to 3-oxoacyl-[acyl-carrier-protein] reductase from E. c
9874_at	4817.1	P	weak similarity to human transcription regulator Staf-5
9875_at	666.1	P	questionable ORF
9876_at	8447.2	P	has homology to the Dictyostelium and human actin-binding protein c
9877_at	4651.4	P	component of a nuclear-localized tRNA splicing complex
9878_at	539.2	P	weak similarity to rabbit trichohyalin
9879_f_at	22175.3	P	strong similarity to IMP dehydrogenases, Pur5p and YML056c
9880_at	1778.7	P	Calcineurin subunit A\; type 2B protein serine\/threonine phosphatase
9881_at	2113.9	P	questionable ORF
9882_at	1765.7	P	hypothetical protein
9883_at	1414.2	P	ExtraCellular Mutant
9884_at	4681.2	P	hypothetical protein
9885_at	12789.6	P	ornithine aminotransferase
9886_at	6391.1	P	Putative snRNP protein containing Sm-like domain\; coprecipitates w
9887_at	5964.6	P	Mitochondrial 60S ribosomal protein L4
9888_at	2707	P	hypothetical protein
9889_i_at	26329.7	P	Ribosomal protein S1A (rp10A)
9890_s_at	14288.8	P	Ribosomal protein S1A (rp10A)
9891_at	3655.1	P	regulator of silent mating loci
9892_at	3294.7	P	ExtraCellular Mutant
9893_at	586.3	P	questionable ORF
9894_at	24.6	A	hypothetical protein
9850_at	1024.7	A	weak similarity to hexokinases
9851_at	14490.4	P	36 kDa subunit (D subunit of VO sector) of the vacuolar H(+) ATPase
9852_at	20014.7	P	60S ribosomal subunit protein L6B (L17B) (rp18) (YL16)
9853_at	7186.8	P	60 kDa nuclear FK506 binding protein
9854_at	9660.4	P	3-hydroxy-3-methylglutaryl-coenzyme A (HMG-CoA) reductase isozym
9855_at	1594.3	P	zinc-finger transcription factor of the Zn(2)-Cys(6) binuclear cluster d
9856_at	11900.2	P	Protein involved in desensitization to alpha-factor pheromone
9857_at	457.6	A	Nuclear protein
9858_at	5566.8	P	similarity to YPR117w
9859_at	3265	P	weak similarity to human G/T mismatch binding protein
9860_at	1616.2	P	strong similarity to YPR172w
9861_at	573.9	P	Nap1p-binding protein
9862_at	359.7	A	questionable ORF
9863_at	4917.2	P	cell division control protein
9864_at	335.9	A	similarity to C.carbonum toxD protein
9865_f_at	3798.8	P	member of the seripauperin protein\/gene family (see Gene_class PA
9866_i_at	573	A	questionable ORF
9867_s_at	676.1	P	questionable ORF
9868_at	1841.3	P	hypothetical protein identified by SAGE
9869_at	8754.6	P	identified by SAGE
9870_s_at	1947	P	Mitochondrial ribosomal protein MRPL15 (YmL15)
9871_at	616.8	P	non-annotated SAGE orf Found forward in NC_001144 between 230
9872_at	3168.3	A	non-annotated SAGE orf Found forward in NC_001144 between 320
9826_at	2683.9	P	non-annotated SAGE orf Found forward in NC_001144 between 341
9827_at	4498.3	P	non-annotated SAGE orf Found forward in NC_001144 between 433
9828_at	3343.1	P	non-annotated SAGE orf Found forward in NC_001144 between 449
9829_at	2507.7	P	non-annotated SAGE orf Found forward in NC_001144 between 449
9830_at	554.4	P	non-annotated SAGE orf Found forward in NC_001144 between 449
9831_at	686.5	A	non-annotated SAGE orf Found forward in NC_001144 between 603
9832_at	63.2	A	non-annotated SAGE orf Found reverse in NC_001144 between 789

9833_at	84.9	A	non-annotated SAGE orf Found reverse in NC_001144 between 867
9834_at	7.2	A	non-annotated SAGE orf Found forward in NC_001144 between 925
9835_at	7304.4	P	non-annotated SAGE orf Found forward in NC_001144 between 198
9836_at	25750.9	P	non-annotated SAGE orf Found forward in NC_001144 between 199
9837_s_at	8032.2	P	non-annotated SAGE orf Found forward in NC_001144 between 451
9838_s_at	24322.6	P	non-annotated SAGE orf Found forward in NC_001144 between 453
9839_s_at	14539.5	P	non-annotated SAGE orf Found forward in NC_001144 between 455
9840_f_at	3.7	A	non-annotated SAGE orf Found reverse in NC_001144 between 596
9841_at	489.1	A	non-annotated SAGE orf Found forward in NC_001144 between 687
9842_at	4859.4	P	non-annotated SAGE orf Found reverse in NC_001144 between 849
9843_at	150.1	A	non-annotated SAGE orf Found reverse in NC_001144 between 906
9844_at	11575.1	P	non-annotated SAGE orf Found reverse in NC_001144 between 529
9845_at	5944.7	P	non-annotated SAGE orf Found reverse in NC_001144 between 121
9846_at	3.8	A	non-annotated SAGE orf Found reverse in NC_001144 between 228
9847_at	3483	P	non-annotated SAGE orf Found forward in NC_001144 between 371
9848_at	394.2	P	non-annotated SAGE orf Found forward in NC_001144 between 373
9849_at	3055	P	non-annotated SAGE orf Found forward in NC_001144 between 390
9804_at	610.6	P	non-annotated SAGE orf Found forward in NC_001144 between 441
9805_at	659.9	P	non-annotated SAGE orf Found reverse in NC_001144 between 576
9806_at	19595.3	P	non-annotated SAGE orf Found reverse in NC_001144 between 578
9807_at	885.4	A	non-annotated SAGE orf Found reverse in NC_001144 between 669
9808_at	1286.6	P	non-annotated SAGE orf Found reverse in NC_001144 between 708
9809_at	51.4	A	non-annotated SAGE orf Found forward in NC_001144 between 787
9810_at	116.8	A	non-annotated SAGE orf Found forward in NC_001144 between 789
9811_at	463.2	A	non-annotated SAGE orf Found reverse in NC_001144 between 315
9812_at	307.1	P	non-annotated SAGE orf Found reverse in NC_001144 between 136
9813_at	856.3	P	non-annotated SAGE orf Found reverse in NC_001144 between 223
9814_at	323.2	P	non-annotated SAGE orf Found forward in NC_001144 between 293
9815_at	599.5	P	non-annotated SAGE orf Found reverse in NC_001144 between 368
9816_s_at	1535.1	P	non-annotated SAGE orf Found forward in NC_001144 between 458
9817_at	748.6	A	non-annotated SAGE orf Found reverse in NC_001144 between 460
9818_at	81.8	A	non-annotated SAGE orf Found forward in NC_001144 between 677
9819_at	429.3	A	non-annotated SAGE orf Found reverse in NC_001144 between 884
9820_s_at	716.7	A	non-annotated SAGE orf Found forward in NC_001144 between 288
9821_at	12.6	A	non-annotated SAGE orf Found reverse in NC_001144 between 156
9822_at	190.9	A	non-annotated SAGE orf Found forward in NC_001144 between 171
9823_at	15340.4	P	non-annotated SAGE orf Found reverse in NC_001144 between 185
9824_at	2870.5	P	non-annotated SAGE orf Found reverse in NC_001144 between 388
9825_s_at	1204.2	P	non-annotated SAGE orf Found reverse in NC_001144 between 468
9779_at	1579.5	A	non-annotated SAGE orf Found forward in NC_001144 between 514
9780_at	576.4	P	non-annotated SAGE orf Found forward in NC_001144 between 573
9781_at	137.8	A	non-annotated SAGE orf Found reverse in NC_001144 between 658
9782_at	22.2	A	non-annotated SAGE orf Found forward in NC_001144 between 672
9783_at	2595.9	P	non-annotated SAGE orf Found forward in NC_001144 between 710
9784_at	1432.5	P	non-annotated SAGE orf Found reverse in NC_001144 between 712
9785_at	1001.2	A	non-annotated SAGE orf Found forward in NC_001144 between 949
9786_at	1317.5	P	non-annotated SAGE orf Found forward in NC_001144 between 949
9787_at	4868.2	P	non-annotated SAGE orf Found forward in NC_001144 between 964
9788_at	2116.4	P	non-annotated SAGE orf Found forward in NC_001144 between 988
9789_at	2571.5	P	non-annotated SAGE orf Found forward in NC_001144 between 103
9790_i_at	3.7	A	Centromere
9791_f_at	10.7	A	Centromere

9792_s_at	4679.2	P	CEN12-associated
9793_at	305.3	P	snRNA
9794_at	4655.1	P	snRNA
9795_at	14237.9	P	snRNA
9796_at	2448.4	P	snRNA
9797_i_at	1124.1	P	snRNA
9798_at	17578.6	P	snRNA
9799_at	1433.9	P	snRNA
9800_s_at	1572.5	P	hypothetical protein Y .2
9801_at	594.7	P	similarity to human leukotriene b4 12-hydroxydehydrogenase
9802_at	1554.4	P	required for protein disulfide bond formation in the ER
9803_at	6228.9	P	mitochondrial membrane protein
9757_at	1193.8	P	C-terminal part starting with aa 262 cause growth inhibition when ove
9758_at	12537.4	P	weak similarity to Los1p
9759_at	26968.8	P	Hydroxymethylglutaryl-CoA Synthase
9760_at	11082.1	P	strong similarity to cytochrome-b5- and nitrate reductases
9761_at	16831	P	alpha-tubulin
9762_at	30528.1	P	inorganic phosphate transporter, transmembrane protein
9763_at	212.6	A	hypothetical protein
9764_at	7983	P	Putative small GTPase
9765_at	6285.6	P	mitochondrial NADH ubiquinone 6 oxidoreductase
9766_at	1009	P	hypothetical protein
9767_at	581.4	A	similarity to YMR285c
9768_at	1823.2	P	similarity to YPL184c
9769_g_at	3753.5	P	similarity to YPL184c
9770_at	5443.8	P	questionable ORF
9771_at	3589.4	P	predicted protein is very hydrophobic, has many membrane-spannin
9772_at	8052.3	P	Vanadate resistance protein
9773_at	2083.1	P	hypothetical protein
9774_at	5556.2	P	datin, an oligo(dA).oligo(dT)-binding protein
9775_at	2086.8	P	CTD kinase-I gamma subunit
9776_at	1504.4	P	strong similarity to ubiquitination protein Bul1p
9777_at	29170.5	P	DBF2 Interacting Protein
9778_at	1683.6	P	multicopy suppressor of a sin4 defect
9734_at	1803.8	P	hypothetical protein
9735_at	3516	P	hypothetical protein
9736_at	19386.1	P	Orotate phosphoribosyltransferase 1
9737_at	3677.7	P	signal recognition particle subunit, homologue of mammalian SRP1
9738_at	2535.1	P	Intermediate filament protein involved in organelle inheritance
9739_at	2617.5	P	Nucleoporin
9740_at	5621.7	P	p60 subunit of the yeast omatin Assembly Factor-I (CAF-I)
9741_at	148.1	A	questionable ORF
9742_at	13309.8	P	weak similarity to YMR264w
9743_at	2775.9	P	123 kD regulatory subunit of trehalose-6-phosphate synthase\/phosp
9744_at	1298.9	M	questionable ORF
9745_at	804.7	P	zinc-finger transcription factor of the Zn(2)-Cys(6) binuclear cluster d
9746_at	865.4	P	TFIID subunit
9747_at	2966.8	P	required for Golgi to vacuole trafficking, shares similarity to mammal
9748_at	1060.3	P	similarity to asparagine synthases
9749_at	667.6	P	Endonuclease (with Rad1p) that degrades single-stranded DNA for r
9750_at	425.6	A	questionable ORF
9751_at	11181.1	P	Putative homolog of subunit 5 of bovine prefoldin, a chaperone com

9752_at	6321.9	P	similarity to P.falciparum liver stage antigen LSA-1
9753_at	31208.6	P	proteasome component Y7
9754_at	1971.3	P	subunit of mitochondrial RNase P
9755_at	115.6	A	hypothetical protein
9756_at	113.6	A	questionable ORF
9711_at	1077.6	P	hypothetical protein
9712_at	40.3	A	strong similarity to YML125c, similarity to cytochrome-b5- and nitrat
9713_at	12484.4	P	D-arabinono-1,4-lactone oxidase
9714_at	25542.1	P	alpha-tubulin
9715_at	34.7	A	hypothetical protein
9716_at	31.3	A	hypothetical protein
9717_at	2783.1	P	similarity to N.crassa O-succinylhomoserine (thiol)-lyase
9718_at	3262.2	P	strong similarity to ZMS1 protein
9719_at	2935.3	P	similarity to A.brasilense nifR3 protein
9720_at	1958.1	P	weak similarity to Synechocystis sp. hypothetical protein sll1188
9721_at	29060.9	P	cyclophilin-3 (cyclosporin-sensitive proline rotamase-3)
9722_at	5101.3	P	Bet5p\/18kD component of TRAPP
9723_at	2502.5	P	weak similarity to transcription factor
9724_at	24389.5	P	3-hydroxy-3-methylglutaryl-coenzyme A (HMG-CoA) reductase isozy
9725_at	21975.8	P	Prolyl cis-trans isomerase, also called proline rotamase or peptidylpr
9726_at	33690.9	P	Ribosomal protein L6A (L17A) (rp18) (YL16)
9727_at	13397.3	P	similarity to YOR3141c and YNL087w
9728_at	5008	P	hypothetical protein
9729_at	10033	P	putative dihydroxyacetone kinase
9730_at	6866.8	P	Binds to catalytic subunit of DNA polymerase alpha (Pol1p)
9731_at	1492.2	P	similarity to C.elegans hypothetical protein
9732_at	14165.1	P	weak similarity to YAL042w
9733_at	119.8	A	hypothetical protein
9689_at	1093.2	P	120-kDa (largest) subunit of origin recognition complex (ORC)\; sho
9690_at	568.2	P	GTP-binding protein of the ras superfamily involved in termination of
9691_i_at	28605.3	P	Ribosomal protein S1B (rp10B)
9692_at	2562.9	P	Protein involved in mitochondrial import of fusion proteins
9693_at	1961.7	P	5 to 3 DNA helicase
9694_at	3618.1	P	43-kDa 8-oxo-guanine DNA glycosylase
9695_at	4186.2	P	similarity to C.elegans ZK370.4 protein
9696_at	18945.2	P	Suppressor of mec lethality
9697_at	679.4	A	questionable ORF
9698_at	2637.8	P	Catalytic A subunit of calcineurin, type 2B protein serine\/threonine p
9699_at	25712.5	P	strong similarity to IMP dehydrogenases
9700_at	29626.9	P	strong similarity to IMP dehydrogenases
9701_at	11351.9	P	subunit of signal peptidase complex, homologous to mammalian pro
9702_at	924.4	P	Cytochrome b2 [L--lactate cytochrome-c oxidoreductase]
9703_at	6911.7	P	hypothetical protein
9704_at	19467.9	P	putative integral membrane protein
9705_at	7522.9	P	regulatory protein
9706_at	412.9	P	weak similarity to potato sucrose cleavage protein
9707_at	2949.6	P	RNA splicing and ER to Golgi transport
9708_at	12666.5	P	Glucose Signaling Factor
9709_at	510.2	P	questionable ORF
9710_at	666.7	P	strong similarity to YJR054w
9666_at	2243.2	P	RNA splicing factor associated with U1 snRNP
9667_at	487	P	Component of rDNA transcription factor CF, which also contains Rr

9668_at	511.4	M	Carnitine O-acetyltransferase, peroxisomal and mitochondrial
9669_at	5065.9	P	hypothetical protein
9670_at	2548.2	P	hypothetical protein
9671_at	699.9	A	hypothetical protein
9672_at	4848.6	P	weak similarity to C.elegans hypothetical protein CELW03F8
9673_at	2626.5	P	putative alpha-mannosidase
9674_at	124	A	questionable ORF
9675_at	1947.1	P	similarity to YDR458c
9676_at	1423.6	P	similarity to YDR458c
9677_at	8340.5	P	Interacts with Rad51p by two hybrid analysis. mRNA is induced in me
9678_at	678.1	P	questionable ORF
9679_at	11472.7	P	Nuclear envelope protein with multiple putative transmembrane doma
9680_at	6123.7	P	hypothetical protein
9681_at	3896.8	P	hypothetical protein
9682_at	27694.1	P	Thiol-specific antioxidant
9683_at	5995.1	P	Homeobox-domain containing protein
9684_s_at	34303.5	P	Ribosomal protein S18B
9685_at	3303.4	P	ribosomal protein, mitochondrial
9686_s_at	24594.5	P	Ribosomal protein S17A (rp51A)
9687_at	2669.1	P	weak similarity to Nmd2p
9688_at	10533.5	P	Adenine phosphoribosyltransferase
9643_at	8195.1	P	uracil DNA glycosylase
9644_at	1323.1	P	hypothetical protein
9645_at	9749.2	P	Putative new 37kDa subunit of N-oligosaccharyltransferase complex
9646_at	8978.5	P	similarity to YDR438w
9647_at	613.1	P	Polymerase suppressor 2\; Suppressors of group II intron-splicing de
9648_at	2781.9	P	serine-threonine phosphatase Z
9649_at	3016.9	P	TFIID subunit
9650_at	3550.6	P	similarity to C.elegans hypothetical protein C14B1.5
9651_at	3815.2	P	hypothetical protein
9652_at	44.2	A	questionable ORF
9653_at	25865.3	P	Component of the COPII coat of certain ER-derived vesicles
9654_at	2680.7	P	hypothetical protein
9655_at	2241.8	P	transcription factor
9656_g_at	12451.1	P	transcription factor
9657_i_at	712.7	P	questionable ORF
9658_r_at	556.1	P	questionable ORF
9659_at	1983.5	P	questionable ORF
9660_at	12455.2	P	Mitochondrial ribosomal protein MRPL39 (YmL39)
9661_at	20402.7	P	S-adenoslymethionine: delta 24-methyltransferase
9662_at	1782.4	P	jun-like transcription factor
9663_at	5752.3	P	hypothetical protein
9664_at	706.7	P	similarity to hypothetical S.pombe protein
9665_at	11132.9	P	lactoylglutathione lyase (glyoxalase I)
9620_at	331.4	P	hypothetical protein
9621_at	1012.4	P	hypothetical protein
9622_at	8831.4	P	GTP-binding protein of the rab family\; required for homotypic fusion
9623_at	5792.6	P	protein kinase which functions at the G(sub)2\/M boundary
9624_at	18963.5	P	similarity to hypothetical S.pombe and C.elegans proteins
9625_at	4539.6	P	hypothetical protein
9626_at	9067.4	P	Protein required for sorting proteins to the vacuole
9627_at	4214.3	P	Protein required for protein synthesis

9628_at	10909.9	P	strong similarity to Plb1p
9629_at	362.3	M	hypothetical protein
9630_at	16597.1	P	Phospholipase B (lypophospholipase)
9631_at	12411.8	P	weak similarity to P.aeruginosa regulatory protein mmsR
9632_at	5688.6	P	weak similarity to hypothetical protein YDR352w
9633_at	13840.9	P	high affinity hexose transporter-2
9634_at	13761.1	P	CLU1 is similar to the Dictyostelium cluA gene
9635_at	1595	P	membrane protein required for core glycosylation
9636_at	2719.7	P	weak similarity to S.pombe hypothetical protein SPAC4F10
9637_at	14746.8	P	cytochrome P450 involved in C-22 denaturation of the ergosterol side
9638_at	3077.5	P	displays homologies to several transcription factors
9639_at	187.2	A	DBF2 Interacting Protein\; SNAP 25 homolog
9640_at	150.4	A	similarity to tetratricopeptide-repeat protein PAS10
9641_at	1368.9	P	Binds Sin3p in two-hybrid assay
9642_at	1877.1	P	Multicopy suppressor of fenpropimorph resistance (fen2 mutant), sh
9598_at	1421.4	P	metal-binding transcriptional activator
9599_at	14058.2	P	ubiquitin conjugating enzyme
9600_at	382.6	P	putative mitochondrial GTPase
9601_at	5986.9	P	Mitochondrial ribosomal protein MRPL3 (YmL3)
9602_at	825.1	A	hypothetical protein
9603_at	2179.3	P	C3HC4 zinc-binding integral peroxisomal membrane protein
9604_at	6043.4	P	High level expression reduced Ty3 Transposition
9605_at	633.9	P	42 kDa protein that pysically associates with the PP2A and SIT4 prot
9606_at	1119.8	P	weak similarity to human nuclear autoantigen
9607_at	678.6	P	hypothetical protein
9608_at	3214.2	P	similarity to YKL050c and human restin
9609_at	238	A	questionable ORF
9610_at	2839.3	P	Cytokinesis
9611_at	7554.5	P	Actin-related protein
9612_at	171.8	A	weak similarity to YPR201w
9613_at	2099.8	P	Inner membrane protease (mitochondrial protein)
9614_at	1366	P	homolog of S. pombe cdc25
9615_at	4846.3	P	zinc finger protein
9616_at	13367	P	Homocitrate
9617_at	14537.1	P	suppressor of TFIIB mutations
9618_at	767.9	P	strong similarity to Yet1p
9619_at	795.4	P	weak similarity to Pseudomonas L-fucose dehydrogenase
9575_at	3399	P	Regulator of arginine-responsive genes with ARG81 and ARG82
9576_at	6739.1	P	putative transcriptional activator of alpha-specific genes
9577_at	6757.8	P	hypothetical protein
9578_at	8337.6	P	Nuclear pore complex protein that is member of GLFG repeat-contai
9579_at	1044.4	P	hypothetical protein
9580_at	22815.2	P	weak similarity to A.thaliana PRL1 protein
9581_at	229.6	A	Required for arrest in G1 in response to pheromone
9582_at	741.8	A	questionable ORF
9583_at	144.6	A	Binds Sin3p in two-hybrid assay and is part of large protein complex
9584_at	6059.5	P	vacuolar proton pumping ATPase, 110-kDa subunit\; not in vacuole
9585_at	3204.3	P	Protein required for cell cycle arrest in response to loss of microtubul
9586_at	2107.9	P	mitochondrial ADP\/ATP translocator
9587_at	721.6	A	hypothetical protein
9588_at	11983.1	P	multicopper oxidase
9589_at	2648.8	P	15kDa subunit of the tetrameric tRNA splicing endonuclease

9590_at	2652.8	P	mitochondrial import receptor, heterodimerizes with Tom70p, prefer
9591_at	1254.7	P	component of the cleavage and polyadenylation factor CF I involved
9592_at	4707.3	P	acetylornithine acetyltransferase
9593_at	368.7	P	Regulator of Rim1p, required for IME1 expression
9594_at	1923.1	P	basic, hydrophilic protein of 59 kDa
9595_at	1193.4	P	appears to be required for the completion of nuclear membrane fusi
9596_at	227.2	A	Synthesis Of Var
9597_at	3276.7	P	hypothetical protein
9553_at	546.8	P	weak similarity to mouse transcription factor NF-kappaB
9554_at	884.1	P	hypothetical protein
9555_at	807.1	P	2 Cys2-His2 zinc fingers at c-terminus, glutamine and asparagine ri
9556_at	13671.6	P	hypothetical protein
9557_at	12841.2	P	HMG-1 homolog, mitochondrial
9558_at	7099.8	P	weak similarity to C-terminal part of cytochrome b5 and b2
9559_at	6698	P	strong similarity to hypothetical S. pombe protein
9560_at	549.4	P	weak similarity to human Mi-2 protein
9561_at	358.7	P	questionable ORF
9562_at	2820.5	P	Precocious Dissociation of Sister chromatids
9563_at	1630.8	P	similarity to SNF7 protein
9564_at	849.3	P	chromosome transmission
9565_at	19431.9	P	phosphatidylinositol transfer protein
9566_at	4099.9	P	putative helicase
9567_at	674.7	A	May regulate NAM7 function, possibly at level of mRNA turnover
9568_at	364	A	hypothetical protein
9569_at	25572.3	P	alcohol dehydrogenase isoenzyme III
9570_at	311.3	P	putative pseudogene
9571_at	91.1	A	putative pseudogene
9572_at	8327.9	P	similarity to YKL105c
9573_at	735.1	A	questionable ORF
9574_at	1458.9	P	hypothetical protein
9530_at	3580.5	P	similarity to multidrug resistance proteins
9531_at	7461.2	P	mitochondrial membrane ATPase of the CDC48\/PAS1\/SEC18 (AA
9532_at	838.1	P	strong similarity to B. subtilis conserved hypothetical protein yhfK
9533_at	3750.9	P	nuclear protein localization factor
9534_at	5558.9	P	Protein localizes to actin cortical patches. Probable binding site on a
9535_at	5051.6	P	weak similarity to Pwp2p
9536_at	243.9	P	58 kd component (Cbf3c) of the multisubunit Cbf3 kinetochore prot
9537_at	677.7	P	SNZ1 proximal ORF, stationary phase induced gene
9538_at	1152.3	P	encodes highly conserved 35 kDa protein that shows increased expr
9539_at	1318.4	P	weak similarity to M.genitalium hypothetical protein homolog MG442
9540_at	1601.6	P	hypothetical protein
9541_at	9962.9	P	similarity to P.ciliare possible apospory-associated protein
9542_at	2239.5	P	Homolog of samB gene of Aspergillus nidulans (deletion of samB res
9543_at	727	P	similarity to YBR002c
9544_at	1977	P	strong similarity to YKL121w
9545_at	2866.6	P	hypothetical protein
9546_at	664.5	P	protein kinase
9547_at	1678.9	P	Phosphoglucomutase
9548_at	1380.2	P	Ku80 homolog, exhibits DNA binding activity on its own, associates
9549_at	174.9	A	hypothetical protein
9550_at	17650.4	P	acetolactate synthase
9551_at	7367.6	P	myosin I

9552_at	13656.1	P	similarity to aldehyde dehydrogenase
9507_at	1188.8	P	weak similarity to MSN1 protein
9508_at	2425	P	hypothetical protein
9509_at	3727.8	P	similarity to folylpolyglutamate synthetases and strong similarity to YK
9510_at	324.7	A	similarity to B. subtilis conserved hypothetical proteins yoqW and yoa
9511_at	2268	P	similarity to YKL133c
9512_at	25189.8	P	WD repeat protein (G-beta like protein) that interacts with the transla
9513_at	21069.6	P	WD repeat protein (G-beta like protein) that interacts with the transla
9514_at	210.2	A	component of spindle pole
9515_at	191.4	A	strong similarity to succinate dehydrogenase
9516_at	1713.1	P	similarity to YNL008c
9517_g_at	6446.1	P	similarity to YNL008c
9518_at	1490.2	P	questionable ORF
9519_at	7594.3	P	5-aminoimidazole-4-carboxamide ribonucleotide (AICAR) transformy
9520_at	8590.3	P	Ribosomal protein L15B (YL10) (L13B) (rp15R)
9521_at	788.2	A	hypothetical protein
9522_at	25871.5	P	resistance against Pichia farinosa killer toxin (SMK toxin) when expre
9523_at	542.5	P	weak similarity to YLR031w
9524_at	3956.7	P	transcriptional activator of glycolytic genes
9525_at	2035.5	P	hypothetical protein
9526_at	1220.2	P	Protein involved in silencing HMR, homologous to acetyltransferase
9527_at	5771.9	P	ExtraCellular Mutant
9528_at	5205.1	P	Nuclear pore membrane glycoprotein
9529_at	769.9	P	similarity to D.melanogaster Dreg-2 protein
9484_at	11105.1	P	similarity to human retinoblastoma-binding protein
9485_at	459.7	P	similarity to hypothetical S. pombe protein
9486_at	36.9	A	mRNA is induced early in sporulation
9487_at	2397.2	P	hypothetical protein
9488_at	1122.6	P	hypothetical protein
9489_at	203.2	A	questionable ORF
9490_at	1509.5	P	weak similarity to YIR013c and YLR013w
9491_at	121.9	A	interstrand crosslink repair protein
9492_at	1471.9	M	GTP-binding protein
9493_at	2522.6	P	Serine\/threonine protein kinase, phosphorylates the mitotic activato
9494_at	3845.1	P	hypothetical protein
9495_at	219.9	A	hypothetical protein
9496_at	31448.6	P	Ribosomal protein L13B
9497_i_at	2415	P	Ribosomal protein S16A (rp61R)
9498_f_at	27165	P	Ribosomal protein S16A (rp61R)
9499_at	959.6	A	weak similarity to Mlp1p
9500_at	14090.6	P	mitochondrial cytosolically directed NADH dehydrogenase
9501_at	18810	P	p39 subunit of translation initiation factor eIF3
9502_at	2554	P	hypothetical protein
9503_at	9659.2	P	hypothetical protein
9504_at	15278.8	P	oligosaccharyl transferase glycoprotein complex, delta subunit
9505_at	2806.1	P	Inner membrane protease (mitochondrial protein)
9506_at	354	A	hypothetical protein
9462_at	1474.6	P	mitochondrial inner membrane protease
9463_at	4008.9	P	similarity to Asm4p
9464_at	192.8	A	questionable ORF
9465_at	435.9	A	Involved in proteolytic processing of Rim1p
9466_at	1013.4	P	weak similarity to E.coli hypothetical protein f402

9467_at	971.9	P	weak similarity to S.pombe hypothetical protein SPAC23C11
9468_at	5054.1	P	hypothetical protein
9469_at	1868.1	P	weak similarity to E.coli ribosomal S8 protein
9470_at	79.7	A	questionable ORF
9471_at	12.5	A	Protein homologous to human Sin3 complex component SAP18, po
9472_at	2710.7	P	weak similarity to fruit fly ecdysone-inducible protein
9473_at	3118.3	P	Homologous to E coli dnaJ protein
9474_at	761.8	P	similarity to ATPases
9475_at	508.3	P	hypothetical protein
9476_at	1355	P	Predicted 758 amino acid polypeptide with poly-glutamine and poly-a
9477_at	2273.7	P	involved in plasmid maintenance
9478_at	4893.7	P	similarity to members of the mitochondrial carrier protein family
9479_at	512.1	A	MutL homolog, forms a complex with Pms1p and Msh2p to repair m
9480_at	477.4	P	contains an N-terminal Zn2Cys6 type zinc finger domain, a C-termin
9481_at	324	A	Aldehyde Dehydrogenase (NAD(P)+)
9482_g_at	3074.5	P	Aldehyde Dehydrogenase (NAD(P)+)
9483_at	873.1	P	aldehyde dehydrogenase, (NAD(P)+), likely cytosolic
9439_at	586	P	similarity to YKL124w
9440_at	1031.6	P	similarity to MSN1 protein
9441_at	253	A	questionable ORF
9442_s_at	11184.7	P	flocculent specific protein\; contains >35 repeats of the amino acid se
9443_at	15577.3	P	questionable ORF
9444_at	898.9	P	Cytoplasmic inhibitor of proteinase Pep4p
9445_at	62.9	A	protein of unknown function
9446_at	669.1	P	ExtraCellular Mutant
9447_at	1806.1	P	Protein involved in mitochondrial iron accumulation
9448_at	1910.7	P	similarity to C.elegans hypothetical protein
9449_at	1184.9	P	non-specific DNA binding protein
9450_at	1621.4	P	similarity to YPL228w
9451_at	745.6	P	similarity to YPL229w
9452_at	1716	P	Putative transcriptional repressor with proline-rich zinc fingers
9453_at	3854.9	P	SSO1 and SSO2 encode syntaxin homologs\; act in late stages of se
9454_at	7064.6	P	hypothetical protein
9455_at	1665.4	P	hypothetical protein
9456_at	35845.7	P	constitutively expressed heat shock protein
9457_g_at	23871.9	P	constitutively expressed heat shock protein
9458_at	3486.7	P	hypothetical protein
9459_at	4012	P	weak similarity to bacterial ribosomal protein S17
9460_at	3971.8	P	Glycine decarboxylase complex (P-subunit), glycine synthase (P-su
9461_at	1836.8	P	has DNA helicase signature motifs
9416_at	3823.1	P	hypothetical protein
9417_at	148.2	A	similarity to mouse Tbc1 protein
9418_at	3760.7	P	Mitochondrial ribosomal protein MRPL24 (YmL24)
9419_at	1022.4	P	questionable ORF
9420_i_at	71.3	P	Ribosomal protein L36A (L39) (YL39)
9421_s_at	31854.8	P	Ribosomal protein L36A (L39) (YL39)
9422_at	5904.1	P	similarity to YPL250c
9423_at	1015.5	P	hypothetical protein
9424_at	2918.3	P	Vti1p is a v-SNARE that interacts with two t-SNARES, Sed5p and P
9425_at	2147.6	P	spindle pole body associated protein
9426_at	4767.7	P	G(sub)1 cyclin
9427_at	9214.8	P	putative membrane protein

9428_at	854.2	P	human xeroderma pigmentosum group A DNA repair gene homolog
9429_at	27094.3	P	C-8 sterol isomerase
9430_at	23305.8	P	Mitochondrial outer membrane protein\; forms the outer membrane i
9431_at	1554.5	P	weak similarity to D.melanogaster hypothetical protein DMC39E1
9432_at	26734.5	P	phosphofructokinase beta subunit
9433_at	194.4	A	weak similarity to hypothetical protein YNR014w
9434_at	1357.3	P	Similar to acetyl-coenzyme A carboxylase
9435_at	5300.8	P	mevalonate kinase
9436_at	2851.3	P	hypothetical protein
9437_at	2543.3	P	similarity to P.glauca late embryogenesis abundant protein and YBR
9438_at	1667	P	weak similarity to beta tubulins
9394_at	6608.7	P	weak similarity to myosins
9395_at	808.7	P	S. cerevisiae homologue of S. pombe cdc5+
9396_at	6951.7	P	dnaJ homolog
9397_at	11479.8	P	similarity to GAS1 protein
9398_at	7612.8	P	Serine Protein Kinase
9399_at	26148.2	P	GMP synthase
9400_at	2016.2	P	hypothetical protein
9401_at	1609	P	Establishes Silent omatin
9402_at	27849.6	P	48 kDa Phosphomevalonate kinase
9403_at	12616.2	P	weak similarity to photosystem II protein D2
9404_at	10790	P	similarity to S.pombe dihydrofolate reductase
9405_at	1437.7	P	encodes putative deubiquitinating enzyme
9406_at	773	P	localizes to discrete sites in rad50s mutants. Mre11p, Rad50p, Mer2
9407_at	4174.5	P	Mitochondrial ribosomal protein MRPL44 (YmL44)
9408_at	848.8	P	Mitochondrial ribosomal protein MRPL44 (YmL44)
9409_at	25504.3	P	similarity to ketoreductases
9410_at	1081.9	P	TFIID subunit
9411_at	3257.4	P	Mitochondrial RNA polymerase specificity factor
9412_at	12559.7	P	Protein required for processing of pre-rRNA
9413_f_at	327.6	P	Ribosomal protein S10B
9414_f_at	14329.1	P	Ribosomal protein S10B
9415_at	890.5	P	peripheral vaculor membrane protein\; putative Zn-finger protein
9371_at	474.3	A	involved in cell fusion during mating, also required for the alignment
9372_at	2880.1	P	strong similarity to YOR295w
9373_at	498.2	P	ribonuclease H
9374_at	6721.5	P	Protein involved in RNA processing and export from nucleus
9375_at	13639.6	P	TFIID subunit
9376_at	8609.6	P	similarity to CHS6 protein
9377_at	10098.2	P	Protein required for filamentous growth, cell polarity, and cellular elo
9378_at	4567.4	P	Ribonuclease III
9379_at	1317.1	P	U2 snRNP protein
9380_at	16840	P	DNA-binding protein, mtDNA stabilizing protein, mitochondrial inner
9381_s_at	29189.2	P	Ribosomal protein L20A (L18A)
9382_at	17719.4	P	Zinc- and cadmium-resistance protein
9383_at	520.8	A	similarity to Uth1p, Nca3p, YIL123w and Sun4p
9384_at	3859.3	P	questionable ORF
9385_at	1342.7	P	weak similarity to mouse thyrotropin-releasing hormone receptor
9386_at	11658.8	P	long-chain fatty acid--CoA ligase and synthetase 4
9387_at	9770.5	P	hypothetical protein
9388_at	1997.9	P	similarity to glutamate decarboxylases
9389_at	311.1	A	strong similarity to YKR076w and YGR154c

9390_at	15284.8	P	hyperosmolarity-responsive gene
9391_at	2078.3	P	hypothetical protein
9392_at	1295.9	P	strong similarity to YPL264c
9393_at	383.5	A	hypothetical protein
9349_at	2133.4	P	hypothetical protein
9350_at	28532.3	P	subunit VII of cytochrome c oxidase
9351_at	1114.8	P	translational activator of cytochrome c oxidase subunit II
9352_at	1217	P	hypothetical protein
9353_at	2059.6	P	hypothetical protein
9354_at	13083	P	Translation initiation factor eIF1A
9355_at	8093.8	P	115 kD regulatory subunit of trehalose-6-phosphate synthase\/phosp
9356_at	2389.5	P	similarity to S.pombe scn1 protein
9357_at	2177.9	P	subunit of the histone deacetylase B complex
9358_at	8194.2	P	Cue1p assembles with Ubc7p. Cue1p recruits Ubc7p to the cytosolic
9359_at	1068.1	P	hypothetical protein
9360_at	13458	P	similarity to A.thaliana hyp1 protein
9361_at	2120.2	P	mitochondrial inorganic pyrophosphatase
9362_at	741.3	P	U4\/U6 snRNA-associated splicing factor
9363_at	3551.6	P	weak similarity to C.elegans hypothetical protein CELT23B3
9364_at	1604.5	P	Upstream activation factor subunit
9365_at	511.2	P	Orotate phosphoribosyltransferase 2
9366_at	19665.9	P	desaturase\/hydroxylase enzyme
9367_at	4265.7	P	Negative regulator of cell polarity
9368_at	4830.4	P	Protease involved in ras and a-factor terminal proteolysis
9369_at	4138.5	P	Involved in the ubiquination pathway, possibly by functioning with Rs
9370_at	28834.9	P	ubiquitin-like protein
9326_at	2216.2	P	TFIIF interacting Component of CTD Phosphatase
9327_at	3392.2	P	similarity to phosphomannomutases
9328_at	72.8	A	strong similarity to aminotriazole resistance protein
9329_at	112.4	A	Zinc-cluster protein involved in activating gluconeogenic genes\; relat
9330_at	1941.7	P	hypothetical protein
9331_at	1208.3	P	basic, hydrophilic 67.5 kDa protein
9332_at	702.8	P	Initiator methionine tRNA 2 -O-ribosyl phosphate transferase
9333_at	1347	P	DNA binding protein
9334_at	1308.9	P	similarity to Ccr4p
9335_at	6954.1	P	Mitochondrial ribosomal protein MRPL33 (YmL33) (E. coli L30)
9336_at	1190.8	P	Protein essential for mitochondrial biogenesis
9337_at	1771.4	P	strong similarity to hypothetical S.pombe and C.elegans proteins
9338_at	1927.1	P	hypothetical protein
9339_at	9485.2	P	Putative RNA-dependent helicase
9340_at	144.7	A	questionable ORF
9341_at	1251.7	P	similarity to ser/thr protein kinase
9342_at	16522	P	strong similarity to C.elegans hypothetical protein
9343_at	601.1	P	similarity to amidases
9344_at	366.2	P	Coiled-coil domain protein required for proper nuclear migration durir
9345_at	991	A	questionable ORF
9346_at	28370.3	P	similarity to YGR273c
9347_at	25541.5	P	Probable component of serine palmitoyltransferase, which catalyzes
9348_at	25126.5	P	carboxypeptidase Y (proteinase C)
9304_at	17958	P	hypothetical protein
9305_at	499.5	P	weak similarity to hypothetical protein YJL062w
9306_at	1319	P	phosphoribosylpyrophosphate amidotransferase

9307_at	2478.8	P	mitochondrial ABC transporter protein
9308_at	4042	P	Integral membrane mitochondrial protein
9309_at	3766.1	P	alcohol dehydrogenase II
9310_at	1668.1	P	encodes putative deubiquitinating enzyme
9311_at	1931.4	P	questionable ORF
9312_at	27777.8	P	member of the glucanase gene family
9313_at	782.3	A	Protein with similarity to Gls1p and Gls2p (GB:Z49212)
9314_at	188.6	A	questionable ORF
9315_at	31637.6	P	cell surface glycoprotein 115-120 kDa
9316_at	29975.2	P	Karyopherin
9317_at	7125	P	~100 kDa cytoplasmic protein
9318_at	7280.6	P	similarity to YGR283c
9319_at	3249.1	P	Regulates activity of protein phosphatase 1, Glc7p, which is involvec
9320_at	5733.6	P	hypothetical protein
9321_at	1591.3	P	similarity to YKR089c and YOR081c
9322_at	23772	P	alpha-type of subunit of 20S proteasome
9323_at	21648.3	P	similarity to hypothetical S. pombe protein
9324_at	5965.1	P	similarity to YOR385w and YNL165w
9325_at	1040.7	M	questionable ORF
9281_at	993.9	P	questionable ORF
9282_at	340.2	A	similarity to mucins, glucan 1,4-alpha-glucosidase and exo-alpha-sia
9283_at	17067.3	P	strong similarity to alcohol-dehydrogenase
9284_at	3684	P	Low-affinity Fe(II) transport protein
9285_at	1330.5	P	hypothetical protein
9286_s_at	12645.7	P	strong similarity to hypothetical proteins YPL273w and YLL062c
9287_s_at	403.6	A	strong similarity to YPL280w, YOR391c and YDR533c
9288_s_at	1116	P	strong similarity to phosphopyruvate hydratases
9289_at	369.4	A	strong similarity to YBL108w, YCR103c and YKL223w
9290_f_at	2151.9	P	strong similarity to members of the Srp1p/Tip1p family
9291_at	24169.8	P	protein associated to the ATP synthase
9292_at	576.3	M	hypothetical protein identified by SAGE
9293_at	772.6	P	identified by SAGE
9294_at	23435.3	P	hypothetical protein
9295_g_at	10873.3	P	hypothetical protein
9296_at	371.9	P	non-annotated SAGE orf Found reverse in NC_001145 between 159
9297_at	807.2	P	non-annotated SAGE orf Found reverse in NC_001145 between 390
9298_at	435	P	non-annotated SAGE orf Found forward in NC_001145 between 318
9299_at	386.6	A	non-annotated SAGE orf Found reverse in NC_001145 between 122
9300_at	155.2	A	non-annotated SAGE orf Found reverse in NC_001145 between 503
9301_at	345.4	A	non-annotated SAGE orf Found reverse in NC_001145 between 503
9302_at	46.4	A	non-annotated SAGE orf Found reverse in NC_001145 between 768
9303_at	282.8	A	non-annotated SAGE orf Found forward in NC_001145 between 769
9258_at	16.6	A	non-annotated SAGE orf Found forward in NC_001145 between 460
9259_at	1020	P	non-annotated SAGE orf Found forward in NC_001145 between 171
9260_at	1111.7	A	non-annotated SAGE orf Found reverse in NC_001145 between 347
9261_at	23.1	A	non-annotated SAGE orf Found forward in NC_001145 between 363
9262_at	264.5	P	non-annotated SAGE orf Found forward in NC_001145 between 390
9263_at	922	P	non-annotated SAGE orf Found reverse in NC_001145 between 492
9264_at	1701.9	A	non-annotated SAGE orf Found forward in NC_001145 between 632
9265_at	735.3	P	non-annotated SAGE orf Found forward in NC_001145 between 752
9266_at	1976.1	P	non-annotated SAGE orf Found forward in NC_001145 between 762
9267_at	25279.4	P	non-annotated SAGE orf Found reverse in NC_001145 between 849

9268_at	573.3	P	non-annotated SAGE orf Found forward in NC_001145 between 863
9269_at	2074.8	M	non-annotated SAGE orf Found reverse in NC_001145 between 910
9270_at	29.9	A	non-annotated SAGE orf Found forward in NC_001145 between 272
9271_at	7357.9	P	non-annotated SAGE orf Found reverse in NC_001145 between 426
9272_at	229.9	A	non-annotated SAGE orf Found forward in NC_001145 between 486
9273_at	9.6	A	non-annotated SAGE orf Found reverse in NC_001145 between 501
9274_at	101.1	A	non-annotated SAGE orf Found reverse in NC_001145 between 299
9275_g_at	95.4	A	non-annotated SAGE orf Found reverse in NC_001145 between 299
9276_at	183.4	A	non-annotated SAGE orf Found reverse in NC_001145 between 300
9277_at	146.1	A	non-annotated SAGE orf Found forward in NC_001145 between 115
9278_at	39	A	non-annotated SAGE orf Found forward in NC_001145 between 286
9279_at	564.3	P	non-annotated SAGE orf Found reverse in NC_001145 between 297
9280_at	663.1	P	non-annotated SAGE orf Found reverse in NC_001145 between 433
9234_at	265.3	A	non-annotated SAGE orf Found reverse in NC_001145 between 433
9235_at	1632.2	P	non-annotated SAGE orf Found forward in NC_001145 between 433
9236_at	2586.7	A	non-annotated SAGE orf Found forward in NC_001145 between 434
9237_at	1528.7	P	non-annotated SAGE orf Found forward in NC_001145 between 465
9238_at	501.8	P	non-annotated SAGE orf Found reverse in NC_001145 between 465
9239_at	99.8	A	non-annotated SAGE orf Found forward in NC_001145 between 478
9240_at	275.6	A	non-annotated SAGE orf Found forward in NC_001145 between 480
9241_at	1819.3	P	non-annotated SAGE orf Found forward in NC_001145 between 480
9242_i_at	7.6	A	non-annotated SAGE orf Found forward in NC_001145 between 481
9243_at	42.7	A	non-annotated SAGE orf Found forward in NC_001145 between 481
9244_at	91.4	A	non-annotated SAGE orf Found forward in NC_001145 between 482
9245_at	646.6	A	non-annotated SAGE orf Found reverse in NC_001145 between 511
9246_at	1467.2	P	non-annotated SAGE orf Found reverse in NC_001145 between 556
9247_g_at	1552.1	A	non-annotated SAGE orf Found reverse in NC_001145 between 556
9248_at	799.6	A	non-annotated SAGE orf Found reverse in NC_001145 between 556
9249_i_at	84.7	A	non-annotated SAGE orf Found forward in NC_001145 between 625
9250_f_at	0	A	non-annotated SAGE orf Found forward in NC_001145 between 625
9251_at	452.3	P	non-annotated SAGE orf Found reverse in NC_001145 between 646
9252_at	21379.8	P	non-annotated SAGE orf Found reverse in NC_001145 between 762
9253_at	20270.9	P	non-annotated SAGE orf Found reverse in NC_001145 between 762
9254_at	206	A	non-annotated SAGE orf Found forward in NC_001145 between 837
9255_at	115.1	A	non-annotated SAGE orf Found reverse in NC_001145 between 915
9256_at	18	A	non-annotated SAGE orf Found reverse in NC_001145 between 982
9257_at	10.4	A	non-annotated SAGE orf Found reverse in NC_001145 between 133
9209_at	10562.1	P	non-annotated SAGE orf Found reverse in NC_001145 between 279
9210_at	3403.3	P	non-annotated SAGE orf Found forward in NC_001145 between 498
9211_at	8718.6	P	non-annotated SAGE orf Found reverse in NC_001145 between 624
9212_at	73.1	A	non-annotated SAGE orf Found reverse in NC_001145 between 797
9213_at	3	A	non-annotated SAGE orf Found reverse in NC_001145 between 151
9214_at	17.1	A	non-annotated SAGE orf Found reverse in NC_001145 between 234
9215_at	709.2	A	non-annotated SAGE orf Found forward in NC_001145 between 271
9216_at	154.1	P	non-annotated SAGE orf Found reverse in NC_001145 between 302
9217_at	360.4	A	non-annotated SAGE orf Found forward in NC_001145 between 337
9218_at	588.8	P	non-annotated SAGE orf Found forward in NC_001145 between 426
9219_i_at	238.2	A	non-annotated SAGE orf Found forward in NC_001145 between 483
9220_r_at	363.6	A	non-annotated SAGE orf Found forward in NC_001145 between 483
9221_f_at	2.2	A	non-annotated SAGE orf Found forward in NC_001145 between 483
9222_at	260.1	A	non-annotated SAGE orf Found reverse in NC_001145 between 509
9223_at	366.9	A	non-annotated SAGE orf Found forward in NC_001145 between 611

9224_at	1293.2	P	non-annotated SAGE orf Found reverse in NC_001145 between 623
9225_at	710.1	P	non-annotated SAGE orf Found forward in NC_001145 between 652
9226_at	286.5	M	non-annotated SAGE orf Found forward in NC_001145 between 667
9227_i_at	15584	P	non-annotated SAGE orf Found reverse in NC_001145 between 671
9228_r_at	4402.5	P	non-annotated SAGE orf Found reverse in NC_001145 between 671
9229_i_at	589.2	P	non-annotated SAGE orf Found forward in NC_001145 between 733
9230_r_at	331.1	P	non-annotated SAGE orf Found forward in NC_001145 between 733
9231_s_at	1554.2	P	non-annotated SAGE orf Found forward in NC_001145 between 733
9232_at	162.9	A	non-annotated SAGE orf Found forward in NC_001145 between 733
9233_at	3627.3	P	non-annotated SAGE orf Found forward in NC_001145 between 774
9186_at	4582.7	P	snRNA
9187_i_at	209.3	A	Centromere
9188_at	354	P	snRNA
9189_at	25812	P	snRNA
9190_at	1230.4	P	snRNA
9191_at	4822.1	P	snRNA
9192_at	398.2	P	snRNA
9193_at	3457.7	P	snRNA
9194_at	4040.7	P	snRNA
9195_at	15751.8	P	snRNA
9196_s_at	163.7	A	similarity to M.verrucaria cyanamide hydratase, identical to hypotheti
9197_s_at	3382.9	P	SNZ2 proximal ORF, stationary phase induced gene
9198_s_at	1936.2	P	Snooze: stationary phase-induced gene family
9199_at	3566	P	Hypothetical aryl-alcohol dehydrogenase
9200_at	3861.3	P	histone deacetylase
9201_at	1655.3	P	Member of the AAA-protein family that includes NSFp and PEX1p
9202_at	573.6	P	Protein of the mitochondrial inner membrane with similarity to E. coli
9203_at	12299.1	P	Cell-cycle regulation protein, may be involved in the correct timing o
9204_at	2319.6	P	similarity to YOL003c, YLR246w and C.elegans hypothetical protein
9205_at	894.4	P	FIG4 expression is induced by mating factor.
9206_at	25.4	A	hypothetical protein
9207_at	6729.5	P	strong similarity to YCR094w and YNR048w
9208_at	21961	P	Cell wall beta-glucan assembly
9163_at	5655.6	P	weak similarity to Vcx1p
9164_at	2219.1	P	strong similarity to S.pombe Bem46 protein
9165_at	35.5	A	questionable ORF
9166_at	4.3	A	hexose transport protein
9167_at	2355.5	P	similarity to A.thaliana PRL1/2 protein
9168_at	3081.5	P	prephenate dehydratase
9169_at	9326.9	P	essential for assembly of a functional F1-ATPase
9170_at	2745.5	P	positive regulator of allophanate inducible genes
9171_at	3241.4	P	similarity to C.elegans hypothetical protein
9172_at	7844.6	P	subunit 2 of replication factor RF-A\; 29\% identical to the human p3
9173_at	832	P	hypothetical protein
9174_at	2809.1	P	similarity to S.pombe hypothetical protein SPAC24H6.02c
9175_at	1568	A	Binds Sin3p in two-hybrid assay and is present in a large protein co
9176_at	11164.5	P	similarity to S.pombe and C.elegans hypothetical proteins
9177_at	14959.4	P	43.1 kDa Serine\/threonine\/tyrosine protein kinase
9178_at	3689.6	P	ribosomal protein of the small subunit, mitochondrial
9179_at	10529.8	P	similarity to C-term. of A.nidulans regulatory protein (qutR)
9180_at	885.6	P	similarity to Ypt1p and rab GTP-binding proteins
9181_at	2393.1	P	hypothetical protein

9182_s_at	19337	P	Ribosomal protein S19B (rp55B) (S16aB) (YS16B)
9183_s_at	10920.7	P	Ribosomal protein L18B (rp28B)
9184_at	18808.2	P	Ribosomal protein L18B (rp28B)
9185_at	25505.5	P	hypothetical protein
9140_at	1126.8	P	exhibits homology to Trf4p and Top1p
9141_at	4022.2	P	protein kinase, homologous to Ste20p, interacts with CDC42
9142_at	4181.1	P	similarity to S.pombe hypothetical protein SPAC23D3.13c
9143_at	418.8	A	questionable ORF
9144_at	343.9	P	hypothetical protein
9145_at	1193.8	P	hypothetical protein
9146_at	790.3	P	Multicopy Suppressor of Bud Emergence
9147_at	5090.6	P	Pseudouridine synthase
9148_at	5377	P	N-glycosylated integral plasma membrane protein
9149_at	4561.1	P	Subunit 3 of Replication Factor C\; homologous to human RFC 36 kD
9150_at	2017.8	P	G(sub)1 cyclin that associates with PHO85
9151_at	4383.6	P	strong similarity to C.elegans hypothetical protein
9152_at	15785.9	P	non-clathrin coat protein involved in transport between ER and Golgi
9153_at	1318.8	P	Cold sensitive U2 snRNA Supressor
9154_at	676.5	P	hypothetical protein
9155_at	5457.4	P	Mitochondrial ribosomal protein MRPL10 (YmL10)
9156_at	5746.1	P	Putative integral membrane protein containing novel cysteine motif.
9157_at	2120.4	P	involved in processsing of tRNAs and rRNAs
9158_at	11295.5	P	strong similarity to YDR214w
9159_at	8004.3	P	sterol C-14 reductase
9160_at	2020	P	hypothetical protein
9161_at	3427.3	P	similarity to YLR187w
9162_at	296.4	A	homoserine O-trans-acetylase
9118_at	348.3	A	questionable ORF
9119_at	997.4	P	similarity to human band 3 anion transport protein
9120_at	1829.5	P	similarity to glycerate- and formate-dehydrogenases
9121_at	3049.6	P	topoisomerase I interacting factor 1
9122_at	774.5	P	Protein with coiled-coil domain essential for vesicular transport
9123_at	6679.2	P	contains formin homology domains\; homologous to BNR1 (BNI1 rela
9124_at	1159.3	P	Protein highly homologous to permeases Can1p and Lyp1p for basic
9125_at	1172.4	A	hypothetical protein
9126_at	18459	P	lysine permease
9127_at	3862.5	P	Phosphatidylinositol 4-kinase
9128_at	536.9	A	questionable ORF
9129_at	1576.6	P	similarity to human protein KIAA0174
9130_at	3718.5	P	weak similarity to Sec14p
9131_at	9410.5	P	YIP1-Interacting Factor, shows similarity to NADH dehydrogenases
9132_at	3258.9	P	DNA polymerase II
9133_at	3007.5	P	Fifth largest subunit of origin recognition complex\; contains possible
9134_at	759.4	P	hypothetical protein
9135_at	6945.9	P	Antioxidant protein and metal homeostasis factor, protects against o
9136_at	2610.3	P	hypothetical protein
9137_at	900.7	P	Interacts with SNF1 protein kinase
9138_at	4632.7	P	similarity to bacterial dihydropteroate synthase
9139_at	23341.1	P	strong similarity to nucleic acid-binding proteins
9095_at	403.4	P	hypothetical protein
9096_at	899.5	P	hypothetical protein
9097_at	5282.9	P	ribosomal protein of the large subunit (YmL30), mitochondrial

9098_at	2846.5	P	RNA recognition motif-containing protein that participates in sequenc
9099_at	1007.3	P	protein contains a purine-binding domain, two heptad repeats and a
9100_at	648.6	P	similarity to YDR109c
9101_at	16078.9	P	49-kDa alpha subunit of RNA polymerase A
9102_at	4902.8	P	cysteinyl-tRNA synthetase
9103_at	5581.8	P	similarity to D.melanogaster SET protein
9104_at	954.2	P	hypothetical protein
9105_at	20931.7	P	translation initiation factor 3 (eIF3)
9106_at	15073	P	transmembrane protein
9107_at	1212.5	P	similarity to human hypothetical protein KIAA0404
9108_at	13402.8	P	Glucose-6-phosphate dehydrogenase
9109_at	5308.8	P	strong similarity to K.marxianus LET1 protein
9110_at	8758.6	P	Ca2+-dependent serine protease
9111_at	328.1	P	Yeast putative Transmembrane Protein
9112_at	5279.1	P	component of RNA polymerase II holoenzyme\/mediator complex
9113_at	239.7	A	questionable ORF
9114_at	417.3	P	weak similarity to mouse hemoglobin zeta chain
9115_at	4574.8	P	Is required to link Chs3p and Chs4p to the septins
9116_at	7579.6	P	hypothetical protein
9117_at	8257.9	P	weak similarity to Sec14p
9073_at	1561.1	P	weak similarity to mammalian transcription elongation factor elongin
9074_at	4067.6	P	transcriptional regulator, putative glutathione transferase
9075_at	622.3	P	similarity to dnaJ-like proteins
9076_at	149.8	A	questionable ORF
9077_at	62.2	A	questionable ORF
9078_at	1491.7	P	chaotic nuclear migration\; predicted mass is 67kDa
9079_at	1020.2	P	hypothetical protein
9080_at	357	M	Aut2p interacts with Tub1p and Tub2p\; Aut2p forms a protein compl
9081_at	3695.7	P	functionally related to TFIIB, affects start site selection in vivo
9082_at	7194.9	P	Component of nuclear RNase P and RNase MRP
9083_at	20116.6	P	adenylosuccinate synthetase
9084_at	6989.7	P	mannosyltransferase
9085_at	352.1	A	similarity to E.coli hypothetical protein in serS 5 region
9086_at	3632.2	P	weak similarity to E.coli bis(5 -nucleosyl)-tetraphosphatase
9087_at	4079.6	P	repressor activator protein
9088_at	805.3	P	similarity to hypothetical S. pombe protein
9089_at	900.8	P	23 kDa peroxisome associated protein, binds Pex14p
9090_at	1228.6	P	hypothetical protein
9091_at	6024.6	P	weak simlarity to C.cardunculus cypro4 protein
9092_at	1615	P	hypothetical protein
9093_at	162.9	A	encodes protein with RNA-binding motifs required for MRE2-depend
9094_s_at	31115	P	Heat shock protein of HSP70 family, homolog of SSB1
9050_at	28095.1	P	weak similarity to Colletotrichum gloeosporioides nitrogen starvation-
9051_at	8751.1	P	similarity to M.jannaschii hypothetical protein MJ1073
9052_at	1602.4	P	similarity to structure-specific recognition proteins
9053_at	26.4	A	questionable ORF
9054_g_at	295.5	A	questionable ORF
9055_at	656.1	P	sporulation-specific protein
9056_at	723.5	A	weak similarity to B.subtilis CDP-diacylglycerol--serine O-phosphatid
9057_at	647.9	P	peroxisomal 2,4-dienoyl-CoA reductase
9058_at	2104.9	P	involved in regulation of carbon metabolism
9059_at	983.9	P	strong similarity to human TGR-CL10C

9060_at	2026	P	Activates transcription of glycolytic genes\; homologous to GCR1\; m
9061_at	394.4	A	questionable ORF
9062_at	1942	P	Protein involved in regulation of cell size
9063_at	25.3	A	sporulation-specific protein with a leucine zipper motif, regulated by
9064_at	1892.9	P	hypothetical protein
9065_at	31.2	A	strong similarity to YDL222c and similarity to Sur7p
9066_at	1315	P	hypothetical protein
9067_at	5212.4	P	chitin synthase 1
9068_at	2095.8	P	similarity to Synechocystis hypothetical protein
9069_at	24382.7	P	hypothetical protein
9070_at	9276.2	P	karyopherin alpha homolog of 60 kDa
9071_at	957.4	P	involved in spindle pole body duplication and karyogamy, interacts w
9072_at	861.2	P	hypothetical protein
9028_at	21937.9	P	a deubiquitinating enzyme
9029_at	3718.9	P	ribosomal protein of the large subunit, mitochondrial
9030_at	699.7	P	questionable ORF
9031_at	3616.7	P	protein kinase homolog
9032_at	3137.3	P	weak similarity to S.pombe hypothetical protein
9033_at	3941.4	P	similarity to hypothetical S. pombe protein
9034_at	690.5	P	hypothetical protein
9035_at	26402.9	P	Ribosomal protein S3 (rp13) (YS3)
9036_at	1615.7	P	hypothetical protein
9037_at	3870.4	P	weak similarity to Hkr1p
9038_at	15032.6	P	similarity to S.pombe Rnp24p
9039_at	1273.7	P	hypothetical protein
9040_at	2234.8	P	multicopy suppressor of bem1 mutation, may be involved in G-protei
9041_at	3206.7	P	Component of the anaphase-promoting complex
9042_at	412.7	A	questionable ORF
9043_at	951.4	A	questionable ORF
9044_at	14917.7	P	Phosphatidylserine Decarboxylase 1
9045_at	6795.1	P	similarity to C.elegans ZK688.3 protein and E.coli hpcEp
9046_at	1687	P	CREB like repressor, bZIP protein that binds to CRE motifs, interact
9047_at	2194.3	P	hypothetical protein
9048_at	2716.6	P	similarity to YOR385w and YMR316w
9049_at	1798.8	P	hypothetical protein
9005_at	3405.4	P	translation elongation factor eEF4
9006_s_at	22819.1	P	Ribosomal protein L42A (YL27) (L41A)
9007_at	3937.6	P	Protein kinase
9008_at	4459.9	P	YGP1 encodes gp37, a glycoprotein synthesized in response to nutr
9009_at	1763.5	P	hypothetical protein
9010_at	1808.1	P	hypothetical protein
9011_at	9704.8	P	weak similarity to S.pombe hypothetical protein SPAC10F6
9012_at	12538.5	P	similarity to YHR133c
9013_at	393.5	P	hypothetical protein
9014_at	3564.2	P	membrane-bound casein kinase I homolog
9015_at	9999.9	P	Putative homolog of subunit 4 of bovine prefoldin, a chaperone com
9016_at	1415.4	P	hypothetical protein
9017_at	4776.6	P	31-kDa subunit of RNA polymerase III (C)\; HMG1 like protein
9018_at	1542.8	P	hypothetical protein
9019_at	3751.7	P	weak similarity to S.pombe hypothetical protein
9020_at	1110.8	A	cofactor B
9021_at	3282.8	P	Sm-like protein

9022_at	287.5	P	hypothetical protein
9023_at	1633.9	A	mating a-factor pheromone precursor
9024_at	180.2	A	similarity to YHR131c
9025_at	480.5	M	hypothetical protein
9026_at	871.7	P	Ammonia transport protein
9027_at	12053	P	Adenosine deaminase\/adenine aminohydrolase
8982_i_at	2092.3	A	questionable ORF
8983_s_at	4520.5	P	questionable ORF
8984_at	28686.7	P	70-kDa adenylyl cyclase-associated protein
8985_at	10646	P	putative mitochondrial S4 ribosomal protein
8986_at	1724.9	P	similarity to neurofilament triplet M protein
8987_at	20597.9	P	peptidylprolyl cis-trans isomerase
8988_at	20148.3	P	similarity to C.carbonum toxD gene
8989_at	1887.9	P	hypothetical protein
8990_at	3413.9	P	similarity to A.ambisexualis antheridiol steroid receptor
8991_at	10604.7	P	Mitochondrial import receptor complex protein
8992_at	16986.6	P	sn-1,2-diacylglycerol cholinephosphotransferase
8993_at	2274.8	P	weak similarity to M.pneumoniae uridine kinase udk
8994_at	207.5	A	Similar to human tumor suppressor gene known as TEP1, MMAC1
8995_at	2069.8	P	similarity to C.elegans hypothetical protein
8996_at	339	P	spindle pole body component, associates in a complex with Spc97p
8997_at	9149.7	P	Protein with similarity to mammalian monocarboxylate transporters
8998_at	3655.4	P	similarity to hypothetical S. pombe protein
8999_at	8457.2	P	weak similarity to C.jejuni serine protease
9000_at	614.2	P	hypothetical protein
9001_at	7702.1	P	70 kDa mitochondrial specialized import receptor of the outer membr
9002_at	143.1	A	questionable ORF
9003_at	3171.4	P	weak similarity to M.jannaschii hypothetical protein MJ1257
9004_at	920.1	P	essential suppressor of the respiratory deficiency of a pet mutant
8959_at	216.3	A	carbon-catabolite sensitive malate synthase
8960_at	992.2	P	weak similarity to RING zinc finger protein from Gallus gallus
8961_at	1131.6	P	weak similarity to S.pombe hypothetical protein SPAC23C11
8962_at	2980.3	P	questionable ORF
8963_at	28357	P	subunit common to RNA polymerases I (A) and III (C)
8964_at	16976.5	P	ATP-dependent RNA helicase of DEAD box family
8965_at	15447.1	P	ATP-dependent RNA helicase of DEAD box family
8966_at	26767.7	P	cytochrome b5
8967_at	9823.3	P	weak similarity to fruit fly RNA-binding protein
8968_at	703.3	A	weak similarity to cytochrome-c oxidase
8969_at	5091.1	P	strong similarity to YOR110w
8970_at	2461.2	P	similarity to human AF-9 protein
8971_at	2996.2	P	inositol polyphosphate 5-phosphatase
8972_at	107.4	A	questionable ORF
8973_at	25537.1	P	alpha-isopropylmalate synthase (2-Isopropylmalate Synthase)
8974_at	1817.8	P	member of the leucine zipper family of transcriptional activators
8975_at	7440.7	P	DNA polymerase I alpha subunit, p180
8976_at	6607.7	P	similarity to YKL146w
8977_at	2138.2	P	hypothetical protein
8978_at	9514.8	P	similarity to YNL032w, YNL056w and YDR067c
8979_at	8362.2	P	Ras proto-oncogene homolog
8980_at	2452.5	P	involved in transcriptional regulation of PHO5
8981_at	24890.8	P	Ribosomal protein S7B (rp30)

8936_at	30972.8	P	Ribosomal protein S7B (rp30)
8937_at	2386.5	P	strong similarity to YOR092w
8938_at	1405.4	P	similarity to S.pombe hypothetical protein
8939_at	11.2	A	rab5-like GTPase involved in vacuolar protein sorting and endocytosi
8940_at	193.1	A	similarity to hypothetical C. elegans proteins Y48E1C.2 and Y48E1C.
8941_at	2296.5	P	similarity to chicken h-caldesmon, Uso1p and YKL201c
8942_at	4803.7	P	GTP-binding protein of the rho subfamily of ras-like proteins
8943_at	92.3	A	questionable ORF
8944_at	4037.6	P	topoisomerase II, Top2p localizes to axial cores in meiosis
8945_at	2691.5	P	weak similarity to synaptogamines
8946_at	4540.1	P	hypothetical protein
8947_at	11036.8	P	Protein involved in propagation of M2 dsRNA satellite of L-A virus
8948_at	2067	P	Required for endocytosis and organization of the cytoskeleton
8949_at	2875.2	P	weak similarity to rabbit peroxisomal Ca-dependent solute carrier
8950_at	870.3	P	MutL homolog, similar to Mlh1p, associates with Mlh1p, possibly forr
8951_at	3480.2	P	similarity to ribosomal protein S13
8952_at	5323.4	P	hypothetical protein
8953_at	20894.4	P	tropomyosin I
8954_at	6238.1	P	hypothetical protein
8955_at	649.3	P	similarity to dnaJ protein homolog YDJ1
8956_at	1661.6	P	negative regulator of Ras cAMP pathway, shares weak homology wi
8957_at	8601.6	P	similarity to YHR088w and C.elegans hypothetical protein F44G4.1
8958_at	1194.6	P	Protein of unknown function
8914_at	3694.8	P	mitochondrial lysine-tRNA synthetase
8915_at	3357.2	P	RNase H(35), a 35 kDa ribonuclease H
8916_at	13580.6	P	Dihydrolipoamide acetyltransferase component (E2) of pyruvate deh
8917_at	11230.4	P	translocase of the outer mito. membrane
8918_at	32977.2	P	Ribosomal protein L16B (L21B) (rp23) (YL15)
8919_at	1558.5	P	Fork Head homolog two
8920_i_at	22087.6	P	Ribosomal protein L9B (L8B) (rp24) (YL11)
8921_s_at	24766.3	P	Ribosomal protein L9B (L8B) (rp24) (YL11)
8922_at	24028.4	P	Protein involved in the aging process
8923_at	4011.2	P	similarity to resistance proteins
8924_at	12851.7	P	yeast dnaJ homolog (nuclear envelope protein)\; heat shock protein
8925_at	1997.5	P	weak similarity to Mycoplasma protoporphyrinogen oxidase
8926_at	8560.5	P	RNA-binding (zeta) subunit of translation initiation factor 3 (eIF-3)
8927_at	17795.7	P	90-kDa protein, located in nucleolus, that is homologous to a human
8928_at	2086	P	Actin-related protein
8929_at	6840.9	P	similarity to YIL117c
8930_at	807.6	P	questionable ORF
8931_at	6004.2	P	similarity to YNL032w and YNL099c
8932_at	35189.3	P	Outer mitochondrial membrane porin (voltage-dependent anion char
8933_at	3595.4	P	vacuolar protein
8934_at	1522.1	P	Tyrosine protein phosphatase involved in adaptation response to phe
8935_at	21363.6	P	Cytochrome-c oxidase chain Va
8891_at	1854.5	P	hypothetical protein
8892_at	657.4	P	hypothetical protein
8893_at	3064.5	P	putative zinc finger protein
8894_at	6072.1	P	Required for aspargine-linked glycosylation
8895_at	1012.6	P	similarity to probable transcription factor Ask10p and hypothetical pr
8896_at	3789.9	P	hypothetical protein
8897_at	5951.5	P	strong similarity to human leukotriene-A4 hydrolase

8898_at	392.6	P	questionable ORF
8899_at	1172	P	Bypass of PAM1
8900_at	2191.5	P	weak similarity to Mlp1
8901_at	1458.7	P	weak similarity to M.genitalium alanine--tRNA ligase
8902_at	1230.7	P	90 kd subunit of TFIIIB, also called TFIIIB90 or B or B 90 compone
8903_at	2296.7	P	hypothetical protein
8904_at	8567.2	P	alpha-4-beta-4 subunit of mitochondrial isocitrate dehydrogenase 1
8905_at	5401.2	P	involved in secretion of proteins that lack classical secretory signal se
8906_at	1725.6	P	hypothetical protein
8907_s_at	553.3	A	nearly identical to YNL018c
8908_s_at	276.2	A	nearly identical to YNL019c
8909_at	4133	P	Tyrosine phosphatase
8910_at	24525.7	P	Histone H3 (HHT1 and HHT2 code for identical proteins)
8911_s_at	18928.7	P	Histone H4 (HHF1 and HHF2 code for identical proteins)
8912_at	3966.5	P	Putative mannosyltransferase of the KRE2 family
8913_at	324.3	A	questionable ORF
8868_at	2804.2	P	putative transcription factor
8869_at	4977.5	P	similarity to S.pombe hypothetical protein
8870_at	790.6	P	C-type cyclin associated with the Ssn3p cyclin-dependent kinase
8871_at	1294.6	P	weak similarity to YBR271w and YJR129c
8872_at	2416.2	P	Transcription factor homolog\; similarity to Drosophila melanogaster
8873_at	5018	P	weak similarity to C.burnetii FMU protein
8874_at	2474.7	P	histone deacetylase, shares sequence similarity with Rpd3p, Hos1p,
8875_at	224.8	P	Predicted Ser\/thr kinase
8876_i_at	2743.2	A	hypothetical protein
8877_r_at	235.9	A	hypothetical protein
8878_s_at	24.4	A	hypothetical protein
8879_at	16047.7	P	poly(A)+ RNA-binding protein
8880_at	4500.5	P	Proteinase inhibitor I2B (PBI2), that inhibits protease Prb1p (yscB)
8881_at	678.6	A	translation elongation factor eEF3 homolog
8882_at	464.3	P	questionable ORF
8883_at	173.2	P	encodes a protein with high similarity to phospholipase B
8884_at	1091.4	P	similarity to hypothetical A. thaliana protein T14G11.21
8885_at	13568.2	P	weak similarity to B.subtilis hypothetical protein ykrX
8886_at	446.3	M	peroxisomal NADP-dependent isocitrate dehydrogenase
8887_at	4399.6	P	similarity to YMR119w
8888_at	24677.8	P	sit4 suppressor, dnaJ homolog
8889_at	6811	P	Required for amino acid permease transport from the Golgi to the ce
8890_at	4255.7	P	Mitochondrial ribosomal protein MRP7 (YmL2) (E. coli L27)
8845_at	4145.1	P	hypothetical RNA-binding protein
8846_at	1233.9	M	Member of family of mitochondrial carrier proteins
8847_at	10700.2	P	Significant sequence similarity to RPL7B, but neither can functionall
8848_at	3850.8	P	an ORF of unknown function located in a centromeric region duplicat
8849_at	21449.5	P	citrate synthase. Nuclear encoded mitochondrial protein.
8850_at	711.2	A	Putative transmembrane protein
8851_at	3433.5	P	34-kDa subunit of RNA polymerase III (C)
8852_at	246.5	P	weak similarity to bovine interferon gamma precursor
8853_at	233.1	A	questionable ORF
8854_at	3047.8	P	hydrophilic protein\; has cysteine rich putative zinc finger esential for
8855_at	1694.6	P	Protein involved in autophagocytosis during starvation
8856_at	5782.3	P	weak similarity to human phosphatidylcholine--sterol O-acyltransfera
8857_at	1962.4	P	hypothetical protein

8858_at	1472.6	P	Protein required for accurate mitotic chromosome segregation
8859_at	779.8	P	putative RNA-dependent ATPase
8860_at	2362.4	P	Uridine kinase
8861_at	7098.6	P	similarity to Pho87p and YJL198w
8862_at	509.2	A	weak similarity to hypothetical protein YMR206w
8863_at	3885.3	P	Suppressor of Mitochondrial Mutation in the tRNAasp gene
8864_at	26713.4	P	acetyl-CoA carboxylase
8865_at	14762.2	P	23 kDa mitochondrial inner membrane protein
8866_at	21248.2	P	hypothetical protein
8867_at	2134.9	P	Acyl-CoA cholesterol acyltransferase (sterol-ester synthetase)
8823_at	1697	P	hypothetical protein
8824_at	4931.2	P	hypothetical protein
8825_at	784.1	P	weak similarity to protein phosphatases
8826_at	2441.1	P	73 kDa subunit of the SWI\/SNF transcription activation complex, ho
8827_at	2922.5	P	weak similarity to Rpc31p
8828_at	1597.6	P	questionable ORF
8829_at	4563.6	P	Guanine nucleotide exchange factor for Sar1p.
8830_at	5388.9	P	similarity to human pyridoxal kinase
8831_at	1322.6	P	Cyclophilin
8832_at	4683.8	P	similarity to P.denitrificans cobW protein
8833_at	5219.2	P	ExtraCellular Mutant
8834_at	8673.9	P	A MAP kinase kinase kinase\; activator of Pbs2p
8835_at	6153.7	P	Serine\/threonine protein phosphatase involved in glycogen accumul
8836_at	3671	P	para-aminobenzoate synthase, PABA synthase
8837_at	1252.1	P	shows similarity to glucose-6-phosphate dehydrogenase non-catalyti
8838_at	4161.4	P	Arp Complex Subunit
8839_at	8171.3	P	strong similarity to ribosomal protein S12
8840_at	3428.4	P	strong similarity to Mycoplasma ribosomal protein S19
8841_at	8904	P	putative RNA helicase
8842_at	3601.1	P	weak similarity to Anopheles mitochondrial NADH dehydrogenase su
8843_at	1436.2	P	hypothetical protein
8844_at	4324.2	P	para hydroxybenzoate: polyprenyl transferase
8800_at	1127.9	A	hypothetical protein
8801_at	25986.8	P	mevalonate pyrophosphate decarboxylase
8802_at	25557.6	P	anchorage subunit of a-agglutinin
8803_at	1420.9	P	translational activator of cytochrome c oxidase
8804_at	6733.1	P	strong similarity to S.pombe hypothetical protein SPAC31A2.02
8805_at	578.8	P	similarity to ser/thr protein kinases
8806_at	1523.8	P	strong similarity to YCR094w and YNL323w
8807_at	2505.5	P	small hydrophilic protein, enriched in microsomal membrane fractio
8808_at	12190.4	P	Saccharopine dehydrogenase (NADP+, L-glutamate forming) (sacc
8809_at	2525.9	P	weak similarity to chicken nucleolin
8810_at	7974.9	P	Putative transcription factor
8811_at	10157.8	P	strong similarity to human breast tumor associated autoantigen
8812_at	10626.2	P	strong similarity to human breast tumor associated autoantigen
8813_at	4359.7	P	similarity to C.elegans hypothetical protein CEESL47F
8814_at	9786.1	P	Putative ion transporter similar to the major facilitator superfamily of
8815_at	152.6	A	transmembrane regulator of KAPA\/DAPA transport
8816_at	1647.1	P	dethiobiotin synthetase
8817_at	1294.5	P	7,8-diamino-pelargonic acid aminotransferase (DAPA) aminotransfe
8818_at	561.7	A	similarity to to alpha-1,3-mannosyltransferase
8819_at	1139.9	P	similar to FRE2

8820_at	1694	P	weak similarity to hypothetical protein YDL218w
8821_at	431.9	P	weak similarity to H.influenzae L-lactate permease (lctP) homolog
8822_at	102.4	A	weak similarity to CYC1/CYP3 transcription activator
8776_at	107.6	A	similarity to R.capsulatus 1-chloroalkane halidohydrolase
8777_at	7921	P	strong similarity to YJL222w, YIL173w and Pep1p
8778_at	1478.7	P	strong similarity to Pep1p
8779_at	7568.7	P	similarity to beta-glucan-elicitor receptor - Glycine max
8780_at	863.9	P	similarity to Bul1p
8781_at	93.5	A	similarity to central part of Bul1p
8782_at	167.6	A	strong similarity to Snq2p
8783_at	516.1	P	strong similarity to UDP-glucose 4-epimerase Gal10p
8784_s_at	1219.5	A	strong similarity to E.coli D-mannonate oxidoreductase, identical to
8785_at	3189.1	P	weak similarity to B.subtilis nitrite reductase (nirB)
8786_f_at	2779.3	P	member of the seripauperin protein\/gene family
8787_at	3595.8	P	hypothetical protein identified by SAGE
8788_at	808.2	P	hypothetical protein
8789_s_at	10027.1	P	Aminopeptidase of cysteine protease family
8790_s_at	10747.7	P	protein of unknown function
8791_at	104.5	A	non-annotated SAGE orf Found reverse in NC_001146 between 600
8792_at	386.6	A	non-annotated SAGE orf Found reverse in NC_001146 between 601
8793_at	950.4	P	non-annotated SAGE orf Found reverse in NC_001146 between 118
8794_i_at	454.1	A	non-annotated SAGE orf Found forward in NC_001146 between 440
8795_r_at	923.1	A	non-annotated SAGE orf Found forward in NC_001146 between 440
8796_at	2039.9	P	non-annotated SAGE orf Found forward in NC_001146 between 728
8797_f_at	478	P	non-annotated SAGE orf Found forward in NC_001146 between 101
8798_at	105.4	A	non-annotated SAGE orf Found reverse in NC_001146 between 301
8799_at	838.3	M	non-annotated SAGE orf Found forward in NC_001146 between 499
8752_f_at	402.7	P	non-annotated SAGE orf Found reverse in NC_001146 between 519
8753_at	191.2	A	non-annotated SAGE orf Found forward in NC_001146 between 547
8754_at	48.7	A	non-annotated SAGE orf Found forward in NC_001146 between 568
8755_at	7922.3	P	non-annotated SAGE orf Found forward in NC_001146 between 716
8756_i_at	37814.5	P	non-annotated SAGE orf Found forward in NC_001146 between 949
8757_at	147.5	A	non-annotated SAGE orf Found forward in NC_001146 between 281
8758_g_at	168.5	A	non-annotated SAGE orf Found forward in NC_001146 between 281
8759_at	118.2	A	non-annotated SAGE orf Found reverse in NC_001146 between 351
8760_at	29	A	non-annotated SAGE orf Found reverse in NC_001146 between 412
8761_at	33.9	A	non-annotated SAGE orf Found reverse in NC_001146 between 413
8762_at	1124.6	A	non-annotated SAGE orf Found reverse in NC_001146 between 478
8763_at	1024.1	P	non-annotated SAGE orf Found reverse in NC_001146 between 478
8764_at	1551.4	P	non-annotated SAGE orf Found forward in NC_001146 between 482
8765_at	3522	P	non-annotated SAGE orf Found forward in NC_001146 between 663
8766_at	1801.4	P	non-annotated SAGE orf Found reverse in NC_001146 between 177
8767_at	1509.5	P	non-annotated SAGE orf Found forward in NC_001146 between 140
8768_at	467.9	A	non-annotated SAGE orf Found reverse in NC_001146 between 254
8769_g_at	56.3	A	non-annotated SAGE orf Found reverse in NC_001146 between 254
8770_i_at	413.7	P	non-annotated SAGE orf Found reverse in NC_001146 between 254
8771_r_at	288.4	A	non-annotated SAGE orf Found reverse in NC_001146 between 254
8772_at	6345.2	P	non-annotated SAGE orf Found forward in NC_001146 between 283
8773_at	4954.8	P	non-annotated SAGE orf Found forward in NC_001146 between 465
8774_at	8759	P	non-annotated SAGE orf Found reverse in NC_001146 between 586
8775_at	1751.8	P	non-annotated SAGE orf Found forward in NC_001146 between 890
8729_at	4366.7	P	non-annotated SAGE orf Found forward in NC_001146 between 892

8730_g_at	15014.5	P	non-annotated SAGE orf Found forward in NC_001146 between 892
8731_at	74.2	A	non-annotated SAGE orf Found reverse in NC_001146 between 240
8732_at	21.7	A	non-annotated SAGE orf Found reverse in NC_001146 between 286
8733_at	674.7	P	non-annotated SAGE orf Found forward in NC_001146 between 330
8734_at	36.1	A	non-annotated SAGE orf Found reverse in NC_001146 between 335
8735_at	1142.6	P	non-annotated SAGE orf Found reverse in NC_001146 between 355
8736_at	394.9	P	non-annotated SAGE orf Found forward in NC_001146 between 366
8737_i_at	202.6	A	non-annotated SAGE orf Found reverse in NC_001146 between 546
8738_s_at	818	M	non-annotated SAGE orf Found reverse in NC_001146 between 546
8739_at	170.1	A	non-annotated SAGE orf Found forward in NC_001146 between 553
8740_f_at	117.2	A	non-annotated SAGE orf Found forward in NC_001146 between 563
8741_at	702.7	A	non-annotated SAGE orf Found forward in NC_001146 between 586
8742_at	980.5	P	non-annotated SAGE orf Found forward in NC_001146 between 591
8743_at	456.6	P	non-annotated SAGE orf Found reverse in NC_001146 between 604
8744_at	408.8	A	non-annotated SAGE orf Found reverse in NC_001146 between 661
8745_at	1010.5	P	non-annotated SAGE orf Found reverse in NC_001146 between 663
8746_at	24.1	A	non-annotated SAGE orf Found reverse in NC_001146 between 779
8747_at	644.6	A	non-annotated SAGE orf Found forward in NC_001146 between 915
8748_at	239.3	A	non-annotated SAGE orf Found reverse in NC_001146 between 104
8749_at	44.9	A	non-annotated SAGE orf Found forward in NC_001146 between 116
8750_at	19.2	A	non-annotated SAGE orf Found forward in NC_001146 between 191
8751_at	2600.5	P	non-annotated SAGE orf Found reverse in NC_001146 between 267
8705_at	625.1	P	non-annotated SAGE orf Found reverse in NC_001146 between 342
8706_at	388.2	P	non-annotated SAGE orf Found forward in NC_001146 between 394
8707_at	967	P	non-annotated SAGE orf Found forward in NC_001146 between 449
8708_at	293.4	A	non-annotated SAGE orf Found forward in NC_001146 between 452
8709_at	507.3	M	non-annotated SAGE orf Found reverse in NC_001146 between 614
8710_at	790.1	P	non-annotated SAGE orf Found forward in NC_001146 between 623
8711_i_at	29.4	A	non-annotated SAGE orf Found reverse in NC_001146 between 651
8712_r_at	259.6	A	non-annotated SAGE orf Found reverse in NC_001146 between 651
8713_at	3418.9	P	snRNA
8714_at	282.1	P	snRNA
8715_at	59.2	A	hypothetical protein
8716_s_at	1388.3	P	Hypothetical aryl-alcohol dehydrogenase (AAD)
8717_at	758.8	P	similarity to Pseudomonas alkyl sulfatase
8718_at	279.4	A	similarity to P.putida phthalate transporter
8719_at	43	A	strong similarity to hypothetical protein YIL166c
8720_f_at	1122.2	A	strong similarity to members of the Srp1p/Tip1p family
8721_at	118.9	A	hypothetical protein
8722_at	836.3	P	hypothetical protein
8723_at	8035	P	similarity to subtelomeric encoded proteins
8724_at	4586.6	P	similarity to glucan 1,4-alpha-glucosidase Sta1p and YAR066w
8725_g_at	5258.7	P	similarity to glucan 1,4-alpha-glucosidase Sta1p and YAR066w
8726_at	3294.2	P	similarity to S.fumigata Asp FII
8727_at	15.3	A	strong similarity to Cps1p
8728_at	1086.6	P	similar to FRE2
8683_at	1022.4	P	induced by osmotic stress\; similar to dihydroflavonol 4-reductase fro
8684_at	605.5	A	questionable ORF
8685_at	2064.8	P	Decapping protein involved in mRNA degradation
8686_at	1025.5	P	transcription factor, member of the histone acetyltransferase SAGA
8687_at	11411.4	P	Peroxisomal membrane protein
8688_at	4205.2	P	hypothetical protein

8689_at	552.5	P	CTR9 is required for normal CLN1 and CLN2 G1 cyclin expression
8690_at	2615.9	P	hypothetical protein
8691_at	21453.3	P	6,7-dimethyl-8-ribityllumazine synthase (DMRL synthase)
8692_at	16277.7	P	strong similarity to hypothetical S. pombe protein
8693_at	813.3	P	similarity to YDR435c and C.elegans hypothetical protein
8694_at	1659.3	P	Acetylornithine aminotransferase
8695_at	21719.8	P	mRNA cap binding protein eIF-4E
8696_at	1195.4	P	hypothetical protein
8697_at	2014.8	P	weak similarity to tetracycline resistance proteins
8698_at	2190.3	P	6-phosphofructo-2-kinase
8699_at	2177.3	P	Stoichiometric member of mediator complex
8700_at	182.1	A	questionable ORF
8701_at	4506.5	P	High level expression Reduces Ty3 Transposition
8702_at	785.7	P	similarity to glycophospholipid-anchored surface glycoprotein Gas1p
8703_at	8.7	A	hypothetical protein
8704_at	5467.9	P	ALuminium Resistance 1
8660_at	11015.3	P	similarity to hypothetical S. pombe protein
8661_at	1899.4	P	strong similarity to protein kinase Mck1p
8662_at	27586	P	Ribosomal protein L25 (rpl6L) (YL25)
8663_at	29240.7	P	cytosolic malate dehydrogenase
8664_at	2178.2	P	hypothetical protein
8665_at	6904.7	P	weak similarity to M.jannaschii hypothetical protein
8666_at	13952.7	P	Putative polyadenylated-RNA-binding protein located in nucleus\; sim
8667_at	3438	P	has been localized to both the plasma membrane and the mitochond
8668_at	31793.4	P	Ribosomal protein L18A (rp28A)
8669_at	3587.9	P	similarity to monocarboxylate transporter proteins
8670_at	463.8	P	hypothetical protein
8671_at	754.3	P	weak similarity to human sodium channel alpha chain HBA
8672_at	1373.3	P	43 kDa protein, transcriptional activator
8673_at	1769.9	P	homologous to Trf5p and Top1p, associates with Smc1p and Smc2
8674_at	676.2	P	similarity to human DS-1 protein
8675_at	1136.3	P	Serine\/threonine protein kinase with similarity to Ste20p and Cla4p
8676_at	2460.4	P	Multicopy Suppressor of Bud Emergence
8677_at	11060.8	P	weak similarity to human ubiquitin-like protein GDX
8678_at	5700	P	Involved in RAS localization and palmitoylation
8679_at	37125.3	P	Overexpression yields resistance to Zeocin
8680_at	1620	P	Transcription factor involved in activation of phospholipid synthetic g
8681_at	1555.7	P	weak similarity to human PL6 protein
8682_at	586.4	M	questionable ORF
8638_at	1962.9	P	Putative integral membrane protein containing novel cysteine motif.
8639_at	437.7	P	Involved in meiotic chromosome segregation\; may stabilize homolo
8640_at	11316.3	P	myo-inositol transporter
8641_at	2240.1	P	tRNA 2 -phosphotransferase
8642_at	2286	P	similarity to YOL002c and YDR492w
8643_at	355.6	P	Ser\/Thr protein kinase
8644_at	592.4	A	questionable ORF
8645_at	12956.5	P	similarity to hypothetical S.pombe protein
8646_at	22606.9	P	cytoplasmic tryptophanyl-tRNA synthetase
8647_at	2585.1	P	3,4-dihydroxy-5-hexaprenylbenzoate methyltransferase
8648_at	874.4	P	Helicase in MItochondria
8649_at	773.3	P	Subunit 4 of Replication Factor C\; homologous to human RFC 40 k
8650_at	2983.4	P	similarity to C.elegans hypothetical protein F25H8.1

8651_at	12696.4	P	strong similarity to YBR147w
8652_at	347.1	A	hypothetical protein
8653_at	4307.2	P	MutS homolog encoding major mismatch repair activity in mitosis an
8654_at	2451.5	P	putative transcription factor\; contains a zinc finger
8655_at	2728.6	P	protein disulfide isomerase related protein
8656_at	1094.6	P	similarity to S.pombe hypothetical protein
8657_at	19582.6	P	Alcohol dehydrogenase
8658_at	147	A	hypothetical protein
8659_at	484.8	P	similarity to A.thaliana hyp1 protein
8615_at	1452.2	P	similarity to YOL082w
8616_at	2039.3	P	similarity to YOL083w
8617_at	1309.9	P	encodes a GTPase activating protein, highly homologous to Ira1p, h
8618_at	5234.3	P	strong similarity to X.laevis XPMC2 protein
8619_at	396.1	A	similarity to NADH dehydrogenases
8620_at	1696.9	P	hypothetical protein
8621_at	11737.2	P	strong similarity to C.elegans K12H4.3 protein
8622_at	1000.4	P	Dislikes Extra CIN8, (MDM) Mitochondrial distribution and morpholo
8623_at	1935.2	P	similarity to A.gambiae ATP-binding-cassette protein
8624_at	3182.2	P	hypothetical protein
8625_at	3413.9	P	hypothetical protein
8626_at	1601.1	P	similarity to hypothetical S. pombe protein
8627_at	2071.7	P	hypothetical protein
8628_at	108.9	P	53-kDa coiled-coil protein
8629_at	5193.5	P	Homolog of SIR2
8630_at	537.8	A	Transcription factor (bHLH) involved in interorganelle communicatio
8631_at	3621.5	P	DRAP deaminase
8632_at	1376.8	P	inositol polyphosphate 5-phosphatase
8633_at	8763.6	P	3 (2)5 -bisphosphate nucleotidase
8634_at	2115.3	P	hypothetical protein
8635_at	2343.6	P	Clathrin associated protein, medium subunit
8636_at	14796.5	P	Phosphoribosylpyrophosphate synthetase (ribose-phosphate pyropho
8637_at	2327.8	P	similarity to C.elegans hypothetical protein M02F4.4
8592_at	5142.3	P	Glycerol-3-phosphate dehydrogenase (NAD+)
8593_at	9862.8	P	arginosuccinate synthetase
8594_at	783.5	P	similarity to hypothetical C. elegans protein F02E9.6
8595_at	1841.5	P	phosphoglycerate mutase
8596_at	2299.1	P	similarity to B. subtilis transcriptional activator tenA
8597_at	2653.6	P	weak similarity to transcription factors
8598_at	1685.8	P	hypothetical protein
8599_at	3950.5	P	DNA Damage Responsive
8600_at	11322	P	S-adenosylmethionine decarboxylase
8601_at	4816.5	P	Component of the RNA polymerase II holoenzyme complex, positiv
8602_at	345.8	M	questionable ORF
8603_at	7633.6	P	Glutathione Synthetase
8604_at	1025.6	P	similarity to YAL018c and YOL047c
8605_at	483.4	A	weak similarity to hypothetical proteins YAL018c and YOL048c
8606_at	41.4	A	questionable ORF
8607_at	2087.8	P	similarity to ser/thr protein kinase
8608_at	1904.4	P	44 kDa phosphorylated integral peroxisomal membrane protein
8609_at	2770	P	Endonuclease III-like glycosylase 2
8610_at	2027.2	P	similarity to CCR4 protein
8611_at	2561.7	P	weak similarity to M.sativa nuM1, hnRNP protein from C. tentans an

8612_at	25610.7	P	40S ribosomal protein S15 (S21) (rp52) (RIG protein)
8613_at	25631.8	P	60S acidic ribosomal protein P2A (L44) (A2) (YP2alpha)
8614_at	26131.1	P	alpha-type of subunit of 20S proteasome
8570_at	331.9	A	questionable ORF
8571_at	4967.1	P	weak similarity to YMR317w
8572_at	740.7	A	questionable ORF
8573_at	1003	P	similarity to S.pombe rad18 and rpgL29 genes and other members o
8574_at	1137.9	P	Mitochondrial glutamyl-tRNA synthetase
8575_at	701.6	P	hypothetical protein
8576_at	3178.7	P	weak similarity to Y.lipolytica Sls1 protein precursor
8577_at	21740.7	P	strong similarity to glycoprotein Gas1p
8578_at	4750.3	P	hypothetical protein
8579_at	1980.9	P	bZIP protein
8580_at	7132.4	P	similarity to YPR125w
8581_at	14055.8	P	hypothetical protein
8582_at	3289.2	P	Affects longevity
8583_at	81.2	A	hypothetical protein
8584_at	957.9	P	mitochondrial initiation factor 2
8585_at	6780	P	weak similarity to rat apoptosis protein RP-8
8586_at	4203.3	P	possible component of RCC1-Ran pathway
8587_at	5425.8	P	Tryptophan permease, high affinity
8588_at	6821.4	P	similarity to Rim9p and YFR012w
8589_at	1090.8	P	tSNARE that affects a Late Golgi compartment
8590_at	273.4	M	similarity to YFR013w
8591_at	3225.5	P	Calmodulin-dependent protein kinase
8547_at	90.4	A	weak similarity to YKR015c
8548_at	2650.1	P	hypothetical protein
8549_at	1129.8	P	Hmg-coa Reductase Degradation
8550_at	8987	P	An evolutionarily conserved member of the histone H2A F\/Z family o
8551_at	4271.3	P	strong similarity to phospholipases
8552_at	2667.7	P	putative RNA 3 -terminal phosphate cyclase
8553_at	2259.4	P	Mdm12p is a mitochondrial outer membrane protein. An Mdm12p ho
8554_at	2049.3	P	hypothetical protein
8555_at	3733.8	P	Appears to be a structural component of the chitin synthase 3 comple
8556_at	4451.7	P	topoisomerase I
8557_at	8402.9	P	RNA polymerase II subunit, homologous to S. pombe Rpb11p subur
8558_at	5183.1	P	DNA binding protein involved in transcriptional regulation
8559_at	2608.1	P	similarity to C.elegans hypothetical protein, YDR126w, YNL326c anc
8560_at	9843.5	P	strong similarity to YDR492w and S.pombe hypothetical protein
8561_at	1849	P	negative transcriptional regulator
8562_at	5376	P	Ribosomal RNA Processing
8563_at	5686.9	P	Required for glucosylation in the N-linked glycosylation pathway
8564_at	2287	P	subtilisin-like protease III
8565_at	13397.3	P	weak similarity to hypothetical protein YDR339c
8566_at	633.5	P	ATP dependent DNA ligase
8567_at	1598.2	P	similarity to M.jannaschii hypothetical protein MJ0708
8568_at	15221.7	P	small glutamine-rich tetratricopeptide repeat containing protein
8569_at	4127.5	P	Cell wall integrity and stress response component 1
8525_at	30.9	A	Killed In Mutagen, reduced growth in diepoxybutane and\/or mitomyc
8526_at	5085.9	P	similarity to Tir1p and Tir2p
8527_at	8820.2	P	Cold-shock induced protein of the Srp1p\/Tip1p family of serine-alani
8528_at	1619	P	strong similarity to ATP-dependent permeases

8529_at	535.9	P	similarity to YDR391c
8530_g_at	1227.5	P	similarity to YDR391c
8531_at	2078.5	P	strong similarity to YDR391c
8532_at	2027.8	P	B-type regulatory subunit of protein phosphatase 2A (PP2A)
8533_at	6858.7	P	hypothetical protein
8534_at	3292.5	P	p24 protein involved in membrane trafficking
8535_at	6197.7	P	Mitochondrial membrane protein
8536_at	1452.8	P	Resistance to o-dinitrobenzene, calcium, and zinc
8537_at	1093.2	P	similarity to YDR474c
8538_at	24191.9	P	10 kDa mitochondrial heat shock protein
8539_at	14215.2	P	similarity to Pyrococcus horikoshii hypothetical protein PHBQ041
8540_at	618.5	P	weak similarity to D.melanogaster probable Ca2+ transporter rdgB
8541_at	1714.8	P	hypothetical protein
8542_at	398.7	P	hypothetical protein
8543_at	904.5	P	Homolog of SIR2
8544_at	2374.9	P	Protein required for cell cycle arrest in response to loss of microtubul
8545_at	20421.7	P	Heat shock protein also induced by canavanine and entry into station
8546_at	2429.6	P	bZIP protein, can activate transcription from a promoter containing a
8502_at	379.9	A	hypothetical protein
8503_at	436.1	P	involved in invasive growth upon nitrogen starvation
8504_at	1521.4	P	Metallothionein-like protein
8505_at	1521.5	P	myc-family transcription factor homolog
8506_at	1747.7	P	Protein that complements a drug-hypersensitive mutation
8507_at	1255	P	Protein involved in constitutive endocytosis of Ste3p
8508_at	1539.9	P	Required for mother cell-specific HO expression
8509_at	501.7	P	integral membrane protein\; c-terminal TMD\; located in endosome
8510_at	1459.4	P	cytochrome c mitochondrial import factor
8511_at	2959.5	P	putative repressor protein\; contains nuclear targeting signal
8512_at	8631.6	P	Casein kinase II, beta subunit
8513_at	663	P	Mitochondrial glyoxylase-II
8514_at	489.8	A	questionable ORF
8515_at	3093.4	P	weak similarity to YDR273w
8516_at	3047.8	P	Protein involved in growth regulation
8517_at	3451.7	P	weak similarity to YDR275w
8518_at	27698	P	outer mitochondrial membrane protein, component of the mitochond
8519_at	30273.4	P	RNA helicase
8520_at	6794.2	P	homologous to MTH1\; interacts with the SNF1 protein kinase and TI
8521_at	2632.5	P	RNA trafficking protein\; transcription activator
8522_at	45.6	A	similarity to YER185w, Rta1p
8523_at	253.3	A	hypothetical protein
8524_at	7803.1	P	weak similarity to myosin heavy chain proteins
8480_at	4526.5	P	hypothetical protein
8481_at	1475.3	P	similarity to protamines
8482_at	1278.7	P	similarity to Sis2p protein and C.tropicalis hal3 protein
8483_at	149.7	A	questionable ORF
8484_at	8382.4	P	weak similarity to human phosphorylation regulatory protein HP-10
8485_at	1241.7	P	G2 allele of skp1 suppressor
8486_at	1693	P	encodes component of the spindle midzone
8487_at	2374.6	P	weak similarity to YGL144c
8488_at	963.8	P	hypothetical protein
8489_at	10100.5	P	alpha subunit of casein kinase II
8490_at	2555.4	P	strong similarity to YKR075c

8491_at	24782.5	P	Ribosomal protein L3 (rp1) (YL1)
8492_at	2210.6	P	weak similarity to human retinoblastoma binding protein 2
8493_at	7259.6	P	Cytochrome c1
8494_at	1800.5	P	hypothetical protein
8495_at	12124.1	P	glycosyl transferase
8496_at	62.9	A	hypothetical protein
8497_at	1122.2	A	GTPase activating protein
8498_at	1260.9	P	strong similarity to Thi10p
8499_at	793.1	A	hypothetical protein
8500_at	2099.2	P	hypothetical protein
8501_at	2137.7	P	endoplasmic reticulum t-SNARE, coprecipitates with Sec20p, Tip1p.
8457_at	2949.4	P	similarity to Hbs1p, Sup2p and EF1-alpha
8458_at	639.8	M	similarity to mouse KIN17 protein
8459_at	5010.8	P	weak similarity to YMR172w
8460_at	7130.6	P	Multi-copy suppressor of SOD-linked defects
8461_at	2499.8	P	hypothetical protein
8462_at	10921.8	P	strong similarity to YKR089c
8463_at	1531.5	P	questionable ORF
8464_at	1982	P	weak similarity to YKR091w
8465_at	8572.5	P	hypothetical protein
8466_at	16340.9	P	34-kDa, gamma subunit of oligosaccharyl transferase glycoprotein c
8467_at	5275.2	P	weak similarity to synaptogamines
8468_at	2455.8	P	hypothetical protein
8469_g_at	1816.9	P	hypothetical protein
8470_at	2466.1	P	weak similarity to human calcium influx channel
8471_at	7390.4	P	small GTP-binding protein\; geranylgeranylated\; geranylgeranylation
8472_at	1481.6	P	similarity to ser/thr protein phosphatases
8473_at	1520.5	P	similarity to hypothetical S.pombe protein D83992_G
8474_at	2250.4	P	ExtraCellular Mutant
8475_at	1712.6	P	similarity to S.pombe hypothetical protein SPAC22F3.04
8476_at	4185.9	P	GTP-binding ADP-ribosylation factor
8477_at	9842.9	P	Ribose-5-phosphate ketol-isomerase
8478_at	31957.7	P	Ribosomal protein S7A (rp30)
8479_at	11640.5	P	Ribosomal protein S7A (rp30)
8434_at	945.2	P	hypothetical protein
8435_at	9856	P	nuclear pore complex protein
8436_at	12684.3	P	type 2 membrane protein\; probable secretory protein
8437_at	849.4	A	similarity to mitochondrial carrier proteins
8438_at	8398.7	P	ras proto-oncogene homolog
8439_at	275.7	A	questionable ORF
8440_at	2095.2	P	16-kDa, epsilon subunit of oligosaccharyltransferase complex\; 40\%
8441_at	1159.6	P	hypothetical protein
8442_g_at	1268.6	P	hypothetical protein
8443_at	1030.6	P	member of the syntaxin family of proteins\; predicted C-terminal TMD
8444_at	1013.1	P	weak similarity to human G-0/G-1 switch regulatory protein 8
8445_at	10325.2	P	putative isoform of Leu4p
8446_at	4285.2	P	inositol polyphosphate 5-phosphatase
8447_at	1674.9	P	TFIIIC (transcription initiation factor) subunit, 55 kDa
8448_at	514.7	P	weak similarity to B.subtilis maf protein
8449_at	2709.2	P	similarity to C.elegans hypothetical protein
8450_at	327.6	P	probable transcription factor, asparagine-rich zinc-finger protein, sup
8451_at	494.3	P	hypothetical protein

8452_at	2672.7	P	involved in targeting and fusion of ER to golgi transport vesicles
8453_at	8724.2	P	RNA polymerase III large subunit
8454_at	10688.2	P	Probable 26S protease subunit and member of the CDC48\/PAS1\/S
8455_at	863.8	P	hypothetical protein
8456_at	1941.4	P	similarity to a C.elegans ZK632.3 protein
8412_at	1785.2	P	Similar to mammalian aldo\/keto reductases
8413_at	57.6	A	questionable ORF
8414_at	26859.9	P	profilin (actin-binding protein)
8415_at	3130.9	P	extremely hydrophilic protein
8416_at	2856.9	P	Ubiquitin-specific protease
8417_at	857.4	P	may encode a protein involved in one or more monoxygenase or hyd
8418_at	1604	P	isoamyl acetate hydrolytic enzyme
8419_at	1956.2	P	rho type GTPase activating protein
8420_at	11891.6	P	phosphoribosylamino-imidazole-carboxylase
8421_at	3063.9	P	hypothetical protein
8422_at	1812.6	P	mitochondrial integral membrane protein
8423_at	4201	P	weak similarity to E.coli hypothetical 27K protein
8424_at	5485.3	P	Peripheral membrane protein required for vacuolar protein sorting
8425_s_at	30021.6	P	translation elongation factor 2 (EF-2)
8426_at	58.4	A	GTPase activating protein (GAP)
8427_at	192.2	A	questionable ORF
8428_at	26146.1	P	NAD+-dependent isocitrate dehydrogenase
8429_at	998	P	similarity to YLR361c
8430_at	2823.2	P	hypothetical protein
8431_at	572.2	P	questionable ORF
8432_at	1858.2	P	Transcription factor
8433_at	1885.8	P	Actin-related protein
8389_at	12531.9	P	Succinate-CoA Ligase (ADP-Forming)
8390_at	957.3	P	Thiamin pyrophosphokinase
8391_at	3668.3	P	weak similarity to human DNA-binding protein PO-GA and to bacteri
8392_at	18544.3	P	strong similarity to hypothtical S. pombe protein and to hypothetical
8393_at	902	M	questionable ORF
8394_at	305.5	P	similarity to YHR194w
8395_at	2310.5	P	required for final stages of splicesome maturation\; promotes step 1
8396_at	489.1	P	Involved in plasmid maintenance
8397_at	5613.6	P	ribosomal protein of the large subunit, mitochondrial
8398_at	11642.4	P	second largest subunit of RNA polymerase II
8399_at	532.6	P	hypothetical protein
8400_at	14868.9	P	multidrug resistance transporter
8401_at	1971.2	P	similarity to hypothetical A. thaliana proteins F19G10.15 and T19F06
8402_at	3492.9	P	similarity to 5 -flanking region of the Pichia MOX gene
8403_at	748.5	P	Interacts with C-terminus of CDC12
8404_at	19198.5	P	putative proteasome subunit
8405_at	1291.8	P	Mitochondrial ribosomal protein of small subunit
8406_at	2181.9	P	homologue of human E core protein
8407_at	3974.2	P	Protein involved in mRNA transport from nucleus to cytoplasm
8408_at	720.5	P	similarity to C.elegans cosmid F35C8
8409_at	1673.6	P	transcription factor
8410_at	3406.1	P	strong similarity to S.pombe SPAC13G6.14 protein
8411_at	5779.7	P	hypothetical protein
8366_at	4582.5	P	similarity to E.histolytica surface lectin
8367_at	1181.7	P	hypothetical protein

8368_i_at	14461.8	P	Ribosomal protein S28A (S33A) (YS27)
8369_f_at	26784.2	P	Ribosomal protein S28A (S33A) (YS27)
8370_at	5891.2	P	glutaminyl-tRNA synthetase
8371_at	857.3	P	questionable ORF
8372_at	383.4	M	questionable ORF
8373_at	1865.2	P	sphingoid long chain base (LCB) kinase
8374_at	844.8	P	similarity to finger protein YKL222c, YOR162c and YLR266c
8375_at	412.1	A	strong similarity to YLR270w
8376_at	3808.3	P	Stoichiometric member of mediator complex
8377_at	7248	P	similarity to human and murine C3f protein
8378_at	7489.7	P	ferrochelatase (protoheme ferrolyase)
8379_at	228	P	weak similarity to rat SCP1 protein
8380_at	157.8	A	Regulatory subunit for Glc7p
8381_at	2037.2	P	similarity to BRR5 protein
8382_at	245.2	P	Peroxisomal enoyl-CoA hydratase
8383_at	3841	P	Actin assembly factor
8384_f_at	28416	P	Ribosomal protein S30B
8385_at	152.1	A	hypothetical protein
8386_at	10177.3	P	phosphoserine transaminase
8387_at	1318.9	P	GTP binding protein, almost identical to Gsp1p
8388_at	358.4	A	hypothetical protein
8343_at	12845.3	P	Translation elongation factor Tu, mitochondrial
8344_at	3546	P	Protein that may play a role in polarity establishment and bud formati
8345_at	1657.5	P	weak similarity to chicken nonhistone chromosomal protein HMG-2
8346_at	57.6	A	sporulation-specific exo-1,3-beta-glucanase
8347_at	1058.2	P	contains motifs that are present in a family of DNA-dependent ATPa
8348_i_at	770.5	A	strong similarity to Thi10p
8349_f_at	2192.4	P	strong similarity to Thi10p
8350_at	535.4	M	weak similarity to YPL112c
8351_at	2439.5	P	Transcription factor IIA, large chain
8352_at	521.6	P	possible leucine zipper
8353_at	3187.9	P	Involved in lipoic acid metabolism
8354_at	8510.6	P	hypothetical protein
8355_at	9939.1	P	Multicopy suppressor of BFA (Brefeldin A)-induced lethality\; implicat
8356_at	22.5	A	questionable ORF
8357_at	690.9	A	questionable ORF
8358_at	4276.3	P	Ribose methyltransferase for mitochondrial 21S rRNA
8359_at	7520.5	P	imidazoleglycerol-phosphate dehydratase
8360_at	2786.8	P	questionable ORF
8361_at	15262.1	P	ATP-dependent RNA helicase of DEAD box family\; suppressor of a
8362_at	2383.2	P	hypothetical protein
8363_at	2513.7	P	similarity to Brettanomyces RAD4 and to S.pombe hypothetical prote
8364_at	14090.3	P	second-largest subunit of RNA polymerase III
8365_at	1806.8	P	protein tyrosine phosphatase
8320_at	11172	P	homology to bacterial nicotinate phosphoribosyl transferase
8321_at	20955.9	P	RNA polymerase II subunit
8322_at	1049.4	P	encodes protein with GTP-binding domain related to dynamin
8323_at	11926.7	P	beta subunit of G protein coupled to mating factor receptor
8324_at	697.5	P	Involved in silencing at telomeres, HML and HMR
8325_at	19.5	A	hypothetical protein
8326_at	1746.4	P	similarity to M.xanthus hypothetical protein
8327_at	1348.9	P	Relieves uso1-1 Transport Defect

8328_at	3547.2	P	Subunit 1 of Replication Factor C\; homologous to human RFC 140 k
8329_at	1425.7	P	questionable ORF
8330_at	7346.9	P	dipeptidyl aminopeptidase
8331_at	5707.8	P	hypothetical protein
8332_at	3609.2	P	malonyl-CoA:ACP transferase
8333_at	18.9	A	malonyl-CoA:ACP transferase
8334_at	1475	P	similarity to ADP/ATP carrier proteins
8335_at	2562.3	P	protein of unknown function
8336_at	30420.7	P	16-kDa RNA polymerase subunit (common to polymerases I, II and
8337_at	1069.3	M	questionable ORF
8338_at	17992.4	P	NifU-like protein A
8339_at	2757.7	P	similarity to microtubule-interacting protein Mhp1p
8340_at	2769.7	P	weak similarity to YNR013c
8341_at	7111.2	P	Transcriptional modulator
8342_at	32679.3	P	Transcriptional modulator
8297_at	2864.8	P	protein kinase involved in protein kinase C pathway
8298_at	4749.1	P	GrpE homolog, mitochondrial matrix protein
8299_at	4980.4	P	protein kinase
8300_f_at	18764.7	P	Ribosomal protein L33B (L37B) (rp47) (YL37)
8301_at	19.3	A	encodes snRNA U3, SNR17B also encodes snRNA U3
8302_at	2843.7	P	dihydrofolate reductase
8303_at	46.2	A	homology to human oxysterol binding protein
8304_at	4229.8	P	similarity to hypothetical S. pombe protein
8305_at	3513.9	P	hypothetical protein
8306_at	7364.3	P	similarity to C.elegans ZK1058.5 protein
8307_at	9366.5	P	tetrahydrofolylpolyglutamate synthase
8308_at	578.7	P	Sporulation Specific
8309_at	10776.5	P	similarity to M.jannaschii hypothetical protein MJ0588
8310_at	2534.3	P	Acetyltransferase in the SAS gene family
8311_at	3946.1	P	similarity to hypothetical C. elegans proteins
8312_at	11137.2	P	weak similarity to reductases
8313_at	24705	P	Suppressor of rad53 lethality
8314_g_at	27029.4	P	Suppressor of rad53 lethality
8315_i_at	17357.9	A	questionable ORF
8316_at	828.6	P	subunit of the anaphase promoting complex
8317_at	1888.2	P	CLeavage\/Polyadenylation factor IA subunit\; interacts with Pcf11p i
8318_at	6451.3	P	similarity to thiosulfate sulfurtransferases
8319_at	2990	P	hypothetical protein
8274_at	3647.5	P	hypothetical protein
8275_at	2333	P	Protein involved in protein import into ER
8276_at	15.1	A	hypothetical protein
8277_at	2025.8	P	strong similarity to secretory protein Ssp134p
8278_at	5268.8	P	calcium-binding protein component of spindle pole bodies, localizes
8279_at	1143.8	P	hypothetical protein
8280_at	11417	P	ATPase\; component of the 26S proteasome cap subunit
8281_at	17844	P	translation initiation factor eIF2b gamma subunit\; negative regulator
8282_at	8493.3	P	Subunit of the regulatory particle of the proteasome
8283_at	2923.6	P	similarity to YLR243w
8284_at	239.6	A	questionable ORF
8285_at	1316	P	hypothetical protein
8286_at	7379.6	P	Binds to beta-tubulin and may participate in microtubule morphogene
8287_at	502.2	P	Pentamidine resistance protein

8288_at	13087.6	P	similarity to ser/thr protein kinases
8289_at	1060.5	M	hypothetical protein
8290_at	702.7	P	Required for viability in the absence of the kinesin-related Cin8p mito
8291_at	22641.2	P	Vacuolar H-ATPase 100 kDa subunit of membrane (V0) sector, ess
8292_at	30626.8	P	strong similarity to Rattus tricarboxylate carrier
8293_at	13472.3	P	microtubule-associated protein
8294_at	3147.5	P	similarity to resistance proteins
8295_at	1529.6	P	transfer RNA isopentenyl transferase
8296_at	777.1	P	similarity to A.nidulans palA protein
8252_at	21194	P	Binds to eIF4E, the mRNA cap-binding protein, and represses cap-d
8253_at	341.8	A	questionable ORF
8254_at	2869.3	P	uroporphyrinogen III synthase
8255_at	391.8	M	hypothetical protein
8256_at	3888.7	P	similarity to S.pombe dihydrofolate reductase
8257_at	6197.2	P	weak similarity to phosducins
8258_at	353.3	A	questionable ORF
8259_at	4729.4	P	weak similarity to phosphoglycerate mutases
8260_at	664.8	P	weak similarity to M.jannaschii hypothetical protein MJ0694
8261_at	17112.4	P	similarity to D.melanogaster heat shock protein 67B2
8262_at	12022	P	similarity to D.melanogaster heat shock protein 67B2
8263_at	1333	P	weak similarity to PITSLRE protein kinase isoforms
8264_at	3377.9	P	Disulfide isomerase related protein
8265_at	648	P	similarity to C.elegans hypothetical protein
8266_at	6851.1	P	transcriptional regulator
8267_at	4928.3	P	similarity to cation translocating ATPases
8268_at	1744.4	P	similarity to human and mouse glomerulosclerosis protein Mpv17
8269_f_at	12761.5	P	Ribosomal protein S10A
8270_f_at	36916	P	Ribosomal protein S10A
8271_at	5120.5	P	similarity to human hypothetical protein
8272_at	350	P	weak similarity to SWI/SNF complex 60 KDa subunit from man and r
8273_at	728.6	P	similarity to hypothetical S. pombe protein
8229_at	7892.7	P	similarity to Sdh4p
8230_at	90.4	A	required for meiosis
8231_at	18877.5	P	multiprotein bridging factor
8232_at	2717.9	P	BUD site selection
8233_g_at	3548.4	P	BUD site selection
8234_at	134.3	A	questionable ORF
8235_at	6739.2	P	hypothetical protein
8236_at	7372.3	P	CPA1 leader peptide
8237_at	7595.4	P	Carbamoyl phosphate synthetase, arginine specific
8238_at	1256.6	P	has strong homology to Drosophila ISWI
8239_at	2314.7	P	AIP3 binding protein
8240_at	1889.7	P	hypothetical protein
8241_at	6552.5	P	similarity to human X-linked PEST-containing transporter
8242_at	4553	P	homolog of chloroplast phosphate transporter
8243_at	765.5	P	weak similarity to YIL149c
8244_i_at	25448.3	P	questionable ORF
8245_r_at	1689.6	P	questionable ORF
8246_s_at	30897.8	P	questionable ORF
8247_at	34064.6	P	57 kDa nucleolar protein
8248_at	22208.9	P	similarity to hypothetical S. pombe protein
8249_at	428.1	P	sporulation-specific protein

8250_at	394.4	P	hypothetical protein
8251_at	2469.9	P	hypothetical protein
8206_at	3063.9	P	Protein involved in cobalt accumulation\; dosage dependent suppres
8207_at	11440.1	P	long chain fatty acyl:CoA synthetase
8208_at	593.8	P	hypothetical protein
8209_at	660.1	P	homolog of mammalian splicing factor\/U2 snRNP protein
8210_at	3213.6	P	hypothetical protein
8211_at	2465.3	P	dolichyl phosphate-D-mannose:protein O-D-mannosyltransferase
8212_at	5091.1	P	similarity to hypothetical S.pombe protein SPAC1F12.05
8213_at	26383.4	P	gamma-glutamyl phosphate reductase
8214_at	746.1	P	similarity to YAL028w
8215_at	970.8	A	questionable ORF
8216_at	6872.2	P	myosin-1
8217_at	14989.1	P	vesicle-associated membrane protein (synaptobrevin) homolog
8218_at	3965.9	P	Putative ABC transporter highly similar to Pdr5p
8219_at	1652.9	P	Multicopy suppressor of clathrin deficiency and of ts mutants of IPL1
8220_at	621.2	P	catalytic subunit of mitochondrial DNA polymerase
8221_at	1381.5	P	questionable ORF
8222_at	12620.7	P	27-kDa subunit of the vacuolar ATPase\; E subunit of V1 sector
8223_at	297.7	P	questionable ORF
8224_at	1154.1	P	splicing factor
8225_at	9737.2	P	Cytoplasmic alanyl-tRNA synthetase gene
8226_at	3485.5	P	Appears to function early in (1,6)-beta-D-glucan synthesis pathway
8227_at	1950.4	P	Mutants are defective in Ty1 Enhancer-mediated Activation
8228_at	1797.8	P	similarity to YAL034c
8183_at	20.6	A	strong similarity to E2 ubiquitin-conjugating enzymes
8184_at	9178.4	P	DNA-dependent RNA polymerase I subunit A43
8185_at	28558.2	P	RNA polymerase I subunit 190 (alpha)
8186_at	4979.5	P	weak similarity to YAl037w
8187_at	1584	A	hypothetical protein
8188_at	1102.6	P	TYE7, a 33 kDa serine-rich protein, is a potential member of the bas
8189_at	59.8	A	questionable ORF
8190_at	1248.5	P	deoxycytidyl transferase
8191_at	2801.2	P	Pyruvate kinase, glucose-repressed isoform
8192_at	779.2	A	putative proline-specific permease
8193_at	52.8	A	Protein involved in chromosome segregation, required for microtubu
8194_at	148.1	A	weak similarity to Esp1p and mitochondrial L.illustris cytochrome oxi
8195_at	40.9	A	mRNA is induced in meiosis, encodes a meiosis-specific serine\/thre
8196_at	1713.3	P	hypothetical protein
8197_at	1129.6	P	weak similarity to adenylate cyclases
8198_at	1876.6	P	hypothetical protein
8199_at	9875.3	P	nam9-1 suppressor
8200_at	7677	P	strong similarity to human electron transfer flavoprotein-ubiquinone o
8201_at	4047.7	P	Grd19p that is epitope tagged with the HA epitope at the C-terminus
8202_at	1359.4	P	Component, along with Hap2p and Hap3p, of CCAAT-binding transc
8203_at	7454	P	hypothetical protein
8204_at	4314.6	P	low-Km (high-affinity) cAMP phosphodiesterase
8205_at	20988.9	P	translation initiation factor eIF3 subunit
8161_at	13940.8	P	proteasome component YC1 (protease yscE subunit 1)
8162_at	1425.9	P	Activator of peroxisome proliferation
8163_at	446.3	P	hypothetical protein
8164_at	132.6	A	strong similarity to YAL053w

8165_at	184.5	P	questionable ORF
8166_at	1978.5	P	Calponin homolog
8167_at	458.2	A	encodes a putative 3 ->5 exonuclease
8168_at	33051.2	P	40S ribosomal protein S12
8169_at	7609.9	P	protein of the TCD\/MRS6 family of GDP dissociation inhibitors (Rab
8170_at	916.5	A	similarity to YAL056w
8171_at	3607.6	P	hypothetical protein
8172_at	2226	P	nuclesome assembly protein I
8173_at	6387.1	P	aldehyde dehydrogenase (E.C. 1.2.1.5) (sold by SIGMA under the ca
8174_at	16391.9	P	NADP-specific glutamate dehydrogenase
8175_at	157.5	A	hypothetical protein
8176_at	1276.8	P	Alcohol acetyltransferase
8177_at	239.2	A	strong similarity to aminotriazole resistance protein
8178_at	521.4	A	questionable ORF
8179_at	1682.4	P	weak similarity to Pdr3p
8180_at	335.6	A	similar to FRE2
8181_at	2589.2	P	hypothetical protein
8182_at	8085.4	P	weak similarity to L.mexicana secreted acid phosphatase 2
8138_at	6.7	A	similar to FRE2
8139_at	5067.3	P	strong similarity to hypothetical protein YMR316w
8140_at	431.1	P	photolyase
8141_at	38.5	A	strong similarity to YGL258w
8142_s_at	33.4	A	Protein with similarity to formate dehydrogenases
8143_at	841	P	strong similarity to putative pseudogenes YPL277c and YPL278c
8144_g_at	1485.6	P	strong similarity to putative pseudogenes YPL277c and YPL278c
8145_s_at	3687.6	P	nearly identical to YPL279c
8146_at	516.5	M	hypothetical protein
8147_s_at	100.8	A	strong similarity to members of the Srp1p/Tip1p family
8148_at	326.6	A	hypothetical protein identified by SAGE
8149_at	1681.5	M	identified by SAGE
8150_s_at	446.7	P	Sorting nexin I homologue
8151_s_at	2985.7	P	Thymidylate synthase
8152_f_at	810.9	P	Thymidylate synthase
8153_at	206.4	P	non-annotated SAGE orf Found forward in NC_001147 between 331
8154_at	55.9	A	non-annotated SAGE orf Found reverse in NC_001147 between 359
8155_at	362.6	A	non-annotated SAGE orf Found forward in NC_001147 between 242
8156_g_at	12.3	A	non-annotated SAGE orf Found forward in NC_001147 between 242
8157_at	509.5	P	non-annotated SAGE orf Found forward in NC_001147 between 571
8158_g_at	2895.8	P	non-annotated SAGE orf Found forward in NC_001147 between 571
8159_at	687.5	P	non-annotated SAGE orf Found forward in NC_001147 between 571
8160_at	786.4	A	non-annotated SAGE orf Found reverse in NC_001147 between 882
8112_at	2035	P	non-annotated SAGE orf Found reverse in NC_001147 between 147
8113_at	642.1	P	non-annotated SAGE orf Found reverse in NC_001147 between 241
8114_i_at	16	A	non-annotated SAGE orf Found forward in NC_001147 between 464
8115_f_at	2617.7	P	non-annotated SAGE orf Found forward in NC_001147 between 464
8116_f_at	76.3	A	non-annotated SAGE orf Found reverse in NC_001147 between 599
8117_i_at	134.3	A	non-annotated SAGE orf Found forward in NC_001147 between 703
8118_i_at	478.1	A	non-annotated SAGE orf Found reverse in NC_001147 between 703
8119_f_at	768.7	A	non-annotated SAGE orf Found reverse in NC_001147 between 703
8120_at	2602.3	P	non-annotated SAGE orf Found forward in NC_001147 between 600
8121_at	704.5	P	non-annotated SAGE orf Found reverse in NC_001147 between 852
8122_at	10.2	A	non-annotated SAGE orf Found forward in NC_001147 between 106

8123_at	1189.6	A	non-annotated SAGE orf Found reverse in NC_001147 between 136
8124_at	2426.2	P	non-annotated SAGE orf Found forward in NC_001147 between 185
8125_at	2357.8	P	non-annotated SAGE orf Found forward in NC_001147 between 254
8126_at	495.2	P	non-annotated SAGE orf Found reverse in NC_001147 between 290
8127_at	82.5	A	non-annotated SAGE orf Found reverse in NC_001147 between 316
8128_at	166.1	A	non-annotated SAGE orf Found reverse in NC_001147 between 372
8129_at	1996.8	P	non-annotated SAGE orf Found reverse in NC_001147 between 397
8130_at	484.6	A	non-annotated SAGE orf Found reverse in NC_001147 between 414
8131_at	689.9	P	non-annotated SAGE orf Found forward in NC_001147 between 423
8132_at	3443.2	P	non-annotated SAGE orf Found forward in NC_001147 between 646
8133_at	534.2	A	non-annotated SAGE orf Found forward in NC_001147 between 658
8134_at	80.7	A	non-annotated SAGE orf Found reverse in NC_001147 between 671
8135_at	557.5	A	non-annotated SAGE orf Found forward in NC_001147 between 680
8136_at	765.6	P	non-annotated SAGE orf Found reverse in NC_001147 between 715
8137_at	21605.7	P	non-annotated SAGE orf Found forward in NC_001147 between 738
8088_i_at	17.4	A	non-annotated SAGE orf Found forward in NC_001147 between 792
8089_at	3600.8	P	non-annotated SAGE orf Found forward in NC_001147 between 850
8090_at	500.4	M	non-annotated SAGE orf Found forward in NC_001147 between 918
8091_at	234.8	A	non-annotated SAGE orf Found reverse in NC_001147 between 922
8092_i_at	10376.8	P	non-annotated SAGE orf Found forward in NC_001147 between 100
8093_r_at	5421.9	P	non-annotated SAGE orf Found forward in NC_001147 between 100
8094_f_at	9468.9	A	non-annotated SAGE orf Found forward in NC_001147 between 100
8095_at	117.9	A	non-annotated SAGE orf Found forward in NC_001147 between 301
8096_at	529.4	P	non-annotated SAGE orf Found forward in NC_001147 between 413
8097_i_at	9.8	A	non-annotated SAGE orf Found reverse in NC_001147 between 798
8098_at	157.1	M	non-annotated SAGE orf Found forward in NC_001147 between 980
8099_at	38.9	A	non-annotated SAGE orf Found reverse in NC_001147 between 178
8100_at	72.2	A	non-annotated SAGE orf Found forward in NC_001147 between 187
8101_at	304.7	A	non-annotated SAGE orf Found forward in NC_001147 between 278
8102_at	3081.4	P	non-annotated SAGE orf Found forward in NC_001147 between 136
8103_at	11.7	A	non-annotated SAGE orf Found forward in NC_001147 between 158
8104_at	3629.5	P	non-annotated SAGE orf Found forward in NC_001147 between 159
8105_at	44.9	A	non-annotated SAGE orf Found forward in NC_001147 between 226
8106_at	1521.5	P	non-annotated SAGE orf Found forward in NC_001147 between 418
8107_at	1168.8	P	non-annotated SAGE orf Found forward in NC_001147 between 438
8108_at	302.5	A	non-annotated SAGE orf Found reverse in NC_001147 between 682
8109_at	81.6	A	non-annotated SAGE orf Found reverse in NC_001147 between 682
8110_at	194.9	A	non-annotated SAGE orf Found reverse in NC_001147 between 759
8111_g_at	112.1	A	non-annotated SAGE orf Found reverse in NC_001147 between 759
8063_at	3113.7	P	non-annotated SAGE orf Found reverse in NC_001147 between 775
8064_at	1374.9	A	non-annotated SAGE orf Found reverse in NC_001147 between 836
8065_at	127.8	A	non-annotated SAGE orf Found reverse in NC_001147 between 854
8066_at	757.5	M	non-annotated SAGE orf Found reverse in NC_001147 between 969
8067_i_at	5361.2	P	non-annotated SAGE orf Found reverse in NC_001147 between 974
8068_at	19.6	A	non-annotated SAGE orf Found reverse in NC_001147 between 978
8069_at	255.7	A	non-annotated SAGE orf Found reverse in NC_001147 between 978
8070_at	221.1	P	non-annotated SAGE orf Found reverse in NC_001147 between 979
8071_f_at	632.1	P	non-annotated SAGE orf Found reverse in NC_001147 between 108
8072_i_at	395.3	A	non-annotated SAGE orf Found reverse in NC_001147 between 108
8073_f_at	452.1	A	non-annotated SAGE orf Found reverse in NC_001147 between 108
8074_s_at	2201.6	P	non-annotated SAGE orf Found reverse in NC_001147 between 108
8075_s_at	810.8	P	non-annotated SAGE orf Found reverse in NC_001147 between 109

8076_at	115.2	A	non-annotated SAGE orf Found reverse in NC_001147 between 165
8077_at	21.1	A	non-annotated SAGE orf Found reverse in NC_001147 between 166
8078_at	96.3	A	non-annotated SAGE orf Found reverse in NC_001147 between 167
8079_s_at	205.8	A	non-annotated SAGE orf Found forward in NC_001147 between 270
8080_at	643.7	P	non-annotated SAGE orf Found forward in NC_001147 between 271
8081_at	54.7	A	non-annotated SAGE orf Found forward in NC_001147 between 427
8082_at	160.1	A	non-annotated SAGE orf Found forward in NC_001147 between 430
8083_at	14.4	A	non-annotated SAGE orf Found forward in NC_001147 between 431
8084_at	199.7	A	non-annotated SAGE orf Found forward in NC_001147 between 108
8085_at	1240.3	P	non-annotated SAGE orf Found forward in NC_001147 between 180
8086_at	251.4	A	non-annotated SAGE orf Found forward in NC_001147 between 193
8087_at	689.4	A	non-annotated SAGE orf Found reverse in NC_001147 between 271
8039_at	494.3	P	non-annotated SAGE orf Found reverse in NC_001147 between 301
8040_at	2463	P	non-annotated SAGE orf Found forward in NC_001147 between 524
8041_at	2119	P	non-annotated SAGE orf Found reverse in NC_001147 between 609
8042_at	299.3	A	non-annotated SAGE orf Found forward in NC_001147 between 690
8043_at	39.3	A	non-annotated SAGE orf Found forward in NC_001147 between 692
8044_at	17282.7	P	non-annotated SAGE orf Found forward in NC_001147 between 758
8045_at	179.7	A	non-annotated SAGE orf Found forward in NC_001147 between 778
8046_at	538.1	P	non-annotated SAGE orf Found forward in NC_001147 between 825
8047_at	1746.2	M	non-annotated SAGE orf Found forward in NC_001147 between 877
8048_at	13061.8	P	non-annotated SAGE orf Found forward in NC_001147 between 100
8049_at	91.7	A	non-annotated SAGE orf Found forward in NC_001147 between 107
8050_at	13.2	A	non-annotated SAGE orf Found forward in NC_001147 between 107
8051_i_at	7.3	A	non-annotated SAGE orf Found reverse in NC_001147 between 107
8052_r_at	103.5	A	non-annotated SAGE orf Found reverse in NC_001147 between 107
8053_at	505.7	A	snRNA
8054_at	744.4	P	snRNA
8055_i_at	9.4	A	Centromere
8056_at	2835.8	P	snRNA
8057_i_at	398.7	P	snRNA
8058_r_at	346.3	P	snRNA
8059_at	1496.1	P	snRNA
8060_at	2560.6	P	snRNA
8061_at	2715	P	snRNA
8062_at	12520.8	P	snRNA
8016_at	307	A	snRNA
8017_at	5719.4	P	snRNA
8018_i_at	293.7	P	strong similarity to hypothetical protein YOR389w/putative pseudoge
8019_s_at	740.8	P	strong similarity to hypothetical protein YOR389w/putative pseudoge
8020_s_at	373.7	A	putative formate dehydrogenase/putative pseudogene
8021_at	2011.5	P	strong similarity to amino-acid transport proteins
8022_at	6394.7	P	weak similarity to M.leprae metH2 protein, and strong similarity to hy
8023_at	85.5	A	hypothetical protein
8024_at	14933.7	P	nuclear gene for ATP synthase epsilon subunit
8025_at	3227	P	ATP-binding cassette (ABC) transporter family member
8026_at	1181.5	P	Cortical protein required for cytoplasmic microtubule orientation\; loc
8027_at	1589.6	P	phosphoinositide-specific phospholipase C
8028_at	1043.1	P	weak similarity to C.elegans transcription factor unc-86
8029_at	8391.7	P	dimethyladenosine transferase
8030_at	25753.3	P	dicarboxylic amino acid permease
8031_at	1998.3	P	strong similarity to YMR253c

8032_at	2380.5	P	similarity to Kel2p and Kel3p
8033_at	30268.7	P	mitochondrial and cytoplasmic fumarase (fumarate hydralase)
8034_at	295.3	A	questionable ORF
8035_at	2946.6	P	hypothetical protein
8036_at	1047.2	P	medium subunit of the clathrin-associated protein complex
8037_at	1025.6	P	similarity to B.subtilis transcriptional activator tenA, and strong simila
8038_at	271.7	A	weak similarity to YIL029c
7993_at	3659.8	P	G(sub)1 cyclin
7994_at	668	P	Involved in mitotic cell cycle and meiosis
7995_at	3291.2	P	transcription factor, member of Ada\/Gcn5 protein complex
7996_at	247.8	A	Cik1p homolog
7997_at	15451.1	P	iron-sulfur protein homologous to human adrenodoxin
7998_at	226.8	A	questionable ORF
7999_at	9300.8	P	weak similarity to YMR195w
8000_i_at	29668.7	P	Ribosomal protein L36B (L39) (YL39)
8001_at	239.4	M	similarity to mouse Tbc1 protein
8002_at	1009.8	P	zinc-finger transcription factor of the Zn(2)-Cys(6) binuclear cluster d
8003_at	3576.6	P	similarity to human HAN11 protein and petunia an11 protein
8004_at	9905.1	P	weak similarity to mouse proteinase activated receptor 2
8005_at	7062.4	P	weak similarity to human mutL protein homolog
8006_at	5111.5	P	weak similarity to human UDP-galactose transporter related isozyme
8007_at	2509.5	P	component of signal recognition particle
8008_at	549.7	P	Homolog of the mammalian IQGAP1 and 2 genes\; probable regulat
8009_at	2142.6	P	involvement in microtubule function
8010_i_at	7088.3	P	heat shock protein
8011_at	11306.7	P	YAR1 encodes a 200-amino-acid protein with two ANK repeat motifs
8012_at	1550.2	P	questionable ORF
8013_at	12187.8	P	beta subunit of translation initiation factor eIF-2
8014_at	711.9	P	similarity to Prk1p, and serine/threonine protein kinase homolog fro
8015_at	10387.8	P	strong similarity to TATA-binding protein-interacting protein 49 from r
7970_at	21578.3	P	17-kDa subunit C of vacuolar membrane H(+)-ATPase
7971_at	1028.5	P	hypothetical protein
7972_at	6792.6	P	SSO1 and SSO2 encode syntaxin homologs\; act in late stages of se
7973_at	27135.1	P	alpha subunit of fatty acid synthase
7974_at	70.2	A	Up in StarVation
7975_at	1924.5	P	weak similarity to YMR181c
7976_at	1329.6	P	mRNA capping enzyme beta subunit (80 kDa), RNA 5 -triphosphata
7977_at	4895.5	P	UDP-glucose:dolichyl-phosphate glucosyltransferase
7978_at	28525.7	P	similarity to translation elongation factor eEF3
7979_at	6140.2	P	hypothetical protein
7980_at	2852	P	Protein involved in mitochondrial iron accumulation
7981_at	593.8	P	Induced by osmotic stress
7982_at	393.3	A	similarity to C.perfringens hypothetical protein
7983_at	6538.6	P	Bypass of PAM1
7984_s_at	24499.7	P	Ribosomal protein L1A, forms part of the 60S ribosomal subunit
7985_at	1129.2	P	PHO85 cyclin
7986_at	20279.9	P	GTP binding protein
7987_at	4505.9	P	similarity to human hypothetical protein KIAA0187
7988_at	207.1	A	similarity to YGL133w
7989_at	2056	P	Protein required for assembly of ubiquinol cytochrome-c reductase c
7990_at	2438.3	P	TMP pyrophosphorylase, hydroxyethylthiazole kinase
7991_at	767.9	P	similarity to A.thaliana U2 snRNP protein A

7992_at	7680.7	P	intranuclear protein which exhibits a nucleotide-specific intron-depen
7947_at	7438	P	Nip7p is required for 60S ribosome subunit biogenesis
7948_at	5426	P	component of signal recognition particle
7949_at	507	P	Protein kinase
7950_at	1531	P	similarity to YHL039w
7951_at	8154.7	P	similarity to hypthetical proteins from A. fulgidus, M. thermoautotrop
7952_at	13295.4	P	weak similarity to glycerophosphoryl diester phosphodiesterases
7953_at	807.8	P	questionable ORF
7954_at	4946.9	P	casein kinase I isoform
7955_at	3101.5	P	cAMP-dependent protein kinase catalytic subunit
7956_at	1130.4	P	similarity to cell size regulation protein Rcs1p
7957_at	233.2	A	hypothetical protein
7958_at	31.5	A	hypothetical protein
7959_at	10759.8	P	weak similarity to T.cruzi p284 protein
7960_i_at	4547.8	P	Ribosomal protein L7B (L6B) (rp11) (YL8)
7961_f_at	7872.3	P	Ribosomal protein L7B (L6B) (rp11) (YL8)
7962_s_at	30583.1	P	Ribosomal protein L7B (L6B) (rp11) (YL8)
7963_at	619.8	P	questionable ORF
7964_at	1458.2	P	weak similarity to S.pombe hypothetical protein SPAC8C9
7965_at	1794.2	P	delta-like subunit of the yeast AP-3 adaptin component of the membr
7966_at	1076.1	P	DNA damage checkpoint gene
7967_at	732.6	P	weak similarity to human centromere protein E
7968_at	451.7	A	hypothetical protein
7969_at	337.4	P	strong similarity to YGL082w
7924_at	2961.8	P	polyadenylated RNA-binding protein
7925_at	452.9	P	strong similarity to YGL084c
7926_at	2254.2	P	similarity to Utr1p and YEL041w
7927_at	30363.4	P	mating factor alpha
7928_at	389.7	P	weak similarity to Xenopus protein xlgv7
7929_at	243.5	A	questionable ORF
7930_at	3125.4	P	weak similarity to Pub1p
7931_at	6896.8	P	ribosomal protein L36, mitochondrial
7932_at	6637.4	P	similarity to Taf90p
7933_at	1122.1	P	questionable ORF
7934_at	726.5	P	weak similarity to YKR029c
7935_at	4893.4	P	weak similarity to human l-caldesmon I
7936_at	4203.1	P	protein phosphatase Q
7937_at	7454.3	P	Small subunit of nuclear cap-binding protein complex
7938_at	5815.8	P	putative DNA binding protein which shows similarity in homeobox do
7939_at	4275.3	P	similarity to chinese hamster transferrin receptor protein
7940_at	2060.1	P	N-acetylglucosaminyl-phosphatidylinositol biosynthetic protein
7941_at	455	P	Nuclear import protein
7942_at	3856.7	P	Mitochondrial ribosomal protein MRPL40 (YmL40)
7943_at	2550	P	Putative farnesyl transferase required for heme A synthesis
7944_at	1610.5	P	NAD(P)H dehydrogenase
7945_at	3343.2	P	similarity to C.elegans LIM homeobox protein
7946_at	6933.5	P	INvolved in nuclear mRNA export, binds both poly(A)
7902_at	256.6	A	weak similarity to E.coli bfpB protein
7903_at	892.9	P	DNA polymerase
7904_at	55.3	A	weak similarity to paramyosins
7905_at	41.5	A	weak similarity to YHR207c
7906_at	446.1	A	similarity to mismatch repair protein Mlh1p

7907_at	23859.1	P	Serine and threonine rich protein.
7908_at	1822	P	hypothetical protein
7909_at	778.3	P	Involved in polarity establishment and bud emergence\; interacts wit
7910_at	11787.3	P	cytosolic leucyl tRNA synthetase
7911_at	2049.5	P	weak similarity to YPR151c
7912_at	5366.2	P	weak similarity to human nucleolin
7913_at	1480.6	P	weak similarity to S.pombe hypothetical protein SPAC2G11.15c
7914_at	2172.8	P	weak similarity to YDL010w
7915_at	1386.5	P	kinesin-related protein
7916_at	18989.4	P	vacuolar proteinase A
7917_at	651.7	P	protein kinase, Mec1p and Tel1p regulate rad53p phosphorylation
7918_at	999.9	P	Resistant to Rapamycin Deletion 2
7919_at	2431.7	P	strong similarity to A.thaliana PRL1 and PRL2 proteins
7920_at	309.3	M	similarity to ser/thr protein kinases
7921_at	1869.9	P	involved in autophagy
7922_at	1138.1	P	Phosphopantetheine
7923_at	296.6	P	Pxa1p and Pxa2p appear to be subunits of a peroxisomal ATP-bindi
7879_at	1825.9	P	weak similarity to myosin heavy chain proteins
7880_at	8345.4	P	Homologous to human oxysterol-binding protein\; implicated in ergos
7881_at	7156.4	P	encodes snRNA U3, SNR17A also encodes snRNA U3
7882_f_at	27750	P	Ribosomal protein L33A (L37A) (YL37) (rp47)
7883_at	1160.6	P	questionable ORF
7884_at	2790.7	P	strong similarity to protein kinase Kin4p
7885_at	842.6	P	protein kinase
7886_at	581.1	P	Transcriptional modulator
7887_at	1806.7	P	weak similarity to fruit fly polycomblike nuclear protein
7888_at	2208	P	similarity to microtubule-interacting protein Mhp1p and to hypothetica
7889_at	39.5	A	questionable ORF
7890_at	9710.2	P	NifU-like protein A
7891_at	1243.5	P	similarity to ADP/ATP carrier proteins
7892_at	1900	P	weak similarity to transcription factors
7893_at	4263	P	Putative heme A biosynthetic enzyme involved in forming the formyl
7894_at	29326.9	P	Ribosomal protein L5 (L1a)(YL3)
7895_at	478.1	P	hypothetical protein
7896_at	5853.5	P	TFIIF subunit (transcription initiation factor), 30 kD
7897_at	4137.1	P	TTAGGG repeat binding factor
7898_at	7637.6	P	histone H1
7899_at	4793.3	P	weak similarity to fruit fly TFIID subunit p85
7900_at	4187.4	P	weak similarity to YDR395w and cellular apoptosis susceptibility pro
7901_at	875.1	P	Nuclear import protein
7857_at	382.7	P	similarity to ribonucleases
7858_at	3150.8	P	TFIIH subunit Tfb2\; has homology to CAK and human IIH subunits
7859_at	36.4	A	Meiotic protein required for synapsis and meiotic recombination
7860_at	1433.8	P	Required for sorting and delivery of soluble hydrolases to the vacuol
7861_at	588.2	P	putative ATP-dependent RNA helicase\; Dead box protein
7862_at	1763.5	P	Component of small subunit of the mitochondrial ribosome
7863_at	5679	P	Isopentenyl diphosphate:dimethylallyl diphosphate isomerase (IPP is
7864_at	553.1	P	Protein with similarity to Hda1p, Rpd3p, Hos2p, and Hos1p
7865_at	4915.4	P	has GTPase-activating protein activity toward the essential bud-site
7866_at	849.1	P	questionable ORF
7867_at	605.4	P	similarity to glycerate dehydrogenases
7868_at	4297.6	P	weak similarity to YOR193w

7869_at	8942.4	P	arginase
7870_at	3751.5	P	similarity to C.elegans hypothetical protein, weak similarity to Pho81
7871_at	795.5	P	similarity to aminoglycoside acetyltransferase regulator from P. stuar
7872_at	1965.4	P	hypothetical protein
7873_at	1137.7	P	hypothetical protein
7874_at	19555.6	P	HSP70 family member, highly homologous to Ssa1p and Sse2p
7875_at	3964.3	P	similarity to Smy2p
7876_at	2047.8	P	Aspartyl-tRNA synthetase, mitochondrial
7877_at	3166.6	P	similarity to hypothetical M. tuberculosis protein
7878_at	1007.3	P	questionable ORF
7834_at	6181.3	P	hypothetical protein
7835_at	2505.9	P	similarity to YFR021w
7836_at	896.2	P	weak similarity to Sulfolobus hypothetical protein
7837_at	14418	P	similarity to S.pombe hypothetical protein
7838_at	1106.9	P	Tyrosyl-tRNA synthetase
7839_at	3306.9	P	hypothetical protein
7840_at	1327.9	P	strong similarity to YBR177c
7841_at	12823.7	P	membrane component of ER protein translocation apparatus
7842_at	16136.5	P	similarity to M.jannaschii GTP-binding protein, GTP1/OBG-family, w
7843_at	2681.4	P	sensitive to sulfite
7844_at	11054.8	P	Glutathione oxidoreductase
7845_s_at	30243.8	P	Ribosomal protein S6A (S10A) (rp9) (YS4)
7846_at	4738.4	P	serum response factor-like protein
7847_at	1891.6	P	similarity to aryl-alcohol dehydrogenases
7848_at	8457.1	P	strong similarity to YBR183w
7849_at	5266.4	P	Histone and other Protein Acetyltransferase\; Has sequence homolo
7850_at	3687	P	multidomain vesicle coat protein that interacts with Sec23p
7851_at	1365.3	P	BCK1-like resistance to osmotic shock
7852_at	1055.5	P	54kDa subunit of the tetrameric tRNA splicing endonuclease
7853_at	2807.6	P	putative helicase
7854_i_at	7562.1	P	Ribosomal protein S9A (S13) (rp21) (YS11)
7855_f_at	16015.2	P	Ribosomal protein S9A (S13) (rp21) (YS11)
7856_at	555.4	A	hypothetical protein
7811_at	0.1	P	Ribosomal protein L21B
7812_at	5991.2	P	F(1)F(0)-ATPase complex delta subunit, mitochondrial
7813_at	987.5	P	weak similarity to YBR197c
7814_at	2133.4	P	Required for synthesis of N-acetylglucoaminylphosphatidylinositol, th
7815_at	1132.4	P	similarity to Vps4p and YER047c
7816_at	59.9	A	questionable ORF
7817_at	553.7	P	encodes putative deubiquitinating enzyme
7818_at	1238.1	P	hypothetical protein
7819_at	825	P	weak similarity to Vps9p
7820_at	831.8	P	geranylgeranyl diphosphate synthase
7821_at	888.3	P	hypothetical protein
7822_at	4848.2	P	hypothetical protein
7823_at	2436.9	P	hypothetical protein
7824_at	1801.2	P	soluble, hydrophilic protein involved in transport of precursors for sol
7825_at	1794.2	P	weak similarity to S.pombe peptidyl-prolyl cis-trans isomerase
7826_at	8527.5	P	similarity to hypothetical protein YLR019w, YLL010c and S.pombe h
7827_at	588.1	A	hypothetical protein
7828_at	28158.4	P	cytosolic aldehyde dehydrogenase
7829_at	511.1	P	strong similarity to Mrs2p

7830_at	7683.2	P	similarity to glutaredoxins
7831_at	13337	P	multidrug resistance transporter
7832_at	2955.8	P	Multicopy suppressor of cls2-2\; also suppresses rvs161 mutations
7833_at	3790.2	P	hypothetical protein
7788_at	2114.4	P	hypothetical protein
7789_at	722.2	A	protein of unknown function
7790_at	12445.7	P	mannosylphosphate transferase
7791_at	6380.8	P	hypothetical protein
7792_at	2552.2	P	strong similarity to ADP-ribosylation factors
7793_at	4507.1	P	Protein required for complex glycosylation
7794_at	4941.8	P	MAP kinase-associated protein
7795_at	14533.1	P	Calcium and phospholipid binding protein homologous to translation
7796_at	3446.9	P	hypothetical protein
7797_at	3849.3	P	Elongin C transcription elongation factor
7798_at	1050	P	Vacuolar sorting protein
7799_at	1304.3	P	questionable ORF
7800_at	5640.2	P	RNA recognition motif-containing protein
7801_at	710.4	P	a cyclin(SSN8)-dependent serine\/threonine protein kinase
7802_at	2004.4	P	hypothetical protein
7803_at	2858.8	P	nuclear encoded mitochondrial isoleucyl-tRNA synthetase
7804_at	2070.1	P	hypothetical protein
7805_at	1203.2	P	zinc finger DNA binding factor, transcriptional regulator of sulfur ami
7806_at	28292.1	P	GAL4 enhancer protein, has similarity to human transcription factor
7807_at	4102.9	M	plasma membrane ATPase
7808_at	496	P	questionable ORF
7809_at	1191.3	P	questionable ORF
7810_at	107.2	A	weak similarity to YLR426w
7766_at	13748.8	P	styryl dye vacuolar localization
7767_at	11372.5	P	negative transcriptional regulator, protein kinase homolog
7768_at	4154.7	P	similarity to C.elegans hypothetical protein
7769_at	2046	P	putative ATP-dependent helicase
7770_at	16598.1	P	acetoacetyl CoA thiolase
7771_at	550.4	A	hypothetical protein
7772_at	2191.2	P	serine\/threonine protein kinase homologous to Ran1p
7773_at	211.4	A	questionable ORF
7774_at	840.4	P	(N)egative regulator of (C)ts1 (E)xpression
7775_at	3293.4	P	putative methylenetetrahydrofolate reductase (mthfr)
7776_at	884.5	P	UV endonuclease
7777_at	47.4	A	ExtraCellular Mutant\; similar to SRD1
7778_at	4115.6	P	weak similarity to Smt4p
7779_at	14296.3	P	strong similarity to YFL004w, similarity to YJL012c
7780_at	561.8	P	Important for chromosome segregation
7781_at	62.3	A	strong similarity to Lpd1p and other dihydrolipoamide dehydrogenase
7782_at	1601.8	P	Zinc-finger transcription factor
7783_at	3300.3	P	Homolog of SIR2
7784_at	3001.1	P	hypothetical protein
7785_at	6934.1	P	ribosomal protein S16, mitochondrial
7786_at	11773.4	P	hypothetical protein
7787_at	989.4	P	Component of the TAF(II) complex (TBP-associated protein complex
7743_at	8439.5	P	coatomer complex zeta chain
7744_at	3530.8	P	similarity to M.jannaschii hypothetical protein
7745_at	1440.5	P	kinetochore protein in the DEAH box family

7746_at	832.5	P	hypothetical protein
7747_at	7466.7	P	predicted transmembrane protein
7748_at	718.7	P	weak similarity to Nup2p
7749_at	21861	P	strong similarity to YGR086c
7750_at	769.2	P	Required for activation of RUB1 (ubiquitin-like protein) together with
7751_at	1731.2	P	appears to be functionally related to SNF7
7752_at	1555	P	histone acetyltransferase
7753_at	109.5	A	Mitochondrial isoform of citrate synthase
7754_at	380.7	M	similarity to B.subtilis mmgE protein
7755_at	432.7	A	similarity to sulphate transporter proteins
7756_at	10267.9	P	strong similarity to electron transfer flavoproteins alpha chain
7757_at	452.1	A	polar 32k Da cytoplasmic protein
7758_at	2411.4	P	Isocitrate lyase, may be nonfunctional
7759_at	80.9	A	hypothetical protein
7760_at	1934	P	similarity to transcription factor
7761_at	2182.9	P	similarity to sterol uptake protein Sut1p
7762_at	20499.3	P	RNA polymerase I subunit A135
7763_at	2864.8	P	similarity to ADP/ATP carrier proteins and Graves disease carrier pr
7764_at	466.3	A	hypothetical protein
7765_at	1021.8	P	similarity to transcription factors
7721_at	34.1	A	hypothetical protein
7722_at	239.9	A	similarity to transcription factors
7723_at	16821	P	similar to human translation initiation factor 6 (eIF6)
7724_at	1546.2	P	GDP dissociation factor for Sec4p
7725_at	1197.3	P	p90 subunit of yeast omatin Assembly Factor-I (CAF-I)
7726_at	2058.5	P	essential for initiation of DNA replication\; homolog of S. pombe CDC
7727_at	3856.7	P	hypothetical protein
7728_at	1238.6	A	similarity to human citrate transporter protein
7729_at	890.3	P	weak similarity to fruit fly dorsal protein and Snf5p
7730_at	13924.8	P	similarity to human hypothetical protein
7731_at	2524.2	P	Mitochondrial protein of the CDC48\/PAS1\/SEC18 family of ATPase
7732_at	1995.6	P	novel cyclin gene\; encodes subunits of TFIIK, a subcomplex of tran
7733_at	646.6	P	null mutant is viable\; increased tolerance to dehydration, freezing, a
7734_at	227.9	A	similarity to YNL019c and YNL033w
7735_at	13235.4	P	Ypt Interacting Protein
7736_at	25026.1	P	Ypt Interacting Protein
7737_at	7802.9	P	Gamma-adaptin, large subunit of the clathrin-associated protein (AP
7738_at	464.7	A	similarity to YBL101c
7739_at	1064.2	P	similarity to human zinc-finger protein BR140
7740_at	2232.4	P	yeast homolog of the Drosphila tumor suppressor, lethal giant larva
7741_at	19510.3	P	cytoplasmic and mitochondrial histidine tRNA synthetases
7742_at	2678.6	P	Actin-related protein
7698_at	29856.9	P	glutamine synthetase
7699_at	21944.7	P	54-kDa vacuolar H(+) ATPase subunit of V1 sector
7700_at	7852.3	P	similarity to Erv1p and rat ALR protein
7701_at	314.1	A	questionable ORF
7702_g_at	2875.7	M	questionable ORF
7703_at	408.4	A	questionable ORF
7704_at	1575.1	P	similarity to C.elegans C02C2.6 protein
7705_at	5986.9	P	Translation initiation factor eIF-5
7706_at	2656.7	P	similarity to Jsn1p
7707_i_at	36052.3	P	Ribosomal protein L43A

7708_f_at	25744.8	P	Ribosomal protein L43A
7709_at	847.3	P	questionable ORF
7710_at	315.3	P	similarity to C.elegans hypothetical protein
7711_at	1241.7	P	Required for chromosome segregation
7712_at	829.4	P	alpha subunit of yeast mitochondrial phenylalanyl-tRNA synthetase
7713_at	6685.6	P	similarity to M.domestica NADPH--ferrihemoprotein reductase and m
7714_at	1153.5	P	similarity to Uso1p
7715_at	937.6	P	questionable ORF
7716_at	6908.8	P	N-acetyltransferase
7717_at	15603.5	P	11-kDa nonhistone chromosomal protein
7718_g_at	16938.9	P	11-kDa nonhistone chromosomal protein
7719_at	1796.9	P	questionable ORF
7720_at	31.1	A	MAP kinase
7675_at	647	P	121 kDa component of the Exocyst complex, which is required for e
7676_at	2570.6	P	Component of RNA polymerase transcription initiation TFIIH (factor
7677_at	2061.4	P	Protein involved in snRNP biogenesis
7678_at	10294.5	P	putative mitochondrial carrier protein
7679_at	370	A	questionable ORF
7680_at	9467	P	chorismate mutase
7681_at	534.3	P	weak similarity to Synechococcus sp. DnaJ protein
7682_at	13134	P	cytosine deaminase
7683_at	11170	P	hypothetical protein
7684_at	876.8	A	hypothetical protein
7685_at	1957.5	P	site-specific DNA binding protein, repressor
7686_at	1449	P	ubiquitin-like protein activating enzyme
7687_at	2627.4	P	weak similarity to F.alni nitrogen fixation protein
7688_at	318.6	P	Protein with similarity to Hda1p, Rpd3p, Hos2p, and Hos3p
7689_at	12628.6	P	putrescine aminopropyltransferase (spermidine synthase)
7690_at	1315.2	P	hypothetical protein
7691_at	2351.8	P	strong similarity to YIL029c
7692_at	5246.5	P	member of the NOT complex, a global negative regulator of transcri
7693_at	2587.3	P	18-kDa phosphotyrosine phosphatase of unknown function
7694_at	28046.5	P	Transketolase 1
7695_at	1829.9	P	imparts Far- phenotype
7696_at	38.9	A	questionable ORF
7697_i_at	283.4	P	questionable ORF
7653_s_at	145.5	A	questionable ORF
7654_at	327.2	A	hypothetical protein
7655_at	1292.7	P	weak similarity to human insulin-like growth factor 2 receptor
7656_s_at	32090.9	P	translational elongation factor EF-1 alpha
7657_at	2100.8	P	strong similarity to glycyl-tRNA synthetases
7658_at	4141.3	P	S. pombe dim1+ in budding yeast
7659_at	1518.7	P	hypothetical protein
7660_at	1567.5	P	hypothetical protein
7661_at	1009.9	P	hypothetical protein
7662_at	8141.7	P	transcription factor TFIIB homolog
7663_at	554.6	P	questionable ORF
7664_at	10948.4	P	Signal recognition particle subunit (homolog of mammalian SRP54)
7665_at	1678	P	questionable ORF
7666_at	6006.3	P	hypothetical protein
7667_at	1281.5	P	weak similarity to C.elegans LIM homeobox protein
7668_at	259	A	questionable ORF

7669_at	1005.4	P	weak similarity to zinc-finger proteins
7670_at	2192.3	P	weak similarity to chicken lim-3 protein
7671_at	825.9	P	Suppressor of Ypt3
7672_at	401.6	P	hypothetical protein
7673_at	4185.1	P	hypothetical protein
7674_at	18055.1	P	hypothetical protein
7629_at	658.7	P	questionable ORF
7630_at	4920.5	P	weak similarity to C.elegans hypothetical protein CEC25A1
7631_at	1467.4	P	splicing factor
7632_i_at	38705.3	P	Ribosomal protein L11A (L16A) (rp39A) (YL22)
7633_s_at	35750.7	P	Ribosomal protein L11A (L16A) (rp39A) (YL22)
7634_at	35548.2	P	proteasome subunit
7635_at	540.1	P	Protein with a domain similar to the fork head DNA-binding domain fo
7636_at	1971.8	P	hypothetical protein
7637_at	1577.8	P	protein kinase
7638_at	1493.5	P	Yeast 30kDa Homologue
7639_at	12180.7	P	Subunit of the regulatory particle of the proteasome
7640_at	975.8	P	weak similarity to human nicotinic acetylcholine receptor delta chain
7641_at	6675.1	P	RNA polymerase III (C) subunit
7642_at	320.3	A	kinase required for late nuclear division
7643_at	212.8	P	kinase required for late nuclear division
7644_at	2826	P	similarity to RNA-binding proteins
7645_at	23970.6	P	phosphatidylinositol synthase
7646_at	18427.8	P	similarity to YJR116w
7647_at	5184.3	P	similarity to probable transcription factor Ask10p, and to YNL047c ar
7648_at	196.7	A	hypothetical protein
7649_at	774.1	P	similarity to YLR454w
7650_at	1954.2	P	similarity to M.jannaschii translation initiation factor, eIF-2B
7651_at	1875.9	P	G(sub)2-specific B-type cyclin
7652_at	4268.5	P	B-type cyclin
7607_at	1612.1	P	similarity to B.subtilis transcriptional activator tenA, strong similarity t
7608_at	2198.6	P	putative homolog of human insulin-degrading endoprotease
7609_at	1506.7	A	questionable ORF
7610_at	6357.2	P	High affinity copper transporter into the cell, probable integral memb
7611_at	12272.5	P	suppressor of mrs2-1 mutation
7612_at	1738.2	P	questionable ORF
7613_at	2851.9	P	similarity to C-term. of N.tabacum auxin-induced protein
7614_at	5725.8	P	similarity to carrier protein FLX1
7615_at	6953.2	P	multicopy suppressor of clathrin deficiency
7616_at	1581.3	P	questionable ORF
7617_at	6239.3	P	similarity to N-acetyltransferases
7618_f_at	39744.8	P	Ribosomal protein S23B (S28B) (rp37) (YS14)
7619_s_at	19968.1	P	Ribosomal protein S23B (S28B) (rp37) (YS14)
7620_at	5585.6	P	similarity to C.elegans hypothetical protein
7621_at	26123.1	P	Translocase of the Outer Mitochondrial membrane
7622_at	1348	P	Protein involved in splicing intron a15beta of COX1
7623_at	3041.9	P	DNA polymerase alpha binding protein
7624_at	609.5	P	questionable ORF
7625_at	8089.9	P	weak similarity to Taf90p
7626_at	5238.9	P	NH4+ transporter, highly similar to Mep1p and Mep2p
7627_at	4839.2	P	hypothetical protein
7628_at	2617.5	P	similarity to human BTHS gene involved in Barth syndrome

7584_at	1608.4	P	kinesin-like nuclear fusion protein
7585_at	1272	P	questionable ORF
7586_at	2370.2	P	hypothetical protein
7587_at	4716.9	P	similarity to YDR060w and C.elegans hypothetical protein
7588_at	27384.1	P	asparagine synthetase
7589_at	2400.4	P	questionable ORF
7590_at	4996.6	P	hypothetical protein
7591_at	2954.3	P	hypothetical protein
7592_at	22025.7	P	involved in secretion of proteins that lack classical secretory signal se
7593_at	119.2	A	questionable ORF
7594_at	1379.2	P	weak similarity to YPL159c
7595_at	1545.9	P	hypothetical protein
7596_at	821.3	P	hypothetical protein
7597_at	6388.4	P	similarity to chicken growth factor receptor-binding protein GRB2 hon
7598_at	816.3	P	Regulates proper expression of subunits 6 (Atp6p) and 8 (Atp8p) of t
7599_i_at	139.6	A	similarity to multidrug resistance proteins
7600_s_at	28839.8	P	similarity to multidrug resistance proteins
7601_at	766.3	P	strong similarity to YGR141w
7602_at	1453.1	P	similarity to YGR142w
7603_at	11277.9	P	potential beta-glucan synthase
7604_at	641.1	A	Glycogen phosphorylase
7605_at	3130.3	P	CDC28\/cdc2 related protein kinase
7606_at	2995.5	P	56-kDa subunit of origin recognition complex (ORC)
7561_at	19838.2	P	Translation initiation factor eIF-4B
7562_at	890.7	P	killed in mutagen, sensitive to diepoxybutane and\/or mitomycin C
7563_at	17535.1	P	GTP-binding protein of the rho subfamily of ras-like proteins
7564_at	6843.7	P	14 kDa mitochondrial ribosomal protein\; homologous to E. coli S14 p
7565_at	1048	P	3 phosphoadenylylsulfate reductase
7566_at	190.9	A	negative regulator of URS2 of the HO promoter
7567_at	7334.9	P	hypothetical protein
7568_at	191.3	A	hypothetical protein
7569_at	961.3	P	hypothetical protein
7570_at	1289.6	P	strong similarity to YLR456w
7571_at	5992	P	defective in vacuolar protein sorting
7572_at	586.9	P	weak similarity to Nbp1p
7573_at	1234.5	P	DNA polymerase epsilon, subunit B
7574_at	10527.8	P	Geranylgeranyltransferase Type II beta subunit
7575_at	171.4	A	questionable ORF
7576_at	1241.7	P	associated with the U4\/U6 snRNP
7577_at	393.4	P	hypothetical protein
7578_at	2874.6	P	Along with Uba2p forms a heterodimeric activating enzyme for Smt3p
7579_at	2500.3	P	cytoplasmic GTPase-activating protein
7580_at	7455.3	P	Sm or Sm-like snRNP protein
7581_at	22098.6	P	dolichol phosphate mannose synthase
7582_at	2052.7	P	similarity to human 4-alpha-glucanotransferase (EC 2.4.1.25)/amylo-
7583_at	2392.8	P	Autophagy
7538_at	258	P	Transcription factor IIIA (TFIIIA) with putative Zn-fingers
7539_at	21287.8	P	subunit common to RNA polymerases I, II, and III
7540_at	1209.6	P	similarity to calmodulin and calmodulin-related proteins
7541_at	1779.5	P	Contains 8 copies of the TPR domain
7542_at	4898.2	P	82-kDa subunit of RNA polymerase III (C)
7543_at	22852.3	P	40 kDa ubiquinol cytochrome-c reductase core protein 2

7544_at	716.5	A	similarity to plasma membrane and water channel proteins
7545_at	459.5	A	Histone and other Protein Acetyltransferase\; Has sequence homolog
7546_at	103.7	A	similarity to S.pombe isp4 protein
7547_at	115.2	A	hypothetical protein
7548_at	399.9	P	strong similarity to regulatory protein Mal63p
7549_g_at	11485.8	P	strong similarity to regulatory protein Mal63p
7550_at	184.9	A	questionable ORF
7551_at	4441.7	P	multi-copy suppressor of gal11 null\; member of drug-resistance prot
7552_at	2829.9	P	Similar to transcriptional regulatory elements YAP1 and cad1
7553_at	371.7	A	Required for arsenate but not for arsenite resistance
7554_at	9.4	A	involved in arsenite transport
7555_s_at	4221.5	P	trans-acting positive regulator of the enolase and glyceraldehyde-3-p
7556_at	2267.2	P	non-annotated SAGE orf Found reverse in NC_001148 between 188
7557_at	27218.6	P	non-annotated SAGE orf Found reverse in NC_001148 between 582
7558_at	82.3	A	non-annotated SAGE orf Found forward in NC_001148 between 744
7559_at	412.3	P	non-annotated SAGE orf Found forward in NC_001148 between 744
7560_at	188.5	P	non-annotated SAGE orf Found reverse in NC_001148 between 824
7512_at	1605.4	P	non-annotated SAGE orf Found reverse in NC_001148 between 132
7513_f_at	391.2	P	non-annotated SAGE orf Found forward in NC_001148 between 809
7514_at	779.8	P	non-annotated SAGE orf Found forward in NC_001148 between 810
7515_f_at	54.9	A	non-annotated SAGE orf Found forward in NC_001148 between 853
7516_at	2702.1	P	non-annotated SAGE orf Found reverse in NC_001148 between 212
7517_at	1531.6	P	non-annotated SAGE orf Found reverse in NC_001148 between 278
7518_at	368.5	P	non-annotated SAGE orf Found forward in NC_001148 between 411
7519_at	1319.3	P	non-annotated SAGE orf Found forward in NC_001148 between 431
7520_at	10502.6	P	non-annotated SAGE orf Found reverse in NC_001148 between 592
7521_at	10256.5	P	non-annotated SAGE orf Found reverse in NC_001148 between 624
7522_at	65.8	A	non-annotated SAGE orf Found forward in NC_001148 between 700
7523_at	614.4	P	non-annotated SAGE orf Found forward in NC_001148 between 706
7524_at	2334.4	P	non-annotated SAGE orf Found reverse in NC_001148 between 718
7525_at	1983.5	P	non-annotated SAGE orf Found forward in NC_001148 between 743
7526_i_at	1601.7	P	non-annotated SAGE orf Found reverse in NC_001148 between 773
7527_r_at	314.7	P	non-annotated SAGE orf Found reverse in NC_001148 between 773
7528_f_at	463.4	P	non-annotated SAGE orf Found reverse in NC_001148 between 773
7529_at	287.8	A	non-annotated SAGE orf Found forward in NC_001148 between 819
7530_s_at	1644.8	A	non-annotated SAGE orf Found forward in NC_001148 between 880
7531_at	7032	P	non-annotated SAGE orf Found forward in NC_001148 between 883
7532_at	1556.2	P	non-annotated SAGE orf Found forward in NC_001148 between 897
7533_at	17030.4	P	non-annotated SAGE orf Found forward in NC_001148 between 298
7534_i_at	23.3	A	non-annotated SAGE orf Found reverse in NC_001148 between 700
7535_f_at	13.5	A	non-annotated SAGE orf Found reverse in NC_001148 between 700
7536_at	789.2	P	non-annotated SAGE orf Found forward in NC_001148 between 754
7537_at	942	P	non-annotated SAGE orf Found reverse in NC_001148 between 812
7489_at	280.1	A	non-annotated SAGE orf Found forward in NC_001148 between 860
7490_at	1018	P	non-annotated SAGE orf Found reverse in NC_001148 between 927
7491_at	1267.3	A	non-annotated SAGE orf Found forward in NC_001148 between 147
7492_at	778.4	A	non-annotated SAGE orf Found reverse in NC_001148 between 854
7493_at	16889.3	P	non-annotated SAGE orf Found reverse in NC_001148 between 296
7494_at	538.6	A	non-annotated SAGE orf Found forward in NC_001148 between 297
7495_at	10	A	non-annotated SAGE orf Found reverse in NC_001148 between 411
7496_at	546.4	A	non-annotated SAGE orf Found reverse in NC_001148 between 445
7497_at	5.6	A	non-annotated SAGE orf Found reverse in NC_001148 between 588

7498_at	36.2	A	non-annotated SAGE orf Found reverse in NC_001148 between 588
7499_at	657.8	A	non-annotated SAGE orf Found reverse in NC_001148 between 678
7500_at	492.2	A	non-annotated SAGE orf Found reverse in NC_001148 between 769
7501_at	133.5	A	non-annotated SAGE orf Found forward in NC_001148 between 775
7502_at	1198.4	A	non-annotated SAGE orf Found forward in NC_001148 between 822
7503_i_at	2316.3	P	non-annotated SAGE orf Found reverse in NC_001148 between 880
7504_r_at	664.7	A	non-annotated SAGE orf Found reverse in NC_001148 between 880
7505_at	366.2	A	non-annotated SAGE orf Found reverse in NC_001148 between 921
7506_at	2611.5	P	non-annotated SAGE orf Found reverse in NC_001148 between 324
7507_at	623.8	A	non-annotated SAGE orf Found reverse in NC_001148 between 408
7508_at	826.3	P	non-annotated SAGE orf Found forward in NC_001148 between 408
7509_at	847.5	P	non-annotated SAGE orf Found reverse in NC_001148 between 409
7510_at	1335.4	P	non-annotated SAGE orf Found forward in NC_001148 between 427
7511_at	794.3	A	non-annotated SAGE orf Found forward in NC_001148 between 497
7466_at	182.8	A	non-annotated SAGE orf Found forward in NC_001148 between 560
7467_at	78.9	A	non-annotated SAGE orf Found forward in NC_001148 between 596
7468_at	94.5	A	non-annotated SAGE orf Found forward in NC_001148 between 633
7469_at	160	A	non-annotated SAGE orf Found forward in NC_001148 between 703
7470_at	23075.4	P	non-annotated SAGE orf Found reverse in NC_001148 between 733
7471_at	18	A	non-annotated SAGE orf Found forward in NC_001148 between 780
7472_at	1819.8	P	non-annotated SAGE orf Found forward in NC_001148 between 831
7473_at	2890.5	P	snRNA
7474_at	4187.6	P	snRNA
7475_at	5862.2	P	snRNA
7476_at	3387.2	P	snRNA
7477_at	1631.6	P	snRNA
7478_s_at	1968.5	P	similarity to subtelomeric encoded proteins
7479_at	1391.5	P	hypothetical protein
7480_at	1464.3	P	yeast homolog of the Drosphila tumor suppressor, lethal giant larvae
7481_at	1814.9	P	putative protein kinase
7482_at	2311.1	P	hypothetical protein
7483_at	2014.6	P	Probable cytochrome c subunit, copper binding
7484_at	10695.6	P	suppressor of sed5 ts mutants
7485_at	1779.7	P	ExtraCellular Mutant
7486_at	619.8	A	questionable ORF
7487_at	15876.9	P	mitochondrial F1F0-ATPase alpha subunit
7488_at	3979.3	P	similarity to human and D.melanogaster kynurenine 3-monooxygenas
7443_at	319.8	M	BARREN, a gene with sequence similarity to Drosophila barren and
7444_at	4340.7	P	questionable ORF
7445_at	1598.2	P	similarity to C.albicans hypothetical protein
7446_at	949.4	P	questionable ORF
7447_at	2832.9	P	RNA polymerase II holoenzyme\/mediator subunit
7448_at	21884.8	P	Ribosomal protein L32
7449_at	2956	P	weak similarity to SCS2
7450_at	23598.6	P	methionine aminopeptidase 2
7451_at	940	P	Component of the small subunit of mitochondrial ribosomes
7452_at	2143.6	P	weak similarity to A.thaliana aminoacid permease AAP3
7453_at	807.8	P	putative phosphatidylinositol kinase
7454_s_at	33076.6	P	Ribosomal protein L23A (L17aA) (YL32)
7455_at	784.5	P	involved in sugar metabolism
7456_at	4214.7	P	BEM1-binding protein
7457_at	3185.3	P	component of the anaphase-promoting complex

7458_i_at	558.9	P	questionable ORF
7459_s_at	7742.8	P	questionable ORF
7460_at	7809.7	P	putative Dol-P-Man dependent alpha(1-3) mannosyltransferase invol
7461_at	4799.8	P	hypothetical protein
7462_at	604	P	62-kDa protein
7463_at	3940.9	P	Nucleoporin highly similar to Nup157p and to mammalian Nup155p (
7464_at	6264.4	P	Form a protein complex with Aut2p, to mediate attachment of autop
7465_at	750.3	P	questionable ORF
7421_at	15454	P	cytoplasmic isoleucyl-tRNA synthetase
7422_at	939.1	M	heat-inducible cytosolic member of the 70 kDa heat shock protein fa
7423_at	1251.9	P	splices pre mRNA of the MATa1 cistron
7424_at	301	A	questionable ORF
7425_s_at	29584.1	P	Ribosomal protein S8A (S14A) (rp19) (YS9)
7426_at	1114.4	P	hypothetical protein
7427_at	306.8	A	questionable ORF
7428_at	16644.6	P	ribose-phosphate pyrophosphokinase 4
7429_at	2102.7	P	ubiquitin carboxyl-terminal hydrolase
7430_at	621.8	A	putative transcription factor
7431_at	434.9	A	questionable ORF
7432_at	2585.1	P	Homolog to thiol-specific antioxidant
7433_at	568.5	P	kinesin related protein
7434_at	762	P	questionable ORF
7435_at	5531.5	P	protoplast regeneration and killer toxin resistance gene, may be a p
7436_at	513.5	P	hypothetical protein
7437_at	320.6	P	weak similarity to hypothetical protein YER093c-a
7438_at	2265.3	P	weak similarity to hypothetical protein YER093c-a
7439_at	13576.6	P	isolated as a suppressor of the lethality caused by overexpression of
7440_at	5622	P	strong similarity to hypothetical S.pombe protein
7441_at	2676.9	P	protein phosphatase type 2C
7442_at	2350.9	P	similarity to hypothetical S.pombe protein
7398_at	5047.2	P	Homolog to myb transforming proteins
7399_at	1344.7	P	questionable ORF
7400_at	1474.9	P	SAS3 for Something about silencing, gene 3. Influences silencing at
7401_at	5904.1	P	similarity to S.pombe Z66568_C protein
7402_at	4940.3	P	peripheral membrane protein required for vesicular transport betwee
7403_at	770.8	P	hypothetical protein
7404_at	683.9	A	hypothetical protein
7405_at	7143.8	P	USO1 homolog (S. cerevisiae), cytoskeletal-related transport protei
7406_at	4487.7	P	weak similarity to hypothetical protein YOR054c
7407_at	9796.6	P	44 kDa core protein of yeast coenzyme QH2 cytochrome c reductas
7408_at	318	A	hypothetical protein
7409_at	1910.7	P	ExtraCellular Mutant
7410_at	15789.8	P	uridine permease
7411_at	14718	P	proteasome subunit
7412_at	4308.5	P	encodes the HDEL receptor required for retention of ER proteins
7413_at	22756.2	P	CTP synthase, highly homologus to URA8 CTP synthase
7414_at	2147.4	P	Mitochondrial ribosomal protein MRPL16
7415_at	1613.4	P	clathrin Associated Protein complex Large subunit
7416_at	6514.7	P	Homolog to twitching motility protein (P. aeroginosa)
7417_at	2408.3	P	B subunit of DNA polymerase alpha-primase complex
7418_at	2019.9	P	suppressor of cold-sensitive tub2 mutation\; shown to be a compone
7419_at	9901.5	P	GTP cyclohydrolase II

7420_at	9630	P	weak similarity to hnRNP complex protein homolog YBR233w
7374_at	524.6	P	hypothetical protein
7375_at	32033.8	P	mitochondrial ADP\/ATP translocator
7376_at	2390.2	P	hypothetical protein
7377_at	5354.1	P	involved in mating-type regulation
7378_s_at	37301	P	Ribosomal protein L19B (YL14) (L23B) (rpl5L)
7379_i_at	524.5	P	snRNA-associated protein of the Sm class
7380_f_at	301.2	A	snRNA-associated protein of the Sm class
7381_at	4041.1	P	snRNA-associated protein of the Sm class
7382_at	1390.7	P	Upstream activation factor subunit
7383_at	7952.9	P	Probable proliferating-cell nucleolar antigen (human p120)
7384_at	3592.8	P	Minichromosome maintenance protein, transcription factor
7385_at	21589	P	mitochondrial ATP-dependent protease
7386_at	2304.8	P	transcriptional activator protein of CYC1
7387_at	7714.6	P	67 kDa integral membrane protein
7388_at	779.3	P	AP endonuclease
7389_at	4074.5	P	integral subunit of RNase P and apparent subunit of RNase MRP
7390_at	10703.4	P	carboxypeptidase Y sorting receptor in late Golgi\; Type I integral me
7391_at	8659.4	P	cdc2+\/CDC28 related kinase with positive role in conjugation
7392_at	2585.6	P	acetyl CoA hydrolase
7393_at	2045.1	P	member of yeast Pol I core factor (CF) also composed of Rrn11p, R
7394_at	717.4	A	Probable met-tRNA formyltransferase, mitochondrial
7395_at	148.4	A	questionable ORF
7396_at	7112.9	P	High copy suppresor of choline-transport mutants
7397_at	461.1	A	hypothetical protein
7352_at	3318.8	P	strong similarity to DNA damage responsive Alk1p
7353_at	1122.6	P	putative repressor protein homologous to yeast Tup1p and mammali
7354_at	8571.9	P	contains 3 SH3 domains, interacts with Bee1p
7355_at	5212.7	P	hypothetical protein
7356_at	1394.9	P	Pleiotropic drug resistance protein 3
7357_at	4852.6	P	weak similarity to Papaya ringspot virus polyprotein
7358_s_at	37283.4	P	Histone H2A (HTA1 and HTA2 code for nearly identical proteins)
7359_at	29189.3	P	Histone H2B (HTB1 and HTB2 code for nearly identical proteins)
7360_at	12358.5	P	ExtraCellular Mutant
7361_at	2788.6	P	Neutral trehalase, highly homologous to Nth1p
7362_at	6097.9	P	strong similarity to hypothetical protein YMR101c
7363_at	7255.1	P	hexaprenyl pyrophosphate synthetase
7364_at	5831.5	P	similarity to S.pombe hypothetical protein SPAC18B11.05
7365_at	2357.8	P	strong similarity to hypothetical protein YDR003w
7366_at	2677.9	P	hypothetical protein
7367_at	2700.9	P	Major Facilitator Transporter
7368_i_at	22107.7	P	Histone H3 (HHT1 and HHT2 code for identical proteins)
7369_s_at	20709.3	P	Histone H3 (HHT1 and HHT2 code for identical proteins)
7370_at	34147.3	P	Inorganic pyrophosphatase
7371_at	1487.4	P	hypothetical protein
7372_at	761.1	P	hypothetical protein
7373_at	4247.5	P	Glutaredoxin homolog
7328_at	7397	P	Type II transmembrane protein
7329_at	11961.6	P	strong similarity to hypothetical proteins YDL012c and YDR210w
7330_at	5350.3	P	karyopherin beta 2, yeast transportin
7331_at	566.2	A	galactose-1-phosphate uridyl transferase
7332_at	424	A	UDP-glucose 4-epimerase

7333_at	214.1	A	galactokinase
7334_at	7544.1	P	uracil permease
7335_at	1934.5	P	hypothetical protein
7336_at	14406.4	P	chitin synthase 3
7337_at	1877	P	SCO1 protein homolog (S. cerevisiae)
7338_at	24387.3	P	probable purine nucleotide-binding protein
7339_at	2013.1	P	Nuclear protein that binds to T-rich strand of core consensus sequen
7340_at	674.5	M	hypothetical protein
7341_at	1041.6	P	Probable ser\/thr-specific protein kinase, homolog to YKR2 and YPK
7342_at	8424.4	P	CDP-diacylglycerol synthase, CTP-phosphatidic acid cytidylyltransfe
7343_at	1209.7	P	involved in inositol biosynthesis
7344_i_at	3201.7	A	Ribosomal protein L4A (L2A) (rp2) (YL2)
7345_s_at	31641.6	P	Ribosomal protein L4A (L2A) (rp2) (YL2)
7346_at	1866.9	P	hypothetical protein
7347_at	575.6	A	Probable regulatory Zn-finger protein,\/ homolog to YKL251\/
7348_at	6524	P	nuclear protein arginine methyltransferase (mono- and asymmetricall
7349_at	7271.3	P	pyridoxine (pyridoxiamine) phosphate oxidase
7350_at	10348.2	P	contains 9 or 10 putative membrane spanning regions\; putative Ca2
7351_at	3562.1	P	inner mitochondrial membrane protein
7306_at	5202.9	P	chitin synthase 2
7307_at	29624.3	P	gamma subunit of mitochondrial ATP synthase
7308_at	1189.7	P	integral membrane protein
7309_at	3132.3	P	Fatty acid transporter
7310_at	1008.6	P	Probable membrane-bound small GTPase
7311_at	4115	P	similarity to benomyl/methotrexate resistance protein
7312_at	648.8	P	similarity to chaperonin HSP60 proteins
7313_at	14.1	A	Glc7-interacting protein.
7314_at	2718.4	P	Homolog to quinone oxidoreductase (E. coli)
7315_at	1313.5	P	hypothetical protein
7316_s_at	27766.4	P	Ribosomal protein S11B (S18B) (rp41B) (YS12)
7317_at	2167.2	P	RNA polymerase I enhancer binding protein
7318_at	1372.9	P	Possible regulatory subunit for the PP1 family protein phosphatase G
7319_at	266.4	A	questionable ORF
7320_at	12360.5	P	Homolog to YCR004, obr1 (S. pombe), trp repressor binding protein
7321_at	2828.2	P	similarity to rat regucalcin
7322_at	5619.7	P	Homolog to HSP30 heat shock protein YRO1 (S. cerevisiae) 7
7323_at	2578.6	P	RNA splicing factor
7324_at	970.7	P	Homolog to glucan-1,3--glucosidase (EC 3.2.1.5\; S. cerevisiae) 2
7325_at	1237.4	P	Muddled Meiosis
7326_at	2258.5	P	Ubiquitin-specific protease
7327_at	2243.6	P	Probable protein kinase
7283_at	3622.7	P	origin recognition complex subunit 2
7284_at	5822.9	P	Homolog to ftsJ protein (E. coli) ,\/ YCR054\/
7285_at	11649.8	P	similarity to rat neurodegeneration associated protein 1
7286_at	1024.9	P	Probable phosphopanthethein-binding protein
7287_at	145.2	A	questionable ORF
7288_at	524.2	A	ExtraCellular Mutant
7289_at	2466.3	P	Probable Zn-finger protein
7290_at	33014	P	cell wall mannoprotein
7291_at	17219.3	P	probable amino acid permease for leucine, valine, and isoleucine
7292_at	4483.8	P	Probable amino acid transport protein
7293_at	2438.8	P	osmotolerance protein

7294_at	3446.4	P	hypothetical protein
7295_at	1769.1	P	heat shock protein 26
7296_at	3735.6	P	Putative helicase similar to RAD54
7297_at	4536.1	P	Homolog to aminopeptidase Y (S. cerevisiae)
7298_at	2183.5	P	hypothetical protein
7299_at	185.6	A	ExtraCellular Mutant
7300_at	5139.5	P	hypothetical protein
7301_at	27233.6	P	Homolog to sporulation specific protein SPS2 (S. cerevisiae)
7302_at	20140.6	P	Homolog to sporulation specific protein SPS2 (S. cerevisiae)
7303_at	15378.4	P	Exhibits significant sequence similarity with a subunit of the mammal
7304_at	6254.5	P	cytoplasmic protein involved in protein transport between ER and Go
7305_at	1643.3	P	transcription factor, member of the histone acetyltransferase SAGA
7260_at	26598.9	P	ubiquitin-conjugating enzyme
7261_at	18423.2	P	transcription factor of the TEA\/ATTS DNA-binding domain family, re
7262_at	12760.5	P	mitochondrial C1-tetrahydroflate synthase
7263_at	4311.3	P	mitochondrial ADP\/ATP translocator
7264_at	9706.7	P	Probable transmembrane protein
7265_at	5266.3	P	Subunit 5 of Replication Factor C\; homologous to human RFC 38 k
7266_at	4608.3	P	profilerating cell nuclear antigen (PCNA)\; accessory factor for DNA
7267_at	54	A	questionable ORF
7268_at	4066	P	11-kDa nonhistone chromosomal protein
7269_g_at	1413.3	P	11-kDa nonhistone chromosomal protein
7270_i_at	29605.1	P	questionable ORF
7271_at	82.8	A	questionable ORF
7272_at	4221.7	P	Nuclear protein involved in mitochondrial intron splicing
7273_at	33420.8	P	Acid phosphatase, constitutive
7274_at	1161.3	P	Acid phosphatase, repressible
7275_at	1856.7	P	weak similarity to pig tubulin-tyrosine ligase
7276_at	6439.4	P	hypothetical protein
7277_at	3697	P	hypothetical protein
7278_at	2383.2	P	Myristoylated Serine\/threonine protein kinase involved in vacuolar pr
7279_at	150.2	M	putative transcriptional (co)activator for DNA damage
7280_at	456.7	P	weak similarity to T.brucei mitochondrion hypothetical protein 6
7281_at	267.9	P	questionable ORF
7282_at	17252	P	weak similarity to S.pombe hypothetical protein SPBC3B9.01
7238_at	724.3	P	hypothetical protein
7239_at	3357	P	weak similarity to human U3 snoRNP associated 55 kDa protein
7240_at	4351.3	P	mitochondrial carrier protein
7241_at	2112.2	P	involved in fructose-1,6-bisphosphatase degradation
7242_at	35462.6	P	May be a membrane protein involved in inorganic phosphate transpo
7243_at	631.9	P	weak similarity to N.crassa chitin synthase
7244_at	930.3	P	Probable transcription factor
7245_at	12121.8	P	Calmodulin
7246_at	3153.5	P	beta-1,4-mannosyltransferase
7247_at	19995.1	P	Homolog to serendipity protein (D. melanogaster)
7248_at	5685.2	P	Transcription regulatory protein
7249_at	907.9	A	questionable ORF
7250_at	692	P	Radiation repair protein, putative DNA helicase
7251_at	13823.5	P	alpha aminoadipate reductase
7252_at	850	P	questionable ORF
7253_g_at	954.4	P	questionable ORF
7254_at	157.6	A	transketolase, homologous to tkl1

7255_at	1688.7	P	U1 snRNP A protein
7256_at	1802.1	P	Translational activator of COB mRNA
7257_at	26100.9	P	Glycyl-tRNA synthase
7258_at	3915.4	P	Mitochondrial ribosomal protein MRPL36 (YmL36)
7259_at	1930.7	P	transcription factor tau (TFIIIC) subunit 95
7215_at	85.2	A	questionable ORF
7216_at	1754.2	P	Probable phosphoprotein phosphatase (EC 3.1.3.16)
7217_at	7561	P	56 kD synthase subunit of trehalose-6-phosphate synthase\/phospha
7218_at	29570.2	P	H+-transporting ATPase, vacuolar (EC 3.6.1.35)
7219_at	206.3	A	required for autophagy
7220_at	1501.5	P	imparts Far- phenotype
7221_at	7800.4	P	cytoplasmic protein involved in mother-specific HO expression
7222_at	2131.7	P	Calcium Caffeine Zinc sensitivity
7223_at	365.7	P	Amino acid permease
7224_at	3789.8	P	Negative regulator of swe1 kinase (which regulates cdc28)
7225_at	163.8	A	questionable ORF
7226_at	8895.6	P	subunit of the Cdc28 protein kinase
7227_at	1434.6	P	similar to phosphatidylinositol(PI)3-kinases required for DNA damag
7228_at	4704.3	P	hypothetical protein
7229_at	148.9	A	Unknown
7230_at	2340.5	P	Probable serine-type carboxypeptidase (EC 3.4.16.1)
7231_at	2539.6	P	GTPase activating protein
7232_at	3629.9	P	hypothetical protein
7233_at	6330.2	P	Probable pre-mRNA splicing RNA-helicase
7234_at	16850.8	P	Ominipotent suppressor protein of nonsense codons
7235_at	489.1	P	hypothetical protein
7236_at	5767.9	P	alcohol dehydrogenase isoenzyme V
7237_at	4633.5	P	Probable mitochondrial ribosomal protein S9
7193_at	1129.7	P	strong similarity to hypothetical protein YOL092w
7194_at	399.5	A	Spore-specific protein
7195_at	8186.5	P	D-arabinose dehydrogenase
7196_at	1380.7	P	Probable Zn-finger protein
7197_at	6456.3	P	weak similarity to potato sucrose cleavage protein
7198_at	303.6	P	U4\/U6.U5-associated snRNP protein\; contains a PEST proteolysis
7199_at	6379.7	P	Riboflavin biosynthesis protein
7200_at	16356.8	P	25-kDa RNA polymerase subunit (common to polymerases I, II and
7201_at	4242.8	P	Stress-inducible riboflavin biosynthetic protein homolog
7202_at	427.7	P	weak similarity to myosins
7203_at	899.5	P	hypothetical protein
7204_at	23295	P	hypothetical protein
7205_at	13194.5	P	similarity to human 17-beta-hydroxysteroid dehydrogenase
7206_at	10507.5	P	protein kinase catalytic subunit
7207_at	1045.9	P	Homolog to suppressor of reduced viability of starvation (SUR1, S.
7208_at	22133.1	P	similarity to hypothetical protein YJL171c
7209_at	6873.4	P	Protein that participates in secretory pathway
7210_at	3168.4	P	hypothetical protein
7211_at	10665.1	P	ADP-ribosylation factor-like protein 1
7212_at	875.6	P	General positive regulator of CDC34\; Suppress some cdc34 mutatio
7213_at	7022.2	P	Prephenate dehydrogenase (NADP+)
7214_at	1398.1	P	Pop7 protein, an integral subunit of RNase P and apparent subunit
7170_at	641.8	A	weak similarity to hypothetical protein YLR324w
7171_at	3303.1	P	HSP70 family member, highly homologous to Sse1p

7172_at	2328	P	Suppressor of SEC63 (S.cerevisiae), novel ER translocation compo
7173_at	11415.7	P	glycoprotein complexed with Sec62p and Sec63p in the Sec63 com
7174_at	1231.6	P	Kinesin-related protein suppressing myosin defects (MYO2)
7175_at	2744.2	P	20S proteasome maturation factor
7176_at	42.3	A	questionable ORF
7177_at	4554.1	P	Probable GTP-binding protein
7178_at	3749.1	P	Alpha-Ketoisovalerate Hydroxymethyltransferase
7179_at	15415.3	P	Probable membrane receptor
7180_at	164.3	A	questionable ORF
7181_at	1416.4	P	homolog of Drosophila melanogaster fuzzy onions gene\; integral pro
7182_at	290.1	A	Probable resistance protein
7183_at	1503.7	P	Probable DNA-binding transcription factor, Homolog to SRF\/SL-2
7184_at	7524.4	P	strong similarity to hypothetical protein YPL087w
7185_at	250.7	P	alpha-galactosidase
7186_at	2862.7	P	respiratory chain assembly protein
7187_at	64.5	A	Putative ATPase
7188_at	18737.9	P	probable membrane protein
7189_at	1690	P	splicing factor
7190_i_at	23330.7	P	Ribosomal protein S9B (S13) (rp21) (YS11)
7191_f_at	27419.3	P	Ribosomal protein S9B (S13) (rp21) (YS11)
7192_at	645.7	P	questionable ORF
7147_at	845.7	P	Ribosomal protein L21A
7148_at	3353.7	P	Probable carrier protein, mitochondrial
7149_at	1177.9	P	Stoichiometric member of mediator complex
7150_at	1957.9	P	hypothetical protein
7151_at	3039.8	P	p50 subunit of the yeast omatin Assembly Factor-I (CAF-I) negative r
7152_at	31861.6	P	Glucose-6-phosphate isomerase
7153_at	1272	P	weak similarity to hypothetical protein YPL077c
7154_at	5608.4	P	Probable transcription-associated factor protein, probable -transduci
7155_at	6112.6	P	Putative alpha-1,2-mannosyltransferase
7156_at	842.9	P	contains two SH3 domains
7157_at	4030	P	MCM3 protein homolog (S. cerevisiae)
7158_at	148.3	M	hypothetical protein
7159_at	1671.6	P	Probable serine-active lipase, peroxisomal (EX 3.1.1.-)
7160_at	9916	P	Putative alpha-1,2-mannosyltransferase
7161_g_at	17218.5	P	Putative alpha-1,2-mannosyltransferase
7162_at	4832	P	questionable ORF
7163_at	6528.8	P	probable membrane protein
7164_at	3154	P	Urea amidolyase (contains urea carboxylase and allophanate hydrola
7165_at	133.2	A	hypothetical protein
7166_at	6482.9	P	strong similarity to D.melanogaster cornichon protein
7167_at	631.5	P	regulator of microtubule stability
7168_at	3985.5	P	negative growth regulatory protein
7169_at	4092.6	P	Effector in the expression of PAPS reductase and sulfite reductase
7124_at	1349	P	strong similarity to hypothetical protein YGL056c
7125_at	1498.4	P	highly charged, basic protein
7126_at	865.4	P	strong similarity to hypothetical protein YGL060w
7127_at	586.1	P	autophagy
7128_at	18872.1	P	pyruvate carboxylase
7129_at	3113.5	P	similarity to human acetyl-coenzyme A transporter
7130_g_at	3474.8	P	similarity to human acetyl-coenzyme A transporter
7131_at	16770.2	P	beta subunit of pyruvate dehydrogenase (E1 beta)

7132_at	7348.1	P	Probable AMP-binding protein
7133_at	1799.7	P	hypothetical protein
7134_at	965.5	P	questionable ORF
7135_at	1239.4	P	hypothetical protein
7136_at	300.5	A	questionable ORF
7137_at	1847.5	P	Homolog to ATP-binding protein clpX (E.coli)
7138_at	1112.8	P	similarity to hypothetical A.thaliana protein
7139_at	2493.4	P	Homolog to 1,4-a-glucosidase (S.cerevisiae) (EC 3.2.1.3) 3
7140_at	7250.4	P	hypothetical protein
7141_at	1324.3	P	similarity to human p97 homologous protein
7142_at	617.8	A	questionable ORF
7143_at	1103.5	P	Homolog to human hnRNP complex K protein
7144_at	12930.9	P	similarity to human Arp2/3 protein complex subunit p41-Arc and to hu
7145_at	1835.7	P	similarity to bumetanide-sensitive Na-K-Cl cotransport protein
7146_at	3736.2	P	RNA (guanine-7-)methyltransferase (cap methyltransferase)
7102_at	769.4	P	RNA helicase homolog
7103_at	2580.4	P	strong similarity to general chromatin factor Spt16p
7104_at	2223	P	Probable Zn-finger protein
7105_at	620.2	P	Probable Zn-finger protein
7106_at	4121	P	Probable sugar transport protein
7107_at	4348.7	P	Probable ATP\/GTP-binding protein
7108_at	7492.9	P	UDP-N-acetyl-glucosamine-1-P transferase (GPT)
7109_at	1581.3	P	Probable glutathione peroxidase (EC 1.11.1.9)
7110_at	2146.3	P	Homolog to SNF2\/SWI2 DNA-binding regulatory protein
7111_at	6891.9	P	hypothetical protein
7112_at	13668.9	P	Putative 57 kDa protein with an apparent MW of 70 kDa by SDS-PA
7113_at	9983.1	P	glutamine amidotransferase:cyclase
7114_at	20965.7	P	3-deoxy-D-arabino-heptulosonate 7-phosphate (DAHP) synthase iso
7115_at	444.9	A	hypothetical protein
7116_at	885.8	P	Probable mitochondrial ribosomal protein S5
7117_at	22398.3	P	dUTP pyrophosphatase (dUTPase)
7118_at	1060.4	P	transcription factor, part of Srb\/Mediator complex
7119_at	2348.7	P	probable membrane protein
7120_at	379	P	hypothetical protein
7121_at	890.3	P	Riboflavin synthase alpha-chain
7122_at	2272.2	P	Required for normal 5.8S rRNA processing and for tRNA processing
7123_at	572.9	P	hypothetical protein
7079_at	832.8	P	hypothetical protein
7080_at	4916.6	P	similarity to C.elegans GTPase-activating protein
7081_at	11947.9	P	similarity to hypothetical S. pombe protein
7082_at	6777.6	P	questionable ORF
7083_at	22470.4	P	Serine hydroxymethyltransferase, mitochondrial
7084_at	3209.5	P	Probable small GTP-binding protein
7085_at	15499.8	P	probable membrane protein
7086_at	6877.9	P	Probable mitochondrial protein L37
7087_at	2801.7	P	hypothetical protein
7088_at	726.7	A	Probable ATP\/GTP-binding protein
7089_at	3157.1	P	weak similarity to S.pombe uvi22 protein and hypothetical protein YN
7090_at	1076.2	P	Hsm3p may be a member of the yeast MutS homolog family
7091_at	4632.2	P	similarity to hypothetical protein YJL048c
7092_at	2376.1	P	Probable protein kinase (growth factor & cytokine receptor family)
7093_at	1613.8	P	RAP1-interacting factor, involved in establishment of repressed chro

7094_at	5077.2	P	dual specificity protein phosphatase
7095_at	137.6	A	questionable ORF
7096_at	2623.6	P	C and C subunits of DNA polymerase II
7097_at	3815.1	P	RNA polymerase II-associated, nuclear protein that may serve as bc
7098_at	2874.6	P	hypothetical protein
7099_at	1932.1	P	Probable G-protein, -transducin type
7100_at	4933.8	P	Mitochondrial ribosomal protein MRPL27 (YmL27)
7101_at	14112.2	P	Probable SEC61 protein homolog
7057_at	514.5	P	similarity to AMP deaminase
7058_at	41.7	A	hypothetical protein
7059_at	36012.3	P	Aminopeptidase yscIII
7060_at	5130.9	P	similarity to hypothetical S. pombe protein
7061_at	4275.2	P	clathrin associated protein medium chain
7062_at	3614.9	P	transcriptional activator
7063_at	2834.8	P	metal homeostasis protein\; putative membrane protein
7064_at	13174.4	P	citrate tranporter in mitochondrial inner membrane
7065_at	735.5	P	hypothetical protein
7066_at	2061.6	P	Probable multidrug resistance protein
7067_at	166	A	Probable sulfate transport protein
7068_at	1449.6	P	Putative P-type Cu(2+)-transporting ATPase
7069_at	3138.3	P	Homolog to phosphate-repressible phosphate permease
7070_at	1130.8	P	Maltose fermentation regulatory protein
7071_s_at	438.4	A	maltose permease
7072_s_at	81.9	A	Maltase (EC 3.2.1.20)
7073_at	664.9	A	strong similarity to hypothetical protein YGR293c
7074_f_at	2304	P	YKL224 c homolog
7075_at	150.7	A	hypothetical membrane protein
7076_at	2544.8	P	identified by SAGE
7077_at	8881.8	P	identified by SAGE
7078_at	2340.3	P	hypothetical protein
7033_at	403.8	P	questionable ORF - upstream ORF of ALG1
7034_i_at	14002.1	P	identified by SAGE
7035_s_at	25195.6	P	identified by SAGE
7036_s_at	4479.8	P	Protein involved in targeting of plasma membrane [H+]ATPase
7037_s_at	1113.6	P	Probable aldehyde dehydrogenase (EC 1.2.1.-)
7038_s_at	2721.4	P	Degradation in the Endoplasmic Reticulum
7039_at	123.1	A	probable membrane protein
7040_g_at	448.9	M	probable membrane protein
7041_s_at	5262	P	Probable Zn-finger protein (C2H2 type)
7042_at	1352.2	P	non-annotated SAGE orf Found forward in NC_001134 between 469
7043_at	3848.5	P	non-annotated SAGE orf Found reverse in NC_001134 between 164
7044_at	403.1	A	non-annotated SAGE orf Found reverse in NC_001134 between 164
7045_i_at	381.3	P	non-annotated SAGE orf Found forward in NC_001134 between 490
7046_s_at	19389.1	P	non-annotated SAGE orf Found forward in NC_001134 between 490
7047_at	5605.8	P	non-annotated SAGE orf Found forward in NC_001134 between 680
7048_i_at	1311.6	P	non-annotated SAGE orf Found forward in NC_001134 between 680
7049_s_at	1234.5	P	non-annotated SAGE orf Found forward in NC_001134 between 680
7050_at	8796.7	P	non-annotated SAGE orf Found reverse in NC_001134 between 680
7051_at	11.1	A	non-annotated SAGE orf Found forward in NC_001134 between 362
7052_at	1087.4	A	non-annotated SAGE orf Found reverse in NC_001134 between 101
7053_at	23.7	A	non-annotated SAGE orf Found reverse in NC_001134 between 196
7054_i_at	93	A	non-annotated SAGE orf Found forward in NC_001134 between 592

7055_f_at	864.6	A	non-annotated SAGE orf Found forward in NC_001134 between 592
7056_at	131	A	non-annotated SAGE orf Found forward in NC_001134 between 767
7010_at	606.8	P	non-annotated SAGE orf Found reverse in NC_001134 between 882
7011_g_at	6498.4	P	non-annotated SAGE orf Found reverse in NC_001134 between 882
7012_at	12506.2	P	non-annotated SAGE orf Found reverse in NC_001134 between 883
7013_at	82	A	non-annotated SAGE orf Found reverse in NC_001134 between 101
7014_at	5131.8	P	non-annotated SAGE orf Found reverse in NC_001134 between 115
7015_at	995.3	P	non-annotated SAGE orf Found reverse in NC_001134 between 143
7016_at	2522.9	P	non-annotated SAGE orf Found forward in NC_001134 between 172
7017_at	2141.5	P	non-annotated SAGE orf Found reverse in NC_001134 between 241
7018_at	1109.9	P	non-annotated SAGE orf Found reverse in NC_001134 between 256
7019_at	554.9	P	non-annotated SAGE orf Found forward in NC_001134 between 270
7020_at	16744	P	non-annotated SAGE orf Found reverse in NC_001134 between 305
7021_at	18778.4	P	non-annotated SAGE orf Found reverse in NC_001134 between 373
7022_at	75.5	A	non-annotated SAGE orf Found forward in NC_001134 between 391
7023_at	2075.5	P	non-annotated SAGE orf Found forward in NC_001134 between 407
7024_at	26	A	non-annotated SAGE orf Found reverse in NC_001134 between 480
7025_at	237.8	P	non-annotated SAGE orf Found reverse in NC_001134 between 553
7026_at	1951.2	P	non-annotated SAGE orf Found reverse in NC_001134 between 553
7027_at	3937.6	P	non-annotated SAGE orf Found reverse in NC_001134 between 562
7028_at	45.1	A	non-annotated SAGE orf Found forward in NC_001134 between 592
7029_g_at	243.8	A	non-annotated SAGE orf Found forward in NC_001134 between 592
7030_at	22.3	A	non-annotated SAGE orf Found forward in NC_001134 between 592
7031_at	1360.5	P	non-annotated SAGE orf Found reverse in NC_001134 between 615
7032_at	4882.6	P	non-annotated SAGE orf Found forward in NC_001134 between 649
6985_at	144.1	A	non-annotated SAGE orf Found reverse in NC_001134 between 741
6986_i_at	41.7	A	non-annotated SAGE orf Found forward in NC_001134 between 356
6987_at	289.9	A	non-annotated SAGE orf Found reverse in NC_001134 between 668
6988_at	83.5	A	non-annotated SAGE orf Found forward in NC_001134 between 181
6989_at	760.2	P	non-annotated SAGE orf Found reverse in NC_001134 between 593
6990_at	477.8	A	non-annotated SAGE orf Found forward in NC_001134 between 622
6991_i_at	167.9	P	non-annotated SAGE orf Found reverse in NC_001134 between 694
6992_r_at	1.8	A	non-annotated SAGE orf Found reverse in NC_001134 between 694
6993_f_at	10555.4	A	non-annotated SAGE orf Found reverse in NC_001134 between 694
6994_at	915	P	non-annotated SAGE orf Found reverse in NC_001134 between 747
6995_at	2318.1	P	non-annotated SAGE orf Found forward in NC_001134 between 143
6996_at	322.9	A	non-annotated SAGE orf Found reverse in NC_001134 between 159
6997_at	585.6	P	non-annotated SAGE orf Found forward in NC_001134 between 164
6998_at	239.9	A	non-annotated SAGE orf Found forward in NC_001134 between 165
6999_at	2552.4	P	non-annotated SAGE orf Found forward in NC_001134 between 165
7000_i_at	11.6	A	non-annotated SAGE orf Found reverse in NC_001134 between 197
7001_r_at	30.3	A	non-annotated SAGE orf Found reverse in NC_001134 between 197
7002_at	421.9	P	non-annotated SAGE orf Found reverse in NC_001134 between 235
7003_at	36	A	non-annotated SAGE orf Found reverse in NC_001134 between 351
7004_at	198.9	A	non-annotated SAGE orf Found reverse in NC_001134 between 363
7005_at	234.8	M	non-annotated SAGE orf Found forward in NC_001134 between 419
7006_at	111.6	A	non-annotated SAGE orf Found forward in NC_001134 between 477
7007_at	31.5	A	non-annotated SAGE orf Found forward in NC_001134 between 480
7008_at	3929.6	P	non-annotated SAGE orf Found reverse in NC_001134 between 554
7009_g_at	851	P	non-annotated SAGE orf Found reverse in NC_001134 between 554
6962_at	352.3	A	non-annotated SAGE orf Found reverse in NC_001134 between 554
6963_at	1079.9	P	non-annotated SAGE orf Found forward in NC_001134 between 555

6964_s_at	3665.6	P	non-annotated SAGE orf Found forward in NC_001134 between 555
6965_i_at	67.2	A	non-annotated SAGE orf Found forward in NC_001134 between 555
6966_r_at	230.7	P	non-annotated SAGE orf Found forward in NC_001134 between 555
6967_at	1889.2	P	non-annotated SAGE orf Found reverse in NC_001134 between 624
6968_at	2770.5	P	non-annotated SAGE orf Found reverse in NC_001134 between 681
6969_at	8181.4	P	non-annotated SAGE orf Found reverse in NC_001134 between 681
6970_at	301.2	A	non-annotated SAGE orf Found reverse in NC_001134 between 681
6971_at	973.3	P	non-annotated SAGE orf Found forward in NC_001134 between 697
6972_at	81.6	A	non-annotated SAGE orf Found forward in NC_001134 between 744
6973_at	7.4	A	non-annotated SAGE orf Found forward in NC_001134 between 938
6974_at	32.2	A	non-annotated SAGE orf Found forward in NC_001134 between 978
6975_at	4396.3	P	non-annotated SAGE orf Found forward in NC_001134 between 133
6976_at	13847.2	P	non-annotated SAGE orf Found reverse in NC_001134 between 167
6977_at	2452	P	non-annotated SAGE orf Found forward in NC_001134 between 283
6978_at	394.1	P	non-annotated SAGE orf Found reverse in NC_001134 between 308
6979_at	5640.5	P	non-annotated SAGE orf Found forward in NC_001134 between 333
6980_at	98.6	A	non-annotated SAGE orf Found reverse in NC_001134 between 376
6981_at	4934.8	P	non-annotated SAGE orf Found reverse in NC_001134 between 398
6982_at	420.9	A	non-annotated SAGE orf Found forward in NC_001134 between 479
6983_at	127.1	A	non-annotated SAGE orf Found forward in NC_001134 between 741
6984_at	266.6	P	non-annotated SAGE orf Found forward in NC_001134 between 741
6938_at	1730.3	A	Saccharomyces cerevisiae chromosome II, complete chromosome s
6939_g_at	1224.3	P	Saccharomyces cerevisiae chromosome II, complete chromosome s
6940_s_at	112.4	A	Saccharomyces cerevisiae chromosome II, complete chromosome s
6941_s_at	735.1	P	Saccharomyces cerevisiae chromosome II, complete chromosome s
6942_at	1421.4	A	Saccharomyces cerevisiae chromosome II, complete chromosome s
6943_g_at	679.5	P	Saccharomyces cerevisiae chromosome II, complete chromosome s
6944_at	87.7	A	Saccharomyces cerevisiae chromosome II, complete chromosome s
6945_g_at	3072.5	P	Saccharomyces cerevisiae chromosome II, complete chromosome s
6946_at	3898.6	P	Saccharomyces cerevisiae chromosome II, complete chromosome s
6947_g_at	9367.7	P	Saccharomyces cerevisiae chromosome II, complete chromosome s
6948_i_at	211.4	A	Saccharomyces cerevisiae chromosome II, complete chromosome s
6949_f_at	2845.6	A	Saccharomyces cerevisiae chromosome II, complete chromosome s
6950_at	4516.3	P	snRNA
6951_at	5118.2	P	telomerase RNA component
6952_at	3656	P	telomerase RNA component
6953_at	402.3	A	snRNA
6954_at	363.7	A	snRNA
6955_s_at	114.3	A	putative pseudo-TY5
6956_s_at	746.7	P	Reverse transcriptase
6957_s_at	796.4	P	Bud site selection
6958_s_at	5266.1	P	Mating type protein alpha-2
6959_s_at	3691.9	P	transcripton factor involved in the regulation of the alpha-specific gen
6960_at	4.6	A	questionable ORF
6961_g_at	14532	P	questionable ORF
6915_at	2376	P	catabolic serine (threonine) dehydratase
6916_at	2067	P	weak similarity to yeast translation regulator Gcd6p
6917_at	820.3	P	similarity to myosin heavy chain form b from Chicken and Xenopus
6918_at	3819.2	P	strong similarity to human Rev interacting protein Rip-1
6919_at	1353.6	P	hypothetical protein
6920_at	7326.8	P	Saccharolysin (oligopeptidase yscD)
6921_at	7750.3	P	hypothetical protein

6922_at	2716.1	P	May assist Ste12p in pheromone-dependent expression of KAR3 an
6923_at	1952	P	Methyltransferase
6924_at	4075.2	P	Protease B Non-derepressible
6925_at	1126.2	P	involved in laminarinase resistance
6926_at	8953.9	P	diadenosine 5 ,5 -P1,P4-tetraphosphate phosphorylase I
6927_at	11350.7	P	hypothetical protein
6928_at	43.2	A	strong similarity to sporulation-specific protein Sps2p
6929_at	797	P	hypothetical protein
6930_at	1193.2	P	weak similarity to human ORF
6931_at	58.6	A	questionable ORF
6932_at	3429	P	hypothetical protein
6933_at	27282.4	P	protein disulfide isomerase
6934_at	553.2	P	questionable ORF
6935_at	1877.4	M	questionable ORF
6936_g_at	10370.3	P	questionable ORF
6937_at	19051	P	Glucokinase
6893_at	1236.4	P	regulatory protein
6894_at	1434.5	P	Membrane transporter
6895_at	16357.2	P	SRO9 may overlap in function with tropomyosin and may be involved
6896_at	10108.4	P	similarity to hypothetical protein YDR514c
6897_at	12201	P	Glutaredoxin (thiol-transferase)
6898_at	5099.9	P	similarity to hypothetical S.pombe protein
6899_at	4353.7	P	Transcription regulator
6900_at	599.6	P	possesses a SAM (sterile alpha motif)\; interacts with G protein and
6901_at	3776.2	P	involved in pre-rRNA processing and ribosome assembly
6902_at	26850.3	P	histidinol dehydrogenase
6903_at	888	P	Microtubule-binding protein
6904_at	9784.9	P	weak similarity to glutenins, high molecular weight chain
6905_at	2355.5	P	serine\/threonine-rich membrane protein
6906_at	1039.8	P	Protein involved in the integration of lipid signaling pathways with cell
6907_at	3591.9	P	Amino acid permease
6908_at	339.1	M	questionable ORF
6909_at	16004.1	P	beta-IPM (isopropylmalate) dehydrogenase
6910_at	12932.4	P	NifS-like protein
6911_at	1727.2	P	hypothetical protein
6912_at	1648.9	P	Cell cycle regulated protein required for axial bud formation\; co-asse
6913_at	2627.9	P	part of budding protein Bud3p due to frameshift in DNA sequence
6914_at	16605.7	P	Protein with RNA recognition motifs
6870_at	1324.8	P	strong similarity to Saccharomyces pastorianus hypothetical protein L
6871_at	22782.1	P	Small regulatory subunit of Acetolactate synthase
6872_at	401.9	P	Calcofluor White Hypersensitivity
6873_at	668.3	P	questionable ORF
6874_at	2392.7	P	strong similarity to Saccharomyces pastorianus hypothetical protein L
6875_at	641.6	P	17-kDa phosphatidylserine synthase
6876_at	3360.1	P	strong similarity to Saccharomyces pastorianus hypothetical protein L
6877_at	5406.7	P	Protein involved in retention of membrane proteins, including Sec12
6878_at	9.6	A	similarity to Dom34p
6879_at	258.1	A	hypothetical protein
6880_at	7629.8	P	conserved potential GTP-ginding protein
6881_at	3523.4	P	Mitochondrial ribosomal protein MRPL32 (YmL32)
6882_at	16081	P	FMN-binding protein
6883_at	15119.6	P	non-mitochondrial citrate synthase

6884_at	549.5	A	hypothetical protein
6885_at	6550.4	P	Ser\/Thr protein kinase
6886_at	11840.4	P	Reduced viability on starvation protein RVS161
6887_at	530.3	P	strong similarity to Y.lipolytica GPR1 protein and Fun34p
6888_at	6336.2	P	Active transport ATPase
6889_at	63.5	A	weak similarity to M.leprae B1496_F1_41 protein
6890_at	8135	P	3-phosphoglycerate kinase
6891_at	601.5	P	DNA polymerase IV
6892_at	1567.3	P	hypothetical protein
6848_at	1642.3	P	hypothetical protein
6849_at	11084.6	P	similarity to hypothetical S.pombe protein
6850_at	2267	P	Transcription regulator
6851_at	1346	P	MAK32 sugar kinase
6852_at	319.3	A	Transcription regulator
6853_at	7252.1	P	MAK31 snRNP
6854_at	589.3	P	Protein induced by heat shock, ethanol treatment, and entry into stat
6855_at	69.2	A	hypothetical protein
6856_at	3075.9	P	Membrane transporter
6857_at	1219.6	P	Asn-tRNA synthetase
6858_f_at	28808.3	P	Proteolipid associated with plasma membrane H(+)-ATPase (Pma1p
6859_at	688.2	A	hypothetical protein
6860_at	1073	P	Membrane phospho-diesterase
6861_at	284.3	P	GTPase (RAS-related)
6862_at	624.2	P	Amino acid permease
6863_at	13198.1	P	required for mitochondrial DNA replication
6864_at	21645.9	P	required for mitochondrial DNA replication
6865_at	3311.4	P	weak similarity to S.pombe hypothetical protein SPBC4C3.06
6866_at	23973.2	P	Ribosomal protein S14A (rp59A)
6867_at	850.5	P	Beige Protein Homologue 1
6868_at	6060.1	P	similarity to mouse nuclear receptor co-repressor N-Cor
6869_at	16382.9	P	Probable subunit of 1,3-beta-glucan synthase\; homolog of ELO1
6825_at	2280.3	P	Component of the exosome 3->5 exoribonuclease complex with Rrp
6826_at	5664.2	P	ribokinase
6827_at	4311.7	P	May collaborate with Pho86p and Pho84p in inorganic phosphate upt
6828_at	584.5	P	GTP\/GDP exchange factor for Rsr1 protein
6829_at	35.9	A	questionable ORF
6830_at	1139.6	P	TATA binding protein-associated factor (TAF)
6831_at	3578.5	P	hypothetical protein
6832_at	2928	P	involved in manganese homeostasis
6833_at	343.3	A	Protease
6834_at	8053.9	P	required for respiration and maintenance of mitochondrial genome
6835_at	6819.3	P	Protein carboxyl methylase
6836_at	324.6	A	questionable ORF
6837_at	13130.1	P	Acyl-CoA cholesterol acyltransferase (sterol-ester synthetase)
6838_at	81	A	questionable ORF
6839_at	3452.9	P	weak similarity to ankyrins
6840_at	3871.1	P	a subunit of RSC, a fifteen-protein chromatin remodeling complex ar
6841_at	13604.6	P	threonine synthase
6842_at	607.5	P	CTR86 shares a terminator region with THR4. CTR86 contains aGCI
6843_at	2332.8	P	regulatory protein
6844_at	6600.7	P	weak similarity to hypothetical protein YDL177c
6845_at	4888.4	P	regulatory protein

6846_at	5086.2	P	hypothetical protein
6847_g_at	9285.6	P	hypothetical protein
6803_at	2104.6	P	similarity to Ytp1p protein
6804_at	578.9	A	questionable ORF
6805_at	1773.2	P	G10-like protein
6806_at	5250.7	P	Transcription factor (fork head domain)
6807_at	577.2	P	Zn finger protein, putative ATPase
6808_at	4971.7	P	Intracellular transport protein
6809_at	1308.5	A	similarity to hypothetical S.pombe protein
6810_g_at	1518.3	P	similarity to hypothetical S.pombe protein
6811_at	5442.1	P	cyclophilin homolog
6812_at	1149.8	P	(required for) Integrity of Mitochondrial Genome 2
6813_at	7483.5	P	regulatory protein
6814_at	1380.8	P	protein kinase
6815_at	18030.6	P	shows similarity to glucose-6-phosphate dehydrogenase non-catalyti
6816_at	3177.8	P	ERS1 protein, ER defect supressor
6817_at	2735.2	P	hypothetical protein
6818_at	7687.5	P	Necessary for accurate chromosome transmission during cell divisio
6819_at	1449.5	P	weak similarity to A.thaliana protein phosphatase 2C
6820_at	2106.5	P	activation mediator subcomplex of RNA polymerase I holoenzyme
6821_at	4487.4	P	weak similarity to Rbk1p
6822_at	3269.5	P	Thioredoxin type II
6823_at	9077.8	P	glucose repression regulatory protein, exhibits similarity to beta subu
6824_at	571.1	A	hypothetical protein
6780_at	3752.8	P	hypothetical protein
6781_at	1527	P	questionable ORF
6782_at	5644.2	P	nucleic acid-binding protein
6783_at	7638.1	P	Actin binding protein
6784_at	2289.3	P	predicted GPI-anchored cell wall protein
6785_at	3412.8	P	hypothetical protein
6786_at	47.6	A	Putative serine\/threonine protein kinase most similar to cyclic nucle
6787_at	465.8	P	mutS homolog, forms a complex with Msh2p to repair insertion-dele
6788_at	1967.5	P	nuclear protein that negatively regulates basal transcription
6789_at	3681.4	P	Cell Division Cycle mutant
6790_at	481.8	P	hypothetical protein
6791_s_at	2.1	A	Homeobox-domain containing protein which, together with alpha2, r
6792_s_at	73.5	A	Homeobox-domain containing protein which, together with alpha2, r
6793_at	640.6	M	permease involved in the uptake of glycerophosphoinositol (GroPIns
6794_at	311.6	A	strong similarity to Pep1p
6795_at	1290.6	P	strong similarity to Pep1p
6796_at	140.6	A	strong similarity to Pep1p
6797_at	2858	P	Alcohol dehydrogenase
6798_f_at	1740.1	P	member of the seripauperin protein\/gene family (see Gene_class P
6799_at	1757.1	P	Alcohol dehydrogenase
6800_at	1019.4	P	Transcription regulator
6801_at	107.8	A	hypothetical protein
6802_at	440.6	P	hypothetical protein
6755_i_at	70.5	A	hypothetical protein
6756_at	331.5	P	high-temperature lethal
6757_i_at	3.7	A	Homeobox-domain containing protein which, together with alpha2, r
6758_at	200.8	P	hypothetical protein identified by SAGE
6759_at	9618.5	P	identified by SAGE

6760_g_at	26528.9	P	identified by SAGE
6761_at	890.1	P	similarity to starvation induced pSI-7 protein of C. fluvum
6762_s_at	1274.4	P	Ser\/Thr protein kinase
6763_at	5137.6	P	homologous to mouse and human Tsg101 tumor susceptibility genes
6764_g_at	2099	P	homologous to mouse and human Tsg101 tumor susceptibility genes
6765_at	383.7	A	non-annotated SAGE orf Found forward in NC_001135 between 414
6766_at	523.1	A	non-annotated SAGE orf Found forward in NC_001135 between 157
6767_at	808.4	A	non-annotated SAGE orf Found forward in NC_001135 between 171
6768_at	3683.5	P	non-annotated SAGE orf Found reverse in NC_001135 between 175
6769_at	130.3	P	non-annotated SAGE orf Found forward in NC_001135 between 289
6770_i_at	958.8	A	non-annotated SAGE orf Found forward in NC_001135 between 127
6771_s_at	272.5	A	non-annotated SAGE orf Found forward in NC_001135 between 127
6772_at	110.8	A	non-annotated SAGE orf Found forward in NC_001135 between 127
6773_at	872.8	P	non-annotated SAGE orf Found forward in NC_001135 between 185
6774_at	334	P	non-annotated SAGE orf Found forward in NC_001135 between 109
6775_at	18194.7	P	non-annotated SAGE orf Found reverse in NC_001135 between 130
6776_at	711	P	non-annotated SAGE orf Found reverse in NC_001135 between 171
6777_at	1317.2	P	non-annotated SAGE orf Found reverse in NC_001135 between 172
6778_i_at	637.6	A	non-annotated SAGE orf Found reverse in NC_001135 between 204
6779_r_at	113	P	non-annotated SAGE orf Found reverse in NC_001135 between 204
6731_at	304.7	M	non-annotated SAGE orf Found reverse in NC_001135 between 286
6732_at	13110.6	P	non-annotated SAGE orf Found reverse in NC_001135 between 162
6733_at	23934.4	P	non-annotated SAGE orf Found reverse in NC_001135 between 162
6734_at	24.6	A	non-annotated SAGE orf Found reverse in NC_001135 between 205
6735_i_at	314.8	M	non-annotated SAGE orf Found forward in NC_001135 between 258
6736_r_at	79.3	A	non-annotated SAGE orf Found forward in NC_001135 between 258
6737_at	304	A	non-annotated SAGE orf Found reverse in NC_001135 between 895
6738_at	394	A	non-annotated SAGE orf Found reverse in NC_001135 between 926
6739_at	71.8	A	non-annotated SAGE orf Found forward in NC_001135 between 154
6740_at	923.2	M	non-annotated SAGE orf Found forward in NC_001135 between 240
6741_at	12.3	A	non-annotated SAGE orf Found reverse in NC_001135 between 414
6742_at	1366	A	non-annotated SAGE orf Found reverse in NC_001135 between 416
6743_at	317.3	P	non-annotated SAGE orf Found reverse in NC_001135 between 123
6744_at	1484.3	A	non-annotated SAGE orf Found forward in NC_001135 between 125
6745_at	1765.1	P	non-annotated SAGE orf Found reverse in NC_001135 between 168
6746_at	667.8	P	non-annotated SAGE orf Found forward in NC_001135 between 288
6747_at	6049.2	P	non-annotated SAGE orf Found reverse in NC_001135 between 209
6748_at	287.9	A	non-annotated SAGE orf Found reverse in NC_001135 between 213
6749_at	155.7	A	non-annotated SAGE orf Found forward in NC_001135 between 265
6750_i_at	1081.2	A	TY5-1
6751_at	730.1	P	snRNA
6752_i_at	0.8	A	Centromere
6753_at	7022.6	P	snRNA
6754_at	42.4	A	snRNA
6708_at	1492.2	P	snRNA
6709_i_at	328.9	A	strong similarity to sugar transport proteins
6710_at	851.2	P	Hypothetical aryl-alcohol dehydrogenase
6711_at	14.1	A	strong similarity to hypothetical protein YPR079w
6712_at	1855.6	P	hypothetical protein
6713_at	1908.9	P	Protein similar to LIM-domain proteins and to rho\/rac GTPase-activa
6714_at	417.9	P	hypothetical protein
6715_at	610.3	P	similarity to E.coli hypothetical protein and to chlorohydrolases

6716_at	6002.1	P	hypothetical protein
6717_at	19298.7	P	p-nitrophenyl phosphatase
6718_at	2555.4	P	Two-component phosphorelay intermediate
6719_at	1403.4	P	protein of unknown function
6720_at	709.6	P	hypothetical protein
6721_at	16718	P	3.6-kDa protein, probably membrane-located
6722_at	1388.9	P	hypothetical protein
6723_at	2356.4	P	phosphotyrosine-specific protein phosphatase
6724_at	477.2	P	similarity to A.klebsiana glutamate dehydrogenase
6725_at	7003.9	P	Homothallic switching endonuclease
6726_at	6500.4	P	ADP-ribosylation factor GTPase-activating protein (ARF GAP)
6727_at	3266.5	P	similarity to Cdc11p, Cdc3p and human CDC10 protein
6728_at	1999.1	P	Possible RNA binding protein. Homolog of Whi3.
6729_at	1050.5	P	weak similarity to mucin
6730_at	1704.7	P	strong similarity to hypothetical protein YNL194c and similarity to YM
6686_at	118.3	A	questionable ORF
6687_at	4319.6	P	binds to single-stranded TG1-3 telomere G-tails
6688_at	6954.4	P	strong similarity to S.equisimilis hypothetical protein
6689_at	5494.6	P	strong similarity to S.equisimilis hypothetical protein
6690_at	332.9	A	weak similarity to hypothetical protein YNR061c
6691_at	4947.2	P	Mitochondrial inner membrane protein involved in import of proteins
6692_at	469.3	P	similarity to Jun activation domain binding protein homologue of A. th
6693_at	1796.9	P	NAD-dependent glutamate dehydrogenase
6694_at	19.6	A	strong similarity to putative protein kinase NPR1
6695_at	5594	P	has an RNA recognition domain in the N-terminal region
6696_at	27334.2	P	Integral membrane component of the endoplasmic reticulum
6697_at	335	A	similarity to hypothetical protein YNL176c
6698_at	292.3	A	GABA-specific transport protein
6699_at	2194.2	P	similarity to hypothetical S. pombe protein
6700_at	20443.6	P	HMG-like nuclear protein
6701_at	3032.6	P	Nuclear-export-signal (NES)-containing protein
6702_at	734.9	P	weak similarity to transporter proteins
6703_at	481.1	A	phorphobilinogen deaminase (uroporphyrinogen synthase), the third
6704_at	208	P	similarity to hypothetical protein YDR233c
6705_at	2404.6	P	similarity to Skt5p
6706_at	2742.8	P	Mitochondrial ribosomal protein MRPL11 (YmL11)
6707_at	7766.7	P	strong similarity to human D1075-like protein
6663_at	1738.6	M	6-O-methylguanine-DNA methylase
6664_at	309.5	A	similarity to sugar transporter proteins
6665_at	8060.2	P	high copy suppressor of abf2 lacking the HMG1-like mitochondrial H
6666_at	1555.6	P	Anti-silencing protein that causes depression of silent loci when over
6667_at	1099.6	A	hypothetical protein
6668_at	25960.1	P	involved in protein transport from endoplasmic reticulum to Golgi
6669_at	501.7	P	glucose transporter
6670_at	1965	P	similarity to N.crassa hypothetical 32 kDa protein
6671_at	925.1	P	ADP-ribosylation factor
6672_s_at	22043.9	P	Ribosomal protein L35A
6673_at	5322.6	P	ubiquitin fusion degradation protein
6674_at	959.3	P	hypothetical protein
6675_at	1366.7	P	hypothetical protein
6676_at	5047.7	P	serine-threonine protein phosphatase 2A
6677_at	430.2	P	questionable ORF

6678_at	89.8	A	hypothetical protein
6679_at	22499.8	P	encodes a protein with three regions (ABC) that is spliced to yield th
6680_s_at	2220.6	P	Ribosomal protein L41A (YL41) (L47A)
6681_at	838.6	P	weak similarity to S.pombe hypothetical protein SPAC23H3
6682_at	27451.5	P	homocitrate synthase, highly homologous to YDL131W
6683_g_at	30893.6	P	homocitrate synthase, highly homologous to YDL131W
6684_at	2547.8	P	ATPase inhibitor
6685_at	2700.2	P	hypothetical protein
6641_at	1892.1	P	PHO85 cyclin
6642_at	6994.5	P	D-Lactate Dehydrogenase (Cytochrome)
6643_at	741.7	P	similarity to hypothetical protein YCR059c
6644_at	284.8	P	hypothetical protein
6645_at	1065.9	P	strong similarity to hypothetical protein YIL079c and weak similarity t
6646_at	15082.7	P	mitochondrial enzyme D-lactate ferricytochrome c oxidoreductase
6647_at	3875.7	P	hypothetical protein
6648_at	1199.2	A	questionable ORF
6649_at	11370	P	Glutamate synthase (NADPH)
6650_at	808.6	P	zinc-finger transcription factor of the Zn(2)-Cys(6) binuclear cluster d
6651_at	327.1	P	protein of unknown function
6652_at	7179.6	P	Long-chain alcohol dehydrogenase (glutathione-dependent formalde
6653_at	2335.1	P	Asparagine-rich protein
6654_at	5615	P	weak similarity to Pyrococcus horikoshii hypothetical protein PHBJ01
6655_at	7720.4	P	nuclear protein that negatively regulates basal transcription
6656_at	4312.7	P	DNA ligase
6657_at	22.6	A	questionable ORF
6658_at	89	A	hypothetical protein
6659_at	2582.9	P	strong similarity to hypothetical protein YLR206w and to human KIAA
6660_at	3160.5	P	Putative RNA helicase of DEAD box family, required for Rap1p local
6661_at	3184.1	P	MEK homolog
6662_at	3227.7	P	questionable ORF
6618_at	13825.7	P	hypothetical protein
6619_at	481.5	A	weak similarity to Pas7p
6620_at	4225.6	P	G(sub)2-specific B-type cyclin
6621_at	772	P	MutS homolog involved in chromosome exchange
6622_at	12712.8	P	Something About Silencing 10
6623_at	672.5	M	questionable ORF
6624_at	821.5	A	questionable ORF
6625_at	6776.4	P	RNA polymerase III (C) subunit, homologus to human BN51 protein
6626_at	257.6	P	hypothetical protein
6627_at	4301.4	P	similarity to human mRNA clone RES4-25
6628_at	5834.8	P	Subunit of the regulatory particle of the proteasome
6629_at	541.4	P	weak similarity to Orc3p
6630_at	20049.5	P	alpha subunit of the coatamer complex\; gamma-alpha-COP
6631_at	6630.2	P	hypothetical protein
6632_at	8506.6	P	Cytoplasmic chaperonin subunit required for actin cytoskeleton asse
6633_at	1596.9	P	Cardiolipin synthase
6634_at	1674.6	P	Biotin:apoprotein ligase
6635_at	20352.9	P	RNA polymerase II large subunit
6636_at	685.5	P	hypothetical protein
6637_at	971.8	P	suppressor of snf3 mutant
6638_at	29356.2	P	ADP-ribosylation factor 2
6639_at	9767.6	P	Rho GDP dissociation inhibitor with activity toward Rho1p

6640_at	2089.4	P	serine-threonine protein phosphatase 2A
6595_at	3082	P	hypothetical protein
6596_at	3034.9	P	Acts together with Cdc4p and Cdc34p to control the G1-S phase trai
6597_at	26482.1	P	homocitrate synthase, highly homologous to YDL182W
6598_at	8669.2	P	ATPase stabilizing factor
6599_at	29159.2	P	Ribosomal protein P1B (L44) (YP1beta) (Ax)
6600_at	925.2	P	Ribosomal protein P1B (L44) (YP1beta) (Ax)
6601_at	3269	P	hypothetical protein
6602_at	12248	P	vacuolar H+\/Ca2+ exchanger
6603_at	2719.3	P	G1 cyclin
6604_at	21884	P	Microsomal protein of CDC48\/PAS1\/SEC18 family of ATPases\; fu
6605_at	20223.1	P	Yeast member of the Histidine Triad protein family (HIT)
6606_at	869.6	A	Yeast member of the Histidine Triad protein family (HIT)
6607_at	3321.7	P	similarity to aldose reductases
6608_at	2937.7	P	similarity to hypothetical protein YJL151c
6609_at	13330.4	P	Ubiquitin-specific protease
6610_at	2489.7	P	hypothetical protein
6611_at	2356.1	P	Mitochondrial protein that regulates mitochondrial iron accumulation i
6612_at	1430.1	P	similarity to bovine Graves disease carrier protein
6613_at	166.3	A	questionable ORF
6614_at	5085.4	P	similarity to hypothetical S. pombe protein
6615_at	8617.4	P	Protein with homology to mammalian Nup107p
6616_at	492.4	P	hypothetical protein
6617_at	21.9	A	weak similarity to Rhizobium nodulation protein nodG
6573_at	285	P	similarity to hypothetical protein YDR425w
6574_at	6202.1	P	similarity to C-terminus of human TRP-185 protein
6575_at	5344.7	P	Component of the exosome 3->5 exoribonuclease complex with Rrp
6576_at	1642	P	hypothetical protein
6577_at	851.1	P	strong similarity to thiamine-repressed protein Thi4p
6578_at	1373.8	P	serine-threonine kinase, subunit of transcription factor TFIIK, a subc
6579_at	386.2	M	cox1 pre-mRNA splicing factor
6580_at	150.8	A	Homeobox-domain containing protein which is a positive regulator of
6581_at	776.5	A	protein of unknown function
6582_at	323.4	P	similarity to H.influenzae sialoglycoprotease (gcp)
6583_at	5082.6	P	UDP-N-acetylglucosamine pyrophosphorylase
6584_at	1086	P	largest and catalytic subunit of DNA polymerase III (delta)
6585_at	1655.9	P	protein kinase
6586_at	12199.7	P	similarity to E.coli arsenical pump-driving ATPase
6587_at	4974.2	P	weak similarity to myosin heavy chain proteins
6588_at	1439.6	P	hypothetical protein
6589_at	12661.2	P	Subunit of the regulatory particle of the proteasome
6590_at	1036.9	P	questionable ORF
6591_at	16309.4	P	dolichyl phosphate-D-mannose:protein O-D-mannosyltransferase
6592_at	179.3	A	questionable ORF
6593_at	2468.3	P	dolichyl phosphate-D-mannose:protein O-D-mannosyltransferase
6594_at	4924.2	P	Signal recognition particle subunit
6550_at	755.2	P	weak similarity to mouse FAF1 protein
6551_at	3625.9	P	beta subunit of farnesyltransferase
6552_at	4609.9	P	hypothetical protein
6553_at	1123.5	P	Suppressor of thermosensitive mutations in the DNA polymerase del
6554_at	1125.3	P	Living Under Cap-binding complex expression
6555_at	21976.7	P	similarity to hypothetical Synechocystis protein

6556_at	141.8	A	strong similarity to NADH dehydrogenase (ubiquinone)
6557_at	22162.5	P	suppressor of the cold-sensitive snRNP biogenesis mutant brr1-1
6558_i_at	31592	P	Ribosomal protein S16B (rp61R)
6559_f_at	19279.3	P	Ribosomal protein S16B (rp61R)
6560_at	35817.8	P	Ribosomal protein L13A
6561_at	29048.4	P	Acidic ribosomal protein P1A (YP1alpha) (A1)
6562_at	2800	P	positive regulatory factor with thiamin pyrophosphate-binding motif fo
6563_at	1270.7	P	MDS1 related protein kinase
6564_at	185.9	A	MDS1 related protein kinase
6565_at	8726	P	malate dehydrogenase
6566_at	1713.8	P	Required for the vacuolar morphogenesis in yeast
6567_at	2619.6	P	hypothetical protein
6568_f_at	33282.8	P	Ribosomal protein L31A (L34A) (YL28)
6569_at	15582.9	P	Ribosomal protein L31A (L34A) (YL28)
6570_at	2373.6	P	weak similarity to spindle pole body protein NUF1
6571_at	1504.9	P	weak similarity to Cyprinus carpio calcium channel protein
6572_at	3415.7	P	weak similarity to hypothetical protein YMR040w
6527_at	2685.1	P	questionable ORF
6528_at	2034.1	P	Bromodomain protein, homolog of Bdf1
6529_at	725.1	P	translational activator of cytochrome b
6530_at	307.5	A	questionable ORF
6531_at	11059.8	P	Subunit VIIa of cytochrome c oxidase
6532_at	15406	P	Mitochondrial form of NADP-specific isocitrate dehydrogenase
6533_at	1390.1	P	40 kDa farnesylated protein associated with peroxisomes
6534_at	11524	P	ubiquitin-conjugating enzyme
6535_at	3849	P	weak similarity to human estrogen-responsive finger protein
6536_at	215.6	A	questionable ORF
6537_f_at	38507.9	P	Ribosomal protein S29B (S36B) (YS29)
6538_at	15420.3	P	similarity to C.elegans hypothetical protein
6539_at	703.5	A	A mutation in this gene results in RADiation sensitivity and recombin
6540_at	984.2	P	Integrin analogue gene
6541_at	1078.4	P	hypothetical protein
6542_at	1323.4	P	transcription factor
6543_at	32927.6	P	mannose-1-phosphate guanyltransferase, GDP-mannose pyrophos
6544_at	3246.1	P	hypothetical protein
6545_at	9003.8	P	hypothetical protein
6546_at	13735.7	P	putative 1-acyl-sn-gylcerol-3-phosphate acyl transferase
6547_at	5246.2	P	Protein homologous to human La (SS-B) autoantigen
6548_at	1167	P	questionable ORF
6549_at	1137	A	KRE9 homolog
6504_at	3119.3	P	SIT4 suppress mutations in DBF2
6505_at	16591.1	P	hypothetical protein
6506_at	9426.9	P	homologous to Yml37p, component of the 37 S subunit of mitochon
6507_at	1137.3	P	FAD synthetase
6508_at	1324	P	Necessary for the stability and\/or processing of some large mitochor
6509_at	794.1	P	snRNA-associated protein
6510_at	3048.8	P	regulator of silent mating loci
6511_at	1155	P	questionable ORF
6512_at	10292.2	P	N-terminal acetyltransferase
6513_at	10042.1	P	questionable ORF
6514_at	6431	P	similarity to mucin proteins
6515_at	2971.9	P	strong similarity to glucan 1,4-alpha-glucosidase

6516_at	3056.5	P	strong similarity to RIB2 protein
6517_at	2505.1	P	G-protein coupled receptor
6518_at	177	A	questionable ORF
6519_at	2549.5	P	similarity to H.influenzae hypothetical protein HI0174
6520_at	516	A	questionable ORF
6521_at	6785.1	P	DEAD box protein 10
6522_at	2402.7	P	RNA splicing factor
6523_at	11348.3	P	actin-related protein
6524_at	1171.1	P	serine\/threonine\/tyrosine protein kinase (dual specificity), able to au
6525_at	613.2	P	hypothetical protein
6526_at	205.4	A	questionable ORF
6482_at	1702.2	P	ser/thr protein kinase of the DEAD/DEAH box family
6483_at	808.3	P	strong similarity to acid phosphatase
6484_at	42.1	A	questionable ORF
6485_at	6674.8	P	glycerol-3-phosphate dehydrogenase
6486_at	437.3	P	Similar to GPM1 (phosphoglycerate mutase)
6487_at	2438.1	P	involved in ubiquitin degradation pathway
6488_at	7173.1	P	similarity to Osh1p
6489_at	764.5	P	p24 protein involved in membrane trafficking
6490_at	1546.7	P	serine\/threonine protein kinase
6491_at	104.7	A	questionable ORF
6492_at	15752.9	P	similarity to rat synaptic glycoprotein SC2
6493_at	21919.3	P	nucleolar protein, homologous to mammalian fibrillarin
6494_at	2172.4	P	Protein involved in hexose metabolism
6495_at	12835.6	P	strong similarity to hypothetical protein YBR016w and YDR210w
6496_at	641.8	M	questionable ORF
6497_at	2565.4	P	similarity to hypothetical protein YBR014c and glutaredoxins
6498_at	1236.7	P	questionable ORF
6499_at	4364.2	P	subunit of the anaphase promoting complex (APC)
6500_at	5699.8	P	Probable 26S protease subunit and member of CDC48\/PAS1\/SEC1
6501_at	453.6	P	serine-threonine protein phosphatase
6502_at	974	P	Stoichiometric member of mediator complex
6503_at	18365.2	P	ATP synthase delta subunit
6459_at	1511.1	P	Mitotic omosome Determinant\; similar to S. pombe RAD21\; may fur
6460_at	891.2	P	HMG1-box containing protein
6461_at	1020.3	P	similarity to hypothetical protein YFR048w, YDR282c and S.pombe h
6462_at	3174.5	P	neutral trehalase (alpha,alpha-trehalase)
6463_at	28765	P	Yeast Ran Binder #1\; suppressor of FUS1\; homolog of mouse HTF
6464_at	1506.9	P	strong similarity to hypothetical protein YBR005w
6465_at	2080.2	P	RecA homolog (similar to DMC1, RAD51, and RAD55), interacts wit
6466_at	1636	P	required for sorting of Mod5p
6467_at	2635	P	gene dosage suppressors of the conditional growth defect of several
6468_at	3852.5	P	n-(5 -phosphoribosyl)-anthranilate isomerase
6469_at	712.9	M	questionable ORF
6470_at	814.3	P	galactokinase
6471_at	119.7	A	hypothetical protein
6472_at	11167.3	P	ABC transporter
6473_i_at	35792.3	P	Ribosomal protein L4B (L2B) (rp2) (YL2)
6474_at	667.1	P	similarity to human hypothetical KIAA0186 protein
6475_at	383.5	P	weak similarity to chicken neurofilament triplet M protein
6476_at	364.9	A	hypothetical protein
6477_at	3987.6	P	hypothetical protein

6478_at	5178.8	P	Shows homology to basic leucine zipper family of transcription factor
6479_at	191.5	A	strong similarity to hypothetical protein YBR042c
6480_at	2945.7	P	glycine cleavage T protein (T subunit of glycine decarboxylase comp
6481_at	207.8	A	weak similarity to uridine kinases and phosphoribulokinases
6436_at	2099.3	P	DEAD-box protein, putative RNA helicase
6437_at	388.8	P	cik1 suppressor
6438_at	25222.6	P	seryl-tRNA synthetase
6439_at	563.2	A	hypothetical protein
6440_at	2690	P	strong similarity to DNA-binding protein Reb1p
6441_at	2570.2	P	Loss Upsets Vacuole
6442_at	1506	P	regulatory subunit for protein phosphatase Glc7p
6443_at	575.6	P	hypothetical protein
6444_at	790.5	P	Protein involved in the same pathway as Rad26p, has beta-transduc
6445_at	1365.6	P	hypothetical protein
6446_at	18198.6	P	strong similarity to S.pombe obr1
6447_at	29133.2	P	strong similarity to putative heat shock protein YRO2
6448_at	1351.6	P	Transcriptional activator of lysine pathway genes with 2-aminoadipat
6449_at	2790.4	P	identified by SAGE expression analysis
6450_at	19485.7	P	DAHP synthase\; a.k.a. phospho-2-dehydro-3-deoxyheptonate aldol
6451_at	5707.8	P	similarity to enoyl CoA hydratase
6452_at	29384.2	P	lysyl-tRNA synthetase
6453_at	638.8	P	P-type ATPase involved in Na+ efflux
6454_g_at	6632	P	P-type ATPase involved in Na+ efflux
6455_s_at	7856.9	P	plasma membrane protein\; putative Na+ pump\; P-type ATPase
6456_at	4835.2	P	weak similarity to bacterial ribosomal S10 proteins
6457_at	330.5	A	hypothetical protein
6458_at	535.6	P	Suppressor of SNf
6413_at	4360.6	P	Coproporphyrinogen III oxidase
6414_at	7683.7	P	strong similarity to S.acidocaldarius transcription elongation factor tfs
6415_at	9401.6	P	Valine transporter
6416_at	10022.4	P	uroporphyrinogen decarboxylase
6417_at	21.1	A	questionable ORF
6418_at	1226.7	P	similarity to C.elegans K06H7.3 protein
6419_at	22512.6	P	triosephosphate isomerase
6420_at	4436.8	P	similarity to hypothetical A. thaliana protein BAC F7G19
6421_at	784.9	P	cyclin-like kinase required for late nuclear division
6422_at	377.1	A	questionable ORF
6423_at	1624.1	P	ubiquitin-conjugating enzyme, E2
6424_at	5979.7	P	strong similarity to SPS2 protein
6425_at	5846.4	P	hypothetical protein
6426_at	522.5	P	weak similarity to L.lactis mleR protein
6427_at	1095.9	P	TriGlyceride Lipase
6428_at	2028.6	P	ubiquitin-conjugating enzyme
6429_at	1887	P	similarity to mouse putative CCAAT binding factor CBF1 and CBF2
6430_at	2302.4	P	similarity to E.coli modF and photorepair protein phrA
6431_at	24151.6	P	Probable component of serine palmitoyltransferase, which catalyzes
6432_at	6631.9	P	weak similarity to glia maturation factor beta
6433_at	21619.2	P	Ribosomal protein S13 (S27a) (YS15)
6434_at	699	P	hypothetical protein
6435_at	776.4	P	similarity to hypothetical protein YER139c
6391_at	544.2	P	similarity to YNL099c
6392_at	2164.8	P	involved in genome stability

6393_at	1366.7	P	ubiquitin isopeptidase
6394_at	403.2	P	hypothetical protein
6395_at	7017.7	P	similarity to O.aries arylalkylamine N-acetyltransferase
6396_at	1885.2	P	inositolphosphotransferase 1
6397_at	2188.4	P	component of SWI\/SNF global transcription activator complex
6398_at	6701	P	Trehalose-6-phosphate phosphatase
6399_at	2901.1	P	protein phosphatase type 2A
6400_at	129.4	A	RecA homolog (related to DMC1, RAD51, RAD57), interacts with Ra
6401_at	23112.7	P	putative cell surface glycoprotein
6402_at	1902.1	P	Preferential Use of Neither donor locus during mating type switching.
6403_at	2667.1	P	cytochrome c oxidase-specific assembly factor
6404_at	626.7	P	vacuolar protein sorting
6405_at	2641.6	P	Asparagine and serine-rich protein
6406_at	1065.1	P	Involved in telemere length regulation, may be functional in telemere
6407_at	8759.8	P	similarity to hypothetical S.pombe protein
6408_at	8705.5	P	similarity to hypothetical C.elegans protein
6409_at	1670.9	P	coordinates regulation of alpha-factor receptor signalling and inductio
6410_at	13368.3	P	endoplasmic reticulum protein that is part of the Sec61 trimeric comp
6411_at	5238.8	P	involved in processing rRNA precursor species to mature rRNAs
6412_at	1443.5	P	involved in 3 splice site choices and 2nd step of splicing
6368_at	1428.3	P	weak similarity to Streptococcus transposase
6369_at	4079.3	P	weak similarity to YRO2 protein
6370_at	30181.8	P	strong similarity to human RNase L inhibitor and M.jannaschii ABC tr
6371_at	21786.5	P	ubiquitin-conjugating enzyme
6372_at	3351.1	P	similarity to P.falciparum ATPase 2
6373_g_at	8933.9	P	similarity to P.falciparum ATPase 2
6374_at	1577.3	P	questionable ORF
6375_at	1506.9	P	hypothetical protein
6376_at	647.5	P	putative zinc finger protein
6377_at	4852	P	Homolog of the human GTBP protein, forms a complex with Msh2p
6378_at	9591.8	P	similarity to Legionella glutaredoxin-like protein
6379_at	22986.7	P	Homolog of mammalian 14-3-3 proteins
6380_at	10434.2	P	similarity to Dictyostelium development-specific membrane protein
6381_at	7710.2	P	weak similarity to proliferation-associated protein
6382_at	145	A	hypothetical protein
6383_at	2990.3	P	Protein of the pheromone pathway
6384_at	618.7	P	hypothetical protein
6385_at	4502.7	P	similarity to mouse hypothetical protein
6386_at	627.4	M	Actin-related protein
6387_at	780.3	P	strong similarity to Emp70 protein
6388_at	1023.2	P	Probably has role late in meiosis following DNA replication
6389_at	326.8	P	similarity to Mpa43p
6390_at	683	P	DNA replication fork blocking protein
6346_at	715	P	strong similarity to alanine transaminase
6347_at	164.8	A	questionable ORF
6348_at	581	P	42-kDa nuclear protein
6349_at	247	A	questionable ORF
6350_at	5953.8	P	similarity to bacterial ribosomal L34 proteins
6351_at	1738.1	P	similarity to bacterial ribosomal L1 proteins
6352_at	3208.7	P	similarity to mouse ligatin, a trafficking receptor for phosphoglycopro
6353_at	740.3	P	subunit of the anaphase promoting complex (APC)
6354_at	7047.9	P	similarity to B.subtilis tetracyclin resistance

6355_at	7168	P	N2,N2-dimethylguanosine-specific tRNA methyltransferase
6356_at	3336.2	P	weak similarity to YNC2beta protein
6357_at	1218.2	P	Serine\/threonine protein kinase
6358_at	1051.3	P	helix-loop-helix protein
6359_at	117.3	A	hypothetical protein
6360_at	29.9	A	ExtraCellular Mutant
6361_at	3641.8	P	similarity to hypothetical protein YLR246w and YOL003c
6362_at	25457.2	P	pentafunctional arom polypeptide (contains: 3-dehydroquinate synth
6363_at	4292.7	P	weak similarity to Sec27p, YMR131c and human retinoblastoma-bin
6364_at	7682.6	P	fibrim homolog (actin-filament bundling protein)
6365_at	796.3	P	weak similarity to sea urchin myosin heavy chain
6366_at	354.4	P	similarity to hypothetical protein YJL149w
6367_at	340.4	P	strong similarity to hypothetical protein YLR108c
6323_at	25087.3	P	questionable ORF
6324_g_at	34195.5	P	questionable ORF
6325_at	5496	P	Metal resistance protein with similarity to human cystic fibrosis protei
6326_at	447.9	A	questionable ORF
6327_at	2851.2	P	Reduced growth phenotype
6328_at	1188.3	P	Hyperrecombination protein that suppresses intrachromosomal excis
6329_at	11170.3	P	ubiquitin-like protein
6330_at	5119	P	ubiquitin-like protein
6331_at	3821.1	P	weak similarity H.influenzae protoporphyrinogen oxidase (hemK) hon
6332_at	1793.7	P	hypothetical protein
6333_at	687.3	P	Member of beta-transducin-related (WD-40) protein family
6334_at	4765.3	P	mating-type regulation protein
6335_at	12409.8	P	aspartyl protease related to Yap3p
6336_at	1068	P	TFIID subunit
6337_at	1939.7	P	transcriptional activator
6338_at	1400.6	P	Ethanolamine Kinase
6339_at	9865.5	P	dihydrolipoyl transsuccinylase component of alpha-ketoglutarate deh
6340_at	90	A	questionable ORF
6341_at	2969.5	P	Protein with variable number of tandem repeats of a 64 amino-acid
6342_at	863.2	P	member of the CCCH zinc finger protein family that has two or more
6343_at	3491.1	P	weak similarity to C.elegans hypothetical protein CET26E3
6344_at	3416.1	P	hypothetical protein
6345_at	10811.4	P	questionable ORF
6300_g_at	26285.8	P	questionable ORF
6301_at	21190.2	P	cyclophilin peptidyl-prolyl cis-trans isomerase
6302_at	29634	P	RNA polymerase I subunit A14
6303_at	1675.1	P	questionable ORF
6304_at	14378.6	P	aspartic beta semi-aldehyde dehydrogenase
6305_at	1863.3	P	Leucine permease transcriptional regulator
6306_at	865.9	P	Ssy1p controls expression of several transporter genes, including B
6307_at	2471.2	P	protein phosphatase Two C-Interacting protein
6308_at	747.5	P	Nap1p-binding protein
6309_at	1768.8	P	weak similarity to S.pombe hypothetical protein
6310_at	1254.6	P	Hydrophilic protein involved at the late stage of secretion
6311_at	3857	P	weak similarity to hypothetical C.elegans protein
6312_at	2317.5	P	107 kDa component of the Exocyst complex\; required for exocytosis
6313_at	6228.7	P	TFIID subunit
6314_at	8830.4	P	Cell cycle protein necessary for passage through START
6315_at	678.2	P	Binds Sin3p in two-hybrid assay

6316_at	10053.1	P	Guanine nucleotide exchange protein for ARF
6317_at	4377	P	Similar to HSP26\; expression is regulated by stress conditions
6318_at	12217.2	P	putative translation factor
6319_at	710.2	P	Regulator of arginine-responsive genes with ARG80 and ARG81
6320_at	9617.1	P	Non-histone protein
6321_at	3417.1	P	similarity to S.pombe hypothetical protein SPAC2F7.15
6322_at	1089.2	P	transcription factor\; genetic and mutant analyses suggest that Ngg1
6278_at	17232.7	P	ubiquitin-conjugating enzyme
6279_at	13927.8	P	succinate dehydrogenase membrane anchor subunit
6280_at	205.9	P	hypothetical protein
6281_at	582.4	P	hypothetical protein
6282_at	1394.3	P	Sister chromatid cohesion protein
6283_at	970.4	P	Involved in silencing at telomeres, HML and HMR
6284_at	2962.5	P	Protein that affects bud emergence, intrachromosomal recombinatio
6285_at	1061.6	P	weak similarity to thioredoxin
6286_at	2389.8	P	Aip Three Complex\; interacts with AIP3, localized to the nucleus
6287_at	618.5	A	strong similarity to Msf1p
6288_at	414.1	P	hypothetical protein
6289_at	509.9	A	questionable ORF
6290_at	14045.7	P	Cytoplasmic chaperonin of the Cct ring complex (previously called T
6291_at	2020.4	P	Hydrophilic suppressor of ypt1 involved in vesicle trafficking between
6292_at	11610.1	P	strong similarity to TATA-binding protein-interacting protein 49 - rat
6293_at	1109.5	P	Homolog of SIR2
6294_at	659.5	P	nucleoporin
6295_at	249	A	questionable ORF
6296_at	8626.5	P	Mitochondrial RNA helicase of the DEAD box family
6297_at	2616	P	RNA-binding protein involved in cleavage step of mRNA 3 -end form
6298_at	3333.3	P	similarity to C.elegans hypothetical protein T05G5.5
6299_at	644.7	P	cytochrome b translational activator
6255_at	696.4	P	hypothetical protein
6256_at	474.5	A	questionable ORF
6257_at	908.9	P	similarity to hypothetical protein YLR238w
6258_at	4014.8	P	component of spindle pole
6259_at	1471.6	P	hypothetical protein
6260_at	136.1	A	questionable ORF
6261_at	3243.3	P	Involved in ubiquinone biosynthesis
6262_at	1571.2	P	similarity to A.eutrophus cation efflux system membrane protein czcl
6263_at	3170.7	P	EST1-like bcy1 Suppressor
6264_at	2625.3	P	Ume6p is a C6 zinc finger URS1-binding protein that is a key regulat
6265_at	3076.2	P	Phosphatidylinositol 4-phosphate kinase
6266_at	1373.1	P	questionable ORF
6267_at	19869.5	P	strong similarity to hypothetical protein YBR016w
6268_at	6102.9	P	Translation initiation factor eIF-2B epsilon subunit
6269_at	20178.3	P	chaperonin subunit alpha
6270_at	438.5	P	regulatory protein involved in control of sterol uptake
6271_at	8729.6	P	similarity to hypothetical protein YNL281w
6272_at	382.8	A	hypothetical protein
6273_at	1000.2	P	positive transcriptional regulator of ADH2 and peroxisomal protein ge
6274_at	852.4	P	cell cycle arrest protein
6275_at	231.9	A	Septin-related protein expressed during sporulation
6276_at	486.8	P	hypothetical protein
6277_at	461.5	M	questionable ORF

6232_at	770.5	P	weak similarity to the beta subunit of an ER luminal alpha-glucosidas
6233_at	5452.1	P	strong similarity to hypothetical protein YLR225c
6234_at	222.3	A	similarity to Ifh1p
6235_at	22354.9	P	Histone H2B (HTB1 and HTB2 code for nearly identical proteins)
6236_i_at	37130	A	Histone H2A (HTA1 and HTA2 code for nearly identical proteins)
6237_at	15949	P	cytosolic adenylate kinase
6238_at	506.7	P	regulator of silent mating loci
6239_at	1131.7	P	Component of pre-mRNA cleavage and polyadenylation factor I, inte
6240_at	1239.2	P	hypothetical protein
6241_at	471.6	A	questionable ORF
6242_at	3330.3	P	hypothetical protein
6243_at	10424.6	P	5-aminolevulinate synthase
6244_at	33060.5	P	similarity to hypothetical protein YDL204w
6245_at	18412	P	homoaconitase
6246_at	2308.1	P	U1 snRNP protein that shares 50\% sequence similarity with Prp39p
6247_at	1639.5	P	similarity to hypothetical A. thaliana protein
6248_at	2208.6	P	Mitochondrial ribosomal protein MRPL7 (YmL7)
6249_at	22548	P	encodes a subunit of yeast coatomer
6250_at	3698.4	P	hypothetical protein
6251_at	644.8	P	Snurp = Small nuclear ribonucleoprotein particle of MW 56 kDa. Ass
6252_at	16.9	A	questionable ORF
6253_at	511.4	P	putative amidase
6254_at	824.4	P	Required for the first step of splicing in vitro
6209_at	1158.1	P	69-kDa protein containing tetratricopeptide repeat (TPR)
6210_at	8287	P	galactosyltransferase
6211_at	6291.7	P	involved in targeting and fusion of ER to golgi transport vesicles
6212_at	1048.8	P	strong similarity to Sks1p
6213_at	2182.4	P	strong similarity to E.coli thermoresistant gluconokinase
6214_at	777	P	weak similarity to cytochrome b
6215_at	390	P	hypothetical protein
6216_at	3505.9	P	coiled-coil protein multicopy suppressor of loss of PP2A
6217_at	1054.6	P	Negative effect on expression of several genes transcribed by RNA
6218_at	143.3	A	zinc finger DNA binding factor, transcriptional regulator of sulfur ami
6219_at	373.7	P	Protein necessary for stability of ARS-CEN plasmids\; suggested to
6220_at	1529.9	P	weak similarity to hypothetical S.pombe hypothetical protein SPBC29
6221_at	376	P	catalase A
6222_at	822.9	P	Transcription regulator
6223_at	1282	P	Mitochondrial heat shock protein 78 kDa
6224_at	131.5	A	bZIP protein
6225_at	3238.3	P	hypothetical protein
6226_at	1678.9	P	Exo-1,3-b-glucanase
6227_at	6807.9	P	hypothetical protein
6228_at	1193.9	P	DNA-damage inducible gene
6229_at	3657.9	P	Ankyrin repeat-containing protein
6230_at	978.6	P	C3HC4 zinc-binding integral peroxisomal membrane protein
6231_at	2736.1	P	similarity to hypothetical C.elegans protein
6187_at	3201	P	weak similarity to human TAFII100 and other WD-40 repeat containi
6188_at	1992.7	P	mitochondrial tryptophanyl-tRNA synthetase
6189_at	537.2	A	questionable ORF
6190_at	4221.8	P	Copper-transporting P-type ATPase with similarity to human Menkes
6191_at	348.8	A	questionable ORF
6192_at	2115.5	P	Cytoplasmic glyoxylase-II

6193_at	687.9	P	weak similarity to YOR042w
6194_at	438.1	A	hypothetical protein
6195_at	1285.7	P	weak similarity to YOR042w
6196_at	27338.9	P	strong similarity to Hordeum vulgare blt101 protein
6197_at	791	P	Protein is 61\% identical to Msn3p
6198_at	238.2	A	hypothetical protein
6199_at	841.9	P	hypothetical protein
6200_at	6828	P	Putative 3 ->5 exoribonuclease\; component of exosome complex o
6201_at	2914.1	P	hypothetical protein
6202_at	1283.7	P	similarity to hypothetical protein YDL001w, YFR048w and S.pombe
6203_at	1289.8	P	eukaryotic initiation factor 2 alpha (eIF2-alpha) kinase
6204_at	6592.5	P	Diacylglycerol Pyrophosphate Phosphatase
6205_at	459.9	A	Synaptonemal complex protein, component of the central element
6206_at	2553.2	P	hypothetical protein
6207_at	1391	P	similarity to inositolmonophosphatases
6208_at	348.8	P	hypothetical protein
6163_at	380.9	P	hypothetical protein
6164_at	29.6	A	questionable ORF
6165_at	3355.5	P	similarity to B.subtilis helicases
6166_at	4564.9	P	signal recognition particle receptor - alpha subunit
6167_at	6210.7	P	putative protein phosphatase
6168_at	17374.3	P	dihydrosphingosine phosphate lyase (also known as sphingosine ph
6169_at	472.2	A	weak similarity to Uso1p, YPR179c and fruit fly tropomyosin
6170_at	5263.2	P	hypothetical protein
6171_at	7735.6	P	Syringomycin response protein 2
6172_at	8190.8	P	ATP synthase subunit 5\; oligomycin sensitivity-conferring protein
6173_at	2207.1	P	involved in protein transport step at the Brefeldin A blocks
6174_at	7607.2	P	gamma-glutamyl kinase
6175_at	3721.8	P	Component of pre-mRNA cleavage factor II (CFII)\; 150-kDa protein
6176_at	10543.9	P	weak similarity to human GPI-anchor biosynthesis protein
6177_at	1660.3	P	similarity to transcriptional regulator proteins
6178_at	17998.8	P	Cyclophilin D, Peptidyl-prolyl cis-trans isomerase D
6179_at	4084.9	P	Yeast member of the Histidine Triad protein family (HIT)
6180_i_at	260	M	Yeast member of the Histidine Triad protein family (HIT)
6181_r_at	57.6	A	Yeast member of the Histidine Triad protein family (HIT)
6182_f_at	390.4	A	Yeast member of the Histidine Triad protein family (HIT)
6183_at	2258.2	P	weak similarity to S.pombe hypothetical protein SPAC6F6
6184_at	3440.2	P	similarity to Pmt1p, Pmt2p, Pmt3p and Pmt5p
6185_at	3618.1	P	RNA polymerase II holoenzyme component
6186_at	13049	P	GTPase-interacting component 2
6140_at	6291.7	P	Suppresor of mar1-1 (sir2) mutation
6141_at	1277.8	P	Component of transcription initiation factor IIb, 75 kDa subunit
6142_i_at	484.7	P	high copy suppressor of G beta subunit temperature sensitive mutati
6143_f_at	1929.9	P	high copy suppressor of G beta subunit temperature sensitive mutati
6144_at	996.5	P	Phosphatidylinositol(3)-phosphate binding
6145_at	239.2	A	weak similarity to hypothetical S.pombe protein
6146_at	215.4	A	hypothetical protein
6147_at	2204.8	P	hypothetical protein
6148_at	216.3	A	hypothetical protein
6149_at	1228	P	Involved in minichromosome maintenance
6150_at	1909.5	P	hypothetical protein
6151_at	678.1	P	similarity to hypothetical S. pombe protein and weak similarity to bovi

6152_at	17809.9	P	Asparaginase I, intracellular isozyme
6153_at	2872.2	P	Mitochondrial ribosomal protein MRPL35 (YmL35)
6154_at	22749.9	P	subunit e of mitochondrial F1F0-ATPase
6155_at	181.1	A	cytosolic and peripheral membrane protein with three zinc fingers\; c
6156_at	1886.7	P	weak similarity to beta transducin from S. pombe and other WD-40 r
6157_at	759.4	P	weak similarity to S.pombe hypothetical protein SPAC1B9
6158_at	1425.4	P	strong similarity to YHR080c, similarity to YFL042c and YLR072w
6159_at	761.5	P	questionable ORF
6160_at	12340.1	P	Skp1p encodes Cbf3d, a 29 Kd kinetochore protein subunit of CBF3
6161_at	848.2	P	48-kDa peroxisomal integral membrane protein
6162_at	1775.5	P	similarity to hypothetical S. pombe protein
6117_at	5098.2	P	Protein involved in the attachment of glycosylphosphatidylinositol (G
6118_at	767.8	P	similarity to E.coli hypothetical protein and weak similarity to RNA hel
6119_at	4286.5	P	similarity to hypothetical S. pombe protein
6120_at	1220.9	P	similarity to nuclear Sth1p, Snf2p and related proteins
6121_at	9562.9	P	Multicopy suppressor of snf1 mutation
6122_at	1659.2	P	weak similarity to B.subtilis hypothetical protein X
6123_at	2809.1	P	Mitochondrial ribosomal protein MRPS28 (E. coli S15)
6124_at	2327.7	P	similarity to Erc1p
6125_at	10070.6	P	weak similarity to hypothetical protein YOR004w
6126_at	68.8	A	questionable ORF
6127_at	31368.7	P	strong similarity to arginine-tRNA ligase
6128_f_at	22789	P	Hexose transporter
6129_f_at	21711.5	P	Hexose transporter
6130_at	412.9	A	hypothetical protein
6131_at	35103.9	P	High-affinity glucose transporter
6132_at	2652.1	P	similarity to hypothetical S.pombe protein
6133_at	6656.9	P	37 kDa mitochondrial ribosomal protein
6134_at	2104.8	P	similarity to hypothetical protein YHR097c
6135_at	4401	P	GPI-anchored aspartic protease
6136_at	1381	P	protein of unknown function
6137_at	4181.5	P	required for bud growth
6138_at	1870.5	P	weak similarity to hypothetical proteins YOL092w, YBR147w and Y
6139_at	14592.9	P	Thioredoxin reductase
6095_at	4973.6	P	anthranilate phosphoribosyl transferase
6096_at	226.4	A	questionable ORF
6097_at	828.2	P	component of the spindle pole body that interacts with Spc42p, calm
6098_at	791.6	P	hypothetical protein
6099_at	1458.4	P	strong similarity to hypothetical protein YHR108w and weak similarity
6100_at	1659.1	P	hypothetical protein
6101_at	19.9	A	questionable ORF
6102_at	3248.1	P	hypothetical protein
6103_at	2674.7	P	91 kDa tau91 subunit of transcription factor IIIC (TFIIIC)
6104_at	802	P	Establishes Silent omatin
6105_at	4347	P	Homolog of DSS1\; similar to hypothetical protein from S. pombe
6106_at	2298.8	P	Member of the beta transducin family
6107_at	2865.7	P	weak similarity to Streptococcus M protein
6108_at	228.9	A	similarity to YOL106w and YER181c
6109_at	5305.1	P	hypothetical protein
6110_at	9632	P	homologous to the aldo-keto reductase protein family
6111_at	467.4	A	DNA repair protein
6112_at	1968.8	P	hypothetical protein

6113_at	59.9	A	similarity to chitinases
6114_at	1556	P	similarity to hypothetical S. pombe protein
6115_at	4845.6	P	strong similarity to human BDR-1 protein and other calcium binding p
6116_at	260.1	A	similarity to hypothetical A. thaliana protein BAC F21M12
6072_at	880.2	P	Mitochondrial protein of the CDC48\/PAS1\/SEC18 ATPase family, r
6073_at	2976.2	P	adrenodoxin oxidoreductase homolog
6074_at	7602.3	P	ATP synthase subunit f
6075_at	1980	P	Sm-like protein
6076_at	1076.3	P	Contains a Rho-GAP domain and two LIM domains. Has strong simil
6077_at	10917.2	P	similarity to Pdc6p, Thi3p and to pyruvate decarboxylases
6078_at	14566.3	P	Nuclear RNA-binding RNA annealing protein
6079_at	8248.7	P	Nuclear RNA-binding RNA annealing protein
6080_at	10741.3	P	Ribosomal protein P2B (YP2beta) (L45)
6081_at	35.1	A	weak similarity to S.pombe paramyosin
6082_at	13897.1	P	strong similarity to Y.lipolytica GPR1 gene
6083_at	379	A	MMS and UV Sensitive\; Mus81p and Rad54p are found together in a
6084_at	728.4	P	similarity to Itr1p and Itr2p and E.coli araE
6085_at	23440.4	P	involved in endocytosis
6086_at	2081.1	P	GTPase activating protein (GAP) for RHO1
6087_at	1348.6	P	Protein with homology to mammalian ubiquitin activating (E1) enzym
6088_at	2262.3	P	strong similarity to hypothetical protein YOR013w
6089_at	1121.3	P	transcription factor, member of the histone acetyltransferase SAGA
6090_at	478.6	P	mRNA (identified by a library screen) that causes growth arrest when
6091_at	5731.9	P	probable 26S protease subunit and member of the CDC48\/PAS1\/S
6092_at	5732.3	P	Sxm1p
6093_at	737	P	hypothetical protein
6094_at	3241.8	P	repressor of class II transcription
6049_at	9218.7	P	similarity to human KIAA0007 gene
6050_at	9830.8	P	Hypoxanthine Phosphoribosyltransferase
6051_at	7049	P	similarity to C. fasciculata inosine-uridine preferring nucleoside hydro
6052_at	33.7	A	Cytochrome P450 56, Dit2p catalyzes oxidation of N-formyl tyrosine
6053_at	691	A	questionable ORF
6054_at	289.3	A	first enzyme in dityrosine synthesis in the outer layer of the spore wa
6055_at	10459.9	P	dissociable subunit of RNA polymerase II
6056_at	1455.5	P	263-amino acid mitochondrial ribosomal large subunit protein\; simila
6057_at	1678	P	probable multidrug resistance transporter
6058_at	3037.6	P	weak similarity to Myo1p
6059_at	9705.7	P	glycinamide ribotide transformylase
6060_at	915.5	P	similarity to Nfi1p
6061_at	9681.1	P	farnesyl cysteine-carboxyl methyltransferase
6062_at	4911.9	P	weak similarity to Der1p
6063_at	788.4	A	weak similarity to NADH dehydrogenase
6064_at	1503.6	P	questionable ORF
6065_at	1045.7	P	Protein required for retention of luminal ER proteins
6066_at	3372.6	P	strong similarity to bacterial leucyl aminopeptidase
6067_at	1559	P	SYnthetic lethal with cdcForty
6068_at	658.2	P	questionable ORF
6069_i_at	31402.8	P	Ribosomal protein L12B (L15B) (YL23)
6070_s_at	30767.7	P	Ribosomal protein L12B (L15B) (YL23)
6071_at	388.8	P	similar to E. coli DinB and S. cerevisiae REV1
6026_at	4582	P	Type 1 membrane protein with EF hand motif
6027_at	355.6	P	hypothetical protein

6028_at	2577.5	P	SNF1 protein kinase substrate
6029_at	2111.5	P	Transcriptional activator involved in resistance to 1,10-phenanthrolin
6030_at	13744	P	putative light chain of dynein
6031_at	777.3	P	similarity to hypothetical protein YDL113c
6032_at	148.9	A	questionable ORF
6033_at	12387.1	P	Subunit of the regulatory particle of the proteasome
6034_at	5006.5	P	hypothetical protein
6035_at	23986.5	P	Translation initiation factor 3 p33 subunit
6036_at	2634.6	P	similarity to C.perfringens hypothetical hypA protein
6037_at	154.7	A	questionable ORF
6038_at	15331.6	P	nuclear shuttling protein with an RNA recognition motif
6039_g_at	31000.8	P	nuclear shuttling protein with an RNA recognition motif
6040_i_at	37970.3	P	questionable ORF
6041_at	5122.1	P	similarity to S.pombe hypothetical protein
6042_at	2429.3	P	similarity to YOL141w and hypothetical C.elegans protein
6043_at	1602.7	M	serine-threonine phosphatase Z
6044_at	1269.3	A	hypothetical protein
6045_at	808.4	P	strong similarity to hypothetical protein YML018c
6046_at	918.1	A	Loss of rDNA silencing
6047_at	1275.3	P	Pachytene CHeckpoint
6048_at	2770.5	P	Adenine phosphoribosyltransferase
6003_at	30.1	A	questionable ORF
6004_at	2426.6	P	RNA polymerase II holoenzyme component
6005_at	1046.9	P	similarity to hypothetical protein YGL144c and YDL109c
6006_at	446.9	A	questionable ORF
6007_at	133.7	A	ExtraCellular Mutant
6008_at	1852.8	P	transcription factor, member of ADA and SAGA, two transcriptional a
6009_at	2627.3	P	hypothetical protein
6010_at	2478.8	P	strong similarity to Yox1p
6011_at	3396.1	P	similarity to human sphingomyelin phosphodiesterase
6012_at	1535	P	strong similarity to thiol-specific antioxidant proteins
6013_at	22711.5	P	guanylate kinase
6014_at	40.8	A	questionable ORF
6015_at	2948.9	P	Na+\/H+ exchanger
6016_at	12723.8	P	hect-domain-containing protein, required for G2\/M transition\; simila
6017_at	833.1	P	similarity to hypothetical protein YML034w and YML033w
6018_at	1013.2	P	weak similarity to YNL326c
6019_at	1083.2	P	TFIIH subunit Tfb3 , contains ring finger motif\; similar to mammaliar
6020_r_at	985.2	A	a-factor mating pheromone precursor
6021_f_at	46.5	A	a-factor mating pheromone precursor
6022_at	2700.1	P	Mitochondrial ribosomal protein MRPL28 (YmL28)
6023_at	2353.2	P	Nuclear-localized protein containing zinc finger motifs
6024_at	1559.4	P	negative regulator of prp genes
6025_at	10112	P	Protein arginine methyltransferase
5980_at	2782.3	P	similarity to ser/thr protein kinase
5981_at	945.8	A	questionable ORF
5982_at	1454.4	P	tSNARE that affects a Late Golgi compartment
5983_at	1055.6	P	hypothetical protein
5984_at	494.1	P	similarity to chromosome segregation protein Cse1p
5985_at	34200.5	P	Ribosomal protein L27B
5986_at	3517.4	P	similarity to P.falciparum 41-2 protein antigen
5987_at	1672	P	essential splicing factor

5988_at	1574.5	P	similarity to C-terminal region of YOR019w
5989_at	492.6	A	hypothetical protein
5990_at	9656	P	hypothetical protein
5991_at	3422.4	P	protein serine\/threonine kinase
5992_at	1997	P	RNAse MRP protein component
5993_at	837.2	P	weak similarity to YHR150w
5994_at	1171.7	A	MAP kinase-associated protein
5995_at	4895.4	P	repressible alkaline phosphatase
5996_at	672.4	A	hypothetical protein
5997_at	9676	P	alpha-1,2-mannosyltransferase
5998_at	523.9	P	May interact with actin as a component or controller of the assembly
5999_at	2049.4	P	similarity to trichohyalin
6000_at	2590.5	P	weak similarity to Snf7p
6001_at	12649.2	P	3,4-dihydroxy-2-butanone 4-phosphate synthase
6002_at	3840	P	Protein required in the absence of Cin8p
5958_at	1054	P	hypothetical protein
5959_at	1708.8	P	Ser\/Thr protein kinase
5960_at	551.6	A	questionable ORF
5961_at	15406.1	P	strong similarity to hypothetical protein YOL002c
5962_at	1820.1	P	hypothetical protein
5963_at	3639.7	P	hypothetical protein
5964_at	329.8	P	Vacuolar sorting protein
5965_at	3667	P	similarity to hypothetical human and C.elegans proteins
5966_at	28058.4	P	myo-inositol transporter
5967_at	4929	P	membrane glycoprotein, sorted by HDEL retrieval system
5968_at	730.1	P	weak similarity to hypothetical C.elegans protein, M.genitalium pepti
5969_at	35409.1	P	60S ribosomal protein L37B (L43) (YL35)
5970_at	218.1	A	similarity to hypothetical protein YLR183c
5971_at	15642.4	P	S-adenosylmethionine synthetase
5972_at	1494.1	P	Lipid phosphate phosphatase
5973_at	8254.5	P	similarity to hypothetical T.brucei protein
5974_at	1802.3	P	high copy suppressor of ts mutations in DNA polymerase alpha
5975_at	2453.3	P	similarity to FET3, YFL041w and F.floriforme diphenol oxidase
5976_at	4076.5	P	putative serine\/threonine kinase
5977_at	13816.6	P	high-affinity glutamine permease
5978_at	527.6	P	questionable ORF
5979_at	8582.2	P	may be involved in function and\/or structure of the eukaryotic kineto
5935_at	5073.6	P	weak similarity to C. elegans protein F25H9.7 and to the human com
5936_at	3496.1	P	questionable ORF
5937_at	12734	P	Glutaredoxin (thioltransferase) (glutathione reductase)
5938_at	2785.9	P	strong similarity to hypothetical protein YCL036w
5939_at	942	P	regulates the copper-dependent mineralization of copper sulfide com
5940_at	4724.9	P	strong similarity to glucokinase
5941_at	4044.4	P	weak similarity to hypothetical S.pombe protein
5942_at	1882.8	P	Protein disulfide isomerase homolog
5943_at	9485.4	P	FKBP (FK506 binding protein) 13\; peptidylprolyl cis-trans isomerase
5944_at	1448.5	P	weak similarity to transcription factors of the zinc finger class
5945_at	471.1	A	questionable ORF
5946_at	41.5	A	Middle\/late gene of meiosis
5947_at	566.3	P	serine\/threonine kinase homologous to Ste20p\; expressed in middl
5948_at	1494.5	P	similarity to hypothetical human protein and YIL044c
5949_at	241.9	A	hypothetical protein

5950_at	954.6	A	questionable ORF
5951_at	4544.9	P	weak similarity to Plasmodium yoelii rhoptry protein
5952_at	1480.6	P	similarity to Lre1p
5953_at	18073.4	P	ubiquinol-cytochrome c oxidoreductase subunit 7 (14 kDa)
5954_at	2949.9	P	5 ,5 -P-1,P-4-tetraphosphate phosphorylase II
5955_at	6658.5	P	similarity to hypothetical A. thaliana and C. elegans proteins
5956_at	212.6	P	weak similarity Plasmodium repeat organellar protein
5957_at	22208.2	P	strong similarity to hypothetical proteins YPL280w, YOR391c and Y
5913_at	751	P	similarity to YOR383c,Sta1p and pig mucin
5914_at	717.1	A	hypothetical protein
5915_at	50.8	A	sugar transporter-like protein
5916_at	342.7	A	questionable ORF
5917_at	5259.3	P	Phenylacrylic acid decarboxylase
5918_at	8940.8	P	similarity to E.coli hypothetical 55.3 kDa protein in rfah-rfe intergenic
5919_at	429.8	A	hypothetical protein
5920_at	1622	P	similarity to dihydroflavonol-4-reductases
5921_at	15038.9	P	hypothetical protein identified by SAGE
5922_s_at	8875.6	P	homing endonuclease with protein splicing activity
5923_at	4120.9	P	identified by SAGE
5924_at	649.1	P	identified by SAGE
5925_at	925.2	P	identified by SAGE
5926_g_at	925.2	A	identified by SAGE
5927_at	4236.4	P	Involved in pre-tRNA splicing and in uptake of branched-chain amino
5928_at	649.7	P	non-annotated SAGE orf Found forward in NC_001136 between 169
5929_at	1543.3	P	non-annotated SAGE orf Found reverse in NC_001136 between 340
5930_at	949.1	P	non-annotated SAGE orf Found reverse in NC_001136 between 372
5931_at	2476.5	P	non-annotated SAGE orf Found forward in NC_001136 between 578
5932_at	2047.7	P	non-annotated SAGE orf Found reverse in NC_001136 between 603
5933_at	1124.3	P	non-annotated SAGE orf Found forward in NC_001136 between 691
5934_at	2925.8	P	non-annotated SAGE orf Found reverse in NC_001136 between 110
5887_i_at	9730.5	A	non-annotated SAGE orf Found reverse in NC_001136 between 148
5888_at	75.1	A	non-annotated SAGE orf Found reverse in NC_001136 between 169
5889_at	45.9	A	non-annotated SAGE orf Found reverse in NC_001136 between 436
5890_i_at	17.9	A	non-annotated SAGE orf Found forward in NC_001136 between 437
5891_f_at	0	A	non-annotated SAGE orf Found forward in NC_001136 between 437
5892_at	954.2	A	non-annotated SAGE orf Found reverse in NC_001136 between 512
5893_at	2.6	A	non-annotated SAGE orf Found forward in NC_001136 between 629
5894_at	182.2	A	non-annotated SAGE orf Found reverse in NC_001136 between 130
5895_at	1528.7	P	non-annotated SAGE orf Found forward in NC_001136 between 319
5896_at	683.9	A	non-annotated SAGE orf Found forward in NC_001136 between 541
5897_at	1298	P	non-annotated SAGE orf Found reverse in NC_001136 between 769
5898_at	872.4	P	non-annotated SAGE orf Found reverse in NC_001136 between 104
5899_i_at	1.3	A	non-annotated SAGE orf Found forward in NC_001136 between 130
5900_at	89.4	A	non-annotated SAGE orf Found forward in NC_001136 between 130
5901_at	2563.5	P	non-annotated SAGE orf Found forward in NC_001136 between 192
5902_at	70.1	A	non-annotated SAGE orf Found forward in NC_001136 between 217
5903_at	264.2	A	non-annotated SAGE orf Found forward in NC_001136 between 241
5904_at	8734	P	non-annotated SAGE orf Found forward in NC_001136 between 370
5905_i_at	556.7	P	non-annotated SAGE orf Found forward in NC_001136 between 370
5906_r_at	1172.3	P	non-annotated SAGE orf Found forward in NC_001136 between 370
5907_at	26.2	A	non-annotated SAGE orf Found forward in NC_001136 between 473
5908_at	12488.3	P	non-annotated SAGE orf Found forward in NC_001136 between 509

5909_at	109.8	A	non-annotated SAGE orf Found reverse in NC_001136 between 542
5910_at	2703.9	P	non-annotated SAGE orf Found forward in NC_001136 between 654
5911_at	367.8	P	non-annotated SAGE orf Found reverse in NC_001136 between 683
5912_at	716.4	A	non-annotated SAGE orf Found forward in NC_001136 between 886
5864_at	1069.7	P	non-annotated SAGE orf Found forward in NC_001136 between 930
5865_at	331.8	A	non-annotated SAGE orf Found reverse in NC_001136 between 971
5866_at	1045.7	P	non-annotated SAGE orf Found reverse in NC_001136 between 971
5867_at	1394.2	P	non-annotated SAGE orf Found reverse in NC_001136 between 101
5868_at	902.5	P	non-annotated SAGE orf Found forward in NC_001136 between 102
5869_at	269.1	A	non-annotated SAGE orf Found reverse in NC_001136 between 107
5870_at	68.7	A	non-annotated SAGE orf Found reverse in NC_001136 between 114
5871_at	33	A	non-annotated SAGE orf Found reverse in NC_001136 between 116
5872_at	1792.8	P	non-annotated SAGE orf Found forward in NC_001136 between 122
5873_at	686	P	non-annotated SAGE orf Found reverse in NC_001136 between 127
5874_at	775.6	M	non-annotated SAGE orf Found forward in NC_001136 between 138
5875_s_at	1123.6	A	non-annotated SAGE orf Found forward in NC_001136 between 138
5876_at	9091.4	P	non-annotated SAGE orf Found reverse in NC_001136 between 141
5877_i_at	1515.7	P	non-annotated SAGE orf Found reverse in NC_001136 between 340
5878_r_at	4926.2	A	non-annotated SAGE orf Found reverse in NC_001136 between 340
5879_at	1626.4	P	non-annotated SAGE orf Found forward in NC_001136 between 160
5880_at	798.8	P	non-annotated SAGE orf Found reverse in NC_001136 between 217
5881_at	467.3	A	non-annotated SAGE orf Found forward in NC_001136 between 309
5882_at	697.5	P	non-annotated SAGE orf Found forward in NC_001136 between 681
5883_i_at	166.5	P	non-annotated SAGE orf Found forward in NC_001136 between 871
5884_r_at	50.1	A	non-annotated SAGE orf Found forward in NC_001136 between 871
5885_at	1521.3	P	non-annotated SAGE orf Found forward in NC_001136 between 937
5886_at	945.4	P	non-annotated SAGE orf Found forward in NC_001136 between 102
5841_at	802.6	P	non-annotated SAGE orf Found forward in NC_001136 between 102
5842_at	73.4	A	non-annotated SAGE orf Found reverse in NC_001136 between 104
5843_at	12	A	non-annotated SAGE orf Found forward in NC_001136 between 109
5844_at	41.2	A	non-annotated SAGE orf Found reverse in NC_001136 between 116
5845_at	1288.9	M	non-annotated SAGE orf Found reverse in NC_001136 between 120
5846_at	953.6	P	non-annotated SAGE orf Found forward in NC_001136 between 148
5847_at	32	A	non-annotated SAGE orf Found reverse in NC_001136 between 484
5848_at	14.7	A	non-annotated SAGE orf Found reverse in NC_001136 between 485
5849_at	2180.7	P	non-annotated SAGE orf Found reverse in NC_001136 between 169
5850_at	302.7	P	non-annotated SAGE orf Found forward in NC_001136 between 362
5851_at	425.1	A	non-annotated SAGE orf Found reverse in NC_001136 between 366
5852_at	358.7	A	non-annotated SAGE orf Found reverse in NC_001136 between 369
5853_at	97.2	A	non-annotated SAGE orf Found reverse in NC_001136 between 386
5854_at	1436.1	M	non-annotated SAGE orf Found reverse in NC_001136 between 471
5855_at	124.4	A	non-annotated SAGE orf Found forward in NC_001136 between 542
5856_at	290.4	P	non-annotated SAGE orf Found reverse in NC_001136 between 545
5857_g_at	62.1	A	non-annotated SAGE orf Found reverse in NC_001136 between 545
5858_at	233.9	A	non-annotated SAGE orf Found reverse in NC_001136 between 545
5859_at	85.9	A	non-annotated SAGE orf Found reverse in NC_001136 between 721
5860_g_at	414.3	A	non-annotated SAGE orf Found reverse in NC_001136 between 721
5861_at	1008.3	A	non-annotated SAGE orf Found reverse in NC_001136 between 721
5862_at	511.6	P	non-annotated SAGE orf Found reverse in NC_001136 between 909
5863_at	591.7	P	non-annotated SAGE orf Found reverse in NC_001136 between 118
5817_at	1101.5	M	non-annotated SAGE orf Found reverse in NC_001136 between 125
5818_at	43.2	A	non-annotated SAGE orf Found reverse in NC_001136 between 125

5819_at	3268.1	P	non-annotated SAGE orf Found reverse in NC_001136 between 135
5820_at	648.1	P	non-annotated SAGE orf Found reverse in NC_001136 between 138
5821_at	23.6	A	non-annotated SAGE orf Found reverse in NC_001136 between 139
5822_at	117.5	A	non-annotated SAGE orf Found reverse in NC_001136 between 151
5823_at	698	A	non-annotated SAGE orf Found reverse in NC_001136 between 151
5824_i_at	3.6	A	non-annotated SAGE orf Found forward in NC_001136 between 174
5825_r_at	8.6	A	non-annotated SAGE orf Found forward in NC_001136 between 174
5826_at	1116.7	P	non-annotated SAGE orf Found reverse in NC_001136 between 235
5827_at	37.2	A	non-annotated SAGE orf Found reverse in NC_001136 between 286
5828_at	2956.6	P	non-annotated SAGE orf Found forward in NC_001136 between 371
5829_at	604.4	M	non-annotated SAGE orf Found reverse in NC_001136 between 423
5830_at	266.7	A	non-annotated SAGE orf Found reverse in NC_001136 between 428
5831_at	256.1	A	non-annotated SAGE orf Found reverse in NC_001136 between 463
5832_i_at	248.3	P	non-annotated SAGE orf Found reverse in NC_001136 between 541
5833_r_at	187.1	A	non-annotated SAGE orf Found reverse in NC_001136 between 541
5834_s_at	1027.8	P	non-annotated SAGE orf Found reverse in NC_001136 between 541
5835_i_at	109.9	A	non-annotated SAGE orf Found reverse in NC_001136 between 541
5836_at	17	A	non-annotated SAGE orf Found reverse in NC_001136 between 558
5837_at	66.2	A	non-annotated SAGE orf Found reverse in NC_001136 between 664
5838_at	2979.9	P	non-annotated SAGE orf Found reverse in NC_001136 between 678
5839_at	4094.6	P	non-annotated SAGE orf Found forward in NC_001136 between 733
5840_at	5582.5	P	non-annotated SAGE orf Found reverse in NC_001136 between 792
5792_at	2041.8	P	non-annotated SAGE orf Found reverse in NC_001136 between 812
5793_at	229.3	M	non-annotated SAGE orf Found forward in NC_001136 between 909
5794_i_at	12063.7	P	non-annotated SAGE orf Found forward in NC_001136 between 945
5795_at	136.2	M	non-annotated SAGE orf Found reverse in NC_001136 between 976
5796_at	258.4	A	non-annotated SAGE orf Found forward in NC_001136 between 979
5797_at	51	A	non-annotated SAGE orf Found forward in NC_001136 between 101
5798_at	1671.2	A	non-annotated SAGE orf Found forward in NC_001136 between 101
5799_at	2009.9	P	non-annotated SAGE orf Found forward in NC_001136 between 110
5800_at	8017	P	non-annotated SAGE orf Found reverse in NC_001136 between 123
5801_at	37.2	A	non-annotated SAGE orf Found forward in NC_001136 between 135
5802_at	12.3	A	non-annotated SAGE orf Found forward in NC_001136 between 136
5803_at	683.7	M	non-annotated SAGE orf Found reverse in NC_001136 between 150
5804_at	4130.5	P	snRNA
5805_i_at	6	A	Centromere
5806_i_at	907.4	P	snRNA
5807_at	31466.1	P	snRNA
5808_i_at	49.7	A	questionable ORF
5809_i_at	1170.6	A	similarity to subtelomeric encoded proteins
5810_s_at	5108.4	P	similarity to subtelomeric encoded proteins
5811_at	304.1	A	similarity to YJR108w
5812_at	190	A	hypothetical protein
5813_at	7760.5	P	strong similarity to Aip2p
5814_at	364.2	P	hypothetical protein
5815_at	59	A	weak similarity to YKL083w
5816_at	7731	P	Histone and other Protein Acetyltransferase\; Has sequence homolo
5769_at	1781.7	P	probably multidrug resistance protein
5770_at	1106.4	P	similarity to YBL089w
5771_at	7228.2	P	arginine permease
5772_at	787	P	Non-membrane-embedded, PEST sequence-containing protein
5773_at	1054.9	P	Kinesin-related protein involved in establishment and maintenance o

5774_at	8547.1	P	vacuolar protease B
5775_at	6442.6	P	high copy suppressor of imp1 mutation, may be required for the func
5776_at	1262.4	M	hypothetical protein
5777_at	17336.4	P	Phosphoacetylglucosamine Mutase
5778_at	262.8	M	hypothetical protein
5779_at	4661.9	P	subunit of a cytoplasmic histone acetyltransferase
5780_at	5894.7	P	DNA polymerase V that has motifs typical of DNA polymerase family
5781_i_at	29855.2	P	Ribosomal protein L12A (L15A) (YL23)
5782_at	1192.4	P	glucose-repressible protein
5783_at	7471	P	ATPase family gene
5784_at	6169.5	P	Vacuolar H-ATPase D subunit of the V1 catalytic sector
5785_at	6025.2	P	Mitochondrial ribosomal protein L2 of the large subunit
5786_f_at	1153.1	A	member of the seripauperin protein\/gene family (see Gene_class PA
5787_at	364.3	P	hypothetical protein
5788_at	15556.1	P	strong similarity to Osm1p
5789_at	13255.9	P	Threonine Aldolase
5790_at	1068.8	P	weak similarity to cytochrome c oxidase III of T.brucei kinetoplast
5791_at	2404	P	hypothetical protein
5747_at	8850.5	P	weak similarity to Mad1p
5748_at	17545.7	P	Guanosine diphosphatase of Golgi membrane
5749_at	445.3	A	strong similarity to Utr1p
5750_at	30010	P	weak similarity to Bacillus 1,3-1,4-beta-glucanase
5751_at	604	P	iso-2-cytochrome c
5752_at	6201.6	P	similarity to K.oxytoca enolase-phosphatase E-1
5753_at	17095.5	P	ubiquitin-like protein
5754_at	7969.4	P	Mannan 8\; Protein of the endoplasmic reticulum with a role in retent
5755_at	72.2	A	protein of unknown function
5756_at	21764.5	P	Translation initiation factor eIF-5A
5757_at	677.1	M	weak similarity to Sauroleishmania mitochondrial hypothetical ORF-5
5758_at	5873.2	P	Member of complex that acts at ARS s to initiate replication
5759_at	16431.5	P	P-type ATPase
5760_at	209.7	A	ExtraCellular Mutant
5761_at	1986.7	P	similarity to hypothetical protein YNR027w
5762_at	356	P	hypothetical protein
5763_at	28588.5	P	Vacuolar ATP synthase 17-kDa proteolipid C subunit of VO sector\; c
5764_at	33159.3	P	strong similarity to high mobility group-like protein Nhp2p
5765_at	815.3	P	hypothetical protein
5766_at	26557	P	Rieske iron-sulfur protein of the mitochondrial cytochrome bc1 compl
5767_at	224.6	P	hypothetical protein
5768_at	709.1	P	ARF GTP\/GDP exchange factor
5724_at	439	A	orotidine-5 -phosphate decarboxylase
5725_at	1940.4	P	similarity to O.formigenes oxalyl-CoA decarboxylase
5726_at	315.9	A	Protein involved in DNA repair
5727_at	3253.8	P	weak similarity to Rad50p
5728_i_at	33702.8	P	Proteolipid associated with plasma membrane H(+)-ATPase (Pma1p
5729_f_at	29114.8	P	Proteolipid associated with plasma membrane H(+)-ATPase (Pma1p
5730_at	12362.6	P	hypothetical protein
5731_at	1095.7	P	similarity to human nucleotide pyrophosphatase
5732_at	4805.4	P	weak similarity to Spa2p
5733_at	739.1	P	hypothetical protein
5734_at	3185.6	P	An armadillo repeat-containing protein localized on the vacuolar mem
5735_at	702	P	1,4-glucan-6-(1,4-glucano)-transferase

5736_at	53	A	hypothetical protein
5737_at	23452.4	P	transcriptional activator of amino acid biosynthetic genes
5738_at	61.2	A	hypothetical protein
5739_at	9117.8	P	similarity to S.pombe pac2 protein
5740_at	2278.2	P	similarity to peroxisomal membrane and mitochondrial carrier protein
5741_at	1020.3	P	hypothetical protein
5742_at	1270.3	P	Shows sequence similarity to GOG5, a gene involved in vanadate re
5743_at	4294.3	P	Putative homolog of subunit 2 of bovine prefoldin, a chaperone comp
5744_at	25059.3	P	oligosaccharyl transferase glycoprotein complex, beta subunit
5745_at	25755.4	P	hypothetical protein
5746_at	9393.8	P	Alpha-1,3-mannosyltransferase
5701_at	6429.9	P	weak similarity to chicken microfibril-associated protein
5702_at	21315.2	P	mannose-6-phosphate isomerase
5703_at	17535.8	P	similarity to hypothetical E.coli and C.elegans proteins
5704_at	1402.2	P	similarity to Gda1p
5705_at	14080.6	P	similarity to P.polycephalum myosin-related protein mlpA
5706_at	917.3	P	Required for viability in the absence of the kinesin-related mitotic mo
5707_at	16167	P	putattive ORF identified by SAGE
5708_at	2905.5	P	SEC3 encodes the 144 kD and 91 kD components of the Exocyst co
5709_at	20396.8	P	May coordinate the Ran-dependent (GSP1\/GSP2) association and c
5710_at	4532.6	P	similarity to L.pneumophila dlpA protein
5711_at	2778.2	P	Cold-shock induced protein of the Srp1p\/Tip1p family of serine-alani
5712_at	15032.2	P	22.6 kDa proteasome subunit
5713_at	2017.6	P	helicase-like protein
5714_at	2384.1	P	protoporphyrinogen oxidase
5715_at	193.8	A	Acyl-CoA synthetase (fatty acid activator 2)
5716_at	611.4	P	BInding to Microtubules
5717_at	14274.3	P	ATP-dependent metalloprotease
5718_at	3457.8	P	component of spindle pole
5719_at	9424.3	P	putative neutral sphingomyelinase
5720_at	20390.7	P	homologous to Sbh1p
5721_at	7470.6	P	nucleotide binding regulatory protein
5722_at	6210.3	P	component of the regulatory module of the 26S proteasome, homolo
5723_at	1250.9	P	subunit of RNA polymerase II holoenzyme\/mediator complex
5678_at	14604.5	P	delta 1-pyrroline-5-carboxylate reductase
5679_at	552.4	P	similarity to carnitine O-acetyltransferase Yat1p
5680_at	28301.9	P	gamma subunit of translational initiation factor eIF-2
5681_at	19209.6	P	phosphatidylserine synthase
5682_at	4382.4	P	glucose repression protein
5683_at	908	P	similarity to Mig1p
5684_at	3327.9	P	Associated with U1 snRNP as part of the Sm-core that is common to
5685_at	7432.3	P	similarity to mouse nucleolin
5686_at	9430.6	P	ras-like GTPase, highly homologous to YPT32
5687_at	2093	P	Putative participant in 3 mRNA processing
5688_at	1723.3	P	weak similarity to Nmd2p, Kex1p and hamster nucleolin
5689_at	1847.7	P	hypothetical protein
5690_at	4238.4	P	hypothetical protein
5691_at	29200.6	P	strong similarity to members of the ABC transporter family
5692_at	320.7	A	strong similarity to hypothetical protein YGL224c
5693_at	234.7	A	hypothetical protein
5694_at	661.8	M	Homologous to VRG4
5695_at	744.6	P	positive nitrogen regulatory protein

5696_at	977.6	P	weak similarity to DNA repair protein Rad2p and Dsh1p
5697_at	2539.6	P	responsible for the reduction of methionine sulfoxide
5698_at	16467.1	P	putative S-adenosyl-L-homocysteine hydrolase
5699_at	13499.3	P	hypothetical protein
5700_at	153	A	Required for full sporulation. Dispensable for axial cores but requirec
5655_n_at	3.8	A	Required for full sporulation. Dispensable for axial cores but requirec
5656_at	796.4	P	weak similarity to transcription factor Sko1p
5657_at	819.2	P	hypothetical protein
5658_at	1508.1	P	member of the AAA ATPase family of proteins
5659_at	12339.2	P	Homologous to E. coli DnaJ\; contains leucine zipper-like motif
5660_at	5150.5	P	putative ORF identified by SAGE
5661_at	12320.6	P	strong similarity to hypothetical S.pombe protein YER049W
5662_at	6393.3	P	hypothetical protein
5663_at	454.7	P	similarity to C.elegans hypothetical protein
5664_at	6809.8	P	Aspartate kinase (L-aspartate 4-P-transferase) (EC 2.7.2.4)
5665_at	2615	P	strong similarity to mitochondrial phosphate carrier protein
5666_at	187.4	P	Glc7-interacting protein\; shares homology with PIG2\; contains cons
5667_at	28274.4	P	ATP phosphoribosyltransferase
5668_at	17350.7	P	purine-cytosine permease
5669_g_at	24670.8	P	purine-cytosine permease
5670_i_at	29694.7	P	Ribosomal protein L34A
5671_s_at	23394.4	P	Ribosomal protein L34A
5672_at	22054.2	P	Inhibitor of cell Growth\; heat shock inducible
5673_at	4105.1	P	cytochrome c oxidase assembly factor
5674_at	892.6	P	PHO85 cyclin
5675_at	2285	P	purine-cytosine permease
5676_at	1005.6	P	purine-cytosine permease
5677_at	1808.4	P	Protein homologous to beta-keto-acyl synthase
5633_at	3508.3	P	DL-glycerol-3-phosphatase
5634_at	7135.1	P	Suppressor of the Transcriptional (T) defect of Hpr1 (H) by Overexpr
5635_at	11786.8	P	similarity to hypothetical protein YIL056w
5636_at	1118.9	P	isocitrate lyase
5637_at	891.1	P	strong similarity to cell division control protein Cdc4p
5638_g_at	2389.2	P	strong similarity to cell division control protein Cdc4p
5639_at	469.5	A	hypothetical protein
5640_at	943.5	P	strong similarity to hypothetical protein YIL057c
5641_at	869.7	P	putative zinc finger protein
5642_at	10416.6	P	N-acetyl-gamma-glutamyl-phosphate reductase and acetylglutamate
5643_at	15972.6	P	ribonucleotide reductase
5644_at	1152.5	P	hypothetical protein
5645_at	37162.8	P	Homolog of S. pombe Nrf1 (97\% identical in predicted amino acid s
5646_at	13561	P	aldehyde dehydrogenase (NAD+)
5647_s_at	25789.6	P	40S ribosomal protein S24A
5648_at	1208.3	P	Protein tyrosine phosphatase
5649_at	1741.8	P	similarity to killer toxin Khr1p
5650_at	683.3	P	hypothetical protein
5651_at	1683.4	P	similarity to E.coli X-Pro aminopeptidase II
5652_at	1888.5	P	hypothetical protein
5653_at	6962	P	hypothetical protein
5654_at	1132.1	P	strong similarity to phosphoglycerate dehydrogenases
5610_at	2327.3	P	similarity to M.sexta steroid regulated MNG10 protein
5611_at	22828	P	hypothetical protein

5612_at	1212	P	questionable ORF
5613_at	195.2	A	weak similarity to myosins
5614_at	15757.8	P	threonine deaminase
5615_at	1602.5	P	similarity to E.coli prolyl-tRNA synthetase
5616_at	9688.9	P	homologous to Sbh2p
5617_at	5176.9	P	Derepression Of Telomeric silencing
5618_at	11341.1	P	Protein phosphatase type 2C
5619_at	14817.1	P	anthranilate synthase Component I
5620_at	19891.6	P	vitamin B12-(cobalamin)-independent isozyme of methionine synthas
5621_at	2536.6	P	hypothetical protein
5622_at	1739.8	P	weak similarity to S.epidermidis PepB protein
5623_at	2389.5	P	similarity to hypothetical protein YBL059w
5624_at	2749.9	P	similarity to hypothetical protein YBL059w
5625_at	13812.1	P	20S proteasome subunit (beta3)
5626_at	8461.8	P	RecA homolog\; Rad51p colocalizes to ~65 spots with Dmc1p prior t
5627_at	607.1	P	sporulation-specific homolog of csd4
5628_at	99.1	A	weak similarity to ribosomal S3 proteins
5629_at	434	M	ubiquitin carboxyl-terminal hydrolase
5630_at	3838.6	P	ribose-phosphate pyrophosphokinase 2
5631_at	3892.1	P	ubiquitin-conjugating enzyme
5632_at	1726.3	P	Protein involved in targeting of plasma membrane [H+]ATPase
5588_at	1956.2	P	member of 70 kDa heat shock protein family
5589_at	564.2	P	hypothetical protein
5590_at	11421.1	P	Nucleoporin similar to Nup157p and to mammalian Nup155p
5591_at	337.9	A	hypothetical protein
5592_at	7669.1	P	homologous to S. pombe RAE1 gene\; 2-hybrid analysis demonstrat
5593_at	1862	P	putative transcriptional activator of FLO1
5594_at	330.1	P	putative transcriptional activator of FLO1
5595_at	19016.9	P	Karyopherin beta 4
5596_at	341.1	P	transcription factor
5597_at	2657.5	P	U6 snRNA associated protein
5598_at	3096	P	similarity to Emp70p
5599_at	4903.9	P	Protein which binds Bem1p and contains a proline-rich sequence, ar
5600_at	7059.8	P	sporulation-specific protein
5601_at	1299.6	A	zinc-finger protein
5602_at	2334.9	P	Transmembrane osmosensor
5603_at	2302.4	P	weak similarity to E.herbicola tyrosine permease
5604_at	23.7	A	questionable ORF
5605_at	26253.6	P	Likely to be involved in regulating INO1 expression, suppressor of a
5606_at	539.5	A	hypothetical protein
5607_at	7123	P	Zinc-finger-containing protein with similarity to Gcs1p and Sps18p
5608_at	729.6	P	plasma membrane-bound casein kinase I homolog
5609_at	1557.1	P	weak similarity to Dictyostelium WD40 repeat protein 2
5565_at	8073.7	P	Rsp5p encodes a hect (homologous to E6-AP C terminus) and enco
5566_at	12614	P	weak similarity to E.coli colicin N
5567_at	2918.5	P	Lethal with conditional pap1 allele
5568_at	1534.2	P	hypothetical protein
5569_at	1007.3	M	DNA polymerase alpha suppressing protein kinase
5570_at	2018.3	P	similarity to Msn2p and weak similarity to Msn4p
5571_at	17158.6	P	Ribosomal protein S26B
5572_at	4673.3	P	Paralog of MDS3
5573_at	2033.5	P	protein phosphatase type I

5574_at	12282.7	P	protein phosphatase type I
5575_at	1855.1	P	weak similarity to S.pombe SPBC13G1 and C.elegans F26F2.d hypo
5576_at	94.1	A	hypothetical protein
5577_at	16484.4	P	GDP dissociation inhibitor
5578_at	1146.4	P	weak similarity to Mycoplasma hominis P120 protein
5579_at	400.2	P	similarity to hypothetical protein YDR066c
5580_at	1923.8	P	hypothetical protein
5581_at	22219.1	P	cytochrome oxidase assembly factor
5582_at	1110.5	P	3-methyladenine DNA glycosylase
5583_at	3428.1	P	DNA Damage Inducible
5584_at	3378.6	P	Putative Ubiquitin-specific protease
5585_at	9305.1	P	Iron permease
5586_at	7799.2	P	Sm-like protein
5587_at	3251.6	P	weak similarity to mouse NAD(P)H dehydrogenase (quinone)
5542_at	14685.5	P	TATA-binding protein (tfIId)
5543_at	875.2	P	Protein with coiled-coil domain
5544_at	2554.1	P	strong similarity to putative cell surface glycoprotein Sed1p
5545_at	2216.5	P	Ubiquitin-specific protease
5546_at	14420	P	weak similarity to E.coli hypothetical protein f470
5547_at	750.7	A	translational activator of cytochrome c oxidase subunit III
5548_at	15360.7	P	Required for correct assembly of the cytochrome c oxidase and the
5549_at	7967.1	P	Rho-type GTPase activating protein (GAP)
5550_at	16363	P	similarity to hypothetical C. elegans protein C27H6.5
5551_at	536.6	P	hypothetical protein
5552_at	2097.9	P	weak similarity to Afr1p
5553_at	4324.7	P	Transcriptional regulator which functions in modulating the activity of
5554_at	1914.8	P	non-specific DNA binding protein (sin1)
5555_at	514.8	P	Nucleotide excision repair protein
5556_at	3498.6	P	weak similarity to E.coli cation transport protein
5557_at	1853.3	P	transcriptional regulator
5558_at	23788.7	P	Poly(A) binding protein, cytoplasmic and nuclear
5559_at	5726	P	similarity to ATPase P.falciparum ATPase 2
5560_at	1536.8	P	Serine\/threonine protein kinase
5561_at	1859.3	P	tRNA nucleotidyltransferase (tRNA CCA-pyrophosphorylase)
5562_at	1753.9	P	Repressor of PHR1 transcription\; binds to PHR1 URS
5563_at	1083.2	P	Adenylate kinase (mitochondrial GTP:AMP phosphotransferase)
5564_at	1202.5	P	DNA repair helicase component of transcription factor b
5520_at	1001.9	P	putative ATP-dependent RNA helicase
5521_at	941.6	P	checkpoint protein
5522_at	4008	P	similarity to Legionella glutaredoxin-like protein
5523_at	272.1	M	similarity to hypothetical protein YHR209w
5524_at	3279.4	P	DNA Helicase I
5525_at	26178.6	P	Ribosomal protein L23B (L17aB) (YL32)
5526_at	19520.5	P	alpha subunit of pyruvate dehydrogenase (E1 alpha)
5527_at	69.4	A	meiosis-specific protein related to RecA and Rad51p. Dmc1p coloca
5528_at	400.7	M	meiosis-specific protein related to RecA and Rad51p. Dmc1p coloca
5529_at	1152.6	P	Meiosis-specific protein required for spore formation
5530_at	178.8	M	questionable ORF
5531_at	1571.2	P	hypothetical protein
5532_at	5098.4	P	similarity to human 5,10-methenyltetrahydrofolate synthetase
5533_at	532.2	A	similarity to multidrug resistance proteins Pdr3p and Pdr1p
5534_at	628.6	P	strong similarity to Rtm1p

5535_at	6397.1	P	weak similarity to hypothetical protein YMR316w
5536_at	513.1	P	similarity to killer toxin KHS precursor
5537_at	682.2	P	hypothetical protein
5538_at	4820.1	P	Translocase in inner membrane of mitochondria involved in mitochor
5539_at	490.5	A	hypothetical protein
5540_at	43.9	A	hypothetical protein identified by SAGE
5541_at	340.8	P	questionable ORF
5497_at	843.4	P	questionable ORF
5498_at	58.1	A	questionable ORF
5499_at	364.3	A	questionable ORF
5500_at	231.9	A	questionable ORF
5501_at	62.2	A	questionable ORF
5502_at	1894.3	P	questionable ORF
5503_at	86.2	A	questionable ORF
5504_at	603.1	A	questionable ORF
5505_at	134.9	A	hypothetical protein
5506_s_at	1598.5	P	ubiquitin-conjugating enzyme\; ubiquitin-protein ligase
5507_at	1365.7	P	non-annotated SAGE orf Found forward in NC_001137 between 671
5508_at	42.1	A	non-annotated SAGE orf Found reverse in NC_001137 between 159
5509_at	630.7	P	non-annotated SAGE orf Found reverse in NC_001137 between 187
5510_at	534.3	P	non-annotated SAGE orf Found reverse in NC_001137 between 251
5511_at	571.2	M	non-annotated SAGE orf Found reverse in NC_001137 between 288
5512_at	1013.4	P	non-annotated SAGE orf Found reverse in NC_001137 between 550
5513_at	22.8	A	non-annotated SAGE orf Found reverse in NC_001137 between 900
5514_at	13678.4	P	non-annotated SAGE orf Found reverse in NC_001137 between 314
5515_at	1668.7	P	non-annotated SAGE orf Found reverse in NC_001137 between 642
5516_at	14353.3	P	non-annotated SAGE orf Found reverse in NC_001137 between 673
5517_at	26442.9	P	non-annotated SAGE orf Found reverse in NC_001137 between 122
5518_at	552.6	P	non-annotated SAGE orf Found forward in NC_001137 between 251
5519_at	187.8	P	non-annotated SAGE orf Found reverse in NC_001137 between 258
5473_at	1768.1	P	non-annotated SAGE orf Found reverse in NC_001137 between 308
5474_at	153.2	A	non-annotated SAGE orf Found reverse in NC_001137 between 314
5475_at	1613.4	P	non-annotated SAGE orf Found forward in NC_001137 between 401
5476_at	8767.7	P	non-annotated SAGE orf Found reverse in NC_001137 between 407
5477_at	11779.2	P	non-annotated SAGE orf Found reverse in NC_001137 between 499
5478_i_at	3386.5	P	non-annotated SAGE orf Found reverse in NC_001137 between 561
5479_r_at	1607.9	P	non-annotated SAGE orf Found reverse in NC_001137 between 561
5480_f_at	70.3	A	non-annotated SAGE orf Found reverse in NC_001137 between 561
5481_at	1368.3	A	non-annotated SAGE orf Found reverse in NC_001137 between 848
5482_at	497.4	P	non-annotated SAGE orf Found reverse in NC_001137 between 118
5483_at	9975.3	P	non-annotated SAGE orf Found forward in NC_001137 between 251
5484_at	150.1	A	non-annotated SAGE orf Found forward in NC_001137 between 303
5485_at	428.5	A	non-annotated SAGE orf Found reverse in NC_001137 between 545
5486_at	473.5	P	non-annotated SAGE orf Found reverse in NC_001137 between 156
5487_at	492.4	A	non-annotated SAGE orf Found reverse in NC_001137 between 460
5488_at	83	A	non-annotated SAGE orf Found reverse in NC_001137 between 117
5489_at	382.9	P	non-annotated SAGE orf Found reverse in NC_001137 between 117
5490_at	10.9	A	non-annotated SAGE orf Found reverse in NC_001137 between 135
5491_at	11	A	non-annotated SAGE orf Found reverse in NC_001137 between 137
5492_at	26.4	A	non-annotated SAGE orf Found reverse in NC_001137 between 144
5493_at	113.6	A	non-annotated SAGE orf Found forward in NC_001137 between 167
5494_at	445.1	M	non-annotated SAGE orf Found reverse in NC_001137 between 177

5495_at	165.2	A	non-annotated SAGE orf Found forward in NC_001137 between 194
5496_g_at	871.1	A	non-annotated SAGE orf Found forward in NC_001137 between 194
5449_at	216	A	non-annotated SAGE orf Found reverse in NC_001137 between 225
5450_g_at	148	A	non-annotated SAGE orf Found reverse in NC_001137 between 225
5451_at	0.9	A	non-annotated SAGE orf Found forward in NC_001137 between 249
5452_at	18.2	A	non-annotated SAGE orf Found forward in NC_001137 between 284
5453_at	599.4	A	non-annotated SAGE orf Found forward in NC_001137 between 284
5454_at	1146.6	P	non-annotated SAGE orf Found forward in NC_001137 between 289
5455_at	662.7	P	non-annotated SAGE orf Found reverse in NC_001137 between 311
5456_at	13.6	A	non-annotated SAGE orf Found reverse in NC_001137 between 312
5457_at	387.8	A	non-annotated SAGE orf Found forward in NC_001137 between 382
5458_at	6.1	A	non-annotated SAGE orf Found forward in NC_001137 between 434
5459_at	23	A	non-annotated SAGE orf Found forward in NC_001137 between 434
5460_at	1486.1	P	non-annotated SAGE orf Found reverse in NC_001137 between 467
5461_at	374	A	non-annotated SAGE orf Found reverse in NC_001137 between 504
5462_at	301.3	A	non-annotated SAGE orf Found forward in NC_001137 between 564
5463_r_at	2778.4	P	non-annotated SAGE orf Found reverse in NC_001137 between 523
5464_i_at	11217.9	A	non-annotated SAGE orf Found reverse in NC_001137 between 523
5465_f_at	7775.6	P	non-annotated SAGE orf Found reverse in NC_001137 between 523
5466_i_at	246	A	non-annotated SAGE orf Found reverse in NC_001137 between 523
5467_f_at	17924.5	P	non-annotated SAGE orf Found reverse in NC_001137 between 523
5468_at	211.2	A	non-annotated SAGE orf Found forward in NC_001137 between 774
5469_at	283.2	A	non-annotated SAGE orf Found forward in NC_001137 between 849
5470_at	1577	P	non-annotated SAGE orf Found forward in NC_001137 between 898
5471_at	1658.1	P	non-annotated SAGE orf Found forward in NC_001137 between 122
5472_at	217.5	A	non-annotated SAGE orf Found reverse in NC_001137 between 212
5436_i_at	4.8	A	non-annotated SAGE orf Found reverse in NC_001137 between 212
5437_s_at	26.5	A	non-annotated SAGE orf Found reverse in NC_001137 between 212
5438_at	411.5	A	non-annotated SAGE orf Found reverse in NC_001137 between 250
5439_at	132.8	A	non-annotated SAGE orf Found forward in NC_001137 between 272
5440_at	702.7	P	non-annotated SAGE orf Found forward in NC_001137 between 367
5441_at	2789.6	P	non-annotated SAGE orf Found forward in NC_001137 between 412
5442_at	653.3	A	non-annotated SAGE orf Found forward in NC_001137 between 422
5443_g_at	169.1	A	non-annotated SAGE orf Found forward in NC_001137 between 422
5444_at	856.6	A	non-annotated SAGE orf Found forward in NC_001137 between 422
5445_i_at	5331.8	P	non-annotated SAGE orf Found reverse in NC_001137 between 441
5446_r_at	12.5	A	non-annotated SAGE orf Found reverse in NC_001137 between 441
5447_at	5678.4	P	non-annotated SAGE orf Found forward in NC_001137 between 546
5448_at	5569.3	P	snRNA
5412_at	193	A	snRNA
5413_at	4438.2	P	RNase P RNA
5414_i_at	1	A	Centromere
5415_r_at	1.3	A	Centromere
5416_at	2020.2	P	snRNA R14
5417_at	18107	P	snRNA U4
5418_at	770.5	P	snRNA
5419_at	569.6	P	small cytoplasmic RNA
5420_s_at	1546.6	P	weak similarity to hypothetical E.coli protein
5421_i_at	12.3	A	similarity to mouse period clock protein
5422_s_at	2053.5	A	similarity to mouse period clock protein
5423_s_at	2023.4	P	strong similarity to aryl-alcohol dehydrogenases
5424_at	93.7	A	Hypothetical aryl-alcohol dehydrogenase (AAD)

5425_at	285	A	Amino acid permease
5426_at	915.1	P	similarity to channel proteins
5427_at	610.9	A	dihydroxyacetone kinase
5428_at	109.2	A	strong similarity to Mal63p, YPR196w and Mal13p
5429_at	188.7	A	putative pseudogene
5430_at	750.1	A	ALuminium Resistance 2
5431_at	1313.8	P	weak similarity to Npl6p
5432_at	4272.3	P	47 kDa type I transmembrane protein localized to the Golgi
5433_at	3167.2	P	similarity to S.pombe hypothetical protein SPAC2F7.18c
5434_at	2544.8	P	weak similarity to middle part of C.elegans myosin heavy chain A
5435_at	26265.2	P	phosphomannomutase
5389_at	2816.4	P	weak similarity to human dystrophin
5390_at	5938.2	P	multicopper oxidase, type 1 integral membrane protein
5391_at	43	A	similarity to yeast glucose transport proteins
5392_at	14506.6	P	Actin
5393_at	26082.9	P	Ras-like GTP-binding protein\; most similar to mammalian Rab1A pr
5394_at	25579.9	P	beta-tubulin
5395_at	4606.8	P	mitochondrial RNA polymerase II
5396_at	17063.4	P	Ribosomal protein L22B (L1c) (rp4) (YL31)
5397_at	512.9	P	similarity to hypothetical S. pombe protein and to C.elegans F35D11
5398_at	1223.2	P	Trehalose-associated protein kinase related to S. pombe cek1+
5399_at	5.6	A	questionable ORF
5400_at	570.8	A	similarity to several transaminases
5401_at	1389.9	P	Cyclin-dependent kinase-activating kinase
5402_at	2220.6	P	ABC ATPase
5403_at	1308	P	weak similarity to P.falciparum Pfmdr2 protein
5404_at	128	A	alpha-factor pheromone receptor\; seven-transmembrane domain pr
5405_at	3982.1	P	Negatively regulates COPII vesicle formation
5406_at	795.6	P	Probable chromatin protein because of homology to Drosophila Ena
5407_at	1876.1	P	similarity to repeat structures in a Plasmodium falciparum protein (M
5408_at	20031.1	P	Phenylalanyl-tRNA synthetase, beta subunit, cytoplasmic
5409_at	1359.7	A	transcriptional activator with GATA-1-type Zn finger DNA-binding mo
5410_f_at	2069.5	P	member of the seripauperin protein\/gene family (see Gene_class P
5411_at	152.8	A	hypothetical protein
5367_at	31568.8	P	dihydrolipoamide dehydrogenase precursor (mature protein is the E3
5368_at	4333.2	P	snRNP G protein (the homologue of the human Sm-G)
5369_at	4517.8	P	similarity to hypothetical S. pombe protein and to hypothetical C.eleg
5370_at	3650	P	DnaJ homolog involved in mitochondrial biogenesis and protein foldi
5371_at	538.6	A	weak similarity to YDR504c
5372_at	2463.5	P	12 kDa heat shock protein
5373_at	1379.9	P	weak similarity to Dictyostelium protein kinase
5374_at	25.1	A	questionable ORF
5375_at	141.3	A	hypothetical protein
5376_at	45.1	A	High-affinity hexose transporter
5377_at	572.6	P	Involved in ammonia regulation of GAP1 activity
5378_at	14019.7	P	questionable ORF
5379_at	1587.8	P	beta subunit of large (heterotrimeric) G-proteins (beta-transducin)
5380_at	2747.6	P	omosome segregation protein
5381_at	10682.2	P	weak similarity to Mms19p
5382_at	5007.7	P	hypothetical protein
5383_at	6170.5	P	Ras-like small GTP-binding protein
5384_at	15632.8	P	strong similarity to hypothetical protein YPL019c

5385_at	232.7	P	meiosis specific protein, E.coli MutS protein, localizes to discrete sit
5386_at	6022.5	P	ATP-dependent RNA helicase
5387_at	2961.3	P	Depressed growth-rate protein
5388_at	9005.7	P	weak similarity to rabbit triadin Spp41p
5344_at	5137.2	P	96 kDa nucleoporin-interacting component
5345_at	2723.8	P	hypothetical protein
5346_at	11620.5	P	Similar to S. pombe PAD1 gene product
5347_at	1213	P	similarity to hypothetical A. thaliana proteins
5348_at	8662.1	P	similarity to X-Pro dipeptidases
5349_at	1961.4	P	weak similarity to YER176w
5350_at	410.3	P	weak similarity to human centromere protein E
5351_at	15806.4	P	Member of ATP-binding cassette (ABC) family of proteins
5352_at	17433.5	P	encodes putative deubiquitinating enzyme
5353_at	2995.3	P	ochre suppressor tyr-tRNA
5354_at	647.1	A	similarity to hypothetical protein YOL019w
5355_at	1659.7	P	similarity to YOL017w
5356_at	321.6	P	Calmodulin-dependent protein kinase
5357_at	936.3	P	Glycogen synthase (UDP-gluocse--starch glucosyltransferase)
5358_at	2232.6	P	similarity to mammalian neurofilament proteins and to Dictyostelium
5359_at	602.1	P	hypothetical protein
5360_at	10019	P	similarity to human glutaminyl-peptide cyclotransferase
5361_at	1764.4	P	type II PI(4)P5-kinase (PIP4,5 kinase) similar to human PIP5K-II
5362_at	1797.5	P	hypothetical protein
5363_at	1806.2	P	similarity to hypothetical protein YPL100w
5364_at	273.5	M	similarity to Rod1p
5365_at	90.3	A	poly(A) binding protein\; related to PES4 protein homolog YHR015w
5366_s_at	4417.7	P	similarity to Acanthamoeba myosin heavy chain IC and weak similari
5322_at	2468.1	P	Histidinolphosphatase
5323_at	746.6	A	hypothetical protein
5324_at	619.1	A	hypothetical protein
5325_at	3865.8	P	soluble tyrosine-specific protein phosphatase
5326_at	703.4	P	Regulator of expression of the PTR2, GAP1, and BAP2 genes\; invo
5327_at	1209.7	P	subunit of assimilatory sulfite reductase
5328_at	3790.4	P	nuclear protein related to ScII (chicken), XCAPE (xenopus), and cut
5329_s_at	5544.8	P	Ribosomal protein L2A (L5A) (rp8) (YL6)
5330_at	1432	P	weak similarity to S.pombe polyadenylate-binding protein, YPR112c
5331_at	22548.3	P	Ribosomal protein L29 (YL43)
5332_at	13868.7	P	ubiquinol-cytochrome c oxidoreductase subunit 6 (17 kDa)
5333_at	2261.6	P	myc-type helix-loop-helix transcription factor
5334_at	659	P	hypothetical protein
5335_at	1720.8	P	cell division control protein
5336_at	5182.6	P	Rsc8 is the eighth largest subunit of RSC, a fifteen-protein chromati
5337_at	1383.7	P	strong similarity to mouse lymphocyte specific helicase
5338_at	1938.8	P	similarity to hypothetical protein YGL228w
5339_at	2500.2	P	155 kDa SIT4 protein phosphatase-associated protein
5340_at	854.1	P	weak similarity to dnaJ-like heat shock proteins
5341_at	2783.3	P	hypothetical protein
5342_at	1275	P	hypothetical protein
5343_at	29700.3	P	similarity to hypothetical protein YBR281c
5299_at	1271.6	P	similarity to mitochondrial citrate transport proteins
5300_at	1118.9	P	hypothetical protein
5301_at	9685.3	P	strong similarity to human quinolinate phosphoribosyltransferase

5302_at	1463.3	P	similarity to hypothetical S.pombe protein SPAC12G12.14 and to YD
5303_at	3865.1	P	mitochondrial ribosomal protein (precursor)
5304_at	22077	P	proteasome subunit necessary for peptidyl glutamyl peptide hydrolyzi
5305_at	12506.8	P	Coatomer (COPI) complex delta subunit
5306_at	4510.1	P	cytoplasmic 32 - 34 kDa protein
5307_at	2717.8	P	Hexokinase I (PI) (also called Hexokinase A)
5308_at	256.7	A	hypothetical protein
5309_at	22.5	A	questionable ORF
5310_at	7925.5	P	strong similarity to beta-cystathionases
5311_at	178.3	P	weak similarity to Cha4p
5312_s_at	1351.4	P	hypothetical protein
5313_s_at	3275.4	P	Mob1p-like protein
5314_at	577.4	A	hypothetical protein
5315_at	360.4	A	questionable ORF
5316_at	1117.1	P	questionable ORF
5317_s_at	734.3	P	similarity to hypothetical protein YLR072w
5318_s_at	11161	P	bZIP (basic-leucine zipper) protein
5319_at	4582.2	P	non-annotated SAGE orf Found reverse in NC_001138 between 763
5320_at	181.1	A	non-annotated SAGE orf Found forward in NC_001138 between 101
5321_at	1045.8	P	non-annotated SAGE orf Found forward in NC_001138 between 234
5274_at	1546.9	P	non-annotated SAGE orf Found reverse in NC_001138 between 444
5275_i_at	101.6	A	non-annotated SAGE orf Found reverse in NC_001138 between 101
5276_r_at	25.6	A	non-annotated SAGE orf Found reverse in NC_001138 between 101
5277_at	11127.6	P	non-annotated SAGE orf Found reverse in NC_001138 between 224
5278_at	1827.4	P	non-annotated SAGE orf Found forward in NC_001138 between 226
5279_at	456	A	non-annotated SAGE orf Found reverse in NC_001138 between 184
5280_i_at	11.5	A	non-annotated SAGE orf Found reverse in NC_001138 between 580
5281_f_at	173	A	non-annotated SAGE orf Found reverse in NC_001138 between 580
5282_at	1020.4	A	non-annotated SAGE orf Found reverse in NC_001138 between 480
5283_at	351.5	P	non-annotated SAGE orf Found forward in NC_001138 between 485
5284_at	1017.8	P	non-annotated SAGE orf Found forward in NC_001138 between 487
5285_at	2316.6	P	non-annotated SAGE orf Found reverse in NC_001138 between 111
5286_at	311	P	non-annotated SAGE orf Found forward in NC_001138 between 119
5287_at	704.8	P	non-annotated SAGE orf Found forward in NC_001138 between 184
5288_at	63	A	non-annotated SAGE orf Found forward in NC_001138 between 265
5289_at	492.6	A	non-annotated SAGE orf Found forward in NC_001138 between 279
5290_at	23.3	A	non-annotated SAGE orf Found forward in NC_001138 between 975
5291_at	687.1	P	non-annotated SAGE orf Found forward in NC_001138 between 161
5292_at	694.3	P	non-annotated SAGE orf Found reverse in NC_001138 between 181
5293_g_at	262.1	A	non-annotated SAGE orf Found reverse in NC_001138 between 181
5294_at	370.2	A	ARS605 Found forward in NC_001138 between 135973 and 136029
5295_f_at	2.6	A	ARS607 Found forward in NC_001138 between 199390 and 199446
5296_i_at	322.4	A	ARS608 Found forward in NC_001138 between 216458 and 216508
5297_at	14.7	A	Protein with strong similarity to subtelomerically-encoded proteins in
5298_at	22.5	A	similarity to hypothetical protein YER187w
5251_f_at	2929.4	P	strong similarity to members of the Srp1/Tip1 family
5252_at	277.9	A	GPI-anchored aspartic protease
5253_g_at	538.4	P	GPI-anchored aspartic protease
5254_i_at	45	A	strong similarity to hypothetical protein YOR387c
5255_s_at	211.6	A	strong similarity to hypothetical protein YOR387c
5256_at	2785.6	P	similarity to Mnn1p
5257_at	7695	P	alcohol dehydrogenase isoenzyme IV

5258_at	7049.1	P	high-affinity zinc transport protein
5259_at	2965.7	P	putative transcription factor, has five zinc fingers
5260_at	29792	P	Hexokinase II (PII) (also called Hexokinase B)
5261_at	5113.5	P	Protein involved in interorganelle communication between mitochon
5262_at	438.4	P	C4 zinc finger DNA-binding protein of low sequence specificity in vitr
5263_at	322.2	M	hypothetical protein
5264_at	42.5	A	Required for ZIPpering up meiotic chromosomes during chromoson
5265_at	2390	P	3 ,5 -Cyclic-nucleotide phosphodiesterase, low affinity
5266_at	2912.3	P	similarity to hypothetical protein YHR036w
5267_at	1604.6	P	weak similarity to C.elegans dom-3 protein
5268_at	22143.8	P	strong similarity to glutamine--tRNA ligase
5269_at	1040.4	P	Nuclear protein
5270_at	1665.5	P	tRNA-specific adenosine deaminase 1 (TAD1)\; Tad1p\/scADAT1
5271_at	6193	P	weak similarity to Drosophila ANK protein
5272_at	2074.1	P	similarity to Cse1p
5273_at	755.2	A	Doc1p and Cdc26p are associated with the anaphase-promoting con
5229_at	282.9	M	questionable ORF
5230_at	5330.9	P	Protein required for accurate mitotic chromosome segregation
5231_at	775.9	A	transcriptional activator protein of CYC1
5232_at	2895.8	P	strong similarity to gidA E.coli protein
5233_at	66.2	A	questionable ORF
5234_at	24283.2	P	glycinamide ribotide synthetase and aminoimidazole ribotide syntheta
5235_at	1558.6	P	113kD component of the Exocyst complex, which contains the gene
5236_n_at	1024.5	P	weak similarity to P.falciparum dihydropteroate synthase
5237_at	2089.5	P	weak similarity to P.falciparum dihydropteroate synthase
5238_at	7835.4	P	hypothetical protein
5239_at	152.2	A	hypothetical protein
5240_at	931.8	P	SAP4 is related to SAP155, SAP185, and SAP190, all of which asso
5241_at	8159.9	P	mRNA (identified by a library screen) that causes growth arrest when
5242_at	626.9	P	TOR inhibitor
5243_at	17332.3	P	9.5-kDa zeta subunit of oligosaccharyltransferase complex
5244_at	2063.3	P	similarity to N.crassa cytochrome-c oxidase chain V
5245_at	19967.2	P	May regulate Golgi function and glycosylation in Golgi
5246_at	4537.4	P	strong similarity to hypothetical protein YER037w
5247_at	1787.6	P	weak similarity to Clostridium regulatory protein
5248_at	26	A	hypothetical protein
5249_at	2300.6	P	Ngg1p-interacting factor 3
5250_at	12983.6	P	weak similarity to V.alginolyticus bolA protein
5206_at	1181.6	P	hypothetical protein
5207_at	184.6	A	questionable ORF
5208_at	414.1	A	questionable ORF
5209_at	1314.7	P	Kinesin-related protein
5210_at	2207	P	Cyclin-like protein that interacts with Pho85p in affinity chromatograp
5211_at	51.4	A	questionable ORF
5212_at	5412.4	P	antiviral protein, mRNA is induced early in meiosis
5213_at	540.6	P	hydrophilic protein, heptad repeat motif
5214_at	3486.7	P	similarity to M.jannaschii hypothetical proteins MJ1157 and MJ1478
5215_at	2521.9	P	ras-like GTPase, highly homologous to YPT31
5216_at	5997.3	P	Protein containing zinc fingers very similar to zinc fingers in Mig1p
5217_at	1076.5	P	Member of a family of proteins, including Sip1p and Gal83p, that inte
5218_at	7077.8	P	transcription factor
5219_at	10865.3	P	presumed vesicle coat protein

5220_at	108.1	A	fatty-acyl coenzyme A oxidase
5221_at	3078	P	questionable ORF
5222_at	1124.4	P	carboxypeptidase B-like processing protease
5223_at	29110.4	P	aromatic amino acid aminotransferase
5224_at	1083.5	P	Member of the MCM\/P1 family of proteins involved in DNA replicatio
5225_at	27649.6	P	type I transmemebrane protein, component of COPII-coated, ER-de
5226_at	694	M	questionable ORF
5227_at	13000.5	P	weak similarity to Yip1p
5228_at	2688.4	P	Mck1 Dosage Suppressor 3\; negative regulator of early meiotic gene
5183_at	7360.6	P	hypothetical protein
5184_at	9561.2	P	translational activator of GCN4 through activation of GCN2 in respon
5185_at	424.1	P	Protein with similarity to Hda1p, Rpd3p, Hos1p, and Hos3p
5186_at	2803.8	P	questionable ORF
5187_at	171.5	A	IME4 appears to activate IME1 in response to cell-type and nutritiona
5188_at	15591.6	P	subunit VIa of cytochrome c oxidase, may specifically interact with A
5189_at	983.2	P	Protein phosphatase 2A regulatory subunit B
5190_i_at	1550.1	A	Ribosomal protein S26A
5191_f_at	20149.2	P	Ribosomal protein S26A
5192_at	310.1	P	hypothetical protein
5193_at	14070.1	P	subunit IV of cytochrome c oxidase
5194_at	6112.2	P	similarity to hypothetical protein Fcy21p and weak similarity to FCY2
5195_at	3098.6	P	weak similarity to dehydrogenases
5196_at	1192.6	P	strong similarity to Emericella nidulans cystathionine beta-lyase
5197_at	4.5	A	hypothetical protein
5198_at	121.3	A	questionable ORF
5199_at	1392.5	P	Glycine-threonine-serine repeat protein
5200_at	1112.3	P	Protein kinase
5201_at	1217.7	P	ser/thr protein kinase
5202_at	1495.2	P	questionable ORF
5203_at	13312.9	P	multicopy suppressor of POP2
5204_at	1589.4	P	weak similarity to Oryctolagus calcium channel BIII
5205_at	139.2	A	involved in meiotic recombination and chromosome metabolism
5161_at	1495.6	P	weak similarity to C.elegans hypothetical protein R08D7.1
5162_at	10890.5	P	DNA strand-transfer protein exoribonuclease I\; catalyzes the formati
5163_at	8392.2	P	nuclear pore complex protein with GLFG repetitive sequence motif
5164_at	6082.5	P	Contains domains found in the DEAD protein family of ATP-depende
5165_at	28	A	hypothetical protein
5166_at	786.9	P	Protein involved in translation initiation
5167_at	278.5	A	questionable ORF
5168_at	6556.7	P	Ca++-Pump, ATPase
5169_at	1785.9	P	Activator of transcription
5170_at	897.5	P	questionable ORF
5171_at	2236.5	P	similarity to S.pombe hypothetical protein SPAC31A2.10
5172_at	1267	P	Required for X-ray damage repair, mitotic recombination, and full me
5173_at	1635.8	P	Involved in sterol uptake
5174_at	8656.5	P	hypothetical protein
5175_at	438	P	similarity to hypothetical protein YLR047c and Fre2p
5176_at	1767.8	P	hypothetical protein
5177_at	21.3	A	Serine\/threonine protein kinase
5178_at	5317.1	P	similarity to V.vinifera dihydroflavonol 4-reductase
5179_at	905.5	P	vacuolar alpha mannosidase
5180_at	836.5	P	polypeptide subunit of a yeast type 1 protein geranylgeranyltransfera

5181_at	3346.6	P	aminoadipate-semialdehyde dehydrogenase small subunit (alpha-am
5182_at	292.7	A	questionable ORF
5137_at	3023.4	P	Peroxisomal peripheral membrane protein (peroxin) involved in impo
5138_at	1251.9	P	negative regulator of URS2 of the HO promoter
5139_at	5342.8	P	Shows similarity to the Snf2p family of DNA-dependent ATPases
5140_at	534.8	M	questionable ORF
5141_at	20814.5	P	Chorismate synthase
5142_i_at	8108.1	P	Ribosomal protein L9A (L8A) (rp24) (YL11)
5143_at	394.5	M	hypothetical protein
5144_at	1296	P	transport protein that interacts with Sec20p\; required for protein tran
5145_at	803.3	P	strong similarity to hypothetical protein YDL109c
5146_at	1217.4	P	Mitochondrial polypeptide chain release factor
5147_at	1802.7	P	Most likely an alpha 1,2 mannosyltransferase utilized for the additio
5148_at	2237.8	P	similarity to human human E6-associated protein
5149_at	3091.1	P	weak similarity to Lactobacillus putative histidine protein kinase Sppk
5150_at	1887.2	P	strong similarity to hypothetical protein YPL221w
5151_at	17.9	A	hypothetical protein
5152_at	10103.1	P	encodes beta -subunit of yeast coatomer
5153_at	1121.1	P	weak similarity to E.coli ftsJ protein
5154_at	670.4	P	PHO85 cyclin
5155_at	1158.1	P	similarity to hypothetical protein YPL216w
5156_at	47	A	questionable ORF
5157_at	1235.4	P	weak similarity to S.pombe hypothetical protein C3H1.12C
5158_at	3283.1	P	mRNA guanylyltransferase (mRNA capping enzyme), alpha subunit
5159_at	449.5	P	hypothetical protein
5160_at	1653.2	P	weak similarity to rat cysteine string protein
5115_at	2062.8	P	SOH1 encodes a novel 14-kD protein with limited sequence similarit
5116_at	14028.5	P	required for inositol prototrophy
5117_at	3913.9	P	putative methylenetetrahydrofolate reductase (mthfr)
5118_at	616.6	P	similarity to S.pombe hypothetical protein
5119_at	26948.1	P	Ribosomal protein S2 (S4) (rp12) (YS5)
5120_at	9962.6	P	nuclear polyadenylated RNA binding protein
5121_at	716.3	P	hypothetical protein
5122_at	19498.8	P	pre-mRNA processing factor involved in disassembly of spliceosome
5123_at	1676.9	P	multicopy suppressor of a cytochrome b mRNA translation defect, e
5124_at	274.5	A	questionable ORF
5125_at	844.4	P	hypothetical protein
5126_at	2747	P	beta-transducin homolog
5127_at	4326	P	associates with Snf1p
5128_at	2745	P	weak similarity to H.influenzae permease
5129_at	1778.2	P	weak similarity to YOR165w
5130_at	3522.1	P	TATA-binding protein-associated-factor
5131_at	7398.9	P	hypothetical protein
5132_at	1452.8	P	hypothetical protein
5133_at	174.4	A	questionable ORF
5134_at	922.1	P	weak similarity to hypotetical S.pombe protein
5135_at	2831.4	P	strong similarity to hypothetical protein YBR238c
5136_at	15370.6	P	light chain for myosin Myo2p
5092_at	24763.8	P	Associated with tRNA and amino acyl-tRNA synthetases\; has affinity
5093_at	562.3	P	similarity to glucose transport proteins
5094_at	29536.7	P	Ribosomal protein L28 (L29) (rp44) (YL24)
5095_at	1479.6	P	questionable ORF

5096_at	5177.3	P	strong similarity to hypothetical protein YBR242w
5097_at	3011.9	P	nuclear pore protein, homologous to sec13
5098_at	6599.3	P	similarity to putative human GTP-binding protein MMR1
5099_at	544.3	P	hypothetical protein
5100_at	13924.1	P	pheromone response pathway suppressor
5101_at	846.2	P	similarity to copper homeostasis protein Cup9p
5102_at	1255.6	P	cytosolic and peripheral membrane protein
5103_at	1081.3	P	135-kDa protein that is subunit of poly(A) ribonuclease
5104_at	5207.9	P	component of spindle pole
5105_at	3644.5	P	Nuclear pore complex protein with GLFG motif
5106_at	2047.1	P	35 kDa nucleotide binding protein
5107_at	321.8	P	Ligase Interacting Factor 1\; physically interacts with DNA ligase 4 pr
5108_at	29380.4	P	alpha mating factor
5109_at	4476.4	P	questionable ORF
5110_at	5266.5	P	Similar to ubiquitin conjugating protein family
5111_at	1053.5	P	Coiled-coil protein involved in spindle-assembly checkpoint
5112_at	2426.9	P	weak similarity to Staphylococcus aureus nuclease (SNase)
5113_at	4365	P	strong similarity to hypothetical protein YPL189w
5114_at	936.8	P	suppressor of GTPase mutant
5069_at	8725.6	P	strong similarity to hypothetical protein YPL191c
5070_at	442.7	P	hypothetical protein
5071_at	6070.5	P	strong similarity to C.elegans R07E5.13 protein
5072_at	3035.4	P	hypothetical protein
5073_at	13892.6	P	ATP-dependent RNA helicase CA3 of the DEAD\/DEAH box family
5074_at	8542.5	P	Transporter (permease) for choline and nitrogen mustard\; share hor
5075_i_at	27996.3	P	Ribosomal protein L7A (L6A) (rp11) (YL8)
5076_f_at	22136	P	Ribosomal protein L7A (L6A) (rp11) (YL8)
5077_at	538.6	A	Mitotic Membrane Component
5078_at	10.7	A	questionable ORF
5079_at	4351.1	P	heat shock transcription factor
5080_at	1833.3	P	questionable ORF
5081_at	1943.9	P	Putative transcription factor that binds the consensus site PyPuCAC
5082_at	9735.9	P	RNA polymerase II subunit
5083_at	77.4	A	questionable ORF
5084_at	5104.5	P	probable ribosomal protein L12
5085_at	6305.2	P	weak similarity to H.influenzae hypothetical protein
5086_at	3168.2	P	hypothetical protein
5087_at	3886.1	P	glycosyltransferase
5088_at	1465.6	P	similarity to YLR276c and YKR024c
5089_at	1470.5	P	pseudouridine synthase 2
5090_at	11104.3	P	pyruvate carboxylase
5091_at	264.9	A	Death Upon Overexpression
5047_at	1908.5	P	strong similarity to hypothetical protein YBR216c
5048_at	229.5	A	similarity to rat branched-chain alpha-ketoacid dehydrogenase kinas
5049_at	4949.2	P	ubiquitin conjugating (E2) enzyme, separate domains of Rad6p inter
5050_at	1307.4	P	hypothetical protein
5051_at	5579.4	P	homologue of pombe SDS23\; localizes to spindle pole body
5052_at	28014.7	P	delta-9-fatty acid desaturase
5053_at	9214.5	P	strong similarity to D.melagonaster cni protein
5054_at	1442	P	strong similarity to hypothetical proteins YAR031w, YGL051w, YAR
5055_at	357.3	P	questionable ORF
5056_at	1161.6	P	strong similarity to YAR033w protein

5057_at	2399.6	P	hypothetical protein
5058_at	1392.3	P	mRNA cap-binding protein (eIF-4F), 130K subunit
5059_at	22207	P	ATPase
5060_at	2290.6	P	similarity to hypothetical S. pombe protein
5061_at	317.3	P	hypothetical protein
5062_at	922.3	P	hypothetical protein
5063_at	2141.8	P	component of the cleavage and polyadenylation factor CF I involved
5064_at	2515.3	P	RNA polymerase II elongation factor
5065_at	544.3	P	questionable ORF
5066_at	214.9	A	weak similarity to YJL109c
5067_at	14954	P	delta-aminolevulinate dehydratase (porphobilinogen synthase)
5068_at	7552.2	P	similarity to V. vinifera dihydroflavonol reductase
5024_at	2032.7	P	membrane-bound mannosyltransferase
5025_at	13514.7	P	similarity to E.coli hypothetical 23K protein
5026_at	1453.9	P	Mtf1 Two Hybrid Clone 2
5027_at	797.3	P	C2H2 zinc finger protein which resembles the mammalian Egr and W
5028_at	376.4	A	questionable ORF
5029_at	226.6	A	Meiosis-specific gene required for the pairing of homologous chromo
5030_at	329.5	A	adhesion subunit of a-agglutinin
5031_at	27882.6	P	Ribosomal protein L24A (rp29) (YL21) (L30A)
5032_at	29197.5	P	Large ribosomal subunit protein L30 (L32) (rp73) (YL38)
5033_at	4254.5	P	weak similarity to human chromatin assembly factor I p150 chain
5034_at	6858.5	P	glucanase gene family member
5035_at	5609.9	P	glucosidase I
5036_at	31799.4	P	tryptophan synthetase
5037_at	821.5	P	Probable transcription factor, polyglutamine domain protein
5038_at	1920.4	A	questionable ORF
5039_at	6774	P	weak similarity to Vsp27p
5040_at	14025.1	P	required for protein glycosylation
5041_at	2422.2	P	DNA damage-responsive protein
5042_at	12299	P	hypothetical protein
5043_at	9536.2	P	beta (38kDa) subunit of casein kinase II (CKII)
5044_at	1383.2	P	Homolog of E. coli Hsc20 co-chaperone protein
5045_at	1108.8	P	arginyl-tRNA-protein transferase
5046_at	2991.2	P	pleiotropic drug resistance regulatory protein
5002_at	363.7	P	hypothetical protein
5003_at	5986.7	P	similarity to Drosophila pumilio protein and Mpt5p protein
5004_at	6505.1	P	zinc-finger transcription factor of the Zn(2)-Cys(6) binuclear cluster d
5005_at	26400.6	P	Sterol C-24 reductase
5006_at	13069.4	P	Proteasome subunit YC7alpha\/Y8 (protease yscE subunit 7)
5007_at	2198.8	P	similarity to hypothetical S. pombe protein
5008_at	16343.4	P	isopropylmalate isomerase
5009_at	16329.5	P	plasma membrane H+-ATPase
5010_at	554.6	A	questionable ORF
5011_at	3208.3	P	putative vacuolar Ca2+ ATPase
5012_at	920.6	P	weak similarity to Xenopus kinesin-related protein Eg5
5013_at	1880	P	weak similarity to Tup1p
5014_at	891.5	P	protein required for Clb2 and Ase1 degradation
5015_at	2452.6	P	p24 protein involved in membrane trafficking
5016_at	20342.4	P	putative 3-beta-hydroxysteroid dehydrogenase
5017_at	2671.6	P	similarity to C.elegans hypothetical M142.5 protein
5018_at	3265.2	P	similarity to C.elegans hypothetical M142.5 protein

5019_at	1010.4	P	similarity to hypothetical S. pombe protein
5020_at	1200.9	P	similarity to D.melanogaster lin19 protein
5021_at	1553.6	P	strong similarity to hypothetical protein YLR324w
5022_at	2301.5	P	transcription initiation factor TFIIF middle subunit
5023_at	665.2	A	RNA splicing factor associated with U5 snRNP
4979_at	4349.9	P	choline phosphate cytidylyltransferase (also called phosphoethanola
4980_at	7191.7	P	ATPase stabilizing factor
4981_at	1900.2	P	Putative t-SNARE of the plasma membrane
4982_at	1810.6	P	strong similarity to hypothetical protein YLR328w
4983_g_at	2607	P	strong similarity to hypothetical protein YLR328w
4984_at	1500.8	P	questionable ORF
4985_at	1907.8	P	similarity to E.nidulans cysteine synthase
4986_at	1718.5	P	Associated with U1 snRNP (no counterpart in mammalian U1 snRN
4987_at	9909.7	P	putative integral membrane protein
4988_at	726.3	P	similarity to hypothetical protein YGR031w
4989_at	583.9	P	weak similarity to M.jannaschii hypothetical protein MJ1317
4990_at	2338.9	P	hypothetical protein
4991_at	403.9	P	questionable ORF
4992_at	1518.7	P	gamma-aminobutyrate (GABA) transaminase (4-aminobutyrate amin
4993_at	16328	P	Vacuolar H-ATPase 14 kDa subunit (subunit F) of the catalytic (V1) s
4994_at	1231.8	P	similarity to M.leprae yfcA protein
4995_at	354	A	questionable ORF
4996_at	344	P	acts in concert with Mid2p to transduce cell wall stress signals
4997_at	5079.8	P	weak similarity to Methanobacterium thermoautotrophicum hypotheti
4998_at	615.7	A	questionable ORF
4999_at	9554.9	P	hypothetical protein
5000_i_at	25210.7	P	Ribosomal protein S25A (S31A) (rp45) (YS23)
5001_f_at	24161.7	P	Ribosomal protein S25A (S31A) (rp45) (YS23)
4956_at	2868.6	P	40 kDa putative membrane-spanning ATPase
4957_at	1612.4	P	integral subunit of RNase P and apparent subunit of RNase MRP
4958_at	2627.4	P	similarity to hypothetical protein YGR015c and weak similarity H.influ
4959_at	3375.2	P	catalytic component of 1,3-beta-D-glucan synthase
4960_at	5355.4	P	hypothetical protein
4961_at	534.6	A	hypothetical protein
4962_at	468.6	P	Cwh8p contains 3 short stretches of amino acids that are characteris
4963_at	32766.2	P	Acyl-CoA-binding protein (ACBP)\/Diazepam binding inhibitor (DBI)\/
4964_at	7244.3	P	strong similarity to hypothetical protein YLR350w
4965_at	413.3	P	questionable ORF
4966_at	542.4	P	MAP protein kinase homolog involved in pheromone signal transduct
4967_at	3455.8	P	Among a group of genes whose products are necessary for bud-site
4968_at	904	P	hypothetical protein
4969_at	421.1	P	strong similarity to transaldolase
4970_at	5065.5	P	zinc finger protein\; negative regulator of meiosis\; directly repressed
4971_at	604.1	P	questionable ORF
4972_at	532.5	P	hypothetical protein
4973_at	2645.7	P	transcription factor tau (TFIIIC) subunit 131
4974_at	2439.6	P	ubiquitin fusion degradation protein
4975_at	10206.7	P	Protein that suppresses ts allele of CDC4 when overexpressed
4976_at	2085.4	P	questionable ORF
4977_at	205.8	A	questionable ORF
4978_at	362	A	similarity to ser/thr protein kinases
4934_at	420.9	A	hypothetical protein

4935_at	4726.1	P	similarity to C.elegans E04D5.1 protein
4936_at	10521.6	P	high affinity methionine permease
4937_at	2880.8	P	Member of RSC complex
4938_at	1501.6	P	Required for amino acid permease transport from the Golgi to the ce
4939_at	1229.1	P	similarity to mouse calcium-binding protein
4940_at	143.1	M	a sporulation-specific homologue of the yeast CDC3\/10\/11\/12 famil
4941_at	24539.4	P	C-4 sterol methyl oxidase
4942_at	18903.2	P	5 -phosphoribosylformyl glycinamidine synthetase
4943_at	6421.6	P	Cytochrome OXidase gene 18
4944_at	9058.1	P	Zn-finger protein, transcriptional regulator
4945_at	1257	P	questionable ORF
4946_at	4465.7	P	similarity to P.putida phthalate transporter
4947_at	344	A	similarity to hypothetical protein YBR105c
4948_at	874.6	P	weak similarity to transcription factors
4949_at	2383	P	weak similarity to Rod1p
4950_at	181.5	A	questionable ORF
4951_at	990	A	GDP-GTP Exchange Protein (GEP) for the Rho1p Small GTP-bindin
4952_at	1189.3	P	similarity to hypothetical protein YLR373c
4953_at	1740.6	P	factor stimulating decay of mRNAs containing premature stop codon
4954_at	1141.7	P	questionable ORF
4955_at	1462	P	Homolog of human core snRNP protein D1, involved in snRNA matu
4911_at	680.9	P	RNA splicing factor
4912_at	5752.7	P	Mitochondrial ribosomal protein MRPL25 (YmL25)
4913_at	7948.4	P	peroxisome associated protein containing a PTS1 signal
4914_at	5283.9	P	Polypeptide 3 of a Yeast Non-native Actin Binding Complex, homolo
4915_at	4339.5	P	hypothetical protein
4916_at	9353.9	P	Twinfilin A, an actin monomer sequestering protein
4917_at	1672.6	P	weak similarity to mammalian myosin heavy chain
4918_at	13862.3	P	20 kDa mitochondrial outer membrane protein import receptor
4919_at	2908	P	translation initiation factor eIF2B, 71 kDa (delta) subunit\; translation
4920_at	1976.6	P	35 kDa mitochondrial ribosomal small subunit protein
4921_i_at	33457.5	P	60S ribosomal protein L11B (L16B) (rp39B) (YL22)
4922_at	11137.7	P	strong similarity to hypothetical protein YPL004c
4923_at	91.1	A	Third, minor isozyme of pyruvate decarboxylase
4924_at	356.8	A	cytoplasmic catalase T
4925_at	494.4	P	weak similarity to rat tropomyosin
4926_at	11435.7	P	hypothetical protein
4927_at	1689.4	P	pre-mRNA splicing protein
4928_at	2316.3	P	Serine\/threonine protein kinase
4929_at	4693.7	P	similarity to hypothetical S.pombe protein
4930_at	28023.3	P	mitochondrial and cytoplasmic valyl-tRNA synthetase
4931_at	8601	P	Putative 3 ->5 exoribonuclease\; component of exosome complex o
4932_at	1571.6	P	similarity to bovine Graves disease carrier protein
4933_at	7991	P	transcriptional activator of the SKN7 mediated two-component regu
4888_at	1921.2	P	Esp1 promotes sister chromatid separation by mediating dissociatio
4889_at	1803.2	P	involved in controlling telomere length
4890_at	2085.5	P	Mac1-dependent regulator
4891_at	5416.5	P	weak similarity to B.subtilis YqgP
4892_at	1507.8	P	hypothetical protein
4893_at	1740.3	P	similarity to zebrafish essential for embryonic development gene pes
4894_at	1100	M	subunit of RNA polymerase II holoenzyme\/mediator complex
4895_at	5728.6	P	Protein involved in vacuolar H-ATPase assembly or function

4896_at	19642.7	P	hypothetical protein
4897_at	278.6	A	questionable ORF
4898_at	2833.4	P	G(sub)2-specific B-type cyclin
4899_at	653.7	P	B-type cyclin
4900_at	244.9	P	weak similarity to YLR099c and YDR125c
4901_at	1533.7	P	weak similarity to mosquito carboxylesterase
4902_at	1094.3	P	mitochondrial protein with homology to the mammalian SURF-1 gene
4903_at	443.4	P	Duo1 And Mps1 interacting
4904_at	343.3	A	questionable ORF
4905_g_at	2781.9	P	questionable ORF
4906_at	65.4	A	questionable ORF
4907_at	1252	P	transcriptional regulator, interacts with histones, primarily histone H3
4908_at	3196.4	P	hypothetical protein
4909_f_at	35662.9	P	Ribosomal protein S23A (S28A) (rp37) (YS14)
4910_at	1791.3	P	Contains GLFG repeats in N-terminal half and heptad repeats in C-te
4865_at	2504.6	P	required for ER to golgi vesicle docking
4866_at	2794.9	P	ammonia permease
4867_at	1252.1	P	hypothetical protein
4868_at	3279.5	P	serine\/threonine phosphatase
4869_at	25624.2	P	asparagine synthetase
4870_at	5541.7	P	similarity to S.pombe hypothetical protein SPAC24H6.11c
4871_at	233.2	A	weak similarity to hypothetical protein YPR156c
4872_at	1378	P	weak similarity to mouse T10 protein
4873_at	6259.8	P	hypothetical protein
4874_at	1065.8	P	SYnthetic lethal with cdcForty
4875_at	556.4	P	weak similarity to myosin heavy chain proteins
4876_at	513.7	P	strong similarity to Nce2p
4877_at	3941	P	mitochondrial protein, prohibitin homolog\; similar to S. cerevisiae Ph
4878_at	608.3	A	Member of ubiquitin-conjugating protein family
4879_at	2355.1	P	hypothetical protein
4880_at	12509.3	P	proteasome component Y13
4881_at	16067.2	P	weak similarity to chicken growth factor receptor-binding protein GRE
4882_g_at	4556.7	P	weak similarity to chicken growth factor receptor-binding protein GRE
4883_at	1483.1	P	questionable ORF
4884_i_at	14430.9	P	similarity to multidrug resistance proteins
4885_at	54.3	A	questionable ORF
4886_at	689.4	P	110 kDa subunit of the centromere binding factor CBF3
4887_at	1587.2	P	strong similarity to hypothetical protein YPR157w
4842_at	3095.1	P	similarity to hypothetical protein YPR158w
4843_at	8345.3	P	encodes a predicted type II membrane protein highly homologous to
4844_at	743.5	P	component of the biosynthetic pathway producing the thiazole precur
4845_at	4424.1	P	similarity to C.elegans hypothetical protein
4846_at	4733.3	P	hypothetical protein
4847_at	3590.9	P	N alpha-acetyltransferase that acts on methionine termini
4848_at	7774.2	P	Ribosomal protein L24B (rp29) (YL21) (L30B)
4849_at	2051	P	hypothetical protein
4850_at	821.9	P	hypothetical protein
4851_i_at	13972.4	P	questionable ORF
4852_s_at	3337.9	P	questionable ORF
4853_at	1190.5	P	GTP-binding protein of the ras superfamily involved in bud site select
4854_at	193.3	A	hypothetical protein
4855_at	483	P	strong similarity to hypothetical proteins YKR076w and YMR251w

4856_at	29040.9	P	Cystathionine beta-synthase
4857_at	1426.9	P	hypothetical protein
4858_at	5933.6	P	Phosphatidyl-ethanolamine N-methyltransferase
4859_at	2616	P	involved in mRNA transport
4860_at	21731.1	P	nuclear localization sequence binding protein
4861_at	547	A	questionable ORF
4862_at	1262.7	P	hypothetical protein
4863_at	6156.5	P	mRNA cap-binding protein (eIF-4F), 150K subunit , highly homologo
4864_at	1867.5	P	GTP-binding protein
4819_at	10.5	A	questionable ORF
4820_at	2853.3	P	hypothetical protein
4821_at	2200.8	P	Involved in biosynthetic pathway for cell wall beta-glucans
4822_at	8060.1	P	Clathrin light chain
4823_at	940.4	P	hypothetical protein
4824_at	3521.6	P	similarity to Rib2p
4825_at	1196.8	P	phosphatidylserine decarboxylase located in vacuole or Golgi
4826_at	2654.2	P	mitochondrial methionyl-tRNA synthetase
4827_at	3765.9	P	Golgi membrane protein
4828_at	8351.1	P	strong similarity to human GTP-binding protein
4829_at	895.8	P	Essential for the expression and activity of ubiquinol-cytochrome c re
4830_at	15990	P	Squalene monooxygenase
4831_at	73.2	A	questionable ORF
4832_at	6196.5	P	Alcohol acetyltransferase
4833_at	11690	P	Poly(A)-binding protein binding protein
4834_at	1521.1	P	hypothetical protein
4835_at	26413.3	P	Ribonucleotide Reductase
4836_at	15757.2	P	similarity to YHR004c-a
4837_at	2689.4	P	questionable ORF
4838_at	11999.9	P	7.3 kDa subunit 9 of the ubiquinol cytochrome c oxidoreductase com
4839_at	4380.6	P	Ubiquitin-protein ligase
4840_at	13779.4	P	tyrosyl-tRNA synthetase, cytoplasmic
4841_at	3143.2	P	Transcription factor TFIIF large subunit
4797_at	11866.3	P	HMG1\/2 homolog
4798_at	319.5	A	Serine\/threonine protein kinase required for cell cycle arrest in resp
4799_at	15119.3	P	similarity to Aspergillus fumigatus rAsp
4800_at	214.5	A	questionable ORF
4801_at	6601.9	P	histidine permease
4802_i_at	925.1	A	Glyceraldehyde-3-phosphate dehydrogenase 3
4803_at	3670.4	P	Protein X component of mitochondrial pyruvate dehydrogenase com
4804_at	1284.4	P	xylulokinase
4805_at	7334.8	P	homolog of RNAse PH
4806_at	852.1	P	weak similarity to Tetrahymena acidic repetitive protein arp1
4807_at	6222.8	P	involved in nitrosoguanidine resistance
4808_at	5286.9	P	hypothetical protein
4809_at	5758.5	P	dolichyl phosphate-D-mannose:protein O-D-mannosyltransferase
4810_at	1621.1	P	weak similarity to rape guanine nucleotide regulatory protein
4811_at	1739.6	P	strong similarity to translation elongation factor eEF1 alpha chain Ca
4812_at	1959.9	P	phosphorylcholine transferase\; or cholinephosphate cytidylyltransfer
4813_at	4313.7	P	weak similarity to X.laevis protein-tyrosin-phosphatase cdc homolog
4814_at	28891.9	P	encodes the cytoplasmic trifunctional enzyme C1-tetrahydrofolate sy
4815_at	608.4	P	similarity to S.pombe hypothetical protein D89234
4816_at	2724.9	P	similarity to Xenopus transcription factor Oct-1.17

4817_at	1370.5	P	electron-transferring flavoprotein, beta chain
4818_at	6871.9	P	phosphoserine phosphatase
4774_at	13944.9	P	thioredoxin
4775_at	7302.7	P	similarity to M.jannaschii GTP-binding protein and to M.capricolum hy
4776_at	6094.6	P	zinc finger protein
4777_at	284.2	P	weak similarity to S.pombe hypothetical protein SPAC18B11.03c
4778_at	549.3	P	involved in 7-aminocholesterol resistance
4779_f_at	29615.8	P	Ribosomal protein S0A
4780_at	28515.8	P	Ribosomal protein S0A
4781_at	1883.8	P	strong similarity to hypothetical S. pombe protein
4782_at	1911.4	P	Participates in synthesis of N-acetylglucoaminylphosphatidylinositol,
4783_at	1648.6	P	putative calcium channel
4784_at	845.9	P	omosome region maintenance protein
4785_at	551	P	questionable ORF
4786_at	6104.4	P	Mitochondrial ribosomal protein MRPL9 (YmL9) (E. coli L3) (human
4787_at	981.3	P	similarity to hypothetical protein YHR149c
4788_at	3350.7	P	translational activator of cytochrome c oxidase subunit III
4789_at	1433.1	P	weak similarity to hypothetical protein YFR021w
4790_at	705.3	P	strong similarity to drug resistance protein SGE1
4791_at	167.6	A	weak similarity to human p55CDC and Cdc20p
4792_at	42.8	A	hypothetical protein
4793_at	5558.3	P	De-repression of ITR1 Expression
4794_at	1175.1	P	questionable ORF
4795_at	2799.9	P	57 kDa nuclear protein
4796_at	603.4	P	questionable ORF
4751_at	13192.7	P	mitochondrial protein, prohibitin homolog\; homolog of mammalian
4752_at	7452.6	P	possible homolog of human 26S proteasome regulatory subunit p28
4753_at	12362.2	P	Positive regulatory protein of phosphate pathway
4754_at	31561.9	P	Flavohemoglobin
4755_at	7438.2	P	hypothetical protein
4756_at	252.7	A	questionable ORF
4757_at	895.8	P	weak similarity to YOR019w
4758_at	1243.8	P	protein containing kelch repeats, similar to YHR158c and YPL263c
4759_at	1221.1	P	weak similarity to hypothetical protein YHR160c
4760_at	23709.9	P	phosphofructokinase alpha subunit
4761_at	2460.8	P	Yeast Assembly Polypeptide, member of AP180 protein family, bind
4762_at	325.2	A	questionable ORF
4763_at	497.3	A	strong similarity to hypothetical protein YHR162w
4764_at	6192.9	P	Succinate-CoA Ligase (ADP-Forming)
4765_at	7194.2	P	similarity to hypothetical S.pombe protein
4766_at	3599.3	P	RNA polymerase III transcription factor with homology to TFIIB
4767_at	603.9	A	hypothetical protein
4768_at	1890.8	P	similar to SOL3
4769_at	437.9	P	Mga1p shows similarity to heat shock transcription factor
4770_at	1339.8	P	weak similarity to human cleavage stimulation factor 64K chain
4771_at	3205.4	P	hypothetical protein
4772_at	1857.8	P	histone acetyltransferase
4773_at	11686.7	P	Proteasome subunit
4729_i_at	24070.1	P	enolase I
4730_s_at	18171.6	P	enolase I
4731_at	4029.2	P	COQ6 monooxygenase
4732_at	792.2	A	6-phosphogluconate dehydrogenase

4733_at	4851.7	P	similarity to C.elegans C16C10.1
4734_at	1700.3	P	homolog of xeroderma pigmentosum group G (XPG) protein, copufu
4735_at	647.6	M	questionable ORF
4736_at	28312.8	P	similarity to allantoate transport protein
4737_at	5447.8	P	putative beta adaptin component of the membrane-associate clathrin
4738_at	2369.7	P	ser/thr protein kinase
4739_at	1420	P	weak similarity to E.coli lipase like enzyme
4740_at	27617.1	P	methionyl tRNA synthetase
4741_at	277.8	A	questionable ORF
4742_at	3267.2	P	hypothetical protein
4743_at	7225.6	P	GTP-cyclohydrolase I
4744_at	3151.4	P	weak similarity to S.pombe hypothetical protein SPAC17A5
4745_at	310.3	A	questionable ORF
4746_at	2134	P	Member of CDC48\/PAS1\/SEC18 family of ATPases
4747_at	887.4	P	strong similarity to S.pombe RNA helicase
4748_at	4379.3	P	similarity to hypothetical S.pombe protein SPAC12G12.02
4749_at	55.8	A	similarity to hypothetical protein YMR295c
4750_at	4446.1	P	Component of the TAFII complex required for activated transcription
4705_at	5069.9	P	hypothetical protein
4706_at	6806	P	ribonuclease H
4707_at	6896	P	similarity to hypothetical S.pombe protein
4708_at	823.9	P	similarity to C.elegans LET-858
4709_at	27553.5	P	glucanase gene family member
4710_at	17497.6	P	weak similarity to Cbf5p
4711_at	4001.3	P	ABC transporter
4712_at	31812.3	P	Cell wall endo-beta-1,3-glucanase
4713_at	5325.3	P	similarity to hypothetical protein YMR310c
4714_at	9594.6	P	similarity to mouse Surf-4 protein
4715_at	29558.4	P	Zuotin, putative Z-DNA binding protein
4716_at	7856.8	P	Biotin synthase
4717_at	260.6	P	strong similarity to maltase
4718_at	511	P	maltose pathway regulatory protein
4719_at	752.7	P	alpha-glucoside transporter
4720_at	597.3	A	hypothetical protein
4721_at	52.2	A	hypothetical protein
4722_s_at	545.7	P	strong similarity to hypothetical protein YBR300c
4723_f_at	1717.9	P	strong similarity to members of the Srp1p/Tip1p family
4724_i_at	10248.2	P	hypothetical protein
4725_f_at	93.5	A	hypothetical protein
4726_at	158.7	A	identified by SAGE
4727_s_at	6090.8	P	Protein essential for mitochondrial biogenesis and cell viability
4728_at	268.9	A	non-annotated SAGE orf Found reverse in NC_001139 between 110
4681_at	1701.5	P	non-annotated SAGE orf Found reverse in NC_001139 between 323
4682_at	13248.7	P	non-annotated SAGE orf Found reverse in NC_001139 between 836
4683_at	3824.6	P	non-annotated SAGE orf Found reverse in NC_001139 between 836
4684_at	1488.2	P	non-annotated SAGE orf Found reverse in NC_001139 between 904
4685_at	4572.6	P	non-annotated SAGE orf Found reverse in NC_001139 between 905
4686_s_at	3167.4	P	non-annotated SAGE orf Found reverse in NC_001139 between 939
4687_at	1450.9	P	non-annotated SAGE orf Found reverse in NC_001139 between 225
4688_at	23.9	A	non-annotated SAGE orf Found forward in NC_001139 between 323
4689_at	913.4	P	non-annotated SAGE orf Found reverse in NC_001139 between 324
4690_at	394.1	P	non-annotated SAGE orf Found forward in NC_001139 between 363

4691_at	36.7	A	non-annotated SAGE orf Found forward in NC_001139 between 437
4692_f_at	389.5	P	non-annotated SAGE orf Found reverse in NC_001139 between 536
4693_i_at	93.3	A	non-annotated SAGE orf Found reverse in NC_001139 between 931
4694_at	401.8	A	non-annotated SAGE orf Found reverse in NC_001139 between 974
4695_at	1100.2	A	non-annotated SAGE orf Found forward in NC_001139 between 299
4696_at	19098.3	P	non-annotated SAGE orf Found forward in NC_001139 between 312
4697_at	1642.7	P	non-annotated SAGE orf Found forward in NC_001139 between 326
4698_at	3796.7	P	non-annotated SAGE orf Found reverse in NC_001139 between 366
4699_at	1043.3	P	non-annotated SAGE orf Found forward in NC_001139 between 393
4700_at	894.6	M	non-annotated SAGE orf Found forward in NC_001139 between 400
4701_at	13415.2	P	non-annotated SAGE orf Found reverse in NC_001139 between 554
4702_at	4120.3	P	non-annotated SAGE orf Found forward in NC_001139 between 669
4703_at	245.3	A	non-annotated SAGE orf Found forward in NC_001139 between 670
4704_at	531.1	P	non-annotated SAGE orf Found reverse in NC_001139 between 736
4658_at	2105.5	P	non-annotated SAGE orf Found forward in NC_001139 between 772
4659_at	1497.3	P	non-annotated SAGE orf Found forward in NC_001139 between 777
4660_i_at	580.5	M	non-annotated SAGE orf Found forward in NC_001139 between 783
4661_r_at	6.8	A	non-annotated SAGE orf Found forward in NC_001139 between 783
4662_at	19154.8	P	non-annotated SAGE orf Found forward in NC_001139 between 827
4663_at	3389	P	non-annotated SAGE orf Found forward in NC_001139 between 836
4664_at	623.8	P	non-annotated SAGE orf Found reverse in NC_001139 between 853
4665_at	14.5	A	non-annotated SAGE orf Found reverse in NC_001139 between 949
4666_r_at	4710	P	non-annotated SAGE orf Found reverse in NC_001139 between 970
4667_at	198.4	P	non-annotated SAGE orf Found forward in NC_001139 between 973
4668_at	260.6	A	non-annotated SAGE orf Found forward in NC_001139 between 974
4669_i_at	49.6	A	non-annotated SAGE orf Found reverse in NC_001139 between 103
4670_f_at	20687.5	P	non-annotated SAGE orf Found reverse in NC_001139 between 103
4671_at	1139.5	P	non-annotated SAGE orf Found reverse in NC_001139 between 103
4672_at	16.9	A	non-annotated SAGE orf Found forward in NC_001139 between 110
4673_at	483	P	non-annotated SAGE orf Found reverse in NC_001139 between 255
4674_at	329.1	P	non-annotated SAGE orf Found forward in NC_001139 between 255
4675_at	1320.8	A	non-annotated SAGE orf Found forward in NC_001139 between 384
4676_at	53.3	A	non-annotated SAGE orf Found reverse in NC_001139 between 394
4677_at	17.9	A	non-annotated SAGE orf Found forward in NC_001139 between 773
4678_at	25	A	non-annotated SAGE orf Found forward in NC_001139 between 106
4679_at	221.1	A	non-annotated SAGE orf Found forward in NC_001139 between 108
4680_at	32.6	A	non-annotated SAGE orf Found reverse in NC_001139 between 101
4631_at	209.1	A	non-annotated SAGE orf Found reverse in NC_001139 between 745
4632_g_at	53.8	A	non-annotated SAGE orf Found reverse in NC_001139 between 745
4633_at	911.1	A	non-annotated SAGE orf Found reverse in NC_001139 between 746
4634_at	641.5	A	non-annotated SAGE orf Found reverse in NC_001139 between 933
4635_g_at	1378.4	A	non-annotated SAGE orf Found reverse in NC_001139 between 933
4636_i_at	100.9	A	non-annotated SAGE orf Found reverse in NC_001139 between 934
4637_r_at	72.7	A	non-annotated SAGE orf Found reverse in NC_001139 between 934
4638_i_at	21.6	A	non-annotated SAGE orf Found reverse in NC_001139 between 148
4639_f_at	245.2	A	non-annotated SAGE orf Found reverse in NC_001139 between 148
4640_at	518.3	P	non-annotated SAGE orf Found forward in NC_001139 between 319
4641_s_at	698.5	P	non-annotated SAGE orf Found forward in NC_001139 between 319
4642_i_at	4.1	A	non-annotated SAGE orf Found reverse in NC_001139 between 401
4643_f_at	24.1	A	non-annotated SAGE orf Found reverse in NC_001139 between 401
4644_i_at	136	A	non-annotated SAGE orf Found forward in NC_001139 between 405
4645_at	121.8	A	non-annotated SAGE orf Found reverse in NC_001139 between 544

4646_at	142.6	A	non-annotated SAGE orf Found forward in NC_001139 between 619
4647_at	246.2	A	non-annotated SAGE orf Found forward in NC_001139 between 700
4648_i_at	6	A	non-annotated SAGE orf Found reverse in NC_001139 between 701
4649_r_at	301.1	M	non-annotated SAGE orf Found reverse in NC_001139 between 701
4650_f_at	98.5	A	non-annotated SAGE orf Found reverse in NC_001139 between 701
4651_at	1733.5	P	non-annotated SAGE orf Found reverse in NC_001139 between 707
4652_at	2979.1	P	non-annotated SAGE orf Found reverse in NC_001139 between 707
4653_at	999.4	P	non-annotated SAGE orf Found reverse in NC_001139 between 708
4654_at	41.8	A	non-annotated SAGE orf Found reverse in NC_001139 between 711
4655_at	80.7	A	non-annotated SAGE orf Found reverse in NC_001139 between 801
4656_f_at	56.9	A	non-annotated SAGE orf Found forward in NC_001139 between 818
4657_at	212.2	P	non-annotated SAGE orf Found reverse in NC_001139 between 823
4608_g_at	523.7	A	non-annotated SAGE orf Found reverse in NC_001139 between 823
4609_at	491.7	A	non-annotated SAGE orf Found reverse in NC_001139 between 919
4610_at	454.8	A	non-annotated SAGE orf Found reverse in NC_001139 between 994
4611_at	31.6	A	non-annotated SAGE orf Found reverse in NC_001139 between 994
4612_at	12.9	A	non-annotated SAGE orf Found reverse in NC_001139 between 994
4613_at	1487.3	P	non-annotated SAGE orf Found forward in NC_001139 between 233
4614_at	1065.1	P	non-annotated SAGE orf Found reverse in NC_001139 between 525
4615_at	1222.5	P	non-annotated SAGE orf Found forward in NC_001139 between 944
4616_at	786.9	P	non-annotated SAGE orf Found forward in NC_001139 between 129
4617_at	2936.7	P	non-annotated SAGE orf Found reverse in NC_001139 between 139
4618_at	1798.3	P	non-annotated SAGE orf Found reverse in NC_001139 between 163
4619_at	615	P	non-annotated SAGE orf Found reverse in NC_001139 between 199
4620_at	999.3	A	non-annotated SAGE orf Found reverse in NC_001139 between 249
4621_at	1190.5	P	non-annotated SAGE orf Found forward in NC_001139 between 274
4622_at	3564.6	P	non-annotated SAGE orf Found forward in NC_001139 between 318
4623_at	9589.1	P	non-annotated SAGE orf Found reverse in NC_001139 between 474
4624_at	518.4	P	non-annotated SAGE orf Found forward in NC_001139 between 512
4625_at	21464.7	P	non-annotated SAGE orf Found reverse in NC_001139 between 533
4626_at	4386.1	P	non-annotated SAGE orf Found forward in NC_001139 between 576
4627_at	2986.9	P	non-annotated SAGE orf Found reverse in NC_001139 between 604
4628_at	526.2	P	non-annotated SAGE orf Found forward in NC_001139 between 682
4629_at	258.3	P	non-annotated SAGE orf Found reverse in NC_001139 between 727
4630_at	2791.4	P	non-annotated SAGE orf Found forward in NC_001139 between 733
4585_at	1450.8	P	non-annotated SAGE orf Found forward in NC_001139 between 757
4586_at	266.5	P	non-annotated SAGE orf Found forward in NC_001139 between 787
4587_at	448.7	A	non-annotated SAGE orf Found forward in NC_001139 between 788
4588_at	247.5	P	non-annotated SAGE orf Found forward in NC_001139 between 810
4589_g_at	590.8	P	non-annotated SAGE orf Found forward in NC_001139 between 810
4590_at	1069	P	non-annotated SAGE orf Found forward in NC_001139 between 810
4591_at	3454.6	P	non-annotated SAGE orf Found forward in NC_001139 between 810
4592_at	44.5	A	non-annotated SAGE orf Found forward in NC_001139 between 867
4593_at	111.3	A	non-annotated SAGE orf Found reverse in NC_001139 between 878
4594_at	93.5	A	non-annotated SAGE orf Found forward in NC_001139 between 965
4595_at	509.7	A	non-annotated SAGE orf Found reverse in NC_001139 between 974
4596_at	20.1	A	non-annotated SAGE orf Found forward in NC_001139 between 100
4597_at	724.9	P	non-annotated SAGE orf Found forward in NC_001139 between 101
4598_g_at	484.5	A	non-annotated SAGE orf Found forward in NC_001139 between 101
4599_i_at	539.8	A	non-annotated SAGE orf Found forward in NC_001139 between 101
4600_at	1999.2	P	non-annotated SAGE orf Found forward in NC_001139 between 101
4601_at	1014.6	P	non-annotated SAGE orf Found forward in NC_001139 between 105

4602_at	4893.9	P	non-annotated SAGE orf Found reverse in NC_001139 between 105
4603_at	2342.4	P	snRNA
4604_i_at	1203	P	snRNA
4605_s_at	2195.2	P	snRNA
4606_at	1376	P	snRNA
4607_at	2723.4	P	snRNA
4561_s_at	800.8	P	snRNA
4562_at	273.8	A	similarity to C.carbonum toxin pump
4563_f_at	5416.4	P	strong similarity to members of the Srp1p/Tip1p family
4564_at	172.2	M	similarity to subtelomeric encoded proteins
4565_at	228.4	A	ExtraCellular Mutant
4566_at	195.8	A	similarity to subtelomeric encoded proteins
4567_at	563.1	A	weak similarity to Drosophila hypothetical protein 6
4568_at	3136	P	similarity to C.carbonum toxin pump
4569_at	2945.2	P	weak similarity to YPL208w
4570_at	258.5	P	Cytochrome B pre-mRNA processing protein
4571_at	432.4	A	hypothetical protein
4572_at	1204.1	P	very low affinity methionine permease
4573_at	1268.6	P	ABC transporter
4574_at	22123.1	P	Single-strand nucleic acid binding protein
4575_i_at	31999	P	Ribosomal protein L8A (rp6) (YL5) (L4A)
4576_at	1678	P	glyerol kinase (converts glycerol to glycerol-3-phosphate
4577_at	5431.7	P	SNARE protein with a C-terminal membrane anchor
4578_at	1391.5	P	ExtraCellular Mutant
4579_at	7706.3	P	hypothetical protein
4580_at	2684.6	P	Putative integral membrane protein containing novel cysteine motif.
4581_at	20721.3	P	Meiotic regulatory protein\; Cys-His zinc fingers
4582_at	3324.1	P	hypothetical protein
4583_at	3989.2	P	transcriptional regulator
4584_at	523.6	P	RNA binding domain (N-term) with asparagine rich region?
4539_at	972.1	P	hypothetical protein
4540_at	35.3	A	Encodes one of the earliest meiosis-specific recombination functions
4541_at	1517.1	P	weak similarity to Pseudomonas gamma-butyrobetaine hydroxylase
4542_at	6852.2	P	negative regulator of phospholipid biosynthesis
4543_at	1015.5	P	Similiar to clathrin coat proteins
4544_at	170	M	Dimerization cofactor of homeodomian protein NF1-alpha
4545_at	2571.3	P	Probable transmembrane protein PTM1
4546_at	1300.1	P	Urea transporter
4547_at	33550.6	P	Ribosomal protein S20
4548_at	460.2	A	GTP-binding protein and glycogen phosphorylase (weak)
4549_at	4523.7	P	similarity to C.elegans hypothetical protein F21D5.2
4550_at	14.3	A	UDP Glucose pyrophosphorylase
4551_at	14170.3	P	ribose-phosphate pyrophosphokinase 3
4552_at	176.5	A	similarity to C.elegans hypothetical protein
4553_at	361	P	bZip DNA binding proteins
4554_at	6055.2	P	Potential formate transporter nirC
4555_at	3444.3	P	serine\/threonine protein kinase
4556_at	1330.8	P	hypothetical protein
4557_at	33.5	A	hypothetical protein
4558_at	2267.3	P	mitochondrial ribosomal protein, homologous to E. coli ribosomal pro
4559_at	2305.4	P	YKL008c
4560_at	3702.2	P	SH3 domain

4515_i_at	22718.7	A	Ribosomal protein L14B
4516_f_at	21629.2	P	Ribosomal protein L14B
4517_at	5929.6	P	60kD chaperonin (weak)
4518_at	11132.9	P	8.5 kDa subunit of the ubiqunol-cytochrome c oxidoreductase comple
4519_at	1237.8	P	Mitochondrial carrier protein\/Grave s disease carrier protein
4520_at	5608.7	P	thiF, moeB, ubiquitin activating enzyme (all weak)
4521_at	958.5	P	similarity to YLL010c, YLR019w
4522_at	2986.5	P	alpha subunit of G protein coupled to mating factor receptors
4523_at	20371.3	P	May act cooperatively with Mrs5p in mitochondrial protein import or o
4524_at	2076.2	P	Zinc finger (Cys(2)-His(2))
4525_at	34584.8	P	cytochrome P450 lanosterol 14a-demethylase
4526_at	7558.9	P	Manganese-containing superoxide dismutase
4527_at	6676.8	P	similarity to S.pombe hypothetical protein
4528_i_at	19774.8	P	Ribosomal protein L27A
4529_f_at	16413.6	P	Ribosomal protein L27A
4530_at	647.6	P	Seryl-tRNA synthetase
4531_at	2252.6	P	Vacuolar protein sorting
4532_at	7249.5	P	subunit of the major N alpha-acetyltransferase, complexes with the
4533_at	110.2	A	Encodes a 33.4 kDa basic protein that localizes to the nucleus. Thou
4534_at	1371.4	M	PolyA-binding protein
4535_at	1009.2	P	SH3 domain in C-terminus
4536_at	1741.1	P	strong similarity to S.douglasii YSD83
4537_at	7843	P	argininosuccinate lyase
4538_at	29178.3	P	Asparaginyl-tRNA synthetase
4493_at	26134.7	P	Aminoacyl tRNA-synthetase
4494_at	24121.8	P	40S Ribosomal protein S27B (rp61) (YS20)
4495_at	84.9	A	ExtraCellular Mutant
4496_at	272.4	P	RAS-related protein
4497_at	1033.7	P	Class II Myosin
4498_at	3147	P	53 kDa subunit of the mitochondrial processing protease
4499_at	29411.3	P	homoserine kinase
4500_at	25417.7	P	proteolipid protein of the proton ATPase
4501_at	9054.3	P	Subunit of 26S Proteasome (PA700 subunit)
4502_at	3275.2	P	Dipeptidyl aminopeptidase B (DPAP B)
4503_at	2405	P	Thymidylate synthase (putative\; weak)
4504_at	8289.4	P	putative protein kinase
4505_at	2178.1	P	Pif1p, mitochondrial DNA repair and recombination protein
4506_at	6290.1	P	ethionine resistance protein
4507_at	1849.5	P	Pro1p (Gamma-glutamyl kinase)
4508_at	1329.3	P	hypothetical protein
4509_at	419.7	A	Sec23p (weak)
4510_at	757.8	P	similarity to hypothetical protein YGL247w
4511_at	2875.4	P	delta-1-pyrroline-5-carboxylate dehydrogenase
4512_at	1173.3	P	Killed in Mutagen, sensitive to Diepoxybutane and\/or Mitomycin C
4513_at	8247.8	P	Aldehyde dehydrogenases
4514_at	36326.3	P	13-kDa vacuolar H-ATPase subunit
4469_at	1857.3	P	weak similarity to Hit1p
4470_at	5973.1	P	RNA polymerase II holoenzyme\/mediator subunit
4471_at	16924.8	P	NADP-cytochrome P450 reductase
4472_s_at	3440.1	P	2-deoxyglucose-6-phosphate phosphatase
4473_i_at	4.5	A	2-deoxyglucose-6-phosphate phosphatase
4474_at	5122.1	P	hypothetical protein

4475_at	3036	P	Inositol monophosphatase
4476_at	9313.7	P	arginine\/alanine aminopeptidase
4477_at	1015.6	P	similarity to multidrug resistance proteins
4478_at	10973.3	P	similarity to S.pombe dihydrofolate reductase and YOR280c
4479_at	890.7	P	questionable ORF
4480_at	4991.2	P	localized to mitochondrial membrane
4481_at	12342.5	P	subunit VI of cytochrome c oxidase
4482_at	6533.7	P	weak similarity to P.yoelii rhoptry protein
4483_s_at	26039.4	P	copper-binding metallothionein
4484_s_at	6396.8	P	weak similarity to YOR262w
4485_at	7284.6	P	Peptidylprolyl isomerase (cyclophilin) ER or secreted
4486_at	2082.5	P	RNA polymerase II transcriptional regulation mediator
4487_at	1219.7	P	weak similarity to Ustilago hordei B east mating protein 2
4488_at	2114	P	required for V-ATPase activity
4489_at	1379.2	P	GTPase-interacting component 1
4490_at	4969.6	P	Protein subunit of nuclear ribonuclease P (RNase P)
4491_at	5039.2	P	weak similarity to translational activator CBS2
4492_at	20502.5	P	Hsp70 Protein
4446_at	5312.7	P	RRP3 is a DEAD box gene homologous to eIF-4a which encodes an
4447_at	2245.6	P	homologous to Ssf2p
4448_at	1225.7	P	hypothetical protein
4449_at	27015.4	P	Deoxyhypusine synthase
4450_at	3149.6	P	3->5 exoribonuclease\; Component of the exosome 3->5 exonucleas
4451_at	4960.9	P	strong similarity to N.crassa met-10+ protein
4452_at	5590.7	P	G1\/S cyclin (weak)
4453_at	11278.4	P	2,3-oxidosqualene-lanosterol cyclase
4454_at	433.9	P	Oxysterol-binding protein
4455_at	3444.9	P	weak similarity to B.subtilis spore outgrowth factor B
4456_at	767.3	P	ribosomal protein of the small subunit, mitochondrial
4457_at	3241.5	P	weak similarity to C.elegans hypothetical protein CEW09D10
4458_at	6267.6	P	hypothetical protein
4459_at	916	P	Ire1p is a transmembrane protein that has both serine-threonine kina
4460_i_at	42.9	A	Ire1p is a transmembrane protein that has both serine-threonine kina
4461_r_at	104.5	A	Ire1p is a transmembrane protein that has both serine-threonine kina
4462_at	1778.1	P	similarity to hypothetical protein YDR326c, YFL042c and YLR072w
4463_at	1688.1	P	weak similarity to human C1D protein
4464_at	5582.5	P	Ser\/Thr protein kinase
4465_at	3517.9	P	hypothetical protein
4466_at	3524.5	P	Transcription factor
4467_at	2966.6	P	weak similarity to fruit fly brahma transcriptional activator
4468_at	3197.7	P	putative RNA binding protein, involved in meiosis-specific splicing of
4423_at	997.2	P	hypothetical protein
4424_at	3785.4	P	similarity to hypothetical protein YNL075w
4425_at	20199.5	P	small nucleolar RNP proteins
4426_at	1960	P	NuBbiN
4427_at	5627.7	P	Arginyl-tRNA synthetase
4428_at	7640.6	P	High-affinity glucose transporter
4429_at	986.9	P	the AHT1 DNA sequence is upstream of HXT4 and contains an HXT
4430_at	18927.8	P	High-affinity hexose (glucose) transporter
4431_at	52.4	A	hypothetical protein
4432_at	435.5	A	hexose transporter
4433_at	1383.1	P	strong similarity to hypothetical protein YDR348c

4434_at	1315.6	P	strong similarity to hypothetical protein YDR348c
4435_at	14656.4	P	binds to Sed5p and Sec23p by distinct domains
4436_at	6893.9	P	ATM\/Mec1\/TOR1+2-related
4437_at	1936.8	P	hypothetical protein
4438_at	3169.8	P	Bad in glucose or big cells
4439_at	1488.5	P	Bad in glucose or big cells
4440_at	1710.9	P	Ser\/Thr protein kinase
4441_at	3777.5	P	functionally redundant and similar in structure to SBE2
4442_at	4108.2	P	Aldo-keto reductase
4443_at	278.1	P	weak similarity to Mvp1p
4444_at	2464.1	P	Thioredoxin reductase
4445_at	2921.2	P	Component of 10 nm filaments of mother-bud neck (septin)
4401_at	13769.1	P	strong similarity to hypothetical protein YDR358w
4402_at	528.1	P	hypothetical protein
4403_at	1842.4	P	p24 protein involved in membrane trafficking
4404_at	1819.7	P	moeB, thiF, UBA1
4405_at	6608.6	P	Cystathionine gamma-synthase
4406_at	7539.6	P	Vacuolar aminopeptidase
4407_at	2014.2	P	SH3 domain
4408_at	2659.8	P	strong similarity to hypothetical protein YNL116w
4409_at	798.6	P	hypothetical protein
4410_at	1008.9	P	71-kDa component of the protein translocase of the outer membrane
4411_at	213.1	P	50-kDa subunit of ORC
4412_at	2412.9	P	trithorax
4413_at	1635.4	P	mutS homolog involved in mitochondrial DNA repair
4414_at	6185.3	P	weak similarity to C.elegans hypothetical protein
4415_at	2230.4	P	similarity to hypothetical C. elegans protein F45G2.a
4416_at	3054.1	P	sn-1,2-diacylglycerol ethanolamine- and cholinephosphotranferase
4417_at	4415.5	P	sn-1,2-diacylglycerol ethanolamine- and cholinephosphotranferase
4418_at	252.1	A	meiosis-specific gene, mRNA is sporulation-specific
4419_at	22.3	A	questionable ORF
4420_at	369.4	A	hypothetical protein
4421_at	3393.6	P	(H)igh copy (S)uppressor of (N)34 dominant negative allele of SEC4.
4422_at	24994.3	P	UPRTase
4378_at	621.5	P	Centractin
4379_at	1025.7	P	weak similarity to T.brucei H+-transporting ATP synthase
4380_at	1367	P	Highly acidic C-terminus
4381_at	10201.7	P	Carboxypeptidase
4382_at	28384.9	P	similarity to hypothetical protein YNL156c
4383_at	522.5	P	hypothetical protein
4384_at	6910.1	P	membrane-bound casein kinase I homolog
4385_at	10976.5	P	17 kDa protein
4386_at	15366.7	P	aromatic amino acid aminotransferase II
4387_at	3526.1	P	hypothetical protein
4388_at	306.6	A	sporulation-specific wall maturation protein
4389_at	156	A	hypothetical protein
4390_at	226.8	A	hypothetical protein
4391_at	9395.1	P	weak similarity to cytochrome-c oxidases
4392_at	21497.5	P	Ser-Thr rich protein
4393_at	9228.5	P	subunit of RNA polymerase II
4394_at	8673.8	P	dCMP deaminase
4395_at	142.3	A	questionable ORF

4396_at	5971.1	P	similarity to pheromone-response G-protein Mdg1p
4397_at	4130.6	P	Mitochondrial ribosomal protein MRPL6 (YmL6)
4398_at	5437.3	P	ribosomal protein (weak similarity)
4399_at	1678.8	P	similarity to hypothetical protein YGR221c
4400_at	675.9	P	weak similarity to YDR479c
4356_at	2816	P	hypothetical protein
4357_at	3456.5	P	20 kDa protein with negatively charged C-terminus required for functi
4358_at	387.5	P	sporulation protein
4359_at	1895	P	Establishes Silent omatin
4360_at	1232.4	P	Snf1-interacting protein Sip3p
4361_at	414.4	A	weak similarity to mouse kinesin KIF3B
4362_at	190.5	A	mRNA is induced early in meiosis
4363_at	1750.8	P	protein containing kelch repeats, similar to YGR238c
4364_at	90.8	A	hypothetical protein
4365_at	138.2	A	weak similarity to hypothetical protein YGR239c
4366_at	2228.3	P	Yeast Assembly Polypeptide, member of AP180 protein family, binds
4367_at	17953.7	P	strong similarity to hypothetical protein YGR243w
4368_at	11891.1	P	shows similarity to glucose-6-phosphate dehydrogenase non-catalyti
4369_at	1655.9	P	DNA replication helicase
4370_at	8613.8	P	RNA splicing factor
4371_at	277	A	Cell division cycle protein
4372_at	1405.5	P	hypothetical protein
4373_at	2913.5	P	GTP-binding protein
4374_at	6626.7	P	DEAD-box protein
4375_at	12946.1	P	putative Upf1p-interacting protein
4376_at	752.3	P	autophagy
4377_at	2090.6	P	spindle pole body component, associates in a complex with Spc98p
4333_at	70	A	hypothetical protein
4334_i_at	19255.2	P	enolase
4335_at	14294.5	P	Putative low-affinity copper transport protein
4336_at	1411	P	Dimethylaniline monoxygenase
4337_at	891	P	weak similarity to Spombe pac2 protein
4338_at	1503.7	P	Zinc finger (6-Cys)
4339_at	25702	P	NAPDH dehydrogenase (old yellow enzyme), isoform 2
4340_at	1439.5	P	hypothetical protein
4341_at	13848.8	P	similarity to mouse TEG-261 protein
4342_at	1339.7	P	hypothetical protein
4343_at	26487	P	Phosphogluconate Dehydrogenase (Decarboxylating)
4344_at	758	P	Involved in the control of meiotic nuclear divisions and spore formatic
4345_at	151.4	P	hypothetical protein
4346_at	3405.7	P	similarity to C.elegans hypothetical protein C10C5.6
4347_at	398.2	P	confers sensitivity to killer toxin
4348_at	6600.6	P	similarity to hypothetical C. elegans proteins F17c11.7
4349_at	121.2	A	similarity to peptidyl-tRNA hydrolases
4350_at	18165.3	P	squalene synthetase
4351_at	3107.1	P	protein of unknown function
4352_at	2071.6	P	hypothetical protein
4353_at	31854	P	GAL4 enhancer protein, homolog of human alpha NAC subunit of th
4354_at	3835.3	P	similarity to hypothetical protein YOR147w
4355_at	4921.4	P	hypothetical protein
4310_at	4267.7	P	hypothetical protein
4311_at	13506	P	hypothetical protein

4312_at	1112.5	P	strong similarity to hypothetical protein YHR199c
4313_at	6113.1	P	strong similarity to hypothetical protein YHR198c
4314_at	13292.2	P	homolog of the mammalian S5a protein, component of 26S proteas
4315_at	4040.4	P	Cytosolic exopolyphosphatase
4316_at	3344.2	P	similarity to S.pombe hypothetical protein SPAC17G6
4317_at	5575.5	P	similarity to alpha-mannosidases
4318_at	2063.8	P	cAMP-dependent protein kinase homolog, suppressor of cdc25ts
4319_at	3230.6	P	Protein with similarity to DNA-binding region of heat shock transcripti
4320_at	3206.8	P	weak similarity to YPL165c
4321_at	23944.9	P	branched-chain amino acid transaminase, highly similar to mammali
4322_at	1157.4	P	UDP-glucose-4-epimerase (GAL10, galE)
4323_f_at	16450.4	P	IMP dehydrogenase\; probable PUR5 gene
4324_s_at	8169.5	P	gene in Y repeat region
4325_at	47	A	questionable ORF
4326_at	1137.3	P	questionable ORF
4327_at	122.3	A	questionable ORF
4328_at	711.8	A	questionable ORF
4329_at	67.4	A	questionable ORF
4330_at	855.9	P	questionable ORF
4331_at	109	A	questionable ORF
4332_at	36.9	A	questionable ORF
4286_s_at	2020.6	P	Highly acidic C-terminus
4287_s_at	552.4	P	similarity to hypothetical protein YER175c
4288_at	2795	P	non-annotated SAGE orf Found reverse in NC_001140 between 345
4289_at	54.6	A	non-annotated SAGE orf Found reverse in NC_001140 between 518
4290_at	654.8	A	non-annotated SAGE orf Found reverse in NC_001140 between 519
4291_i_at	25.7	A	non-annotated SAGE orf Found reverse in NC_001140 between 917
4292_at	639.1	P	non-annotated SAGE orf Found reverse in NC_001140 between 146
4293_at	2437.9	P	non-annotated SAGE orf Found forward in NC_001140 between 370
4294_at	642.2	A	non-annotated SAGE orf Found forward in NC_001140 between 560
4295_at	320.4	P	non-annotated SAGE orf Found forward in NC_001140 between 804
4296_at	552.3	A	non-annotated SAGE orf Found reverse in NC_001140 between 122
4297_at	55.9	A	non-annotated SAGE orf Found forward in NC_001140 between 146
4298_at	150.6	A	non-annotated SAGE orf Found reverse in NC_001140 between 167
4299_at	564.7	M	non-annotated SAGE orf Found reverse in NC_001140 between 225
4300_at	769.4	P	non-annotated SAGE orf Found reverse in NC_001140 between 374
4301_at	43.1	A	non-annotated SAGE orf Found forward in NC_001140 between 508
4302_at	1796.1	P	non-annotated SAGE orf Found forward in NC_001140 between 209
4303_at	1953.4	P	non-annotated SAGE orf Found forward in NC_001140 between 467
4304_f_at	422.3	P	non-annotated SAGE orf Found forward in NC_001140 between 528
4305_at	1873.2	P	non-annotated SAGE orf Found reverse in NC_001140 between 566
4306_i_at	44.4	A	non-annotated SAGE orf Found reverse in NC_001140 between 577
4307_f_at	28.3	A	non-annotated SAGE orf Found reverse in NC_001140 between 577
4308_at	240.8	P	non-annotated SAGE orf Found reverse in NC_001140 between 202
4309_i_at	203.4	A	non-annotated SAGE orf Found forward in NC_001140 between 203
4261_s_at	13.6	A	non-annotated SAGE orf Found forward in NC_001140 between 203
4262_i_at	35.3	A	non-annotated SAGE orf Found forward in NC_001140 between 203
4263_at	482.4	A	non-annotated SAGE orf Found reverse in NC_001140 between 204
4264_at	729.1	P	non-annotated SAGE orf Found reverse in NC_001140 between 422
4265_s_at	627.8	P	non-annotated SAGE orf Found reverse in NC_001140 between 422
4266_at	3334.5	P	non-annotated SAGE orf Found reverse in NC_001140 between 422
4267_at	124.5	A	non-annotated SAGE orf Found reverse in NC_001140 between 458

4268_at	8.5	A	non-annotated SAGE orf Found reverse in NC_001140 between 522
4269_f_at	6683.4	P	non-annotated SAGE orf Found forward in NC_001140 between 530
4270_f_at	67.3	A	non-annotated SAGE orf Found reverse in NC_001140 between 530
4271_at	5.1	A	non-annotated SAGE orf Found reverse in NC_001140 between 531
4272_at	8800.4	P	non-annotated SAGE orf Found reverse in NC_001140 between 111
4273_at	418.8	A	non-annotated SAGE orf Found forward in NC_001140 between 157
4274_at	3693.5	P	non-annotated SAGE orf Found forward in NC_001140 between 175
4275_at	339.3	A	non-annotated SAGE orf Found forward in NC_001140 between 198
4276_at	126.2	A	non-annotated SAGE orf Found reverse in NC_001140 between 410
4277_i_at	19.1	A	Centromere
4278_at	899.8	P	snRNA
4279_at	2206.8	P	snRNA
4280_f_at	3788.6	P	strong similarity to members of the Srp1p/Tip1p family
4281_i_at	3767	A	High-affinity hexose transporter
4282_f_at	342.8	A	High-affinity hexose transporter
4283_at	91.6	A	L-serine dehydratase
4284_at	17	A	serine dehydratase
4285_at	625.7	P	similarity to allantoate permease Dal5p
4237_at	1690.5	P	putative pseudogene
4238_at	1526.5	P	Nit1 nitrilase
4239_at	26.2	A	questionable ORF
4240_at	3634.3	P	hypothetical protein
4241_at	922.2	A	peroxisomal 3-oxoacyl CoA thiolase
4242_at	171	A	Bni1p-related protein, helps regulate reorganization of the actin cytos
4243_at	3332.3	P	similarity to hypothetical protein YKR100c
4244_at	3141.1	P	hypothetical protein
4245_at	563.6	P	Ubiquitin-specific protease
4246_at	2447.9	P	glycerol-3-phosphate dehydrogenase, mitochondrial
4247_at	4475.6	P	transcription factor
4248_at	4280.5	P	Resistant to Rapamycin Deletion
4249_at	2170.3	P	hypothetical protein
4250_at	1203.9	P	similarity to mitochondrial aldehyde dehydrogenase Ald1p
4251_at	363.9	P	Protein required for S-phase (DNA synthesis) initiation or completion
4252_at	2044.8	P	similarity to Mlp1p and myosin heavy chains
4253_i_at	26910.4	A	Ribosomal protein L40A
4254_at	4667.4	P	histidine kinase osmosensor that regulates an osmosensing MAP kin
4255_at	1066.9	P	ExtraCellular Mutant
4256_at	2573.1	P	similarity to E.coli pantothenate synthetase
4257_at	283	A	Dmc1p interacting protein
4258_at	1902.2	P	DNA helicase homolog\; homolog of human XPBC, ERCC3
4259_at	21483.3	P	molecular chaperone
4260_at	2617.4	P	questionable ORF
4215_g_at	2387.7	P	questionable ORF
4216_at	1484.9	P	localizes to the plasma membrane
4217_at	240.7	P	subunit of DNA polymerase-zeta (Pol-zeta), an enzyme whose sole f
4218_at	2182.8	P	Tropomyosin isoform 2
4219_at	4461.5	P	similarity to M.musculus aminopeptidase
4220_at	363.2	A	45-kDa mitochondrial outer membrane protein
4221_at	2129.6	P	similarity to Ymk1p
4222_at	1376.5	P	mitochondrial inner membrane carrier protein for FAD
4223_at	26035.5	P	Ribosomal protein L16A (L21A) (rp22) (YL15)
4224_at	733.6	P	hypothetical protein

4225_at	2260.3	P	similarity to Drosophila fork head protein
4226_at	2478.2	P	similarity to Put3p and to hypothetical protein YJL206c
4227_at	7470	P	similarity to hypothetical human protein
4228_at	1815.9	P	Involved in nucleotide excision repair and regulation of TFIIH
4229_at	2134	P	weak similarity to Smy2p
4230_at	3438.8	P	helicase related protein, snf2 homolog
4231_at	12708.6	P	alpha-ketoglutarate dehydrogenase
4232_at	11196.5	P	similarity to C.perfringens nanH protein
4233_at	21359.5	P	involved in cell cycle regulation and aging
4234_at	756.6	M	hypothetical protein
4235_at	735.6	P	similarity to antibiotic resistance proteins
4236_at	1358.4	P	similarity to antibiotic resistance proteins
4192_at	1490.8	P	inhibitor of ras
4193_at	3550.3	P	ras homolog--GTP binding protein
4194_at	3803.7	P	hydrophobic transmembrane domain
4195_at	3589.8	P	histidinol-phosphate aminotransferase
4196_at	1932.8	P	159-kDa nucleoporin with coiled-coil domain and repeated motifs typ
4197_at	5512.2	P	voltage dependent anion channel (YVDAC2)
4198_at	425.2	A	strong similarity to dual-specificity phosphatase Msg5p
4199_at	937.3	M	similarity to ankyrin and coiled-coil proteins
4200_at	355.7	A	Cytochrome-c oxidase chain Vb
4201_at	2548.5	P	weak similarity to hypothetical C.elegans protein
4202_at	7964.4	P	The Sec23p-Sec24p complex is one of three cytoplamic COPII facto
4203_at	5004.1	P	similarity to hypothetical S. pombe protein
4204_at	427.6	P	6-Phosphofructose-2-kinase
4205_at	410.9	P	weak similarity to probable transcription factor Ask10p
4206_at	982	P	similarity to hypothetical S. pombe protein
4207_at	4742.3	P	weak similarity to Dph2 protein
4208_at	19.3	A	strong similarity to YIL014c-a
4209_at	25.9	A	DNA-binding transcriptional repressor
4210_at	22.9	A	similarity to mouse Gcap1 protein and fruit fly Bkm-like sex-determini
4211_at	1590	P	intracellular glucoamylase
4212_g_at	61.1	A	intracellular glucoamylase
4213_at	1922.5	P	Formation of Mitochondrial Cytochromes 1
4214_at	449.4	P	hypothetical protein
4170_at	8259.1	P	hypothetical protein
4171_at	121.6	A	probable serine\/threonine-protein kinase
4172_at	9811.8	P	Homo-isocitrate dehydrogenase
4173_at	691.1	P	weak similarity to S.pombe hypothetical protein SPBC16A3
4174_at	711.4	P	hypothetical protein
4175_at	4085.9	P	weak similarity to spt5p
4176_at	2679.4	P	similarity to hypothetical S. pombe protein
4177_at	555.9	M	similarity to hypothetical protein YLR036c
4178_at	10134.3	P	weak similarity to A.thaliana aminoacid permease AAP4
4179_at	4682	P	hypothetical protein
4180_at	96.9	A	hypothetical protein
4181_at	2298.6	P	Putative mannosyltransferase of the KRE2 family
4182_at	426.6	M	Functions are similar to those of SIN3 and RPD3
4183_at	6269.2	P	hypothetical protein
4184_s_at	2908.7	P	Ty3-2 orf C fragment
4185_at	1329.4	P	strong similarity to hypothetical protein YDL175c
4186_at	23126.6	P	Threonyl-tRNA synthetase, cytoplasmic

4187_at	722	P	hypothetical protein
4188_at	8795	P	epsilon-COP coatomer subunit Sec28p
4189_at	14107.9	P	RPN2p is a component of the 26S proteosome
4190_at	5695.7	P	strong similarity to E.coli phosphoglycerate dehydrogenase
4191_at	124	A	weak similarity to mouse polycystic kidney disease-related protein
4147_at	144.1	A	Meiosis-specific protein involved in homologous chromosome synaps
4148_at	427.3	P	hypothetical protein
4149_at	14036.4	P	mitochondrial acidic matrix protein
4150_at	4586.4	P	88 kD component of the Exocyst complex, which contains the gene
4151_at	2706.4	P	hypothetical protein
4152_at	5298.1	P	similarity to C.elegans hypothetical protein
4153_at	2371	P	weak similarity to fowlpox virus major core protein
4154_at	1118.5	P	nuclear protein, interacts with Gsp1p and Crm1p
4155_at	14613.3	P	Arp Complex Subunit
4156_at	501.5	P	U1snRNP 70K protein homolog
4157_at	375.6	P	questionable ORF
4158_at	658	P	hypothetical protein
4159_at	330.7	A	hypothetical protein
4160_at	340.1	A	strong similarity to YER067w
4161_at	3181.8	P	similarity to YER064c
4162_at	560.7	P	hypothetical protein
4163_at	485.7	P	weak similarity to fruit fly NADH dehydrogenase
4164_at	20075.8	P	DL-glycerol-3-phosphatase
4165_i_at	34034.5	P	Ribosomal protein L34B
4166_at	26079.4	P	Maintenance of Mitochondrial DNA 1
4167_at	4619.5	P	PHO85 cyclin
4168_at	4149.2	P	Protein required for filamentous growth, cell polarity, and cellular elo
4169_at	7554.6	P	ATPase that leads to neomycin-resistant protein when overexpresse
4124_at	18298.9	P	plasma membrane protein
4125_at	2094.1	P	Met30p contains five copies of WD40 motif and interacts with and re
4126_at	302.1	P	Protein with 30\%% identity to protein corresponding to YER054
4127_at	2808.3	P	weak similarity to zinc finger protein Gcs1p
4128_at	18461.9	P	cytochrome b reductase
4129_at	2183.1	P	similarity to rat branched-chain alpha-ketoacid dehydrogenase kinas
4130_at	14198.3	P	similarity to S.pombe hypothetical protein
4131_at	4758.6	P	weak similarity to T.brucei NADH dehydrogenase
4132_at	13582	P	hypothetical protein
4133_at	2802.5	P	General negative regulator of transcription\; may inhibit RNA polymer
4134_at	288.1	A	hypothetical protein
4135_at	1479.2	P	weak similarity to human cAMP responce element-binding protein
4136_at	2829.8	P	alpha subunit of casein kinase II
4137_at	3963.8	P	beta subunit of capping protein
4138_at	10949.4	P	regulatory subunit of cAMP-dependent protein kinase
4139_at	912.7	A	hypothetical protein
4140_at	1146	P	Suppressor of Mif Two
4141_at	6765	P	integral nuclear membrane protein
4142_at	126.8	A	strong similarity to hypothetical protein YPR071w
4143_at	432.3	M	putative pseudogene
4144_at	16880.3	P	hypothetical protein
4145_at	687.7	P	Irregular
4146_at	23	A	weak similarity to E.gracilis RNA polymerase subunit
4101_at	1211.9	P	hypothetical protein

4102_at	6155.3	P	similarity to mouse MHC H-2K/t-w5-linked ORF precursor
4103_at	7157.9	P	48.8 kDa protein involved in mitochondrial protein import
4104_at	4689.3	P	45 kDa subunit of RNA polymerase II
4105_at	2368.6	P	phosphoribosyl-5-amino-1-phosphoribosyl-4-imidazolecarboxiamide
4106_at	768.4	P	weak similarity to S.pombe hypothetical protein SPAC3F10
4107_at	516.9	P	hypothetical protein
4108_at	1805.1	P	18.3 kD integral membrane protein
4109_at	37.4	A	encodes a-cell barrier activity on alpha factor
4110_at	45.2	A	strong similarity to hypothetical protein YIL102c
4111_at	2386.4	P	similarity to Mnn1p
4112_at	676.5	P	Putative member of the ABC family of membrane transporters
4113_at	227.9	A	hypothetical protein
4114_at	10311.9	P	strong similarity to members of the Srp1p/Tip1p family
4115_at	8169.6	P	Derepression Of Telomeric silencing
4116_at	4152	P	181aa protein - 20.5 kD
4117_at	1340.7	P	181aa protein - 20.5 kD
4118_at	4179	P	Acyl CoA synthase
4119_at	5385.6	P	hypothetical protein
4120_at	610.6	P	similarity to C.elegans hypothetical protein
4121_at	1474.7	P	similarity to Flx1p
4122_at	7235.6	P	similarity to protein disulfide isomerases
4123_at	2042	P	Synaptobrevin (t-SNARE) homolog present on ER vesicles recycling
4079_at	5501.5	P	strong similarity to Nbp35p and human nucleotide-binding protein
4080_at	2189.3	P	phosphatidylinositol 4,5-bisphosphate 5-phosphatase
4081_at	1202	P	similarity to S.pombe hypothetical protein, weak similarity to human
4082_at	858.4	P	similarity to D.melanogaster RNA binding protein
4083_at	2430.9	P	weak similarity to ATP-dependent RNA helicases
4084_at	4683.1	P	weak similarity to mammalian neurofilament triplet H proteins
4085_at	1238.3	P	DnaJ-like protein required for Peroxisome biogenesis\; Djp1p is locat
4086_at	686.9	P	similarity to RNA-binding proteins
4087_at	16862.9	P	polyA-specific ribonuclease
4088_at	665.9	P	hypothetical protein
4089_at	3638.3	P	p48 polypeptide of DNA primase
4090_at	1012.6	P	encodes YU2B, a component of yeast U2 snRNP
4091_at	1547.9	P	hypothetical protein
4092_at	4899.8	P	restores protein transport when overexpressed and rRNA stability to
4093_at	14102.9	P	contains multiple WD repeats and interacts with Qsr1p in two hybrid
4094_at	284.8	A	strong similarity to YLR013w, similarity to YMR136w
4095_at	518.3	P	hypothetical protein
4096_at	784	A	an integral subunit of RNase P but not RNase MRP
4097_at	3124.6	P	weak similarity to YOL036w
4098_at	709.4	P	Transcriptional activator of sulfur amino acid metabolism
4099_at	1210.4	M	bZIP protein\; transcription factor
4100_at	6723.3	P	cell surface flocculin with structure similar to serine\/threonine-rich G
4056_at	868.5	P	hypothetical protein
4057_at	2915.7	P	mitochondrial RNA splicing
4058_at	7699.1	P	signal peptidase subunit
4059_at	1559.9	P	Transcriptional activator for allantoin and GABA catabolic genes, co
4060_at	1046.8	P	G1 Factor needed for normal G1 phase
4061_at	743	P	hypothetical protein
4062_at	4967.5	P	nitrogen starvation-induced protein phosphatase
4063_at	145.5	A	allantoinase

4064_at	401.3	P	allantoin permease
4065_at	437	A	allantoicase
4066_at	701.2	P	involved in nitrogen-catabolite metabolism
4067_at	441.3	P	Malate synthase 2
4068_at	563.4	A	ureidoglycolate hydrolase
4069_at	662.2	P	may be involved in the remodeling chromatin structure
4070_at	2922.9	P	saccharopine dehydrogenase
4071_at	7408.1	P	similarity to human corticosteroid 11-beta-dehydrogenase
4072_at	5267.8	P	similarity to E.coli fabD
4073_at	14417.2	P	putative glutathione-peroxidase
4074_at	3607.1	P	Glutathione transferase
4075_at	812.7	P	GPI-anchored aspartic protease
4076_f_at	662.5	P	similarity to members of the Srp1p/Tip1p family
4077_at	1260.1	P	weak similarity to B.licheniformi hypothetical protein P20
4078_i_at	337	A	putative pseudogene
4032_f_at	164.7	A	putative pseudogene
4033_f_at	15998.3	P	putative pseudogene
4034_at	219.8	A	hypothetical protein
4035_at	270.7	A	questionable ORF
4036_at	192.2	A	questionable ORF
4037_at	82.7	A	questionable ORF
4038_at	472.4	P	questionable ORF
4039_at	222.7	A	questionable ORF
4040_at	523.9	A	questionable ORF
4041_at	74.3	A	hypothetical protein
4042_at	1030.3	P	questionable ORF
4043_s_at	485.7	A	invertase (sucrose hydrolyzing enzyme)
4044_s_at	1904.9	P	Mps One Binder
4045_s_at	498.5	A	Ribonucleotide reductase (ribonucleoside-diphosphate reductase) la
4046_at	20.1	A	non-annotated SAGE orf Found forward in NC_001141 between 197
4047_at	692.9	M	non-annotated SAGE orf Found forward in NC_001141 between 268
4048_at	17.5	A	non-annotated SAGE orf Found forward in NC_001141 between 414
4049_at	782.7	P	non-annotated SAGE orf Found forward in NC_001141 between 438
4050_at	1411.1	P	non-annotated SAGE orf Found forward in NC_001141 between 144
4051_at	165.4	A	non-annotated SAGE orf Found forward in NC_001141 between 173
4052_i_at	0.7	A	non-annotated SAGE orf Found forward in NC_001141 between 324
4053_s_at	9554.6	P	non-annotated SAGE orf Found forward in NC_001141 between 324
4054_at	7321.5	P	non-annotated SAGE orf Found forward in NC_001141 between 350
4055_at	142.2	A	non-annotated SAGE orf Found forward in NC_001141 between 398
4009_at	10968.5	P	non-annotated SAGE orf Found forward in NC_001141 between 269
4010_at	49.6	A	non-annotated SAGE orf Found reverse in NC_001141 between 139
4011_at	1676.8	P	non-annotated SAGE orf Found reverse in NC_001141 between 139
4012_at	114	A	non-annotated SAGE orf Found forward in NC_001141 between 169
4013_i_at	2.7	A	non-annotated SAGE orf Found reverse in NC_001141 between 210
4014_at	2107.3	P	non-annotated SAGE orf Found forward in NC_001141 between 230
4015_at	476.8	P	non-annotated SAGE orf Found forward in NC_001141 between 258
4016_at	1349.4	P	non-annotated SAGE orf Found forward in NC_001141 between 258
4017_at	274.1	M	non-annotated SAGE orf Found reverse in NC_001141 between 324
4018_at	431.3	A	non-annotated SAGE orf Found reverse in NC_001141 between 385
4019_at	1209.9	P	non-annotated SAGE orf Found reverse in NC_001141 between 385
4020_at	2233.5	P	non-annotated SAGE orf Found reverse in NC_001141 between 386
4021_at	200.5	A	non-annotated SAGE orf Found forward in NC_001141 between 387

4022_at	395.7	P	non-annotated SAGE orf Found forward in NC_001141 between 425
4023_s_at	208.4	P	non-annotated SAGE orf Found forward in NC_001141 between 213
4024_at	443.3	P	non-annotated SAGE orf Found reverse in NC_001141 between 306
4025_i_at	1921.5	P	non-annotated SAGE orf Found reverse in NC_001141 between 516
4026_at	50.4	A	non-annotated SAGE orf Found forward in NC_001141 between 122
4027_at	104.3	P	non-annotated SAGE orf Found forward in NC_001141 between 154
4028_at	1282.9	P	non-annotated SAGE orf Found reverse in NC_001141 between 231
4029_at	1743.1	P	non-annotated SAGE orf Found reverse in NC_001141 between 355
4030_at	1334.6	P	non-annotated SAGE orf Found forward in NC_001141 between 385
4031_at	1720.8	P	snRNA
3983_at	151.6	A	cytochrome-c oxidase subunit II
3984_r_at	81.7	A	questionable ORF Found forward in NC_001224 between 74495 and
3985_i_at	154.3	A	questionable ORF Found forward in NC_001224 between 74495 and
3986_f_at	308	A	questionable ORF Found forward in NC_001224 between 74495 and
3987_at	6.5	A	similarity to Podospora cytb intron 1a and coII intron protein 2 Found
3988_at	278.9	A	cytochrome-c oxidase chain III
3989_at	6.6	A	strong similarity to maturase-related hypothetical protein RF2
3990_i_at	11.2	A	similarity to hypothetical protein Sgc2p Found forward in NC_001224
3991_r_at	3.8	A	similarity to hypothetical protein Sgc2p Found forward in NC_001224
3992_f_at	4.7	A	similarity to hypothetical protein Sgc2p Found forward in NC_001224
3993_at	8.5	A	strong similarity to Yeast (S.uvarum) mitochondria RF2 gene and ma
3994_at	1036.4	P	similarity to Sauroleishmania NADH dehydrogenase (ubiquinone) ch
3995_i_at	48.3	A	RF2 protein Found forward in NC_001224 between 8526 and 8736
3996_s_at	1512.5	P	cytochrome-c oxidase subunit I Found forward in NC_001224 betwe
3997_at	613.7	P	questionable ORF Found reverse in NC_001224 between 13748 and
3998_at	736.5	P	COX1 intron 1 protein Found forward in NC_001224 between 13818
3999_at	265.5	P	COX1 intron 2 protein Found forward in NC_001224 between 16473
4000_at	464.5	P	COX1 intron 3 protein Found forward in NC_001224 between 18992
4001_at	19098.3	P	cytochrome-c oxidase subunit I Found forward in NC_001224 betwe
4002_at	177.7	P	DNA endonuclease I-SceII Found forward in NC_001224 between 2
4003_s_at	4210.7	P	cytochrome-c oxidase subunit I Found forward in NC_001224 betwe
4004_at	1248.2	P	probable mRNA maturase aI5-alpha Found forward in NC_001224 b
4005_at	18309.5	P	cytochrome-c oxidase subunit I Found forward in NC_001224 betwe
4006_at	166.2	P	COX1 intron protein aI5-beta Found forward in NC_001224 between
4007_at	789.5	P	cytochrome-c oxidase subunit I Found forward in NC_001224 betwe
4008_at	913.3	P	cytochrome-c oxidase subunit I Found forward in NC_001224 betwe
3956_i_at	218.9	M	F1F0-ATPase complex, F0 subunit 8 Found forward in NC_001224
3957_r_at	303.2	P	F1F0-ATPase complex, F0 subunit 8 Found forward in NC_001224
3958_r_at	55.1	A	similarity to mouse Gcap1 Found forward in NC_001224 between 28
3959_at	294.5	P	F1F0-ATPase complex, FO A subunit Found forward in NC_00122
3960_at	1.6	A	endonuclease SCEI, small subunit Found forward in NC_001224 be
3961_i_at	0.3	A	endonuclease SCEI, small subunit Found forward in NC_001224 be
3962_f_at	1572.3	A	endonuclease SCEI, small subunit Found forward in NC_001224 be
3963_at	1	A	endonuclease SCEI, small subunit Found forward in NC_001224 be
3964_at	0.7	A	endonuclease SCEI, small subunit Found forward in NC_001224 be
3965_i_at	10.9	A	ORF5 Found forward in NC_001224 between 30874 and 31014 with
3966_i_at	28.3	A	similarity to T.brucei mitochondrion protein SGC6 Found reverse in
3967_r_at	10.6	A	similarity to T.brucei mitochondrion protein SGC6 Found reverse in
3968_s_at	1577.9	P	ubiquinol--cytochrome-c reductase subunit (cytochrome B) Found fo
3969_at	52	A	mRNA maturase bI2 Found forward in NC_001224 between 37723 a
3970_s_at	1239.7	P	ubiquinol--cytochrome-c reductase subunit (cytochrome B) Found fo
3971_at	1.1	A	mRNA maturase bI3 Found forward in NC_001224 between 39141 a

3972_s_at	1102.1	P	ubiquinol--cytochrome-c reductase subunit (cytochrome B) Found fo
3973_at	168.4	P	mRNA maturase bI4 Found forward in NC_001224 between 40815 a
3974_at	964.8	P	ubiquinol--cytochrome-c reductase subunit (cytochrome B) Found fo
3975_at	441.4	P	ubiquinol--cytochrome-c reductase subunit (cytochrome B) Found fo
3976_at	27787.7	P	F1F0-ATPase complex, F0 subunit 9 Found forward in NC_001224
3977_i_at	145.4	A	similarity to honeybee mitochondrion NADH dehydrogenase chain 6
3978_r_at	10.7	A	similarity to honeybee mitochondrion NADH dehydrogenase chain 6
3979_i_at	144.3	A	mitochondrial ribosomal protein Found forward in NC_001224 betwe
3980_r_at	10.1	A	mitochondrial ribosomal protein Found forward in NC_001224 betwe
3981_at	70.8	A	probable mRNA maturase in 21S rRNA intron Found forward in NC_
3982_at	59.7	A	kanamycin resistance casette
3932_at	13.6	A	MAL-activator 23 (MAL23) gene
3933_s_at	1436.8	P	Required for the catabolism of melibiose and regulated by several G
3934_at	2432.9	P	Protein that confers resistance to molasses
3935_at	34.6	A	Tropomyosin-related protein with transmembrane domain and basic
3936_at	792	P	invertase (sucrose hydrolyzing enzyme)
3937_g_at	3749.8	P	invertase (sucrose hydrolyzing enzyme)
3938_at	2058	P	Protein involved in targeting of plasma membrane [H+]ATPase
3939_at	659.1	P	Probable aldehyde dehydrogenase (EC 1.2.1.-)
3940_at	734.4	P	Degradation in the Endoplasmic Reticulum
3941_at	1501.9	P	Ser\/Thr protein kinase
3942_at	6202.7	P	bZIP (basic-leucine zipper) protein
3943_i_at	19854.8	P	bZIP (basic-leucine zipper) protein
3944_f_at	8660.4	A	bZIP (basic-leucine zipper) protein
3945_at	2834.2	P	Protein essential for mitochondrial biogenesis and cell viability
3946_at	2404.9	P	Protein essential for mitochondrial biogenesis and cell viability
3947_at	12798.6	P	strong similarity to holacid-halidohydrolase
3948_s_at	2077.7	P	probable serine\/threonine-specific protein kinase (EC 2.7.1.-)
3949_i_at	5415	P	protein of unknown function
3950_at	2099.1	P	Rho family GTPase
3951_at	2127.3	P	2 micron plasmid recombinase
3952_at	8522.7	P	2 micron plasmid rep1 protein
3953_at	11478.6	P	2 micron plasmid D protein
3954_at	9734.9	P	2 micron plasmid rep2 protein
3955_at	383.9	P	2 micron plasmid recombinase
3907_f_at	2766.6	P	strong similarity to subtelomeric encoded proteins
3908_i_at	35	A	Ty1 LTR
3909_f_at	78.3	A	Ty1 LTR
3910_at	200.1	A	Ty1 LTR
3911_at	2.7	A	Ty1 LTR
3912_f_at	21581.6	P	Ty1 LTR
3913_s_at	6218.5	P	Full length Ty1
3914_s_at	37686.7	P	Full length Ty1
3915_s_at	34058.8	P	Full length Ty1
3916_s_at	25953.5	P	Full length Ty1
3917_f_at	13977	P	Full length Ty1
3918_f_at	31533.6	P	Full length Ty1
3919_f_at	18190.3	P	Saccharomyces cerevisiae chromosome I, complete chromosome s
3920_f_at	37010.4	P	Saccharomyces cerevisiae chromosome I, complete chromosome s
3921_s_at	26319.4	P	Saccharomyces cerevisiae chromosome I, complete chromosome s
3922_f_at	20286.9	P	Ty1 LTR
3923_f_at	4129.3	P	tRNA-Ala

3924_f_at	6189.9	P	tRNA-Ser
3925_f_at	15293.2	P	Ty3 LTR Found forward in NC_001133 between 182610 and 182949
3926_f_at	4487.1	P	Ty1 LTR
3927_f_at	8729.3	P	Ty2 LTR
3928_f_at	90.7	A	Ty1 LTR
3929_s_at	1441.8	P	tRNA-Thr
3930_i_at	180.1	A	Ty1 LTR
3931_f_at	551.9	P	Ty1 LTR
3884_f_at	5389.2	P	tRNA-Glu
3885_f_at	9405.1	P	tRNA-Ala
3886_f_at	205.6	P	Ty3 LTR
3887_f_at	1827.8	P	Ty4 LTR
3888_s_at	102.5	A	Saccharomyces cerevisiae chromosome X, complete chromosome s
3889_s_at	526.9	P	Saccharomyces cerevisiae chromosome X, complete chromosome s
3890_s_at	30.9	A	Saccharomyces cerevisiae chromosome X, complete chromosome s
3891_s_at	25	A	Saccharomyces cerevisiae chromosome X, complete chromosome s
3892_s_at	301.9	A	Saccharomyces cerevisiae chromosome X, complete chromosome s
3893_s_at	29.3	A	Saccharomyces cerevisiae chromosome X, complete chromosome s
3894_s_at	48.7	A	Saccharomyces cerevisiae chromosome X, complete chromosome s
3895_s_at	490.9	P	Saccharomyces cerevisiae chromosome X, complete chromosome s
3896_s_at	6	A	Full length Ty4
3897_s_at	28.1	A	Full length Ty4
3898_s_at	0.6	A	Full length Ty4
3899_s_at	288.8	P	Full length Ty4
3900_f_at	5425.8	P	Full length Ty4
3901_f_at	1927.2	P	Ty4 LTR
3902_f_at	7026.6	P	Ty1 LTR
3903_i_at	32.3	A	Ty1 LTR
3904_f_at	598.9	P	Ty1 LTR
3905_s_at	4555.6	P	tRNA-Asp
3906_f_at	5585.8	P	tRNA-Arg
3859_i_at	298.8	A	Ty1 LTR
3860_f_at	14265.7	P	Ty1 LTR
3861_f_at	15603.1	P	Ty1 LTR
3862_f_at	1723	P	tRNA-Arg
3863_f_at	2080.5	P	tRNA-Arg
3864_i_at	374.2	A	Ty1 LTR
3865_f_at	16	A	Ty1 LTR
3866_at	63.4	A	Ty1 LTR
3867_s_at	12777.5	P	tRNA-Val
3868_s_at	355	P	tRNA-Met
3869_f_at	3430.1	A	tRNA-Gly
3870_s_at	3007.1	P	tRNA-Lys
3871_at	4.6	A	Ty4 LTR
3872_i_at	14.6	A	Ty1 LTR
3873_f_at	4.2	A	Ty1 LTR
3874_i_at	0.7	A	Ty1 LTR
3875_f_at	73.4	A	Ty1 LTR
3876_at	883.3	P	Ty4 LTR
3877_at	796.1	P	Ty1 LTR
3878_s_at	7964	P	tRNA-Leu
3879_f_at	16072.9	P	Ty1 LTR

3880_f_at	17754.6	P	Saccharomyces cerevisiae chromosome X, complete chromosome s
3881_f_at	27622.3	P	Full length Ty1
3882_f_at	22388.8	P	Full length Ty1
3883_f_at	13113.7	P	Ty1 LTR
3835_s_at	38253.7	P	Saccharomyces cerevisiae chromosome X, complete chromosome s
3836_f_at	17365.5	P	Full length Ty1
3837_f_at	19659.5	P	Ty1 LTR
3838_s_at	1574.3	P	tRNA-Met
3839_at	1.7	A	Ty1 LTR
3840_f_at	6504.1	P	tRNA-Ser
3841_at	343	A	Ty1 LTR
3842_f_at	3668.9	P	tRNA-Gly
3843_at	502.1	P	Ty1 LTR
3844_f_at	18614.9	P	Ty1 LTR
3845_i_at	76.1	A	tRNA-Arg
3846_f_at	58.3	A	tRNA-Arg
3847_i_at	11	A	Ty1 LTR
3848_f_at	2072.5	P	Ty1 LTR
3849_f_at	266.5	A	Ty1 LTR
3850_at	1353.2	P	Ty1 LTR
3851_s_at	15136.4	P	Protein with similarity to members of the Ybr302p\/Ycr007p\/Cos8p\/
3852_f_at	5410.9	P	Protein with similarity to members of the Ybr302p\/Ycr007p\/Cos8p\/
3853_f_at	553.4	A	strong similarity to subtelomeric encoded proteins
3854_f_at	215	A	strong similarity to Gin11p, YKL225w and other subtelomeric encode
3855_s_at	16.2	A	strong similarity to subtelomeric encoded proteins
3856_at	122.3	A	tRNA-Thr
3857_at	11.6	A	Ty1 LTR
3858_s_at	639	P	tRNA-Asn
3812_at	202.4	A	Ty1 LTR
3813_f_at	5432.8	P	tRNA-Glu
3814_f_at	1717	P	tRNA-Arg
3815_i_at	7.2	A	Ty1 LTR
3816_f_at	367.3	A	Ty1 LTR
3817_f_at	14241.7	P	Ty3 LTR
3818_at	198	M	Ty1 LTR
3819_f_at	9096.7	P	tRNA-Ala
3820_f_at	1028.4	P	Ty1 LTR
3821_f_at	3663.4	P	tRNA-His
3822_f_at	1509.8	P	Ty1 LTR
3823_f_at	6520.6	P	Ty1 LTR
3824_f_at	18550.5	P	Ty1 LTR
3825_at	37.9	A	Ty1 LTR
3826_at	12.6	A	Ty1 LTR
3827_f_at	3923.2	P	tRNA-Arg
3828_f_at	1042.5	P	Ty1 LTR
3829_f_at	23446.7	P	Ty1 LTR
3830_f_at	11174.6	P	tRNA-Ala
3831_s_at	55.9	A	strong similarity to subtelomeric encoded proteins
3832_s_at	20.7	A	strong similarity to subtelomeric encoded proteins
3833_f_at	6.8	A	Ty5 LTR
3834_s_at	15599.6	P	strong similarity to subtelomeric encoded proteins
3789_s_at	15064.5	P	strong similarity to subtelomeric encoded proteins

3790_s_at	14092	P	strong similarity to subtelomeric encoded proteins
3791_s_at	497	P	strong similarity to subtelomeric encoded proteins
3792_s_at	16935.9	P	strong similarity to subtelomeric encoded proteins
3793_f_at	928.4	P	Ty1 LTR
3794_f_at	5884.2	P	tRNA-Ser
3795_at	12.6	A	Ty3 LTR
3796_f_at	3268.3	P	tRNA-Ala
3797_f_at	14382.4	P	Ty1 LTR
3798_s_at	36351.1	P	Saccharomyces cerevisiae chromosome XII, complete chromosome
3799_f_at	12819.6	P	Ty1 LTR
3800_at	56.1	A	Ty1 LTR
3801_f_at	107.4	A	Ty1 LTR
3802_f_at	4426.5	P	Ty3 LTR
3803_f_at	3409.2	P	tRNA-Arg
3804_f_at	11402.1	P	tRNA-Gln
3805_f_at	762.2	P	Ty1 LTR
3806_s_at	19203.7	P	35S ribosomal RNA
3807_s_at	5075.7	P	35S ribosomal RNA
3808_s_at	23584.7	P	35S ribosomal RNA
3809_s_at	24670.8	P	35S ribosomal RNA
3810_s_at	2138.8	P	35S ribosomal RNA
3811_s_at	3385.9	P	35S ribosomal RNA
3764_s_at	3226.8	P	35S ribosomal RNA
3765_s_at	2244.2	P	25S ribosomal RNA
3766_s_at	24755	P	25S ribosomal RNA
3767_s_at	2022.4	P	18S ribosomal RNA
3768_i_at	7301.9	A	5S ribosomal RNA
3769_s_at	3880	P	5S ribosomal RNA
3770_i_at	3632.8	A	5S ribosomal RNA
3771_f_at	22388.8	P	Ty1 LTR
3772_f_at	21519.3	P	Full length Ty1
3773_f_at	27260.4	P	Full length Ty1
3774_f_at	29603.3	P	Saccharomyces cerevisiae chromosome XII, complete chromosome
3775_f_at	20933	P	Ty1 LTR
3776_i_at	8.6	A	Ty1 LTR
3777_f_at	57	A	Ty1 LTR
3778_f_at	14442	P	Ty1 LTR
3779_f_at	16269.5	P	Saccharomyces cerevisiae chromosome XII, complete chromosome
3780_f_at	8110.1	P	Full length Ty1
3781_f_at	19276	P	Full length Ty1
3782_f_at	14591.1	P	Ty1 LTR
3783_at	465.3	A	Ty1 LTR
3784_at	7.3	A	Ty4 LTR
3785_f_at	16379	P	Ty1 LTR
3786_s_at	32292.6	P	TY1B protein Found forward in NC_001144 between 652918 and 65
3787_f_at	14972	P	Saccharomyces cerevisiae chromosome XII, complete chromosome
3788_f_at	35009.4	P	Saccharomyces cerevisiae chromosome XII, complete chromosome
3740_f_at	10915.2	P	Full length Ty1
3741_f_at	15397.4	P	Full length Ty1
3742_f_at	12059.4	P	Ty1 LTR
3743_f_at	9853.3	P	tRNA-Ala
3744_i_at	5914.7	P	Ty3 LTR

3745_f_at	3055.3	P	Ty3 LTR
3746_at	1413	P	Ty1 LTR
3747_at	4.7	A	Ty1 LTR
3748_i_at	8.6	A	Ty1 LTR
3749_r_at	12.2	A	Ty1 LTR
3750_f_at	151.9	P	Ty1 LTR
3751_f_at	11943.6	P	Ty2 LTR
3752_f_at	169.4	A	Ty1 LTR
3753_s_at	1177.5	P	tRNA-Ile
3754_s_at	3373.8	P	tRNA-Ser
3755_f_at	314.9	P	Ty3 LTR
3756_i_at	2.5	A	Ty1 LTR
3757_f_at	299.8	P	Ty1 LTR
3758_f_at	6451.3	P	tRNA-Glu
3759_f_at	5244.1	P	Ty1 LTR
3760_at	1566.2	P	tRNA-Arg
3761_f_at	16648.4	P	Ty2 LTR
3762_s_at	13936.4	P	Saccharomyces cerevisiae chromosome XII, complete chromosome
3763_s_at	6245.2	P	Saccharomyces cerevisiae chromosome XII, complete chromosome
3717_s_at	28300.5	P	Saccharomyces cerevisiae chromosome XII, complete chromosome
3718_s_at	31598.9	P	Saccharomyces cerevisiae chromosome XII, complete chromosome
3719_s_at	17128.3	P	Saccharomyces cerevisiae chromosome XII, complete chromosome
3720_f_at	26045.1	P	Saccharomyces cerevisiae chromosome XII, complete chromosome
3721_s_at	18941.2	P	Full length Ty2
3722_s_at	24189.2	P	Full length Ty2
3723_f_at	19668.3	P	Full length Ty2
3724_f_at	13729.5	P	Ty2 LTR
3725_at	274.4	P	Ty1 LTR
3726_f_at	8747.6	P	Ty2 LTR
3727_f_at	9195.7	P	Full length Ty2
3728_f_at	17194.1	P	Saccharomyces cerevisiae chromosome XII, complete chromosome
3729_f_at	10336.3	P	Ty2 LTR
3730_at	1564.2	P	Ty1 LTR
3731_s_at	1884.4	P	strong similarity to subtelomeric encoded proteins
3732_s_at	1038.8	P	strong similarity to subtelomeric encoded proteins
3733_s_at	3222.4	P	strong similarity to subtelomeric encoded proteins
3734_s_at	5162.8	P	strong similarity to subtelomeric encoded proteins
3735_f_at	19427.9	P	strong similarity to subtelomeric encoded proteins
3736_s_at	3837.8	P	strong similarity to subtelomeric encoded proteins
3737_s_at	2860.5	P	strong similarity to subtelomeric encoded proteins
3738_s_at	21485.5	P	Protein with strong similarity to subtelomerically-encoded proteins su
3739_f_at	24978.9	P	Protein with strong similarity to subtelomerically-encoded proteins su
3695_f_at	2373.9	P	tRNA-Arg
3696_at	212	A	Ty1 LTR
3697_f_at	17590.4	P	Ty2 LTR
3698_f_at	3583	A	tRNA-Gly
3699_f_at	23437.9	P	Ty1 LTR
3700_f_at	15091.2	P	Full length Ty1
3701_f_at	22338.5	P	Ty1 LTR
3702_f_at	21879.9	P	Ty1 LTR
3703_f_at	26414.2	P	Saccharomyces cerevisiae chromosome XIII, complete chromosome
3704_f_at	15172.1	P	Full length Ty1

3705_f_at	23525.4	P	Full length Ty1
3706_f_at	13130.5	P	Ty1 LTR
3707_f_at	6482.3	P	tRNA-Ser
3708_at	22.3	A	Ty4 LTR
3709_f_at	5367.8	P	tRNA-Glu
3710_f_at	9239.6	P	tRNA-Ala
3711_f_at	16597.3	P	Ty1 LTR
3712_s_at	14560.8	P	Full length Ty1
3713_s_at	16508.4	P	Full length Ty1
3714_f_at	11247.9	P	Full length Ty1
3715_f_at	18703.8	P	Ty1 LTR
3716_f_at	3411.2	P	tRNA-His
3671_f_at	14950.6	P	Ty1 LTR
3672_f_at	9063.2	P	Full length Ty1
3673_f_at	15251.6	P	Ty1 LTR
3674_i_at	335	A	Ty1 LTR
3675_r_at	202.9	A	Ty1 LTR
3676_f_at	420.2	M	Ty1 LTR
3677_f_at	415.7	A	Ty1 LTR
3678_at	6	A	Ty1 LTR
3679_at	132.5	A	Ty1 LTR
3680_i_at	90.3	A	Ty1 LTR
3681_s_at	50.7	A	Ty1 LTR
3682_i_at	1.9	A	Ty1 LTR
3683_f_at	285.4	P	Ty1 LTR
3684_f_at	2059.5	P	Ty4 LTR
3685_f_at	4139.9	P	Ty1 LTR
3686_f_at	200.5	M	Ty1 LTR
3687_f_at	2167.9	P	tRNA-Arg
3688_f_at	9892.1	P	tRNA-Ala
3689_f_at	11745.3	P	Ty2 LTR
3690_f_at	2849.6	P	tRNA-Gln
3691_f_at	2337.9	P	Ty4 LTR
3692_at	97.7	A	Ty1 LTR
3693_f_at	511.8	P	Ty1 LTR
3694_at	410.1	A	strong similarity to subtelomeric encoded proteins
3646_s_at	666	P	strong similarity to subtelomeric encoded proteins
3647_f_at	1150.8	P	strong similarity to subtelomeric encoded proteins
3648_f_at	19349.2	P	Protein with similarity to subtelomerically-encoded proteins such as
3649_f_at	888.4	A	tRNA-Gly
3650_f_at	2516.8	P	Ty4 LTR
3651_f_at	16827.9	P	Ty1 LTR
3652_f_at	13895.8	P	Full length Ty1
3653_f_at	16732.3	P	Ty1 LTR
3654_i_at	84.8	A	Ty3 LTR
3655_f_at	57.6	A	Ty3 LTR
3656_f_at	15600.2	P	Ty1 LTR
3657_f_at	15092.3	P	Saccharomyces cerevisiae chromosome XIV, complete chromosom
3658_f_at	9174.5	P	Full length Ty1
3659_f_at	10105.2	P	Full length Ty1
3660_f_at	15076.3	P	Ty1 LTR
3661_at	1631.9	P	Ty3 LTR

3662_f_at	13388.2	P	Ty3 LTR
3663_f_at	2342	P	Ty4 LTR
3664_f_at	14434.4	P	Ty2 LTR
3665_f_at	14200.9	P	Full length Ty2
3666_f_at	14392.3	P	Saccharomyces cerevisiae chromosome XIV, complete chromosom
3667_f_at	17901	P	Ty2 LTR
3668_f_at	10427.4	M	tRNA-Pro
3669_f_at	8389.7	P	Ty1 LTR
3670_f_at	910.1	P	Ty4 LTR
3621_i_at	3	A	Ty3 LTR
3622_f_at	8306.4	P	Ty3 LTR
3623_f_at	13056.1	P	Ty1 LTR
3624_at	2371.7	P	Ty1 LTR
3625_at	852.3	P	Protein with strong similarity to subtelomerically-encoded proteins s
3626_i_at	1807.8	P	Protein with strong similarity to subtelomerically-encoded proteins s
3627_r_at	685.7	A	Protein with strong similarity to subtelomerically-encoded proteins s
3628_f_at	72.3	A	Protein with strong similarity to subtelomerically-encoded proteins s
3629_f_at	705.7	A	strong similarity to subtelomeric encoded proteins
3630_at	35	A	Ty1 LTR
3631_s_at	1643.9	P	Ty4 LTR
3632_at	14.9	A	Ty1 LTR
3633_f_at	811.6	A	tRNA-Gly
3634_f_at	1107.9	P	Ty1 LTR
3635_f_at	18888.2	P	Ty1 LTR
3636_f_at	23759.4	P	Saccharomyces cerevisiae chromosome XV, complete chromosome
3637_f_at	11274.3	P	Full length Ty1
3638_f_at	24257.1	P	Full length Ty1
3639_f_at	21026.9	P	Ty1 LTR
3640_f_at	3282.4	M	tRNA-Gly
3641_f_at	32.2	A	Ty3 LTR
3642_at	18.6	A	Ty1 LTR
3643_i_at	7.1	A	Ty1 LTR
3644_f_at	433.3	A	Ty1 LTR
3645_f_at	3316.5	M	tRNA-Gly
3597_at	32.1	A	Ty1 LTR
3598_f_at	3516.8	P	tRNA-Arg
3599_at	5.7	A	Ty1 LTR
3600_i_at	11.7	A	Ty3 LTR
3601_f_at	24.4	A	Ty3 LTR
3602_at	167.9	A	Ty1 LTR
3603_at	193.3	A	Ty1 LTR
3604_f_at	84.6	A	tRNA-Gly
3605_f_at	272.2	A	Ty1 LTR
3606_f_at	15360.5	P	Ty1 LTR
3607_f_at	11576.8	P	Full length Ty1
3608_f_at	18294.2	P	Ty1 LTR
3609_i_at	58.3	A	Ty1 LTR
3610_f_at	174.5	A	Ty1 LTR
3611_f_at	451.4	A	Ty1 LTR
3612_f_at	16477.6	P	Ty2 LTR
3613_i_at	351.7	A	Ty1 LTR
3614_f_at	733.8	M	Ty1 LTR

3615_i_at	13.6	A	Ty1 LTR
3616_f_at	118.1	P	Ty1 LTR
3617_f_at	1571.3	P	Ty4 LTR
3618_f_at	14619.9	P	Ty2 LTR
3619_f_at	11868.6	P	Full length Ty2
3620_f_at	34153.1	P	Saccharomyces cerevisiae chromosome XV, complete chromosome
3572_f_at	14407	P	Ty2 LTR
3573_f_at	1440.4	P	Ty4 LTR
3574_f_at	4244.8	P	tRNA-Ala
3575_f_at	8707.8	P	Ty3 LTR
3576_f_at	719.8	A	Ty3 LTR
3577_at	312.5	P	Ty1 LTR
3578_f_at	8406.7	P	Ty2 LTR
3579_f_at	22473.5	P	Saccharomyces cerevisiae chromosome XV, complete chromosome
3580_f_at	19873.9	P	Full length Ty2
3581_f_at	8056.9	P	Ty2 LTR
3582_f_at	12139.8	P	Ty1 LTR
3583_i_at	696.9	A	Ty1 LTR
3584_f_at	461.6	P	Ty1 LTR
3585_f_at	11.9	A	Ty3 LTR
3586_f_at	18222.1	P	Ty1 LTR
3587_f_at	20269.3	P	Saccharomyces cerevisiae chromosome XVI, complete chromosome
3588_f_at	15982.7	P	Full length Ty1
3589_f_at	23320.3	P	Full length Ty1
3590_f_at	18910.6	P	Ty1 LTR
3591_f_at	9428.2	P	Ty2 LTR
3592_i_at	109.1	A	Ty1 LTR
3593_f_at	3899.3	P	Ty1 LTR
3594_f_at	6044.2	P	tRNA-Glu
3595_at	76.6	A	Ty1 LTR
3596_f_at	12505.5	P	Ty2 LTR
3548_s_at	1659.3	P	tRNA-Cys
3549_f_at	90.9	A	Ty1 LTR
3550_i_at	3.3	A	Ty1 LTR
3551_f_at	444.6	A	Ty1 LTR
3552_f_at	38	A	Ty1 LTR
3553_f_at	2333.5	P	Ty4 LTR
3554_f_at	3131.7	P	Full length Ty4
3555_s_at	537.1	P	Saccharomyces cerevisiae chromosome XVI, complete chromosome
3556_s_at	203.8	A	Saccharomyces cerevisiae chromosome XVI, complete chromosome
3557_s_at	33.7	A	Saccharomyces cerevisiae chromosome XVI, complete chromosome
3558_f_at	2124.7	P	Ty4 LTR
3559_f_at	20850.2	P	Ty1 LTR
3560_at	362.3	P	Ty1 LTR
3561_f_at	3540.9	M	tRNA-Gly
3562_f_at	3913.6	P	tRNA-Ser
3563_s_at	559	P	tRNA-Thr
3564_f_at	19335.8	P	Ty3 LTR
3565_at	315.4	A	Ty1 LTR
3566_i_at	137.4	A	Ty1 LTR
3567_r_at	11.2	A	Ty1 LTR
3568_f_at	1177.5	P	Ty1 LTR

3569_at	366.2	A	Ty1 LTR
3570_f_at	1115.2	P	Ty1 LTR
3571_f_at	13460.8	P	Ty1 LTR
3524_f_at	6744.8	P	Full length Ty1
3525_f_at	18356.3	P	Full length Ty1
3526_f_at	16027.7	P	Saccharomyces cerevisiae chromosome XVI, complete chromosome
3527_f_at	15464.3	P	Ty1 LTR
3528_f_at	15263.9	P	Ty1 LTR
3529_f_at	23103.5	P	Full length Ty3
3530_f_at	16472.4	P	Ty1 LTR
3531_at	656.1	P	Ty1 LTR
3532_f_at	24361.3	P	Ty1 LTR
3533_f_at	25657.4	P	Full length Ty1
3534_f_at	21602.2	P	Ty1 LTR
3535_i_at	130.4	A	Ty3 LTR
3536_f_at	8927.8	P	Ty3 LTR
3537_f_at	12183.4	P	tRNA-Ala
3538_f_at	4463	M	tRNA-Gly
3539_f_at	1024.1	P	Ty3 LTR
3540_at	251.1	M	Ty4 LTR
3541_at	505.9	A	Ty4 LTR
3542_f_at	16429	P	strong similarity to subtelomeric encoded proteins
3543_s_at	18880.2	P	strong similarity to subtelomeric encoded proteins
3544_at	50.9	A	strong similarity to subtelomeric encoded proteins
3545_i_at	146	A	Ty1 LTR
3546_f_at	5.9	A	Ty1 LTR
3547_f_at	6394.5	P	Ty2 LTR
3500_f_at	4.5	A	Ty1 LTR
3501_f_at	7724.5	P	Ty2 LTR
3502_f_at	23392.2	P	Saccharomyces cerevisiae chromosome II, complete chromosome s
3503_f_at	7850.1	P	Full length Ty2
3504_f_at	7903.3	P	Ty2 LTR
3505_s_at	1117.5	P	Ty1 LTR
3506_s_at	2140	P	Ty4 LTR
3507_at	79.6	A	Ty1 LTR
3508_f_at	3254	A	tRNA-Gly
3509_f_at	5535.5	P	Ty3 LTR
3510_s_at	878.3	P	Ty1 LTR
3511_f_at	17621.7	P	Ty1 LTR
3512_f_at	15494	P	Full length Ty1
3513_f_at	19464.6	P	Ty1 LTR
3514_f_at	6542.8	P	tRNA-Ser
3515_at	969.1	P	Ty1 LTR
3516_f_at	15268.7	P	Ty1 LTR
3517_f_at	10706.4	P	Full length Ty1
3518_f_at	12643	P	Ty1 LTR
3519_f_at	40.2	A	Ty1 LTR
3520_s_at	4889.6	P	tRNA-Val
3521_i_at	14.2	A	Ty1 LTR
3522_f_at	368.6	P	Ty1 LTR
3523_at	527.5	A	Ty1 LTR
3477_at	19.1	A	Ty1 LTR

3478_f_at	17706.5	P	tRNA-Gln
3479_f_at	2665.5	P	tRNA-Arg
3480_at	12.3	A	Ty1 LTR
3481_at	355.8	A	Ty1 LTR
3482_f_at	5516.9	P	tRNA-Glu
3483_f_at	21774	P	Protein with similarity to members of the Cos3\/Cos5\/Cos1\/Cos4\/C
3484_f_at	58.9	A	Ty5 LTR
3485_at	28.2	A	Full length Ty5
3486_at	409.8	A	Full length Ty5
3487_g_at	110.1	A	Full length Ty5
3488_at	110.5	A	Full length Ty5
3489_f_at	1.3	A	Full length Ty5
3490_f_at	2.7	A	Ty5 LTR
3491_f_at	5343.8	P	tRNA-Glu
3492_f_at	2287.6	P	Ty1 LTR
3493_f_at	5886.7	P	Ty1 LTR
3494_f_at	9272.5	P	Ty1 LTR
3495_f_at	852.6	P	Ty1 LTR
3496_f_at	13370.3	P	Ty2 LTR
3497_f_at	19492.8	P	Saccharomyces cerevisiae chromosome III, complete chromosome
3498_f_at	20754.1	P	Full length Ty2
3499_f_at	12440.1	P	Ty2 LTR
3451_f_at	9486.5	M	tRNA-Pro
3452_f_at	13153.5	P	Ty1 LTR
3453_at	244.7	M	strong similarity to subtelomeric encoded proteins
3454_s_at	1329.1	P	tRNA-Asn
3455_f_at	2806.5	A	tRNA-Gly
3456_i_at	38	A	Ty1 LTR
3457_f_at	2256.9	P	Ty1 LTR
3458_f_at	510.1	P	Ty1 LTR
3459_at	259.9	A	Ty1 LTR
3460_at	29.3	A	Ty4 LTR
3461_f_at	16391.8	P	Ty1 LTR
3462_f_at	14385.7	P	tRNA-Gln
3463_at	747.8	P	Ty1 LTR
3464_at	289.6	P	Ty1 LTR
3465_at	29.1	A	Ty5 LTR
3466_i_at	11.5	A	Ty1 LTR
3467_f_at	252.2	A	Ty1 LTR
3468_i_at	20.2	A	Ty1 LTR
3469_f_at	72.2	A	Ty1 LTR
3470_i_at	3718.2	P	Protein with strong similarity to other subtelomerically-encoded prote
3471_f_at	4879.2	P	Protein with strong similarity to other subtelomerically-encoded prote
3472_f_at	3246.9	A	tRNA-Gly
3473_f_at	10840.9	P	tRNA-Ala
3474_f_at	3200	P	Ty1 LTR
3475_f_at	1604.7	P	Ty4 LTR
3476_f_at	5815.1	P	tRNA-Ser
3427_at	210.8	M	Ty1 LTR
3428_f_at	5070	P	Ty1 LTR
3429_f_at	14988.7	P	Ty2 LTR
3430_f_at	24867.5	P	Full length Ty2

3431_f_at	23080.2	P	Saccharomyces cerevisiae chromosome IV, complete chromosome
3432_f_at	6378.8	P	Ty2 LTR
3433_i_at	148.6	A	Ty1 LTR
3434_f_at	239.8	A	Ty1 LTR
3435_f_at	2092.8	P	Ty1 LTR
3436_f_at	11852	P	tRNA-Gln
3437_f_at	1631.7	P	tRNA-Arg
3438_f_at	3573.8	P	tRNA-Arg
3439_f_at	12202.5	P	tRNA-Gln
3440_f_at	13060.6	P	Ty1 LTR
3441_f_at	15727.9	P	Full length Ty1
3442_f_at	17864.8	P	Full length Ty1
3443_f_at	25168.3	P	Saccharomyces cerevisiae chromosome IV, complete chromosome
3444_f_at	14100	P	Ty1 LTR
3445_f_at	2071.5	P	Ty3 LTR
3446_i_at	4.6	A	Ty1 LTR
3447_f_at	654	M	Ty1 LTR
3448_s_at	6073.6	P	Ty3 LTR
3449_i_at	340.6	P	Ty1 LTR
3450_r_at	3.7	A	Ty1 LTR
3404_f_at	2320.1	P	Ty1 LTR
3405_f_at	14301.3	P	tRNA-Gln
3406_f_at	23397.5	P	Ty1 LTR
3407_at	663.5	P	Saccharomyces cerevisiae chromosome IV, complete chromosome
3408_f_at	14021.6	P	Ty1 LTR
3409_f_at	35575.8	P	Saccharomyces cerevisiae chromosome IV, complete chromosome
3410_f_at	7752.2	P	Full length Ty2
3411_f_at	11894.6	P	Ty1 LTR
3412_f_at	12118.7	P	Full length Ty1
3413_f_at	18261.6	P	Full length Ty1
3414_f_at	16475.6	P	Saccharomyces cerevisiae chromosome IV, complete chromosome
3415_i_at	18.2	A	Ty1 LTR
3416_s_at	7249.7	P	Ty1 LTR
3417_f_at	12167	P	Ty3 LTR
3418_f_at	6012.6	P	tRNA-Ser
3419_f_at	8462.9	P	Ty1 LTR
3420_f_at	22608.2	P	Saccharomyces cerevisiae chromosome IV, complete chromosome
3421_f_at	14566.3	P	Full length Ty2
3422_f_at	10440.5	P	Ty1 LTR
3423_f_at	12535.2	P	Ty1 LTR
3424_f_at	10513.5	P	Full length Ty1
3425_f_at	14154	P	Full length Ty1
3426_f_at	13283.7	P	Saccharomyces cerevisiae chromosome IV, complete chromosome
3379_f_at	12791.8	P	Ty1 LTR
3380_i_at	236	P	Ty3 LTR
3381_f_at	44.1	A	Ty3 LTR
3382_f_at	3269	P	tRNA-Gly
3383_f_at	2878.5	P	tRNA-Glu
3384_f_at	6700.3	P	Ty3 LTR
3385_s_at	4807.9	P	tRNA-Val
3386_f_at	17639.8	P	Ty1 LTR
3387_f_at	9737.7	P	Full length Ty1

3388_f_at	19790.2	P	Ty1 LTR
3389_f_at	3936	P	Ty1 LTR
3390_at	133.1	A	Ty3 LTR
3391_f_at	3218.7	P	Ty1 LTR
3392_f_at	21482.4	P	Ty1 LTR
3393_f_at	37772.5	P	Saccharomyces cerevisiae chromosome IV, complete chromosome
3394_f_at	12713.2	P	Full length Ty1
3395_f_at	20980	P	Full length Ty1
3396_f_at	16612	P	Ty1 LTR
3397_f_at	189.9	A	tRNA-Gly
3398_f_at	4388.3	P	tRNA-Ser
3399_f_at	9775.9	P	Ty1 LTR
3400_i_at	66.9	A	Ty1 LTR
3401_f_at	53.2	A	Ty1 LTR
3402_at	153.9	A	Ty1 LTR
3403_f_at	1887.2	P	strong similarity to subtelomeric encoded proteins
3356_f_at	1025.1	P	strong similarity to subtelomeric encoded proteins
3357_at	328.2	A	strong similarity to subtelomeric encoded proteins
3358_f_at	3311.2	A	tRNA-Gly
3359_f_at	12643.8	P	Ty1 LTR
3360_at	21	A	Ty1 LTR
3361_f_at	5653.1	P	tRNA-Ser
3362_at	7	A	Ty1 LTR
3363_at	19.8	A	Ty4 LTR
3364_f_at	12327.8	P	tRNA-Gln
3365_f_at	10110.9	P	Ty1 LTR
3366_at	99.3	A	Ty1 LTR
3367_f_at	890.9	P	Ty1 LTR
3368_f_at	2190.1	P	tRNA-Arg
3369_i_at	4.6	A	Ty1 LTR
3370_f_at	450.6	P	Ty1 LTR
3371_f_at	5636.1	P	tRNA-Glu
3372_f_at	3807.2	P	tRNA-His
3373_at	598.7	P	Ty1 LTR
3374_at	539.6	P	Ty1 LTR
3375_f_at	6435.5	P	Ty3 LTR
3376_f_at	13835.8	P	tRNA-Gln
3377_at	282.8	A	Ty1 LTR
3378_f_at	4405.8	P	tRNA-Ser
3332_i_at	12.8	A	Ty1 LTR
3333_f_at	4047.3	P	Ty1 LTR
3334_at	238	A	Ty1 LTR
3335_at	154.5	A	Ty1 LTR
3336_f_at	1364.8	P	Ty4 LTR
3337_i_at	994.8	A	Ty3 LTR
3338_f_at	6.3	A	Ty3 LTR
3340_f_at	10117.4	P	Ty1 LTR
3342_f_at	6892.2	P	Ty3 LTR
3343_i_at	2682.9	P	Ty1 LTR
3344_f_at	2343.3	P	Ty1 LTR
3345_f_at	4545	P	Ty1 LTR
3346_at	258.7	A	Ty4 LTR

3347_s_at	5558.6	P	Ty1 LTR
3348_f_at	10716.4	P	Ty1 LTR
3350_f_at	21073.3	P	Full length Ty1
3352_s_at	13831.8	P	Ty1 LTR
3354_s_at	693.6	P	Ty1 LTR
3355_s_at	2331.9	P	Ty1 LTR
3307_s_at	305.8	P	Ty1 LTR
3308_s_at	394.8	P	Ty1 LTR
3309_s_at	291.2	A	Ty1 LTR
3310_s_at	1646.6	P	Ty1 LTR
3311_f_at	10832.9	P	Ty1 LTR
3313_f_at	7480.2	P	Ty1 LTR
3315_f_at	28725.7	P	Ty3 LTR
3316_f_at	34382.8	P	Ty3 LTR
3317_f_at	31017.2	P	Ty1 LTR
3319_f_at	27614.7	P	Ty1 LTR
3320_i_at	167.1	A	Ty1 LTR
3321_f_at	236.8	A	Ty1 LTR
3322_at	35.2	A	Ty1 LTR
3323_i_at	3.6	A	Ty5 LTR
3324_at	186	P	Ty5 LTR
3325_f_at	2066.6	P	strong similarity to subtelomeric encoded proteins
3326_at	149.1	A	strong similarity to subtelomeric encoded proteins
3327_f_at	25213.3	P	Protein with strong similarity to subtelomerically-encoded proteins su
3328_at	58.6	A	Ty1 LTR
3329_f_at	1453.4	P	Ty1 LTR
3330_f_at	14167.6	P	Ty2 LTR
3283_f_at	21627.9	P	Saccharomyces cerevisiae chromosome VI, complete chromosome
3284_f_at	15212.1	P	Full length Ty2
3285_f_at	10272.5	P	Ty2 LTR
3286_f_at	1852.2	P	Ty1 LTR
3287_s_at	271.6	P	Ty4 LTR
3288_at	80.6	A	Ty1 LTR
3289_i_at	626.7	A	Ty1 LTR
3290_f_at	163	A	Ty1 LTR
3291_f_at	1858.4	P	Ty1 LTR
3294_at	6.9	A	Ty1 LTR
3296_at	8.2	A	Ty1 LTR
3297_i_at	7.5	A	Ty5 LTR
3298_f_at	3.9	A	Ty5 LTR
3299_f_at	44.1	A	strong similarity to subtelomeric encoded proteins
3301_f_at	1289.2	P	Ty4 LTR
3302_f_at	6453.8	P	Ty1 LTR
3303_f_at	211	P	Ty1 LTR
3304_f_at	472.4	A	Ty1 LTR
3305_at	129.1	A	Ty4 LTR
3306_i_at	1257.6	P	Ty1 LTR
3258_f_at	438.4	P	Ty1 LTR
3259_at	6163	P	Ty1 LTR
3260_f_at	10878.2	P	Ty3 LTR
3262_at	7.4	A	Ty4 LTR
3263_i_at	80.5	A	Ty1 LTR

3264_f_at	392	P	Ty1 LTR
3267_f_at	2732	P	Ty3 LTR
3268_f_at	23066.4	P	Ty1 LTR
3269_f_at	318.6	P	Ty1 LTR
3270_f_at	10651.9	P	Ty1 LTR
3271_i_at	214.1	P	Ty3 LTR
3272_f_at	2199.6	P	Ty3 LTR
3274_at	221.1	A	Ty1 LTR
3276_i_at	17.9	A	Ty1 LTR
3277_f_at	23	A	Ty1 LTR
3279_f_at	8590.7	P	Full length Ty1
3235_f_at	11243.3	P	Ty1 LTR
3236_f_at	12831	P	Full length Ty1
3237_f_at	21252.3	P	Full length Ty1
3239_f_at	18907.8	P	Ty1 LTR
3240_f_at	11580.3	P	Ty2 LTR
3241_f_at	13726.5	P	Full length Ty2
3243_at	3620.6	P	tRNA-Leu
3244_i_at	117.3	A	Ty1 LTR
3245_f_at	453.9	P	Ty1 LTR
3247_s_at	1332.4	P	TY3B protein Found forward in NC_001139 between 707604 and 70
3248_s_at	1863.5	P	Saccharomyces cerevisiae chromosome VII, complete chromosome
3249_s_at	4280.2	P	Saccharomyces cerevisiae chromosome VII, complete chromosome
3250_s_at	2129.2	P	Saccharomyces cerevisiae chromosome VII, complete chromosome
3251_s_at	346	P	Full length Ty3
3252_s_at	4584.7	P	Full length Ty3
3253_f_at	14258.8	P	Full length Ty3
3255_at	619.8	P	Ty1 LTR
3256_at	128.2	A	Ty1 LTR
3257_f_at	5368.2	P	Ty3 LTR
3212_f_at	1251.2	P	Ty1 LTR
3214_at	367.1	P	Ty1 LTR
3215_f_at	272.3	M	Ty1 LTR
3216_at	29.9	A	Ty1 LTR
3218_at	39	A	Ty1 LTR
3222_f_at	17627.9	P	Full length Ty2
3223_f_at	15310.6	P	Ty2 LTR
3225_f_at	11687.5	P	Full length Ty1
3226_f_at	19317.4	P	Ty1 LTR
3228_at	675.3	M	Ty3 LTR
3230_f_at	8428.4	P	Ty1 LTR
3232_f_at	2957.5	P	Ty4 LTR
3233_f_at	24471.3	P	Ty1 LTR
3234_at	10128.7	P	Protein with strong similarity to other subtelomerically-encoded prote
3187_s_at	7788.2	P	strong similarity to subtelomeric encoded proteins
3188_at	1762	M	Protein with similarity to subtelomerically-encoded proteins such as
3189_i_at	59	A	Protein with similarity to subtelomerically-encoded proteins such as
3190_f_at	551.9	P	Protein with similarity to subtelomerically-encoded proteins such as
3191_i_at	36.2	A	Ty5 LTR
3192_f_at	2.3	A	Ty5 LTR
3193_at	132.8	A	strong similarity to subtelomeric encoded proteins
3195_f_at	8898.4	P	Ty3 LTR

3196_f_at	1583.1	P	Ty4 LTR
3199_f_at	15116.5	P	Ty1 LTR
3200_i_at	203.4	A	Ty1 LTR
3201_r_at	30.5	A	Ty1 LTR
3202_f_at	4.1	A	Ty1 LTR
3203_f_at	21720.8	P	Ty1 LTR
3204_at	1090.9	A	Ty1 LTR
3206_at	11.8	A	Ty1 LTR
3207_i_at	545.9	A	Ty1 LTR
3208_f_at	182.3	A	Ty1 LTR
3209_f_at	17637.1	P	Ty1 LTR
3161_f_at	4654.8	P	Ty3 LTR
3162_at	1258.8	P	Ty4 LTR
3163_i_at	118.7	A	Ty1 LTR
3164_f_at	35.8	A	Ty1 LTR
3165_at	10.6	A	Ty4 LTR
3166_i_at	286.4	A	Ty1 LTR
3167_r_at	298.1	A	Ty1 LTR
3168_f_at	197.8	A	Ty1 LTR
3169_f_at	23295.8	P	Ty2 LTR
3170_i_at	69.5	A	Ty1 LTR
3171_r_at	58.1	A	Ty1 LTR
3172_f_at	302.6	A	Ty1 LTR
3173_i_at	28.4	A	Ty1 LTR
3174_f_at	18	A	Ty1 LTR
3175_i_at	686.8	A	Ty1 LTR
3176_f_at	506.1	P	Ty1 LTR
3177_f_at	550.4	A	Ty3 LTR
3178_f_at	157.9	M	Ty1 LTR
3180_f_at	10491.8	P	Full length Ty1
3181_f_at	20094.6	P	Ty1 LTR
3182_i_at	127.2	A	strong similarity to subtelomeric encoded YDR544c
3183_f_at	22811.9	P	strong similarity to subtelomeric encoded proteins
3184_s_at	496.7	P	strong similarity to subtelomeric encoded proteins
3185_s_at	250.2	A	strong similarity to subtelomeric encoded proteins
3133_f_at	2144	P	Ty1 LTR
3136_s_at	8862	P	Saccharomyces cerevisiae chromosome IX, complete chromosome
3137_s_at	2674.8	P	Full length Ty3
3139_f_at	314.3	P	Ty2 LTR
3141_i_at	78.5	A	Ty1 LTR
3142_f_at	3949.4	P	Ty1 LTR
3143_f_at	384.1	P	Ty3 LTR
3144_f_at	1472.8	P	Ty1 LTR
3145_at	721.5	P	Ty1 LTR
3147_at	172.4	A	Ty1 LTR
3148_s_at	11156.4	P	mating hormone a2
3149_at	1331.8	A	Saccharomyces cerevisiae chromosome I, complete chromosome se
3150_at	1415.6	P	Saccharomyces cerevisiae chromosome I, complete chromosome se
3151_g_at	682.9	P	Saccharomyces cerevisiae chromosome I, complete chromosome se
3152_at	2033.1	P	Saccharomyces cerevisiae chromosome I, complete chromosome se
3153_at	228.5	A	Saccharomyces cerevisiae chromosome I, complete chromosome se
3154_at	524.3	P	Saccharomyces cerevisiae chromosome I, complete chromosome se

3155_at	84	A	Saccharomyces cerevisiae chromosome I, complete chromosome se
3156_at	24.6	A	Saccharomyces cerevisiae chromosome I, complete chromosome se
3157_at	601.1	P	Saccharomyces cerevisiae chromosome I, complete chromosome se
3158_at	241	P	Saccharomyces cerevisiae chromosome I, complete chromosome se
3159_at	186.6	A	Saccharomyces cerevisiae chromosome I, complete chromosome se
3088_at	170.9	A	Saccharomyces cerevisiae chromosome I, complete chromosome se
3089_g_at	39.9	A	Saccharomyces cerevisiae chromosome I, complete chromosome se
3090_s_at	804.9	A	Saccharomyces cerevisiae chromosome I, complete chromosome se
3091_at	25.5	A	Saccharomyces cerevisiae chromosome I, complete chromosome se
3092_f_at	0.9	A	Saccharomyces cerevisiae chromosome I, complete chromosome se
3093_f_at	394.3	A	Saccharomyces cerevisiae chromosome I, complete chromosome se
3096_f_at	192.2	P	Saccharomyces cerevisiae chromosome I, complete chromosome se
3097_at	263.1	A	Saccharomyces cerevisiae chromosome I, complete chromosome se
3098_at	66.2	A	Saccharomyces cerevisiae chromosome I, complete chromosome se
3099_at	257	A	Saccharomyces cerevisiae chromosome I, complete chromosome se
3100_s_at	304.3	P	Saccharomyces cerevisiae chromosome I, complete chromosome se
3101_at	555.9	A	Saccharomyces cerevisiae chromosome I, complete chromosome se
3102_s_at	370.7	P	Saccharomyces cerevisiae chromosome I, complete chromosome se
3103_at	150.2	P	Saccharomyces cerevisiae chromosome I, complete chromosome se
3104_at	245.4	A	Saccharomyces cerevisiae chromosome I, complete chromosome se
3105_g_at	21.7	A	Saccharomyces cerevisiae chromosome I, complete chromosome se
3106_s_at	63.2	A	Saccharomyces cerevisiae chromosome I, complete chromosome se
3107_s_at	67.2	A	Saccharomyces cerevisiae chromosome I, complete chromosome se
3108_at	288.9	A	Saccharomyces cerevisiae chromosome X, complete chromosome s
3109_at	459	A	Saccharomyces cerevisiae chromosome X, complete chromosome s
3110_s_at	13.2	A	Saccharomyces cerevisiae chromosome X, complete chromosome s
3111_s_at	406.1	A	Saccharomyces cerevisiae chromosome X, complete chromosome s
3112_s_at	36.1	A	Saccharomyces cerevisiae chromosome X, complete chromosome s
3113_s_at	1218.3	P	Saccharomyces cerevisiae chromosome X, complete chromosome s
3114_s_at	2897.8	P	Saccharomyces cerevisiae chromosome X, complete chromosome s
3115_at	253	A	Saccharomyces cerevisiae chromosome X, complete chromosome s
3116_at	933.4	A	Saccharomyces cerevisiae chromosome X, complete chromosome s
3117_at	805.7	A	Saccharomyces cerevisiae chromosome X, complete chromosome s
3118_at	264.6	A	Saccharomyces cerevisiae chromosome X, complete chromosome s
3119_at	19.5	A	Saccharomyces cerevisiae chromosome X, complete chromosome s
3120_at	201.1	A	Saccharomyces cerevisiae chromosome X, complete chromosome s
3121_at	268.9	A	Saccharomyces cerevisiae chromosome X, complete chromosome s
3122_at	882.6	P	Saccharomyces cerevisiae chromosome X, complete chromosome s
3123_at	99.1	A	Saccharomyces cerevisiae chromosome X, complete chromosome s
3124_at	771.7	A	Saccharomyces cerevisiae chromosome X, complete chromosome s
3125_at	646.5	A	Saccharomyces cerevisiae chromosome X, complete chromosome s
3126_at	667.7	A	Saccharomyces cerevisiae chromosome X, complete chromosome s
3127_at	35.8	A	Saccharomyces cerevisiae chromosome X, complete chromosome s
3128_at	724.8	P	Saccharomyces cerevisiae chromosome X, complete chromosome s
3129_at	478.3	A	Saccharomyces cerevisiae chromosome X, complete chromosome s
3130_at	425.8	A	Saccharomyces cerevisiae chromosome X, complete chromosome s
3131_g_at	1026.2	P	Saccharomyces cerevisiae chromosome X, complete chromosome s
3045_s_at	1581.6	M	Saccharomyces cerevisiae chromosome X, complete chromosome s
3046_at	136.4	A	Saccharomyces cerevisiae chromosome X, complete chromosome s
3047_at	331.1	M	Saccharomyces cerevisiae chromosome X, complete chromosome s
3048_at	8.4	A	Saccharomyces cerevisiae chromosome X, complete chromosome s
3049_at	10.4	A	Saccharomyces cerevisiae chromosome X, complete chromosome s

3050_at	220.3	P	Saccharomyces cerevisiae chromosome X, complete chromosome s
3051_at	297.8	A	Saccharomyces cerevisiae chromosome X, complete chromosome s
3052_at	18.4	A	Saccharomyces cerevisiae chromosome X, complete chromosome s
3053_at	95.3	A	Saccharomyces cerevisiae chromosome X, complete chromosome s
3054_at	146.1	A	Saccharomyces cerevisiae chromosome X, complete chromosome s
3055_g_at	273.3	A	Saccharomyces cerevisiae chromosome X, complete chromosome s
3056_s_at	236.7	A	Saccharomyces cerevisiae chromosome X, complete chromosome s
3057_s_at	2012.7	P	Saccharomyces cerevisiae chromosome X, complete chromosome s
3058_s_at	1335.2	P	Saccharomyces cerevisiae chromosome X, complete chromosome s
3059_at	13.1	A	Saccharomyces cerevisiae chromosome X, complete chromosome s
3060_at	307.3	P	Saccharomyces cerevisiae chromosome X, complete chromosome s
3061_at	17.7	A	Saccharomyces cerevisiae chromosome X, complete chromosome s
3062_at	119.5	A	Saccharomyces cerevisiae chromosome X, complete chromosome s
3063_at	31.1	A	Saccharomyces cerevisiae chromosome X, complete chromosome s
3064_at	269.2	A	Saccharomyces cerevisiae chromosome X, complete chromosome s
3065_g_at	151.6	A	Saccharomyces cerevisiae chromosome X, complete chromosome s
3066_at	50.3	A	Saccharomyces cerevisiae chromosome X, complete chromosome s
3067_g_at	12.3	A	Saccharomyces cerevisiae chromosome X, complete chromosome s
3068_s_at	1006.6	A	Saccharomyces cerevisiae chromosome X, complete chromosome s
3069_s_at	211.3	A	Saccharomyces cerevisiae chromosome X, complete chromosome s
3070_s_at	208.3	A	Saccharomyces cerevisiae chromosome X, complete chromosome s
3071_s_at	551.6	M	Saccharomyces cerevisiae chromosome X, complete chromosome s
3072_s_at	3922.8	P	Saccharomyces cerevisiae chromosome X, complete chromosome s
3073_s_at	243.8	P	Saccharomyces cerevisiae chromosome X, complete chromosome s
3074_at	29	A	Saccharomyces cerevisiae chromosome X, complete chromosome s
3075_at	300.8	A	Saccharomyces cerevisiae chromosome X, complete chromosome s
3076_at	5	A	Saccharomyces cerevisiae chromosome X, complete chromosome s
3077_at	9.5	A	Saccharomyces cerevisiae chromosome X, complete chromosome s
3078_g_at	1458.8	P	Saccharomyces cerevisiae chromosome X, complete chromosome s
3079_s_at	3469.8	P	Saccharomyces cerevisiae chromosome X, complete chromosome s
3080_f_at	6913.6	P	Saccharomyces cerevisiae chromosome X, complete chromosome s
3081_at	535.4	A	Saccharomyces cerevisiae chromosome X, complete chromosome s
3082_at	10.9	A	Saccharomyces cerevisiae chromosome X, complete chromosome s
3083_g_at	48.5	A	Saccharomyces cerevisiae chromosome X, complete chromosome s
3084_s_at	86.2	A	Saccharomyces cerevisiae chromosome X, complete chromosome s
3085_s_at	1012.3	M	Saccharomyces cerevisiae chromosome X, complete chromosome s
3086_s_at	338.4	A	Saccharomyces cerevisiae chromosome X, complete chromosome s
3087_s_at	144	A	Saccharomyces cerevisiae chromosome X, complete chromosome s
3003_s_at	3032.8	P	Saccharomyces cerevisiae chromosome X, complete chromosome s
3004_s_at	2314.8	P	Saccharomyces cerevisiae chromosome X, complete chromosome s
3005_at	121.9	A	Saccharomyces cerevisiae chromosome X, complete chromosome s
3006_at	500.3	A	Saccharomyces cerevisiae chromosome X, complete chromosome s
3007_at	952.6	A	Saccharomyces cerevisiae chromosome X, complete chromosome s
3008_at	312.1	A	Saccharomyces cerevisiae chromosome X, complete chromosome s
3009_g_at	1017.6	P	Saccharomyces cerevisiae chromosome X, complete chromosome s
3010_s_at	22.9	A	Saccharomyces cerevisiae chromosome X, complete chromosome s
3011_s_at	1264.9	M	Saccharomyces cerevisiae chromosome X, complete chromosome s
3012_s_at	1774.8	P	Saccharomyces cerevisiae chromosome X, complete chromosome s
3013_at	118.6	A	Saccharomyces cerevisiae chromosome X, complete chromosome s
3014_at	133.9	A	Saccharomyces cerevisiae chromosome X, complete chromosome s
3015_at	426.5	A	Saccharomyces cerevisiae chromosome X, complete chromosome s
3016_at	525.2	A	Saccharomyces cerevisiae chromosome X, complete chromosome s

3017_g_at	630.4	P	Saccharomyces cerevisiae chromosome X, complete chromosome s
3018_s_at	562.6	P	Saccharomyces cerevisiae chromosome X, complete chromosome s
3019_at	13.4	A	Saccharomyces cerevisiae chromosome X, complete chromosome s
3020_at	5.4	A	Saccharomyces cerevisiae chromosome X, complete chromosome s
3021_at	41.6	A	Saccharomyces cerevisiae chromosome X, complete chromosome s
3022_at	18.9	A	Saccharomyces cerevisiae chromosome X, complete chromosome s
3023_at	25.7	A	Saccharomyces cerevisiae chromosome X, complete chromosome s
3024_g_at	393.3	P	Saccharomyces cerevisiae chromosome X, complete chromosome s
3025_s_at	1378.3	P	Saccharomyces cerevisiae chromosome X, complete chromosome s
3026_at	166.7	A	Saccharomyces cerevisiae chromosome X, complete chromosome s
3027_at	23.3	A	Saccharomyces cerevisiae chromosome X, complete chromosome s
3028_at	8.5	A	Saccharomyces cerevisiae chromosome X, complete chromosome s
3029_at	115.7	A	Saccharomyces cerevisiae chromosome X, complete chromosome s
3030_at	622.4	A	Saccharomyces cerevisiae chromosome X, complete chromosome s
3031_at	149.8	A	Saccharomyces cerevisiae chromosome X, complete chromosome s
3032_at	252.4	A	Saccharomyces cerevisiae chromosome X, complete chromosome s
3033_s_at	379.7	M	Saccharomyces cerevisiae chromosome X, complete chromosome s
3034_at	596.6	A	Saccharomyces cerevisiae chromosome XI, complete chromosome
3035_at	275.7	P	Saccharomyces cerevisiae chromosome XI, complete chromosome
3036_at	402.4	P	Saccharomyces cerevisiae chromosome XI, complete chromosome
3037_at	32.3	A	Saccharomyces cerevisiae chromosome XI, complete chromosome
3038_at	86.1	A	Saccharomyces cerevisiae chromosome XI, complete chromosome
3039_s_at	4561.2	P	Saccharomyces cerevisiae chromosome XI, complete chromosome
3040_at	1055.3	M	Saccharomyces cerevisiae chromosome XI, complete chromosome
3041_at	909.5	A	Saccharomyces cerevisiae chromosome XI, complete chromosome
3042_at	516.9	A	Saccharomyces cerevisiae chromosome XI, complete chromosome
3043_at	218.1	A	Saccharomyces cerevisiae chromosome XI, complete chromosome
3044_at	174.1	A	Saccharomyces cerevisiae chromosome XI, complete chromosome
2960_at	272.3	A	Saccharomyces cerevisiae chromosome XI, complete chromosome
2961_at	1010.6	A	Saccharomyces cerevisiae chromosome XI, complete chromosome
2962_at	1583	P	Saccharomyces cerevisiae chromosome XI, complete chromosome
2963_at	259.9	A	Saccharomyces cerevisiae chromosome XI, complete chromosome
2964_at	31670.3	P	Saccharomyces cerevisiae chromosome XI, complete chromosome
2965_g_at	16639.4	P	Saccharomyces cerevisiae chromosome XI, complete chromosome
2966_s_at	30573.9	P	Saccharomyces cerevisiae chromosome XI, complete chromosome
2967_s_at	14709.2	P	Saccharomyces cerevisiae chromosome XI, complete chromosome
2968_s_at	14021.9	P	Saccharomyces cerevisiae chromosome XI, complete chromosome
2969_s_at	18350.5	P	Saccharomyces cerevisiae chromosome XI, complete chromosome
2970_s_at	30590.7	P	Saccharomyces cerevisiae chromosome XI, complete chromosome
2971_at	633.1	A	Saccharomyces cerevisiae chromosome XI, complete chromosome
2972_at	184.3	M	Saccharomyces cerevisiae chromosome XI, complete chromosome
2973_at	263.8	A	Saccharomyces cerevisiae chromosome XI, complete chromosome
2974_at	44.6	A	Saccharomyces cerevisiae chromosome XI, complete chromosome
2975_at	540	A	Saccharomyces cerevisiae chromosome XI, complete chromosome
2976_at	314	A	Saccharomyces cerevisiae chromosome XI, complete chromosome
2977_at	399.8	A	Saccharomyces cerevisiae chromosome XI, complete chromosome
2978_at	481.3	A	Saccharomyces cerevisiae chromosome XI, complete chromosome
2979_at	23.7	A	Saccharomyces cerevisiae chromosome XI, complete chromosome
2980_at	226.3	A	Saccharomyces cerevisiae chromosome XI, complete chromosome
2981_at	55.8	A	Saccharomyces cerevisiae chromosome XI, complete chromosome
2982_at	131.1	A	Saccharomyces cerevisiae chromosome XI, complete chromosome
2983_at	19.1	A	Saccharomyces cerevisiae chromosome XI, complete chromosome

2984_at	61.1	A	Saccharomyces cerevisiae chromosome XI, complete chromosome
2985_at	28.3	A	Saccharomyces cerevisiae chromosome XI, complete chromosome
2986_at	232	A	Saccharomyces cerevisiae chromosome XI, complete chromosome
2987_at	472.9	P	Saccharomyces cerevisiae chromosome XI, complete chromosome
2988_at	27.1	A	Saccharomyces cerevisiae chromosome XI, complete chromosome
2989_at	278.5	M	Saccharomyces cerevisiae chromosome XI, complete chromosome
2990_g_at	762.4	A	Saccharomyces cerevisiae chromosome XI, complete chromosome
2991_at	1319.2	A	Saccharomyces cerevisiae chromosome XI, complete chromosome
2992_g_at	314.8	A	Saccharomyces cerevisiae chromosome XI, complete chromosome
2993_s_at	314.7	P	Saccharomyces cerevisiae chromosome XI, complete chromosome
2994_s_at	206.5	P	Saccharomyces cerevisiae chromosome XI, complete chromosome
2995_s_at	1223.6	P	Saccharomyces cerevisiae chromosome XI, complete chromosome
2996_s_at	725.4	M	Saccharomyces cerevisiae chromosome XI, complete chromosome
2997_s_at	129.3	P	Saccharomyces cerevisiae chromosome XI, complete chromosome
2998_at	307.9	A	Saccharomyces cerevisiae chromosome XI, complete chromosome
2999_at	330.3	A	Saccharomyces cerevisiae chromosome XI, complete chromosome
3000_at	575.9	A	Saccharomyces cerevisiae chromosome XI, complete chromosome
3001_at	199.1	A	Saccharomyces cerevisiae chromosome XI, complete chromosome
3002_g_at	187.1	A	Saccharomyces cerevisiae chromosome XI, complete chromosome
2917_s_at	64	A	Saccharomyces cerevisiae chromosome XI, complete chromosome
2918_s_at	1064.8	A	Saccharomyces cerevisiae chromosome XI, complete chromosome
2919_s_at	1039.6	P	Saccharomyces cerevisiae chromosome XI, complete chromosome
2920_at	1397.5	A	Saccharomyces cerevisiae chromosome XI, complete chromosome
2921_at	854.2	A	Saccharomyces cerevisiae chromosome XI, complete chromosome
2922_at	593.3	P	Saccharomyces cerevisiae chromosome XI, complete chromosome
2923_at	453.2	M	Saccharomyces cerevisiae chromosome XI, complete chromosome
2924_g_at	263.6	A	Saccharomyces cerevisiae chromosome XI, complete chromosome
2925_s_at	468.1	P	Saccharomyces cerevisiae chromosome XI, complete chromosome
2926_s_at	868.1	M	Saccharomyces cerevisiae chromosome XI, complete chromosome
2927_s_at	894.8	A	Saccharomyces cerevisiae chromosome XI, complete chromosome
2928_at	350.3	A	Saccharomyces cerevisiae chromosome XI, complete chromosome
2929_at	334	A	Saccharomyces cerevisiae chromosome XI, complete chromosome
2930_at	436.5	A	Saccharomyces cerevisiae chromosome XI, complete chromosome
2931_at	160	A	Saccharomyces cerevisiae chromosome XI, complete chromosome
2932_at	456.7	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2933_at	1218.6	P	Saccharomyces cerevisiae chromosome XII, complete chromosome
2934_at	138.3	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2935_at	1143.8	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2936_at	855.2	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2937_at	23.7	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2938_at	6.5	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2939_at	70.8	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2940_at	77.4	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2941_at	28.4	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2942_at	508.2	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2943_at	623	P	Saccharomyces cerevisiae chromosome XII, complete chromosome
2944_g_at	2108.1	P	Saccharomyces cerevisiae chromosome XII, complete chromosome
2945_s_at	1816.2	P	Saccharomyces cerevisiae chromosome XII, complete chromosome
2946_s_at	921	P	Saccharomyces cerevisiae chromosome XII, complete chromosome
2947_s_at	3277.3	P	Saccharomyces cerevisiae chromosome XII, complete chromosome
2948_s_at	1330.2	P	Saccharomyces cerevisiae chromosome XII, complete chromosome
2949_at	62	A	Saccharomyces cerevisiae chromosome XII, complete chromosome

2950_at	353.3	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2951_at	14.3	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2952_at	11.8	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2953_at	14.6	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2954_at	10.5	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2955_at	5.8	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2956_g_at	1686.5	P	Saccharomyces cerevisiae chromosome XII, complete chromosome
2957_at	11.5	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2958_at	36.7	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2959_at	287.2	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2875_at	57.9	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2876_at	34.3	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2877_at	6.1	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2878_at	3.2	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2879_at	179.8	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2880_at	118.9	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2881_at	388.1	M	Saccharomyces cerevisiae chromosome XII, complete chromosome
2882_at	144.8	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2883_at	333.1	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2884_g_at	1190.6	M	Saccharomyces cerevisiae chromosome XII, complete chromosome
2885_s_at	2581.8	M	Saccharomyces cerevisiae chromosome XII, complete chromosome
2886_s_at	699	P	Saccharomyces cerevisiae chromosome XII, complete chromosome
2887_s_at	2975.3	P	Saccharomyces cerevisiae chromosome XII, complete chromosome
2888_at	952.3	P	Saccharomyces cerevisiae chromosome XII, complete chromosome
2889_at	948.3	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2890_at	18.1	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2891_at	557.5	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2892_at	65	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2893_at	24.9	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2894_at	34.2	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2895_at	11.6	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2896_at	19.2	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2897_at	203.3	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2898_at	15.8	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2899_at	208.3	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2900_at	53.8	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2901_at	6.3	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2902_at	9.2	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2903_g_at	377.1	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2904_s_at	2302	P	Saccharomyces cerevisiae chromosome XII, complete chromosome
2905_at	184.3	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2906_at	547.2	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2907_at	33.1	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2908_at	415.4	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2909_at	80.1	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2910_at	131.5	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2911_s_at	4740.5	P	Saccharomyces cerevisiae chromosome XII, complete chromosome
2912_at	26.4	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2913_at	868	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2914_at	7.6	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2915_g_at	448.4	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2916_s_at	381.3	A	Saccharomyces cerevisiae chromosome XII, complete chromosome

2832_s_at	523.1	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2833_s_at	721.6	P	Saccharomyces cerevisiae chromosome XII, complete chromosome
2834_at	375	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2835_at	999	P	Saccharomyces cerevisiae chromosome XII, complete chromosome
2836_g_at	17791	P	Saccharomyces cerevisiae chromosome XII, complete chromosome
2837_s_at	7766.4	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2838_s_at	10786.7	P	Saccharomyces cerevisiae chromosome XII, complete chromosome
2839_s_at	20122.6	P	Saccharomyces cerevisiae chromosome XII, complete chromosome
2840_s_at	23519.5	P	Saccharomyces cerevisiae chromosome XII, complete chromosome
2841_s_at	34587.6	P	Saccharomyces cerevisiae chromosome XII, complete chromosome
2842_at	75.8	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2843_at	59.9	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2844_at	132.7	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2845_g_at	1270.1	P	Saccharomyces cerevisiae chromosome XII, complete chromosome
2846_s_at	1969.1	P	Saccharomyces cerevisiae chromosome XII, complete chromosome
2847_s_at	5778.7	P	Saccharomyces cerevisiae chromosome XII, complete chromosome
2848_s_at	5350.9	P	Saccharomyces cerevisiae chromosome XII, complete chromosome
2849_at	544.1	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2850_g_at	1299.1	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2851_s_at	958.9	P	Saccharomyces cerevisiae chromosome XII, complete chromosome
2852_s_at	854	P	Saccharomyces cerevisiae chromosome XII, complete chromosome
2853_s_at	869.8	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2854_s_at	864.3	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2855_s_at	2961.4	P	Saccharomyces cerevisiae chromosome XII, complete chromosome
2856_at	2110.3	M	Saccharomyces cerevisiae chromosome XII, complete chromosome
2857_at	2465.8	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2858_at	568.3	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2859_at	185.6	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2860_g_at	640.3	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2861_s_at	52.3	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2862_s_at	1112.8	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2863_s_at	680.6	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2864_at	921.9	P	Saccharomyces cerevisiae chromosome XII, complete chromosome
2865_g_at	716	P	Saccharomyces cerevisiae chromosome XII, complete chromosome
2866_s_at	778.7	P	Saccharomyces cerevisiae chromosome XII, complete chromosome
2867_s_at	1250.1	P	Saccharomyces cerevisiae chromosome XII, complete chromosome
2868_s_at	610.9	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2869_s_at	761	P	Saccharomyces cerevisiae chromosome XII, complete chromosome
2870_s_at	1745.8	P	Saccharomyces cerevisiae chromosome XII, complete chromosome
2871_s_at	2425.6	P	Saccharomyces cerevisiae chromosome XII, complete chromosome
2872_at	596.3	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2873_at	409.2	M	Saccharomyces cerevisiae chromosome XII, complete chromosome
2874_g_at	287.8	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2789_s_at	42.1	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2790_s_at	206.7	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2791_s_at	339.1	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2792_s_at	217.9	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2793_s_at	342.3	P	Saccharomyces cerevisiae chromosome XII, complete chromosome
2794_s_at	816.6	P	Saccharomyces cerevisiae chromosome XII, complete chromosome
2795_s_at	3024.8	P	Saccharomyces cerevisiae chromosome XII, complete chromosome
2796_f_at	8808.2	P	Saccharomyces cerevisiae chromosome XII, complete chromosome
2797_at	304	A	Saccharomyces cerevisiae chromosome XII, complete chromosome

2798_g_at	221.1	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2799_at	7.7	A	Saccharomyces cerevisiae chromosome XIII, complete chromosome
2800_at	663.7	A	Saccharomyces cerevisiae chromosome XIII, complete chromosome
2801_at	78.7	A	Saccharomyces cerevisiae chromosome XIII, complete chromosome
2802_at	65.8	A	Saccharomyces cerevisiae chromosome XIII, complete chromosome
2803_at	1173.3	A	Saccharomyces cerevisiae chromosome XIII, complete chromosome
2804_at	1373.9	A	Saccharomyces cerevisiae chromosome XIII, complete chromosome
2805_g_at	2715.5	P	Saccharomyces cerevisiae chromosome XIII, complete chromosome
2806_s_at	3338.8	P	Saccharomyces cerevisiae chromosome XIII, complete chromosome
2807_at	529.5	A	Saccharomyces cerevisiae chromosome XIII, complete chromosome
2808_at	328.9	A	Saccharomyces cerevisiae chromosome XIII, complete chromosome
2809_at	49.3	A	Saccharomyces cerevisiae chromosome XIII, complete chromosome
2810_at	163.5	A	Saccharomyces cerevisiae chromosome XIII, complete chromosome
2811_at	788.5	A	Saccharomyces cerevisiae chromosome XIII, complete chromosome
2812_at	121.2	A	Saccharomyces cerevisiae chromosome XIII, complete chromosome
2813_at	1419.4	P	Saccharomyces cerevisiae chromosome XIII, complete chromosome
2814_at	29.4	A	Saccharomyces cerevisiae chromosome XIII, complete chromosome
2815_at	1858	P	Saccharomyces cerevisiae chromosome XIII, complete chromosome
2816_at	6037	P	Saccharomyces cerevisiae chromosome XIII, complete chromosome
2817_at	5368.1	P	Saccharomyces cerevisiae chromosome XIII, complete chromosome
2818_at	234.6	A	Saccharomyces cerevisiae chromosome XIII, complete chromosome
2819_s_at	2014	P	Saccharomyces cerevisiae chromosome XIII, complete chromosome
2821_at	71.2	A	Saccharomyces cerevisiae chromosome XIII, complete chromosome
2822_at	2336.3	P	Saccharomyces cerevisiae chromosome XIII, complete chromosome
2823_at	1856.9	A	Saccharomyces cerevisiae chromosome XIII, complete chromosome
2824_at	885.1	P	Saccharomyces cerevisiae chromosome XIII, complete chromosome
2825_at	280.3	P	Saccharomyces cerevisiae chromosome XIII, complete chromosome
2826_at	133.4	A	Saccharomyces cerevisiae chromosome XIII, complete chromosome
2827_g_at	384.4	A	Saccharomyces cerevisiae chromosome XIII, complete chromosome
2828_at	15.5	A	Saccharomyces cerevisiae chromosome XIII, complete chromosome
2829_f_at	5508.9	A	Saccharomyces cerevisiae chromosome XIII, complete chromosome
2748_at	24.2	A	Saccharomyces cerevisiae chromosome XIII, complete chromosome
2749_s_at	577.3	P	Saccharomyces cerevisiae chromosome XIII, complete chromosome
2750_at	215.7	A	Saccharomyces cerevisiae chromosome XIII, complete chromosome
2751_at	138.7	A	Saccharomyces cerevisiae chromosome XIII, complete chromosome
2752_at	117.2	A	Saccharomyces cerevisiae chromosome XIII, complete chromosome
2753_at	355.5	A	Saccharomyces cerevisiae chromosome XIII, complete chromosome
2754_at	19.1	A	Saccharomyces cerevisiae chromosome XIII, complete chromosome
2755_at	70.5	A	Saccharomyces cerevisiae chromosome XIII, complete chromosome
2756_at	2222.6	M	Saccharomyces cerevisiae chromosome XIII, complete chromosome
2757_g_at	12953.2	P	Saccharomyces cerevisiae chromosome XIII, complete chromosome
2758_s_at	15075.6	P	Saccharomyces cerevisiae chromosome XIII, complete chromosome
2759_at	67.5	A	Saccharomyces cerevisiae chromosome XIII, complete chromosome
2760_at	691.2	P	Saccharomyces cerevisiae chromosome XIII, complete chromosome
2761_at	163.7	A	Saccharomyces cerevisiae chromosome XIII, complete chromosome
2762_at	31.6	A	Saccharomyces cerevisiae chromosome XIII, complete chromosome
2763_s_at	83	A	Saccharomyces cerevisiae chromosome XIII, complete chromosome
2764_s_at	1168.3	P	Saccharomyces cerevisiae chromosome XIII, complete chromosome
2765_s_at	728	A	Saccharomyces cerevisiae chromosome XIII, complete chromosome
2766_s_at	660.6	P	Saccharomyces cerevisiae chromosome XIII, complete chromosome
2767_at	702.9	A	Saccharomyces cerevisiae chromosome XIII, complete chromosome
2768_at	329.8	A	Saccharomyces cerevisiae chromosome XIII, complete chromosome

2769_at	35.2	A	Saccharomyces cerevisiae chromosome XIII, complete chromosome
2770_at	225.4	A	Saccharomyces cerevisiae chromosome XIII, complete chromosome
2771_at	534.9	A	Saccharomyces cerevisiae chromosome XIII, complete chromosome
2772_at	642.1	A	Saccharomyces cerevisiae chromosome XIII, complete chromosome
2773_at	231.8	A	Saccharomyces cerevisiae chromosome XIII, complete chromosome
2774_at	206.1	A	Saccharomyces cerevisiae chromosome XIII, complete chromosome
2775_at	283	A	Saccharomyces cerevisiae chromosome XIII, complete chromosome
2776_at	414.3	A	Saccharomyces cerevisiae chromosome XIII, complete chromosome
2777_at	67.3	A	Saccharomyces cerevisiae chromosome XIII, complete chromosome
2778_g_at	604.9	M	Saccharomyces cerevisiae chromosome XIII, complete chromosome
2779_s_at	559.3	P	Saccharomyces cerevisiae chromosome XIII, complete chromosome
2780_at	605.7	P	Saccharomyces cerevisiae chromosome XIII, complete chromosome
2781_at	390.2	A	Saccharomyces cerevisiae chromosome XIII, complete chromosome
2782_at	181.7	A	Saccharomyces cerevisiae chromosome XIII, complete chromosome
2783_g_at	1566.9	P	Saccharomyces cerevisiae chromosome XIII, complete chromosome
2784_s_at	117	A	Saccharomyces cerevisiae chromosome XIII, complete chromosome
2785_s_at	979.4	P	Saccharomyces cerevisiae chromosome XIII, complete chromosome
2786_s_at	9969.7	P	Saccharomyces cerevisiae chromosome XIII, complete chromosome
2787_at	68.2	A	Saccharomyces cerevisiae chromosome XIII, complete chromosome
2788_at	241.2	A	Saccharomyces cerevisiae chromosome XIII, complete chromosome
2703_g_at	40.3	A	Saccharomyces cerevisiae chromosome XIII, complete chromosome
2704_s_at	337.7	A	Saccharomyces cerevisiae chromosome XIII, complete chromosome
2705_s_at	19.8	A	Saccharomyces cerevisiae chromosome XIII, complete chromosome
2706_s_at	445.2	A	Saccharomyces cerevisiae chromosome XIII, complete chromosome
2707_s_at	45.1	A	Saccharomyces cerevisiae chromosome XIII, complete chromosome
2708_s_at	514.7	A	Saccharomyces cerevisiae chromosome XIII, complete chromosome
2709_s_at	516.3	M	Saccharomyces cerevisiae chromosome XIV, complete chromosome
2710_s_at	1402.7	A	Saccharomyces cerevisiae chromosome XIV, complete chromosome
2711_s_at	2190.5	P	Saccharomyces cerevisiae chromosome XIV, complete chromosome
2712_s_at	965.3	P	Saccharomyces cerevisiae chromosome XIV, complete chromosome
2713_s_at	2773.1	A	Saccharomyces cerevisiae chromosome XIV, complete chromosome
2714_s_at	12380.1	P	Saccharomyces cerevisiae chromosome XIV, complete chromosome
2715_at	105	A	Saccharomyces cerevisiae chromosome XIV, complete chromosome
2716_at	208.6	A	Saccharomyces cerevisiae chromosome XIV, complete chromosome
2717_at	198.7	A	Saccharomyces cerevisiae chromosome XIV, complete chromosome
2718_at	27.9	A	Saccharomyces cerevisiae chromosome XIV, complete chromosome
2719_at	24.5	A	Saccharomyces cerevisiae chromosome XIV, complete chromosome
2720_at	263.4	A	Saccharomyces cerevisiae chromosome XIV, complete chromosome
2721_at	18.8	A	Saccharomyces cerevisiae chromosome XIV, complete chromosome
2722_g_at	130.3	A	Saccharomyces cerevisiae chromosome XIV, complete chromosome
2723_s_at	17.5	A	Saccharomyces cerevisiae chromosome XIV, complete chromosome
2724_s_at	941.1	P	Saccharomyces cerevisiae chromosome XIV, complete chromosome
2725_s_at	800	A	Saccharomyces cerevisiae chromosome XIV, complete chromosome
2726_s_at	1493.6	P	Saccharomyces cerevisiae chromosome XIV, complete chromosome
2727_s_at	2557.7	P	Saccharomyces cerevisiae chromosome XIV, complete chromosome
2728_s_at	1261	P	Saccharomyces cerevisiae chromosome XIV, complete chromosome
2729_at	736.4	A	Saccharomyces cerevisiae chromosome XIV, complete chromosome
2730_at	5.1	A	Saccharomyces cerevisiae chromosome XIV, complete chromosome
2731_at	330.9	A	Saccharomyces cerevisiae chromosome XIV, complete chromosome
2732_at	15.8	A	Saccharomyces cerevisiae chromosome XIV, complete chromosome
2733_g_at	2556.9	P	Saccharomyces cerevisiae chromosome XIV, complete chromosome
2734_s_at	2814.6	P	Saccharomyces cerevisiae chromosome XIV, complete chromosome

2735_s_at	3082	P	Saccharomyces cerevisiae chromosome XIV, complete chromosom
2736_at	48	A	Saccharomyces cerevisiae chromosome XIV, complete chromosom
2737_at	236.2	A	Saccharomyces cerevisiae chromosome XIV, complete chromosom
2738_at	334.2	A	Saccharomyces cerevisiae chromosome XIV, complete chromosom
2739_g_at	357.4	A	Saccharomyces cerevisiae chromosome XIV, complete chromosom
2740_s_at	48.1	A	Saccharomyces cerevisiae chromosome XIV, complete chromosom
2741_s_at	171.4	A	Saccharomyces cerevisiae chromosome XIV, complete chromosom
2742_s_at	414	M	Saccharomyces cerevisiae chromosome XIV, complete chromosom
2743_at	32.1	A	Saccharomyces cerevisiae chromosome XIV, complete chromosom
2744_at	98.1	A	Saccharomyces cerevisiae chromosome XIV, complete chromosom
2745_g_at	600.5	P	Saccharomyces cerevisiae chromosome XIV, complete chromosom
2660_s_at	557.6	A	Saccharomyces cerevisiae chromosome XIV, complete chromosom
2661_s_at	545.9	A	Saccharomyces cerevisiae chromosome XIV, complete chromosom
2662_s_at	2223.9	M	Saccharomyces cerevisiae chromosome XIV, complete chromosom
2663_s_at	2764.9	P	Saccharomyces cerevisiae chromosome XIV, complete chromosom
2664_at	166.1	A	Saccharomyces cerevisiae chromosome XIV, complete chromosom
2665_at	413.7	A	Saccharomyces cerevisiae chromosome XIV, complete chromosom
2666_s_at	1514.8	A	Saccharomyces cerevisiae chromosome XIV, complete chromosom
2667_s_at	1056.1	P	Saccharomyces cerevisiae chromosome XIV, complete chromosom
2668_s_at	894.1	P	Saccharomyces cerevisiae chromosome XIV, complete chromosom
2669_at	1199.5	A	Saccharomyces cerevisiae chromosome XIV, complete chromosom
2670_at	118.9	A	Saccharomyces cerevisiae chromosome XIV, complete chromosom
2671_at	5.2	A	Saccharomyces cerevisiae chromosome XIV, complete chromosom
2672_at	331.3	A	Saccharomyces cerevisiae chromosome XIV, complete chromosom
2673_at	195.5	A	Saccharomyces cerevisiae chromosome XIV, complete chromosom
2674_at	11.4	A	Saccharomyces cerevisiae chromosome XIV, complete chromosom
2675_at	960.9	P	Saccharomyces cerevisiae chromosome XIV, complete chromosom
2676_at	378.4	A	Saccharomyces cerevisiae chromosome XIV, complete chromosom
2677_at	210.4	A	Saccharomyces cerevisiae chromosome XIV, complete chromosom
2678_at	211.1	A	Saccharomyces cerevisiae chromosome XIV, complete chromosom
2679_at	8.6	A	Saccharomyces cerevisiae chromosome XIV, complete chromosom
2680_at	19.7	A	Saccharomyces cerevisiae chromosome XIV, complete chromosom
2681_g_at	4266.5	P	Saccharomyces cerevisiae chromosome XIV, complete chromosom
2682_s_at	2670	M	Saccharomyces cerevisiae chromosome XIV, complete chromosom
2683_at	64.3	A	Saccharomyces cerevisiae chromosome XIV, complete chromosom
2684_at	504.9	A	Saccharomyces cerevisiae chromosome XIV, complete chromosom
2685_at	807.9	A	Saccharomyces cerevisiae chromosome XIV, complete chromosom
2686_at	442	A	Saccharomyces cerevisiae chromosome XIV, complete chromosom
2687_g_at	6.8	A	Saccharomyces cerevisiae chromosome XIV, complete chromosom
2688_s_at	322.4	A	Saccharomyces cerevisiae chromosome XIV, complete chromosom
2689_s_at	88.2	A	Saccharomyces cerevisiae chromosome XIV, complete chromosom
2690_s_at	38.2	A	Saccharomyces cerevisiae chromosome XIV, complete chromosom
2691_s_at	261.6	A	Saccharomyces cerevisiae chromosome XIV, complete chromosom
2692_at	32.8	A	Saccharomyces cerevisiae chromosome XV, complete chromosome
2693_at	1200	A	Saccharomyces cerevisiae chromosome XV, complete chromosome
2694_at	283	A	Saccharomyces cerevisiae chromosome XV, complete chromosome
2695_at	38	A	Saccharomyces cerevisiae chromosome XV, complete chromosome
2696_at	25	A	Saccharomyces cerevisiae chromosome XV, complete chromosome
2697_g_at	225.9	A	Saccharomyces cerevisiae chromosome XV, complete chromosome
2698_s_at	1593.8	P	Saccharomyces cerevisiae chromosome XV, complete chromosome
2699_at	146.3	A	Saccharomyces cerevisiae chromosome XV, complete chromosome
2700_at	6.2	A	Saccharomyces cerevisiae chromosome XV, complete chromosome

2701_g_at	647.6	A	Saccharomyces cerevisiae chromosome XV, complete chromosome
2702_s_at	408.3	P	Saccharomyces cerevisiae chromosome XV, complete chromosome
2618_s_at	109.3	A	Saccharomyces cerevisiae chromosome XV, complete chromosome
2619_s_at	36.5	A	Saccharomyces cerevisiae chromosome XV, complete chromosome
2620_s_at	234.8	A	Saccharomyces cerevisiae chromosome XV, complete chromosome
2621_s_at	835	P	Saccharomyces cerevisiae chromosome XV, complete chromosome
2622_s_at	2377.1	A	Saccharomyces cerevisiae chromosome XV, complete chromosome
2623_s_at	815.9	A	Saccharomyces cerevisiae chromosome XV, complete chromosome
2624_s_at	3215.1	P	Saccharomyces cerevisiae chromosome XV, complete chromosome
2625_at	188.7	A	Saccharomyces cerevisiae chromosome XV, complete chromosome
2626_at	1494.2	A	Saccharomyces cerevisiae chromosome XV, complete chromosome
2627_at	1374.8	P	Saccharomyces cerevisiae chromosome XV, complete chromosome
2628_s_at	864	A	Saccharomyces cerevisiae chromosome XV, complete chromosome
2629_s_at	910.3	P	Saccharomyces cerevisiae chromosome XV, complete chromosome
2630_s_at	3332.3	P	Saccharomyces cerevisiae chromosome XV, complete chromosome
2631_s_at	1127	P	Saccharomyces cerevisiae chromosome XV, complete chromosome
2632_at	457.6	M	Saccharomyces cerevisiae chromosome XV, complete chromosome
2633_at	391.2	P	Saccharomyces cerevisiae chromosome XV, complete chromosome
2634_at	92	A	Saccharomyces cerevisiae chromosome XV, complete chromosome
2635_at	205	A	Saccharomyces cerevisiae chromosome XV, complete chromosome
2636_at	561	A	Saccharomyces cerevisiae chromosome XV, complete chromosome
2637_g_at	3417.3	P	Saccharomyces cerevisiae chromosome XV, complete chromosome
2638_s_at	9154.1	P	Saccharomyces cerevisiae chromosome XV, complete chromosome
2639_at	10.9	A	Saccharomyces cerevisiae chromosome XV, complete chromosome
2640_at	392.2	A	Saccharomyces cerevisiae chromosome XV, complete chromosome
2641_g_at	1697.2	M	Saccharomyces cerevisiae chromosome XV, complete chromosome
2642_s_at	890.3	P	Saccharomyces cerevisiae chromosome XV, complete chromosome
2643_s_at	7733.7	P	Saccharomyces cerevisiae chromosome XV, complete chromosome
2644_s_at	3091.5	P	Saccharomyces cerevisiae chromosome XV, complete chromosome
2645_s_at	17420.5	P	Saccharomyces cerevisiae chromosome XV, complete chromosome
2646_at	355	A	Saccharomyces cerevisiae chromosome XV, complete chromosome
2647_at	378.5	A	Saccharomyces cerevisiae chromosome XV, complete chromosome
2648_at	15.6	A	Saccharomyces cerevisiae chromosome XV, complete chromosome
2649_at	33.4	A	Saccharomyces cerevisiae chromosome XV, complete chromosome
2650_g_at	170.1	A	Saccharomyces cerevisiae chromosome XV, complete chromosome
2651_s_at	784.3	A	Saccharomyces cerevisiae chromosome XV, complete chromosome
2652_s_at	1279.4	P	Saccharomyces cerevisiae chromosome XV, complete chromosome
2653_at	82.8	A	Saccharomyces cerevisiae chromosome XV, complete chromosome
2654_at	239.5	A	Saccharomyces cerevisiae chromosome XV, complete chromosome
2655_at	1198.4	A	Saccharomyces cerevisiae chromosome XV, complete chromosome
2656_at	1104.1	A	Saccharomyces cerevisiae chromosome XV, complete chromosome
2657_at	393.6	A	Saccharomyces cerevisiae chromosome XV, complete chromosome
2658_at	74.3	A	Saccharomyces cerevisiae chromosome XV, complete chromosome
2659_g_at	236.9	A	Saccharomyces cerevisiae chromosome XV, complete chromosome
2575_s_at	1642.2	P	Saccharomyces cerevisiae chromosome XV, complete chromosome
2576_s_at	1405.5	P	Saccharomyces cerevisiae chromosome XV, complete chromosome
2577_s_at	1015.4	P	Saccharomyces cerevisiae chromosome XV, complete chromosome
2578_s_at	4296.4	P	Saccharomyces cerevisiae chromosome XV, complete chromosome
2579_at	743.4	A	Saccharomyces cerevisiae chromosome XV, complete chromosome
2580_at	335.5	A	Saccharomyces cerevisiae chromosome XV, complete chromosome
2581_at	290.1	M	Saccharomyces cerevisiae chromosome XV, complete chromosome
2582_at	2944.3	A	Saccharomyces cerevisiae chromosome XV, complete chromosome

2583_g_at	2167.5	M	Saccharomyces cerevisiae chromosome XV, complete chromosome
2584_s_at	1336.6	P	Saccharomyces cerevisiae chromosome XV, complete chromosome
2585_s_at	745.8	P	Saccharomyces cerevisiae chromosome XV, complete chromosome
2586_s_at	4232.4	P	Saccharomyces cerevisiae chromosome XV, complete chromosome
2587_at	240.1	A	Saccharomyces cerevisiae chromosome XV, complete chromosome
2588_at	987	P	Saccharomyces cerevisiae chromosome XV, complete chromosome
2589_g_at	7772.2	P	Saccharomyces cerevisiae chromosome XV, complete chromosome
2590_s_at	4739.7	P	Saccharomyces cerevisiae chromosome XV, complete chromosome
2591_s_at	3813.2	P	Saccharomyces cerevisiae chromosome XV, complete chromosome
2592_s_at	11752.4	P	Saccharomyces cerevisiae chromosome XV, complete chromosome
2593_s_at	21802.2	P	Saccharomyces cerevisiae chromosome XV, complete chromosome
2594_at	284.2	A	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2595_at	1924.5	A	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2596_at	505.4	A	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2597_at	417.9	A	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2598_g_at	1381.9	P	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2599_s_at	8812.4	P	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2600_s_at	10604.9	P	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2601_at	607.4	A	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2602_g_at	2481.8	P	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2603_s_at	8814.3	P	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2604_s_at	13596.7	P	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2605_s_at	30226.7	P	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2606_s_at	22077.9	P	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2607_s_at	31299.6	P	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2608_at	537.9	A	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2609_at	971.2	M	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2610_at	45.9	A	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2611_at	1373.3	P	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2612_g_at	144.7	A	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2613_s_at	147.9	A	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2614_s_at	204.6	A	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2615_s_at	337.3	P	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2616_at	15.3	A	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2617_at	352.6	P	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2532_g_at	56.5	A	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2533_s_at	1334.8	P	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2534_s_at	446.1	M	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2535_s_at	3294.3	P	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2536_s_at	1754	P	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2537_s_at	8868.1	P	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2538_s_at	2531.2	P	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2539_at	665.5	A	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2540_at	959.4	A	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2541_at	2.4	A	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2542_at	104	A	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2543_at	394.2	A	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2544_at	41.8	A	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2545_at	92.1	A	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2546_at	37	A	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2547_at	37.4	A	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2548_at	485.7	A	Saccharomyces cerevisiae chromosome XVI, complete chromosome

2549_at	193.2	A	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2550_at	15.6	A	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2551_at	59.7	A	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2552_at	11.9	A	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2553_at	287	A	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2554_at	255.4	A	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2555_at	65.8	A	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2556_at	18.9	A	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2557_at	223.5	A	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2558_at	583	A	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2559_at	1632.5	A	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2560_at	925.1	A	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2561_at	988.4	A	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2562_g_at	335.4	A	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2563_s_at	1042.2	M	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2564_s_at	1356.9	P	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2565_s_at	1370.9	P	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2566_s_at	2973.4	A	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2567_at	519.6	P	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2568_at	1140.9	A	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2569_at	75	A	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2570_at	678.6	P	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2571_s_at	2058	P	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2572_s_at	951.2	P	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2573_at	32.3	A	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2574_at	1837.8	A	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2489_at	0.6	A	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2490_s_at	4017.3	P	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2491_s_at	1837.6	P	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2492_f_at	1247.9	P	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2493_at	780	A	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2494_at	289.9	A	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2495_at	674.3	A	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2496_g_at	418.5	A	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2497_s_at	16.9	A	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2498_s_at	1125.6	A	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2499_s_at	626.1	A	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2500_at	1226.9	P	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2501_g_at	517.8	A	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2502_s_at	728.8	A	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2503_s_at	250.8	A	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2504_s_at	1546	M	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2505_s_at	1164	P	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2506_s_at	1473.7	P	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2507_s_at	427.1	P	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2508_s_at	1996	P	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2509_at	1818.2	A	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2510_at	139.9	A	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2511_g_at	287.5	M	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2512_s_at	360.7	A	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2513_s_at	513.7	P	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2514_s_at	1110.2	P	Saccharomyces cerevisiae chromosome XVI, complete chromosome

2515_s_at	313.8	A	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2516_at	129	A	Saccharomyces cerevisiae chromosome II, complete chromosome s
2517_at	149.2	A	Saccharomyces cerevisiae chromosome II, complete chromosome s
2518_at	366.2	A	Saccharomyces cerevisiae chromosome II, complete chromosome s
2519_at	25	A	Saccharomyces cerevisiae chromosome II, complete chromosome s
2520_at	63.4	A	Saccharomyces cerevisiae chromosome II, complete chromosome s
2521_f_at	888.7	A	Saccharomyces cerevisiae chromosome II, complete chromosome s
2522_at	18.1	A	Saccharomyces cerevisiae chromosome II, complete chromosome s
2523_at	6.2	A	Saccharomyces cerevisiae chromosome II, complete chromosome s
2524_at	25.9	A	Saccharomyces cerevisiae chromosome II, complete chromosome s
2525_at	839.5	A	Saccharomyces cerevisiae chromosome II, complete chromosome s
2526_at	25.1	A	Saccharomyces cerevisiae chromosome II, complete chromosome s
2527_at	69.7	A	Saccharomyces cerevisiae chromosome II, complete chromosome s
2528_at	430.1	A	Saccharomyces cerevisiae chromosome II, complete chromosome s
2529_at	12.4	A	Saccharomyces cerevisiae chromosome II, complete chromosome s
2530_at	473.2	P	Saccharomyces cerevisiae chromosome II, complete chromosome s
2531_at	522.5	A	Saccharomyces cerevisiae chromosome II, complete chromosome s
2446_at	24.4	A	Saccharomyces cerevisiae chromosome II, complete chromosome s
2447_g_at	929.7	M	Saccharomyces cerevisiae chromosome II, complete chromosome s
2448_s_at	911.2	P	Saccharomyces cerevisiae chromosome II, complete chromosome s
2449_s_at	5260	P	Saccharomyces cerevisiae chromosome II, complete chromosome s
2450_s_at	2033.9	P	Saccharomyces cerevisiae chromosome II, complete chromosome s
2451_s_at	12140	P	Saccharomyces cerevisiae chromosome II, complete chromosome s
2452_at	373.6	A	Saccharomyces cerevisiae chromosome II, complete chromosome s
2453_at	448.4	A	Saccharomyces cerevisiae chromosome II, complete chromosome s
2454_at	33.2	A	Saccharomyces cerevisiae chromosome II, complete chromosome s
2455_at	768.3	A	Saccharomyces cerevisiae chromosome II, complete chromosome s
2456_at	416.1	A	Saccharomyces cerevisiae chromosome II, complete chromosome s
2457_at	101.8	A	Saccharomyces cerevisiae chromosome II, complete chromosome s
2458_g_at	6468.5	P	Saccharomyces cerevisiae chromosome II, complete chromosome s
2459_at	1009.8	A	Saccharomyces cerevisiae chromosome II, complete chromosome s
2460_at	329.7	A	Saccharomyces cerevisiae chromosome II, complete chromosome s
2461_at	1754.8	P	Saccharomyces cerevisiae chromosome II, complete chromosome s
2462_g_at	830.2	A	Saccharomyces cerevisiae chromosome II, complete chromosome s
2463_s_at	2766.6	P	Saccharomyces cerevisiae chromosome II, complete chromosome s
2464_s_at	3653.2	P	Saccharomyces cerevisiae chromosome II, complete chromosome s
2465_s_at	4718.8	P	Saccharomyces cerevisiae chromosome II, complete chromosome s
2466_s_at	277.3	P	Saccharomyces cerevisiae chromosome II, complete chromosome s
2467_s_at	3552.8	P	Saccharomyces cerevisiae chromosome II, complete chromosome s
2468_s_at	8041.5	P	Saccharomyces cerevisiae chromosome II, complete chromosome s
2469_s_at	1649.5	P	Saccharomyces cerevisiae chromosome II, complete chromosome s
2470_at	1853.8	P	Saccharomyces cerevisiae chromosome II, complete chromosome s
2471_g_at	754.2	A	Saccharomyces cerevisiae chromosome II, complete chromosome s
2472_s_at	481.8	A	Saccharomyces cerevisiae chromosome II, complete chromosome s
2473_s_at	851.7	A	Saccharomyces cerevisiae chromosome II, complete chromosome s
2474_s_at	499.8	P	Saccharomyces cerevisiae chromosome II, complete chromosome s
2475_s_at	509.3	A	Saccharomyces cerevisiae chromosome II, complete chromosome s
2476_s_at	2051.2	P	Saccharomyces cerevisiae chromosome II, complete chromosome s
2477_s_at	1909.5	P	Saccharomyces cerevisiae chromosome II, complete chromosome s
2478_at	250	A	Saccharomyces cerevisiae chromosome II, complete chromosome s
2479_at	396.5	A	Saccharomyces cerevisiae chromosome II, complete chromosome s
2480_at	126.3	A	Saccharomyces cerevisiae chromosome II, complete chromosome s

2481_at	31.4	A	Saccharomyces cerevisiae chromosome II, complete chromosome s
2482_at	320	A	Saccharomyces cerevisiae chromosome II, complete chromosome s
2483_at	962.9	A	Saccharomyces cerevisiae chromosome II, complete chromosome s
2484_at	8.5	A	Saccharomyces cerevisiae chromosome II, complete chromosome s
2485_at	119.9	A	Saccharomyces cerevisiae chromosome II, complete chromosome s
2486_at	19.3	A	Saccharomyces cerevisiae chromosome II, complete chromosome s
2487_at	1597.9	P	Saccharomyces cerevisiae chromosome II, complete chromosome s
2488_at	50	A	Saccharomyces cerevisiae chromosome II, complete chromosome s
2421_at	94.7	A	Saccharomyces cerevisiae chromosome II, complete chromosome s
2422_at	100.1	A	Saccharomyces cerevisiae chromosome II, complete chromosome s
2423_at	108.8	A	Saccharomyces cerevisiae chromosome II, complete chromosome s
2424_at	345.7	A	Saccharomyces cerevisiae chromosome II, complete chromosome s
2425_at	424.2	A	Saccharomyces cerevisiae chromosome II, complete chromosome s
2426_at	1216.8	A	Saccharomyces cerevisiae chromosome II, complete chromosome s
2427_at	1076.6	A	Saccharomyces cerevisiae chromosome II, complete chromosome s
2428_at	15	A	Saccharomyces cerevisiae chromosome II, complete chromosome s
2429_at	147.8	A	Saccharomyces cerevisiae chromosome II, complete chromosome s
2430_at	2.9	A	Saccharomyces cerevisiae chromosome II, complete chromosome s
2431_at	22.9	A	Saccharomyces cerevisiae chromosome II, complete chromosome s
2432_at	11567.6	P	Saccharomyces cerevisiae chromosome III, complete chromosome s
2433_at	2864.1	P	Saccharomyces cerevisiae chromosome III, complete chromosome s
2434_at	368.1	A	Saccharomyces cerevisiae chromosome III, complete chromosome s
2435_at	137.4	A	Saccharomyces cerevisiae chromosome III, complete chromosome s
2436_g_at	3561.4	P	Saccharomyces cerevisiae chromosome III, complete chromosome s
2437_s_at	10919.7	P	Saccharomyces cerevisiae chromosome III, complete chromosome s
2438_at	8.6	A	Saccharomyces cerevisiae chromosome III, complete chromosome s
2439_g_at	311.3	A	Saccharomyces cerevisiae chromosome III, complete chromosome s
2440_s_at	229.2	A	Saccharomyces cerevisiae chromosome III, complete chromosome s
2441_s_at	256	P	Saccharomyces cerevisiae chromosome III, complete chromosome s
2442_s_at	609.5	P	Saccharomyces cerevisiae chromosome III, complete chromosome s
2443_s_at	594.6	P	Saccharomyces cerevisiae chromosome III, complete chromosome s
2444_s_at	412.7	A	Saccharomyces cerevisiae chromosome III, complete chromosome s
2445_s_at	1684.7	P	Saccharomyces cerevisiae chromosome III, complete chromosome s
2395_at	16.7	A	Saccharomyces cerevisiae chromosome III, complete chromosome s
2396_at	607.3	A	Saccharomyces cerevisiae chromosome III, complete chromosome s
2397_at	63.5	A	Saccharomyces cerevisiae chromosome III, complete chromosome s
2398_g_at	1062.4	P	Saccharomyces cerevisiae chromosome III, complete chromosome s
2399_s_at	1945.4	P	Saccharomyces cerevisiae chromosome III, complete chromosome s
2400_s_at	765.7	P	Saccharomyces cerevisiae chromosome III, complete chromosome s
2401_s_at	1755.9	M	Saccharomyces cerevisiae chromosome III, complete chromosome s
2402_s_at	2357	P	Saccharomyces cerevisiae chromosome III, complete chromosome s
2403_s_at	3168.9	P	Saccharomyces cerevisiae chromosome III, complete chromosome s
2404_s_at	7351.7	P	Saccharomyces cerevisiae chromosome III, complete chromosome s
2405_at	137.1	A	Saccharomyces cerevisiae chromosome IV, complete chromosome s
2406_at	167.1	A	Saccharomyces cerevisiae chromosome IV, complete chromosome s
2407_at	1258.9	A	Saccharomyces cerevisiae chromosome IV, complete chromosome s
2408_at	427.9	A	Saccharomyces cerevisiae chromosome IV, complete chromosome s
2409_at	238.3	A	Saccharomyces cerevisiae chromosome IV, complete chromosome s
2410_g_at	307.5	A	Saccharomyces cerevisiae chromosome IV, complete chromosome s
2411_s_at	1673.4	A	Saccharomyces cerevisiae chromosome IV, complete chromosome s
2412_at	622.5	A	Saccharomyces cerevisiae chromosome IV, complete chromosome s
2413_at	540	A	Saccharomyces cerevisiae chromosome IV, complete chromosome s

2414_at	194.4	A	Saccharomyces cerevisiae chromosome IV, complete chromosome
2415_at	27.2	A	Saccharomyces cerevisiae chromosome IV, complete chromosome
2416_at	514.7	A	Saccharomyces cerevisiae chromosome IV, complete chromosome
2417_at	497.2	A	Saccharomyces cerevisiae chromosome IV, complete chromosome
2418_at	54.5	A	Saccharomyces cerevisiae chromosome IV, complete chromosome
2419_g_at	1141.9	P	Saccharomyces cerevisiae chromosome IV, complete chromosome
2420_s_at	1040.3	P	Saccharomyces cerevisiae chromosome IV, complete chromosome
2352_at	64	A	Saccharomyces cerevisiae chromosome IV, complete chromosome
2353_at	737.3	A	Saccharomyces cerevisiae chromosome IV, complete chromosome
2354_at	56.9	A	Saccharomyces cerevisiae chromosome IV, complete chromosome
2355_at	37.9	A	Saccharomyces cerevisiae chromosome IV, complete chromosome
2356_at	392.8	M	Saccharomyces cerevisiae chromosome IV, complete chromosome
2357_at	206.7	A	Saccharomyces cerevisiae chromosome IV, complete chromosome
2358_at	66.5	A	Saccharomyces cerevisiae chromosome IV, complete chromosome
2359_at	116.5	A	Saccharomyces cerevisiae chromosome IV, complete chromosome
2360_g_at	3168.1	P	Saccharomyces cerevisiae chromosome IV, complete chromosome
2361_s_at	2015.8	P	Saccharomyces cerevisiae chromosome IV, complete chromosome
2362_s_at	2612.3	P	Saccharomyces cerevisiae chromosome IV, complete chromosome
2363_s_at	4333.6	P	Saccharomyces cerevisiae chromosome IV, complete chromosome
2364_s_at	4535.4	P	Saccharomyces cerevisiae chromosome IV, complete chromosome
2365_at	163.8	A	Saccharomyces cerevisiae chromosome IV, complete chromosome
2366_s_at	1245.4	A	Saccharomyces cerevisiae chromosome IV, complete chromosome
2367_s_at	1589.5	P	Saccharomyces cerevisiae chromosome IV, complete chromosome
2368_s_at	201.7	A	Saccharomyces cerevisiae chromosome IV, complete chromosome
2369_s_at	716	P	Saccharomyces cerevisiae chromosome IV, complete chromosome
2370_s_at	216.9	A	Saccharomyces cerevisiae chromosome IV, complete chromosome
2371_at	94.9	A	Saccharomyces cerevisiae chromosome IV, complete chromosome
2372_at	2566.8	A	Saccharomyces cerevisiae chromosome IV, complete chromosome
2373_at	65.6	A	Saccharomyces cerevisiae chromosome IV, complete chromosome
2374_at	1928.7	P	Saccharomyces cerevisiae chromosome IV, complete chromosome
2375_s_at	394.3	A	Saccharomyces cerevisiae chromosome IV, complete chromosome
2376_s_at	456.5	A	Saccharomyces cerevisiae chromosome IV, complete chromosome
2377_at	396.1	A	Saccharomyces cerevisiae chromosome IV, complete chromosome
2378_g_at	2778.7	P	Saccharomyces cerevisiae chromosome IV, complete chromosome
2379_s_at	2358.2	P	Saccharomyces cerevisiae chromosome IV, complete chromosome
2380_s_at	1743.9	P	Saccharomyces cerevisiae chromosome IV, complete chromosome
2381_s_at	2586.9	P	Saccharomyces cerevisiae chromosome IV, complete chromosome
2382_s_at	13159.9	P	Saccharomyces cerevisiae chromosome IV, complete chromosome
2383_at	123	A	Saccharomyces cerevisiae chromosome IV, complete chromosome
2384_at	275.7	A	Saccharomyces cerevisiae chromosome IV, complete chromosome
2385_at	21.9	A	Saccharomyces cerevisiae chromosome IV, complete chromosome
2386_at	178.2	A	Saccharomyces cerevisiae chromosome IV, complete chromosome
2387_at	167.4	A	Saccharomyces cerevisiae chromosome IV, complete chromosome
2388_s_at	273.6	P	Saccharomyces cerevisiae chromosome IV, complete chromosome
2389_s_at	4.6	A	Saccharomyces cerevisiae chromosome IV, complete chromosome
2390_s_at	663.2	A	Saccharomyces cerevisiae chromosome IV, complete chromosome
2391_s_at	159.3	A	Saccharomyces cerevisiae chromosome IV, complete chromosome
2392_s_at	316.9	P	Saccharomyces cerevisiae chromosome IV, complete chromosome
2393_s_at	1497.1	P	Saccharomyces cerevisiae chromosome IV, complete chromosome
2394_s_at	1618.8	P	Saccharomyces cerevisiae chromosome IV, complete chromosome
2309_at	194.8	A	Saccharomyces cerevisiae chromosome IV, complete chromosome
2310_at	16.3	A	Saccharomyces cerevisiae chromosome IV, complete chromosome

2311_at	80.1	A	Saccharomyces cerevisiae chromosome IV, complete chromosome
2312_at	460.4	A	Saccharomyces cerevisiae chromosome IV, complete chromosome
2313_at	1007.7	M	Saccharomyces cerevisiae chromosome IV, complete chromosome
2314_at	2966.3	A	Saccharomyces cerevisiae chromosome IV, complete chromosome
2315_at	373.9	A	Saccharomyces cerevisiae chromosome IV, complete chromosome
2316_at	86.6	A	Saccharomyces cerevisiae chromosome IV, complete chromosome
2317_at	313.5	A	Saccharomyces cerevisiae chromosome IV, complete chromosome
2319_f_at	211.4	A	Saccharomyces cerevisiae chromosome IV, complete chromosome
2320_at	29.6	A	Saccharomyces cerevisiae chromosome IV, complete chromosome
2321_at	268.9	A	Saccharomyces cerevisiae chromosome IV, complete chromosome
2322_at	891.7	P	Saccharomyces cerevisiae chromosome IV, complete chromosome
2323_g_at	1111	P	Saccharomyces cerevisiae chromosome IV, complete chromosome
2324_s_at	548.6	A	Saccharomyces cerevisiae chromosome IV, complete chromosome
2325_s_at	1195.1	A	Saccharomyces cerevisiae chromosome IV, complete chromosome
2326_s_at	1049.9	P	Saccharomyces cerevisiae chromosome IV, complete chromosome
2327_s_at	806.3	P	Saccharomyces cerevisiae chromosome IV, complete chromosome
2328_at	89.1	A	Saccharomyces cerevisiae chromosome IV, complete chromosome
2329_at	447.7	A	Saccharomyces cerevisiae chromosome IV, complete chromosome
2330_g_at	486.7	M	Saccharomyces cerevisiae chromosome IV, complete chromosome
2331_s_at	1604.6	P	Saccharomyces cerevisiae chromosome IV, complete chromosome
2332_s_at	7652.9	P	Saccharomyces cerevisiae chromosome IV, complete chromosome
2333_s_at	2564.4	P	Saccharomyces cerevisiae chromosome IV, complete chromosome
2334_s_at	1683.3	P	Saccharomyces cerevisiae chromosome IV, complete chromosome
2335_s_at	2630	P	Saccharomyces cerevisiae chromosome IV, complete chromosome
2336_at	430.7	A	Saccharomyces cerevisiae chromosome IV, complete chromosome
2337_at	141.9	A	Saccharomyces cerevisiae chromosome IV, complete chromosome
2338_at	99.6	A	Saccharomyces cerevisiae chromosome IV, complete chromosome
2339_at	145.5	A	Saccharomyces cerevisiae chromosome IV, complete chromosome
2340_at	5300.3	A	Saccharomyces cerevisiae chromosome IV, complete chromosome
2341_g_at	1863.7	P	Saccharomyces cerevisiae chromosome IV, complete chromosome
2342_s_at	5065.1	P	Saccharomyces cerevisiae chromosome IV, complete chromosome
2343_at	540	P	Saccharomyces cerevisiae chromosome IV, complete chromosome
2344_g_at	1028	P	Saccharomyces cerevisiae chromosome IV, complete chromosome
2345_s_at	400.7	A	Saccharomyces cerevisiae chromosome IV, complete chromosome
2346_s_at	34.9	A	Saccharomyces cerevisiae chromosome IV, complete chromosome
2347_s_at	270.4	A	Saccharomyces cerevisiae chromosome IV, complete chromosome
2348_s_at	2319.3	A	Saccharomyces cerevisiae chromosome IV, complete chromosome
2349_s_at	723.8	M	Saccharomyces cerevisiae chromosome IV, complete chromosome
2350_s_at	5199.6	P	Saccharomyces cerevisiae chromosome IV, complete chromosome
2351_s_at	2349.2	P	Saccharomyces cerevisiae chromosome IV, complete chromosome
2266_s_at	2920.3	P	Saccharomyces cerevisiae chromosome IV, complete chromosome
2267_s_at	3320.9	P	Saccharomyces cerevisiae chromosome IV, complete chromosome
2268_at	335.7	A	Saccharomyces cerevisiae chromosome V, complete chromosome s
2269_at	122.7	A	Saccharomyces cerevisiae chromosome V, complete chromosome s
2270_at	198.4	M	Saccharomyces cerevisiae chromosome V, complete chromosome s
2271_at	28.7	A	Saccharomyces cerevisiae chromosome V, complete chromosome s
2272_at	833.1	A	Saccharomyces cerevisiae chromosome V, complete chromosome s
2273_at	18.5	A	Saccharomyces cerevisiae chromosome V, complete chromosome s
2274_at	699.9	A	Saccharomyces cerevisiae chromosome V, complete chromosome s
2275_g_at	344.6	A	Saccharomyces cerevisiae chromosome V, complete chromosome s
2276_at	97.7	A	Saccharomyces cerevisiae chromosome V, complete chromosome s
2277_at	392.8	A	Saccharomyces cerevisiae chromosome V, complete chromosome s

2278_at	190.6	A	Saccharomyces cerevisiae chromosome V, complete chromosome s
2279_g_at	1369	P	Saccharomyces cerevisiae chromosome V, complete chromosome s
2280_s_at	3109.4	P	Saccharomyces cerevisiae chromosome V, complete chromosome s
2281_s_at	2825.9	P	Saccharomyces cerevisiae chromosome V, complete chromosome s
2282_s_at	5118.9	P	Saccharomyces cerevisiae chromosome V, complete chromosome s
2283_s_at	3381.8	P	Saccharomyces cerevisiae chromosome V, complete chromosome s
2284_at	58.8	A	Saccharomyces cerevisiae chromosome V, complete chromosome s
2285_at	44.2	A	Saccharomyces cerevisiae chromosome V, complete chromosome s
2286_at	111.8	A	Saccharomyces cerevisiae chromosome V, complete chromosome s
2287_at	729	A	Saccharomyces cerevisiae chromosome V, complete chromosome s
2288_at	245	A	Saccharomyces cerevisiae chromosome V, complete chromosome s
2289_at	87.5	A	Saccharomyces cerevisiae chromosome V, complete chromosome s
2290_at	1707.7	A	Saccharomyces cerevisiae chromosome V, complete chromosome s
2291_g_at	1572.9	A	Saccharomyces cerevisiae chromosome V, complete chromosome s
2294_f_at	1222.5	P	Saccharomyces cerevisiae chromosome V, complete chromosome s
2295_at	44.8	A	Saccharomyces cerevisiae chromosome V, complete chromosome s
2296_at	231.8	M	Saccharomyces cerevisiae chromosome V, complete chromosome s
2297_at	86.9	A	Saccharomyces cerevisiae chromosome V, complete chromosome s
2298_at	192.9	A	Saccharomyces cerevisiae chromosome V, complete chromosome s
2299_at	66.9	A	Saccharomyces cerevisiae chromosome V, complete chromosome s
2300_at	133.7	A	Saccharomyces cerevisiae chromosome V, complete chromosome s
2301_at	36.6	A	Saccharomyces cerevisiae chromosome V, complete chromosome s
2302_at	62	A	Saccharomyces cerevisiae chromosome V, complete chromosome s
2303_f_at	766.6	A	Saccharomyces cerevisiae chromosome V, complete chromosome s
2306_at	677	P	Saccharomyces cerevisiae chromosome V, complete chromosome s
2307_at	266.8	A	Saccharomyces cerevisiae chromosome V, complete chromosome s
2308_at	16.5	A	Saccharomyces cerevisiae chromosome V, complete chromosome s
2223_at	296	A	Saccharomyces cerevisiae chromosome V, complete chromosome s
2224_at	37.7	A	Saccharomyces cerevisiae chromosome V, complete chromosome s
2225_at	279.5	A	Saccharomyces cerevisiae chromosome V, complete chromosome s
2226_at	341.2	A	Saccharomyces cerevisiae chromosome V, complete chromosome s
2227_at	96.5	A	Saccharomyces cerevisiae chromosome V, complete chromosome s
2228_at	32.2	A	Saccharomyces cerevisiae chromosome V, complete chromosome s
2229_at	32	A	Saccharomyces cerevisiae chromosome VI, complete chromosome
2230_at	1251.8	P	Saccharomyces cerevisiae chromosome VI, complete chromosome
2231_at	369.5	A	Saccharomyces cerevisiae chromosome VI, complete chromosome
2232_at	429.6	A	Saccharomyces cerevisiae chromosome VI, complete chromosome
2233_at	496.1	A	Saccharomyces cerevisiae chromosome VI, complete chromosome
2234_at	92	A	Saccharomyces cerevisiae chromosome VI, complete chromosome
2235_at	753	A	Saccharomyces cerevisiae chromosome VI, complete chromosome
2236_at	15.6	A	Saccharomyces cerevisiae chromosome VI, complete chromosome
2237_at	29.6	A	Saccharomyces cerevisiae chromosome VI, complete chromosome
2238_at	430.4	A	Saccharomyces cerevisiae chromosome VI, complete chromosome
2239_at	2804.3	P	Saccharomyces cerevisiae chromosome VI, complete chromosome
2240_at	83.8	A	Saccharomyces cerevisiae chromosome VI, complete chromosome
2241_s_at	1146.8	P	Saccharomyces cerevisiae chromosome VI, complete chromosome
2242_s_at	717	P	Saccharomyces cerevisiae chromosome VI, complete chromosome
2243_s_at	984.3	P	Saccharomyces cerevisiae chromosome VI, complete chromosome
2244_s_at	1477	P	Saccharomyces cerevisiae chromosome VI, complete chromosome
2245_s_at	52.6	A	Saccharomyces cerevisiae chromosome VI, complete chromosome
2246_s_at	1987.6	P	Saccharomyces cerevisiae chromosome VI, complete chromosome
2247_at	506.7	A	Saccharomyces cerevisiae chromosome VII, complete chromosome

2248_at	504.4	A	Saccharomyces cerevisiae chromosome VII, complete chromosome
2249_at	172.3	A	Saccharomyces cerevisiae chromosome VII, complete chromosome
2250_at	2640.8	A	Saccharomyces cerevisiae chromosome VII, complete chromosome
2251_at	948.5	A	Saccharomyces cerevisiae chromosome VII, complete chromosome
2252_g_at	5160.3	P	Saccharomyces cerevisiae chromosome VII, complete chromosome
2253_s_at	1286.3	P	Saccharomyces cerevisiae chromosome VII, complete chromosome
2254_at	25.8	A	Saccharomyces cerevisiae chromosome VII, complete chromosome
2255_at	149	A	Saccharomyces cerevisiae chromosome VII, complete chromosome
2256_at	18.4	A	Saccharomyces cerevisiae chromosome VII, complete chromosome
2257_at	17.8	A	Saccharomyces cerevisiae chromosome VII, complete chromosome
2258_at	319.5	A	Saccharomyces cerevisiae chromosome VII, complete chromosome
2259_at	449.9	A	Saccharomyces cerevisiae chromosome VII, complete chromosome
2260_g_at	113.5	A	Saccharomyces cerevisiae chromosome VII, complete chromosome
2261_s_at	46.5	A	Saccharomyces cerevisiae chromosome VII, complete chromosome
2262_at	4109.7	M	Saccharomyces cerevisiae chromosome VII, complete chromosome
2263_g_at	2134.1	P	Saccharomyces cerevisiae chromosome VII, complete chromosome
2264_s_at	3167.6	P	Saccharomyces cerevisiae chromosome VII, complete chromosome
2265_s_at	3705.3	P	Saccharomyces cerevisiae chromosome VII, complete chromosome
2180_s_at	5333.2	P	Saccharomyces cerevisiae chromosome VII, complete chromosome
2181_s_at	7244.1	P	Saccharomyces cerevisiae chromosome VII, complete chromosome
2182_s_at	16202	P	Saccharomyces cerevisiae chromosome VII, complete chromosome
2183_s_at	22825.3	P	Saccharomyces cerevisiae chromosome VII, complete chromosome
2184_s_at	10442	P	Saccharomyces cerevisiae chromosome VII, complete chromosome
2185_at	635.3	P	Saccharomyces cerevisiae chromosome VII, complete chromosome
2186_at	1146.2	A	Saccharomyces cerevisiae chromosome VII, complete chromosome
2187_at	307.9	A	Saccharomyces cerevisiae chromosome VII, complete chromosome
2188_at	95.5	A	Saccharomyces cerevisiae chromosome VII, complete chromosome
2189_at	249	A	Saccharomyces cerevisiae chromosome VII, complete chromosome
2190_g_at	2345.7	P	Saccharomyces cerevisiae chromosome VII, complete chromosome
2191_s_at	4216.4	P	Saccharomyces cerevisiae chromosome VII, complete chromosome
2192_at	47.1	A	Saccharomyces cerevisiae chromosome VII, complete chromosome
2193_at	216.5	M	Saccharomyces cerevisiae chromosome VII, complete chromosome
2194_at	132.1	A	Saccharomyces cerevisiae chromosome VII, complete chromosome
2195_at	779.3	A	Saccharomyces cerevisiae chromosome VII, complete chromosome
2196_s_at	3526.7	P	Saccharomyces cerevisiae chromosome VII, complete chromosome
2197_s_at	3581.2	P	Saccharomyces cerevisiae chromosome VII, complete chromosome
2198_at	374.4	A	Saccharomyces cerevisiae chromosome VII, complete chromosome
2199_at	88.1	A	Saccharomyces cerevisiae chromosome VII, complete chromosome
2200_at	9	A	Saccharomyces cerevisiae chromosome VII, complete chromosome
2201_at	93.1	A	Saccharomyces cerevisiae chromosome VII, complete chromosome
2202_g_at	134.1	A	Saccharomyces cerevisiae chromosome VII, complete chromosome
2203_s_at	2508.2	P	Saccharomyces cerevisiae chromosome VII, complete chromosome
2204_s_at	973.7	P	Saccharomyces cerevisiae chromosome VII, complete chromosome
2205_at	1770.5	P	Saccharomyces cerevisiae chromosome VII, complete chromosome
2206_g_at	34.7	A	Saccharomyces cerevisiae chromosome VII, complete chromosome
2207_s_at	1485.5	P	Saccharomyces cerevisiae chromosome VII, complete chromosome
2208_s_at	1038.9	P	Saccharomyces cerevisiae chromosome VII, complete chromosome
2209_s_at	977.8	P	Saccharomyces cerevisiae chromosome VII, complete chromosome
2210_s_at	3619.1	P	Saccharomyces cerevisiae chromosome VII, complete chromosome
2211_s_at	3362.8	P	Saccharomyces cerevisiae chromosome VII, complete chromosome
2212_at	584.4	P	Saccharomyces cerevisiae chromosome VII, complete chromosome
2213_at	137.5	A	Saccharomyces cerevisiae chromosome VII, complete chromosome

2214_at	1126.9	P	Saccharomyces cerevisiae chromosome VII, complete chromosome
2215_g_at	5263.5	P	Saccharomyces cerevisiae chromosome VII, complete chromosome
2216_s_at	2918.7	P	Saccharomyces cerevisiae chromosome VII, complete chromosome
2217_s_at	1830.9	P	Saccharomyces cerevisiae chromosome VII, complete chromosome
2218_s_at	5687.6	P	Saccharomyces cerevisiae chromosome VII, complete chromosome
2219_at	39.6	A	Saccharomyces cerevisiae chromosome VII, complete chromosome
2220_at	8.2	A	Saccharomyces cerevisiae chromosome VII, complete chromosome
2221_at	135.3	A	Saccharomyces cerevisiae chromosome VII, complete chromosome
2222_at	40.1	A	Saccharomyces cerevisiae chromosome VII, complete chromosome
2138_at	431.8	P	Saccharomyces cerevisiae chromosome VII, complete chromosome
2139_g_at	393.8	A	Saccharomyces cerevisiae chromosome VII, complete chromosome
2140_s_at	1196.8	A	Saccharomyces cerevisiae chromosome VII, complete chromosome
2141_s_at	1493.4	M	Saccharomyces cerevisiae chromosome VII, complete chromosome
2142_at	531.1	A	Saccharomyces cerevisiae chromosome VII, complete chromosome
2143_at	43.8	A	Saccharomyces cerevisiae chromosome VII, complete chromosome
2144_at	24.9	A	Saccharomyces cerevisiae chromosome VII, complete chromosome
2145_at	10.3	A	Saccharomyces cerevisiae chromosome VII, complete chromosome
2146_at	627.2	A	Saccharomyces cerevisiae chromosome VII, complete chromosome
2147_at	594	A	Saccharomyces cerevisiae chromosome VII, complete chromosome
2148_at	44.5	A	Saccharomyces cerevisiae chromosome VII, complete chromosome
2149_at	59.6	A	Saccharomyces cerevisiae chromosome VII, complete chromosome
2150_g_at	964.1	A	Saccharomyces cerevisiae chromosome VII, complete chromosome
2151_s_at	406.9	A	Saccharomyces cerevisiae chromosome VII, complete chromosome
2152_s_at	615	A	Saccharomyces cerevisiae chromosome VII, complete chromosome
2153_s_at	1994.2	P	Saccharomyces cerevisiae chromosome VII, complete chromosome
2154_s_at	1423.9	P	Saccharomyces cerevisiae chromosome VII, complete chromosome
2155_s_at	1378	P	Saccharomyces cerevisiae chromosome VII, complete chromosome
2156_s_at	1034.6	P	Saccharomyces cerevisiae chromosome VII, complete chromosome
2157_at	322.2	A	Saccharomyces cerevisiae chromosome VII, complete chromosome
2158_at	48.8	A	Saccharomyces cerevisiae chromosome VII, complete chromosome
2159_at	306	A	Saccharomyces cerevisiae chromosome VII, complete chromosome
2160_at	706.2	P	Saccharomyces cerevisiae chromosome VII, complete chromosome
2161_at	193.4	A	Saccharomyces cerevisiae chromosome VII, complete chromosome
2162_g_at	21131.8	P	Saccharomyces cerevisiae chromosome VII, complete chromosome
2163_s_at	29748.6	P	Saccharomyces cerevisiae chromosome VII, complete chromosome
2164_at	542.9	A	Saccharomyces cerevisiae chromosome VII, complete chromosome
2165_g_at	300.8	A	Saccharomyces cerevisiae chromosome VII, complete chromosome
2166_s_at	146.2	A	Saccharomyces cerevisiae chromosome VII, complete chromosome
2167_s_at	960.1	P	Saccharomyces cerevisiae chromosome VII, complete chromosome
2168_s_at	201.5	P	Saccharomyces cerevisiae chromosome VII, complete chromosome
2169_s_at	2873.8	P	Saccharomyces cerevisiae chromosome VII, complete chromosome
2170_s_at	1931.5	P	Saccharomyces cerevisiae chromosome VII, complete chromosome
2171_at	42.3	A	Saccharomyces cerevisiae chromosome VII, complete chromosome
2172_at	220.6	A	Saccharomyces cerevisiae chromosome VII, complete chromosome
2173_g_at	705.2	A	Saccharomyces cerevisiae chromosome VII, complete chromosome
2174_s_at	2504.4	P	Saccharomyces cerevisiae chromosome VII, complete chromosome
2175_s_at	1298.1	P	Saccharomyces cerevisiae chromosome VII, complete chromosome
2176_s_at	1940.5	P	Saccharomyces cerevisiae chromosome VII, complete chromosome
2177_s_at	6522.5	P	Saccharomyces cerevisiae chromosome VII, complete chromosome
2178_at	725.2	P	Saccharomyces cerevisiae chromosome VII, complete chromosome
2179_at	28.2	A	Saccharomyces cerevisiae chromosome VIII, complete chromosome
2100_g_at	2353.8	P	Saccharomyces cerevisiae chromosome VIII, complete chromosome

2101_s_at	692.2	A	Saccharomyces cerevisiae chromosome VIII, complete chromosome
2102_s_at	1021.3	P	Saccharomyces cerevisiae chromosome VIII, complete chromosome
2103_s_at	3800.4	P	Saccharomyces cerevisiae chromosome VIII, complete chromosome
2104_s_at	11668.9	P	Saccharomyces cerevisiae chromosome VIII, complete chromosome
2105_s_at	4751.1	P	Saccharomyces cerevisiae chromosome VIII, complete chromosome
2106_at	165.7	A	Saccharomyces cerevisiae chromosome VIII, complete chromosome
2107_at	594.2	A	Saccharomyces cerevisiae chromosome VIII, complete chromosome
2108_at	77	A	Saccharomyces cerevisiae chromosome VIII, complete chromosome
2109_g_at	427.6	P	Saccharomyces cerevisiae chromosome VIII, complete chromosome
2110_s_at	227.7	A	Saccharomyces cerevisiae chromosome VIII, complete chromosome
2111_s_at	366.6	A	Saccharomyces cerevisiae chromosome VIII, complete chromosome
2112_s_at	281.3	A	Saccharomyces cerevisiae chromosome VIII, complete chromosome
2113_s_at	2418.4	A	Saccharomyces cerevisiae chromosome VIII, complete chromosome
2114_s_at	558.5	P	Saccharomyces cerevisiae chromosome VIII, complete chromosome
2115_at	3.7	A	Saccharomyces cerevisiae chromosome VIII, complete chromosome
2116_at	541.6	P	Saccharomyces cerevisiae chromosome VIII, complete chromosome
2117_at	209.2	A	Saccharomyces cerevisiae chromosome VIII, complete chromosome
2118_at	1191.5	P	Saccharomyces cerevisiae chromosome VIII, complete chromosome
2119_g_at	681	A	Saccharomyces cerevisiae chromosome VIII, complete chromosome
2120_s_at	421.3	A	Saccharomyces cerevisiae chromosome VIII, complete chromosome
2121_s_at	1233.7	A	Saccharomyces cerevisiae chromosome VIII, complete chromosome
2122_s_at	424.7	A	Saccharomyces cerevisiae chromosome VIII, complete chromosome
2123_s_at	526.3	A	Saccharomyces cerevisiae chromosome VIII, complete chromosome
2124_s_at	165.3	A	Saccharomyces cerevisiae chromosome VIII, complete chromosome
2125_s_at	1704.2	P	Saccharomyces cerevisiae chromosome VIII, complete chromosome
2126_s_at	1732.4	P	Saccharomyces cerevisiae chromosome VIII, complete chromosome
2127_s_at	958.3	P	Saccharomyces cerevisiae chromosome VIII, complete chromosome
2128_s_at	898.5	P	Saccharomyces cerevisiae chromosome VIII, complete chromosome
2129_s_at	5013.8	P	Saccharomyces cerevisiae chromosome VIII, complete chromosome
2130_at	2135.3	A	Saccharomyces cerevisiae chromosome VIII, complete chromosome
2131_at	67.3	A	Saccharomyces cerevisiae chromosome VIII, complete chromosome
2132_at	18.3	A	Saccharomyces cerevisiae chromosome VIII, complete chromosome
2133_at	18.7	A	Saccharomyces cerevisiae chromosome VIII, complete chromosome
2134_at	143.1	A	Saccharomyces cerevisiae chromosome VIII, complete chromosome
2135_at	13.9	A	Saccharomyces cerevisiae chromosome VIII, complete chromosome
2136_at	57.4	A	Saccharomyces cerevisiae chromosome VIII, complete chromosome
2137_at	46.2	A	Saccharomyces cerevisiae chromosome VIII, complete chromosome
11394_at	340.2	P	Saccharomyces cerevisiae chromosome VIII, complete chromosome
11395_at	348.4	A	Saccharomyces cerevisiae chromosome VIII, complete chromosome
11396_g_a	771.8	A	Saccharomyces cerevisiae chromosome VIII, complete chromosome
11397_f_at	525.8	A	Saccharomyces cerevisiae chromosome VIII, complete chromosome
11398_s_a	2142.8	A	Saccharomyces cerevisiae chromosome VIII, complete chromosome
11399_s_a	2725.3	P	Saccharomyces cerevisiae chromosome VIII, complete chromosome
11400_s_a	460.1	M	Saccharomyces cerevisiae chromosome VIII, complete chromosome
11401_at	45	A	Saccharomyces cerevisiae chromosome VIII, complete chromosome
11402_at	170.6	A	Saccharomyces cerevisiae chromosome VIII, complete chromosome
11403_at	1447.1	A	Saccharomyces cerevisiae chromosome VIII, complete chromosome
11404_at	45.7	A	Saccharomyces cerevisiae chromosome VIII, complete chromosome
11405_at	2683.5	P	Saccharomyces cerevisiae chromosome VIII, complete chromosome
11406_f_at	112.8	A	Saccharomyces cerevisiae chromosome VIII, complete chromosome
11407_f_at	43.4	A	Saccharomyces cerevisiae chromosome VIII, complete chromosome
11408_f_at	4766.7	P	Saccharomyces cerevisiae chromosome VIII, complete chromosome

11409_f_at	75.9	A	Saccharomyces cerevisiae chromosome VIII, complete chromosome
11410_at	6.4	A	Saccharomyces cerevisiae chromosome VIII, complete chromosome
11411_at	12.1	A	Saccharomyces cerevisiae chromosome IX, complete chromosome
11412_at	48.4	A	Saccharomyces cerevisiae chromosome IX, complete chromosome
11413_s_a	1392.7	P	Saccharomyces cerevisiae chromosome IX, complete chromosome
11414_s_a	16.6	A	Saccharomyces cerevisiae chromosome IX, complete chromosome
11415_f_at	448.7	P	Saccharomyces cerevisiae chromosome IX, complete chromosome
11416_at	1332.9	P	Saccharomyces cerevisiae chromosome IX, complete chromosome
11417_at	97.8	A	Saccharomyces cerevisiae chromosome IX, complete chromosome
11418_at	42.5	A	Saccharomyces cerevisiae chromosome IX, complete chromosome
11419_at	283.3	A	Saccharomyces cerevisiae chromosome IX, complete chromosome
11420_at	91.9	A	Saccharomyces cerevisiae chromosome IX, complete chromosome
11421_at	21.1	A	Saccharomyces cerevisiae chromosome IX, complete chromosome
11422_at	240.1	A	Saccharomyces cerevisiae chromosome IX, complete chromosome
11423_at	78.6	A	Saccharomyces cerevisiae chromosome IX, complete chromosome
11424_g_a	158.8	A	Saccharomyces cerevisiae chromosome IX, complete chromosome
11425_s_a	2565.7	A	Saccharomyces cerevisiae chromosome IX, complete chromosome
11426_s_a	1252.6	P	Saccharomyces cerevisiae chromosome IX, complete chromosome
11427_at	29.6	A	Saccharomyces cerevisiae chromosome IX, complete chromosome
11428_at	314.4	A	Saccharomyces cerevisiae chromosome IX, complete chromosome
11429_at	428.6	A	Saccharomyces cerevisiae chromosome IX, complete chromosome
11430_at	46.5	A	Saccharomyces cerevisiae chromosome IX, complete chromosome
11431_at	41.6	A	Saccharomyces cerevisiae chromosome IX, complete chromosome
11432_at	347.9	A	Saccharomyces cerevisiae chromosome IX, complete chromosome
11433_at	17.7	A	Saccharomyces cerevisiae chromosome IX, complete chromosome
11434_g_a	316.7	M	Saccharomyces cerevisiae chromosome IX, complete chromosome
11435_s_a	1416.9	P	Saccharomyces cerevisiae chromosome IX, complete chromosome
11436_s_a	543	A	Saccharomyces cerevisiae chromosome IX, complete chromosome

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s 1358-3197 of L38424 (-5, -M, -3 represent transcript regions 5 prime, Middle, and 3 prime respectivel
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17-3334 of M24537 (-5, -M, -3 represent transcript regions 5 prime, Middle, and 3 prime respectively)
17-3334 of M24537 (-5, -M, -3 represent transcript regions 5 prime, Middle, and 3 prime respectively)
17-3334 of M24537 (-5, -M, -3 represent transcript regions 5 prime, Middle, and 3 prime respectively)
-2229 of X04603 (-5, -M, -3 represent transcript regions 5 prime, Middle, and 3 prime respectively)
-2229 of X04603 (-5, -M, -3 represent transcript regions 5 prime, Middle, and 3 prime respectively)
-2229 of X04603 (-5, -M, -3 represent transcript regions 5 prime, Middle, and 3 prime respectively)
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nsferase beta subunit
ction
protein of the mitochondrial cytochrome bc1 complex .
MP decarboxylase

1w

es to the spindle pole bodies. Molecular weight is 72 kD

cdc42

revin) homolog, forms a complex with Snc2p and Sec9p
revin) homolog, forms a complex with Snc2p and Sec9p

nsport (E1-E2) ATPases

phology and inheritance

for Tef1p\/Tef2p
for Tef1p\/Tef2p
a C-terminal cysteine-rich region that conforms to the H2 variant of the RING finger Zn2+ binding motif.

NA binding protein, binds URS1 and CAR1

217 and 101354 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the

64 and 23898 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yea

15 and 31373 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yea

994 and 223152 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the

44 and 73614 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yea

298 and 139468 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the

468 and 166617 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the

0 and 3394 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast

29 and 19968 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yea

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555 and 219719 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the

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253 and 223423 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the

333 and 223476 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the

n

ha-1 subunit rbB-I

equences

tty acid tetradecanoic acid (14:0) to that of hexadecanoic acid (16:0)

s in a complex containing other MNN gene products.

prised of six subunits

ha factor

l precursor proteins

in the Golgi

an glycogenin

goid long chain bases into cells

lutamine amidotransferase

1p, Ste11p, and Hog1p

sely resembles Sm-B (Fromont-Racine et al, 1997 Nature Genetics 16:277-282)

3 (Atp8p) of the Fo-F1 ATP synthase
expressed

ction

ay during S-phase
per motif and acidic region\; lexA-Sip4p activates transcription

-nuclear envelope membranes, involved in control of mitotic chromsome transmission

al domain, containing heptad repeats, that binds Nsp1p\; nucleoporin
vate transaminase

egulation

membrane.

n Nup93

n protein
P70 gene family

a subunit)

trn6p and TATA-binding protein
plasma membrane-associated clathrin assembly complex (AP-2)

›f microtubule function

RPO21 CTD (carboxy-terminal domain)\; also called CTDK-I beta subunit

logous to mammalian ribophorin I

?NP)

ex

›mplex. Protein is important for efficient signal peptidase activity.

e ADP-ribosylation factor ARF
with RPD3 gene product

ne B gene ERCC6, that is a putative helicase ntegrity\; may also be involved in tRNA biogenesis

eI endonuclease

n with Syf1p as bait (SYF1 is synthetic lethal with PRP17 KO). A subsequent screen with Isy1p as bait is

ve genes

take

Da subunit

.R243w
d N-methyltransferase)

ich can bind to signal sequence regions of mitochonidrial preproteins. In addition, it has been purified as poly(A) polymerase

and aldehyde reductases

RcsB

n S7

essing of the yeast a-factor precursor

rrin receptor protein

94_SCHPO) and Mrs11p (YHR005c-a)

321 and 159545 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the
250 and 181408 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the
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100 and 116291 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the
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920 and 448102 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the
543 and 549719 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the
016 and 578222 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the
602 and 637835 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the
961 and 728134 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the
313 and 737453 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the

with 100% identity.

OR162c, YOR172w and YLR266c

Cos5p, Ybr302p, Cos3p, Cos1p, Cos4p, Cos8p, Cos6p, Cos9p

nctional enzyme)

way
e b pre-mRNA

es type1 protein phosphatase

oment, see Karos, M. and Fischer, R. (1996). hymA (hypha-like metulae), a new developmental mutant c

transferase, enoyl reductase, dehydratase and malonyl\/palmityl transferase se largest subunit CTD (carboxyl-terminal domain)

complex

inase C, is 90\% identical to Ypk2p

essed
essed

ng

heteromer)

-phosphate synthase)

2

d spindle integrity
othetical protein YOR054c

colocalizes with Myo2p

alizes to the lumen of the endoplasmic reticulum:

B

ucine zipper motifs, coiled-coil region, and some homology to Nup133p

o

-A

lc23p and Cdc27p to catalyze the conjugation of ubiquitin to cyclin B

omain type

ibonucleoprotein particle

ompartment. possible NSF attachment protein receptor (V-SNARE)

tion factor DmS-II

gulator of GCD12, thereby serving indirectly as a positive regulator of GCN4 an glycogenin

phogenesis

argeting and fusion of ER to Golgi transport vesicles

uclear pore distribution, and possibly in the biogenesis of functional tRNA

2p\/Sup2p\/Gst1p\/Sup35p
ologous to L17 of E. coli

at Nopp140, a nonribosomal protein of the nucleolus and coiled bodies.

and adenine biosynthesis genes

18 and 91755 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yea
73 and 94228 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yea
588 and 146755 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the y
218 and 403517 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the y
527 and 618670 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the y
749 and 618886 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the y
01 and 17055 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yea
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00 and 19061 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yea
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275 and 136457 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the y
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759 and 468899 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the y
004 and 527159 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the y
255 and 533518 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the y
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056 and 185205 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the
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740 and 456883 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the
142 and 619375 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the

-L-glycero-4-hexulose-5-epimerase

brane channels\; may be involved in glycerol efflux

al protein

its of G-proteins and the splicing factor Prp4

nsing MAP kinase cascade(suppressor of sensor kinase)

omain type

ired in ER to Golgi transport.

laseVIMP cyclohydrolase

rotubule ends at the spindle pole body

AGA complex

in 4

n of COX1 mRNA and by affecting transcription or stability of COX1 mRNAs

teracts with Sin4p, Gal11p, and a 50 kd polypeptide subunit VI requiring protein

omolog gene

l with polyadenylation factor 1 (PF I)
nt complex

ssible gene

ng with Rrn9p and Rrn10p

.7
bilized cells

. The Exocyst complex contains the gene products encoded by SEC3, SEC5, SEC6, SEC8, SEC10, SE

hthamide biosynthesis

proteins which have a novel highly conserved DNA binding domain

domain

beta-transducin superfamily because of presence of WD-40 repeats

g of a component of the bovine NABC complex

ER

Tub4p-Spc98p-Spc97p complex may be part of the microtubule attachment site at the spindle pole body

with RPD3 gene product

rRNA

ors

omain type

sis and chiasmata formation\; localizes to chromosome cores independently of Mei4p and Spo11p\; mRI

eting subunit

r of GCN4 expression

SC

recombination protein\; mRNA is induced early in sporulation
in the first stages of mating

that of NSP1 and NUP1

eta (importin 90)

g Protein\; high copy suppressor of cik1 and kar3 deletion mutants.
s

acids

ad18

‹

ınction

:homosomes in spread meiotic nuclei but is excluded from the nucleolus

natography

:oli

:oli

:oronin

e catalytic subunit A1\; cytoplasmic

with U4, U5 and U6 snRNAs

e\; required for assembly

'me
omain type

AU)

974 and 231108 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the
496 and 320642 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the
326 and 341589 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the
871 and 434059 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the
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784 and 121936 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the
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and 461 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast tra
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5773 and 1035940 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of th

erexpressed

g regions, several potential glycosylation sites, potential ATP-binding site

9

hatase complex\; homologous to TPS3 gene product

omain type

lian ras inhibitors

epair

prised of six subunits

e reductases

me
rolyl cis-trans isomerase (PPIase)

ws homology to Cdc6p, Cdc18p, and Sir3p and to proteins from K. lactis, S. pombe, and humans
M-phase

phosphatase\; redundant with Cna1\; cytoplasmic

otein SPC25

n6p and Rrn7p, which is required for rDNA transcription by RNA polymerase I eiosis during recombination

ains

efect.

event in vacuole inheritance, for endosome-endosome fusion, and for fusion of endosomes to vacuoles e-chain

ows similarity to Candida albicans corticosteroid-binding protein CBP1

ein phosphatase catalytic subunits

ning family of nucleoporins and is highly homologous to Nup100p

with Sin3p and Stb1p
membrane
le function

entially recognizes the mature regions of precursor proteins associated with ATP-dependent cytosolic ch
in pre-mRNA 3 -end processing

on and may play a role in the organization of the membrane fusion complex

ch

A) family

ctin lies on front surface of subdomain 3 and 4.

tein complex, which binds to the CDE III element of centromeres

ession after entry into stationary phase

sults in mislocalization of septa

with Hdf1p to form major DNA end-binding complex

L132c
aM

tional machinery
tional machinery

lase/IMP cyclohydrolase

essed by a multi copy plasmid

s

r IME1

ssible coiled-coil protein

sparagine domains

ismatched DNA
al acidic domain and a putative coiled coil dimerization domain

equence NNNDSYGS

ecretion

ounit), Glycine cleavage system (P-subunit)

ep12p

mport channel

177c and YPL095c

2p and Xrs2p function in a complex by immunoprecipitation and two-hybrid analyses\; mutations in these

of parental nuclei before nuclear fusion

ngation

membrane protein with low homology to RIM2 hatase complex

surface of the endoplasmic reticulum. Assembly with Cue1p is a prerequisite for the function of Ubc7p

sp5

ted to Gal4p

ng mitosis (but not during conjugation)

the first step in biosynthesis of long-chain sphingolipids d in proper chromosome segregation

alidase

029 and 159169 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the
825 and 390965 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the
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ical protein YFL061w

DnaJ and other DnaJ-like proteins, function partially overlaps that of Mdj1p
cell separation after cytokinesis
ZK757.1

subunit of RF-A

plex with Sin3p and Stb2p

Da subunit

Similarity to SLG1 (WSC1), WSC3 and WSC4

ated protein)
amino acids

ATP-binding site

oxygen toxicity

e-specific regulation of nuclear pre-mRNA abundance
hydrophobic tail, Rad50p interacts with Mre11p and Xrs2p in two-hybrid and immunoprecipitation analys

A

ex with Aut7p\; Aut2p mediates attachment of autophagosomes to microtubules

ent mRNA splicing

-induced glutamine rich protein

yltransferase

ay function in complex with Gcr2p

the transcription factor Ume6 and expressed early in meiosis

ith Cdc31p, localizes to the spindle pole body

in mediated signal transduction

s with Mig1p

ient limitation which is homologous to the sporulation-specific SPS100 gene

prised of six subunits

and PTEN1. Contains sequence motifs characteristic of protein tyrosine phosphatases.

and Tub4p perhaps as part of the microtubule attachment site of the SBP
CT1 and MCT2

rane

is
.c

ming a heterodimer, Pms1p and Msh1p act in concert to bind to a Msh2p-heteroduplex complex contain

ith Spt2p

ydrogenase complex

proliferation-associated nucleolar protein, p120

nnel, or VDAC)

eromone

otein YPR115w, and strong similarity to hypothetical protein YIL105c ent

equences

shuttle craft protein\; similarity to human NFX1 protein\; similarity to human DNA-binding protein tenasci

, Hos2p, and Hos3p

ll surface

y replace the other. Does not correspond to any ribosomal component identified so far, based on its bioc
ted between chromosomes III and XIV (DOM34 homologue on chromosome III is a pseudogene)

function

se

molog of Rsc6p subunit of the RSC chromatin remodeling complex

ation

c domains\; homologous to Sol2p and Sol3p

ubunit 2

, interacts with Sec1p
aropine reductase) (EC 1.5.1.10)

transporters

rase

YEL070w

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m plants

complex

ıilar to vertebrate hnRNP A\/B protein family
lrial membrane

p

enes

Similarity to SLG1 (WSC1), WSC2 and WSC4
gus DNA interactions at telomeres and is required for a telomere activity in distributive segregation\; is as

Da subunit

ıd meiosis, functions with Pms1p and Pms2\/Mlh1p in a complex which interacts with either Pms3\/Msh6

ıomologue of neurofibromin

gy

n between mitochondria, peroxisomes, and nucleus

osphokinase)

e and negative transcriptional regulator of genes involved in mating-type specialization

d D. melanogaster, murine/bovine poly(A) binding protein II, and Nsr1p f the SMC superfamily

of histone variants

omolog exists in S. Pombe which confers a dominant negative phenotype when expressed in S. cerevisia

ex

nit

d YLR246w

cin C

ine-rich proteins

le function
ıary phase
ı Yap recognition site

lliral protein translocation complex, associates with Isp42p

BP in two-hybrid and in in vitro binding studies and Sec22p

omplex

required for membrane association\; also involved in endocytosis post vesicle internalization

identical to vertebrate DAD1 protein

pressor of mutation in the nuclear gene for the core subunit of mitochondrial RNA polymerase

EC18 family of ATPases

roxylase steps of ubiquinone biosynthesis

al H+-transporting ATP synthases
C. elegans protein

of splicing

.21

ion

ses, the SWI2\/SNF2-like proteins

ed in secretion and nuclear segregation

pre-mRNA splicing mutation, prp8-1

in

kDa subunit

III)

n the 2-hybrid system

to half-bridges and interacts with KAR1

in the general control of amino acid biosynthesis

esis

tic motor.
ential for vacuolar acidification and vacuolar H-ATPase activity

ependent translation initiation by interfering with the interaction of eIF4E and eIF4G

ouse

sor of cobalt toxicity

sic region\/helix-loop-helix\/leucine-zipper protein family

ule stability
dase I
eonine protein kinase which interacts with and is believed to phosphorylate Hop1p

oxidoreductase
is functional, migrates at 28 kDa, fractionates predominantly in the cytosolic fraction (however a minor a
cription factor

escort protein)\; component of Rab geranylgeranyl transferase

atalogue number A5550, according to A. Blomberg)

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pothetical protein YLL062c

alizes to the tip of shmoo projections and to the tip of budding cells in a cell-cycle dependent manner arity to hypothetical proteins YOL055c and YPR121w

omain type

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tor of cellular morphogenesis, inducing actin-ring formation in association with cytokinesis

and an acidic C terminus rich in PEST-like sequences

m A. thaliana
rat

ecretion

se

omplex (cytochrome bc1 complex)

dent tRNA pseudouridine synthase activity

hicum and M. jannaschii

rane-associated clathrin assembly complex

main to human proto-oncogene PBX1

n the Rho1p small GTP-binding protein

ng cassette transporter necessary for transport of long-chain fatty acids into peroxisomes

sterol biosynthesis and regulation of Golgi-derived transport vesicle biogenesis

al protein YOR227w

group at position 8 of the porphyrin ring

tein

e.

somerase)

assembly GTPase Cdc42

p
tii

eak similarity to other GTP-binding proteins

gy to known HATs and NATs

ne first intermediate in synthesis of glycosylphosphatidylinositol (GPI) anchors

luble vauolar hydrolases from the late endosome to the vacuole

ypothetical protein SPAC2F7.02c

elongation factor 1-gamma (EF-1gamma)

no acid metabolism, highly homologous to Met32p

BTF3

es

)

UBA3. Related to AOS1 and to N-terminus of UBA1. Collaborates with UBC12 in conjugation of RUB1 tc

otein

:21

s
scription factor TFIIH
ınd toxic levels of ethanol

') complex

e

ıammalian nitric-oxide synthases

xocytosis, and which also contains the gene products encoded by SEC3, SEC5, SEC6, SEC10, SEC15,
b), 37 kDa subunit

ption

ound in the developmental fork head protein of Drosophila melanogaster and in the HNF-3 family of hep

nd YIL105c

to hypothetical proteins YPL258c and YOL055c

rane protein

equences

nolog
:he Fo-F1 ATP synthase

protein

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-1,6-glucosidase (EC 3.2.1.33)

gy to known HATs and NATs

ein family

hosphate dehydrogenase gene families

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Xenopus XCAP-H, and a functional homolog of human BRRN1

ved in the biosynthesis of the lipid-linked oligosaccharide

nup170 mutant can be complemented with NUP155)
hagosomes to microtubules. Aut7p shows homologies to LC3, a microtubule-associated protein from rat

mily

ost-translational regulator of chitin synthase III activity, interacts with Chs3p

the phosphoprotein phosphatase 1 catalytic subuniut encoded by GLC7

HMR.

n ER and Golgi

, Ca++ binding

e

nt of the mitotic spindle

embrane protein 166aa cytoplasmic tail, 1300 aa lumenal domain

rn7p and TATA-binding protein

an retinal transducin\; contains nuclear targeting signal ce of autonomously replicating sequence

1 (S. cerevisiae)
rase, CDP-diglyceride synthetase

ly dimethylating enzyme)

+ binding protein (homology to EF-hand Ca2+ binding site)

lc7p

(E. coli)

lian translation initiation factor 3
lgi\; ATPase
complex

egulator of Ty1 expression

a subunit
polymerase delta, mRNA increases in G1, peaks in S in mitosis, and increases prior to DNA synthesis i

rotein sorting

rt and regulation of Pho81p function

atase complex

e induced checkpoint responses in G1, S\/M, intra S, and G2\/M in mitosis

motif

III)

erevisiae)

ns when over-expressed

f RNase MRP

nent
plex, an integral endoplasmic reticulum membrane protein complex required for translocation of presecr

otein of the mitochondrial outer membrane which can be isolated as part of a high molecular weight com

regulator of ras-mediated cAMP induction\; homologous to beta subunit of GTP-binding proteins

in type

ase)

uman Sop2p-like protein

GE

enzyme

\; associated with RNase MRP and RNase P

L024c

matin

th a positive and negative regulator of a subset of genes, perhaps operating in parallel with Gal11p

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d CIK1

d in organization of actin filaments

Ste11p

lular homeostatis

embles with Bud4p at bud sites

LgYCL010c

LgYCL005w

LgYCL002c
p, in the ER\; localized to Golgi, where it may function in returning membrane proteins to the ER

tionary phase\; located in plasma membrane

)

4p, Rrp41p, Rrp42p and Dis3p (Rrp44p).

take\; protein contains 12 predicted transmembrane domains

nd related to the Swi\/snf Complex.

N4 responsive site suggesting it may also be involved in amino acid biosynthesis.

c domains\; homologous to Sol1p and Sol3p

n

units of G proteins

otide-dependent protein kinase subfamily and the protein kinase C subfamily
tion mispairs\; redundant with Pms3\/Msh6p in repair of insertion-deletion mispairs

epresses transcription of haploid-specific genes in diploid cells
epresses transcription of haploid-specific genes in diploid cells
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epresses transcription of haploid-specific genes in diploid cells

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ating family of proteins

L052w

of the ADP\/ATP carrier (AAC) family
haliana

step in heme biosynthesis

M protein\; putative mitochondrial carrier protein
expressed

e extein AC and the intein B\; AC is a 69K vacuolar (H+)-ATPase, and B is a 50K site-specfic endonucle

o cellular nucleic acid binding proteins

omain type

hyde dehydrogenase)

.9

\0171 protein
lization to telomeres

mbly or function

nsition, assists in mediating the proteolysis of the Cdk inhibitor Sic1p in late G1

ll length homology to mammalian protein VCP\; involved in secretion, peroxisome formation and gene e

iron accumulation

4p, Rrp41p, Rrp43p and Dis3p (Rrp44p).

omplex of TFIIH

PHO5 and other genes

lta gene

r thiamin metabolism

ation defects, which are general properties of the RAD52 epistasis group mutants. rad59 is epistatic to

phorylase

drial ribosomes

ndrial transcripts

utophosphorylate itself as well as Mad1p. A mutation predicted to abolish kinase function not only elimina

18 family of ATPases

nction in chromosome morphogenesis from S phase through mitosis

hypothetical protein SPAC12G12.14

9a and human RanBP1

h Rad 55p by two-hybrid analysis

temperature-sensitive A kinase mutants

s

lex

cin (WD-40) repeats

e semialdehyde as co-inducer\; saccharopine reductase synthesis

ase, phenylalanine-inhibited\; phospho-2-keto-3-deoxyheptonate aldolase\; 2-dehydro-3-deoxyphosphoh

s

s the first step in biosynthesis of long-chain sphingolipids ad51p and Rad57p by two-hybrid analysis

e metabolism during late S phase

on of morphogenesis during conjugation
plex and the Ssh1 trimeric complex

ransporter protein

to repair both single-base and insertion-deletion mispairs, redundant with Msh3p in repair of insertion-de

oteins

ase, 3-dehydroquinate dehydratase (3-dehydroquinase), shikimate 5-dehydrogenase, shikimate kinase,
ding protein

n CFTR and multidrug resistance proteins

sion recombination

nolog

ydrogenase complex in mitochondria

polypeptide, potential Ca2+-binding site, and pleckstrin homology domain
repeats of a novel zinc finger motif consisting of Cys and His residues in the form Cx8Cx5Cx3H [where

AP2, TAT1, PTR2 and YDR046c

s.

1p (Ada3p) is part of two transcriptional adaptor\/HAT (histone acetyltransferase complexes, the 0.8 MD

on, and nuclear division

CP1 or TRiC), distantly related to Tcp1p and to Hsp60
ER and Golgi

nation, prior to polyadenylation

D, rat zinc transport protein ZnT-1 and Cot1p

tor required for both repression and induction of early meiotic genes, and for sporulation\; Ume6p rquire

enes

se from mouse

eracts with Rna14p and Rna15p

U1 snRNP protein and has multiple copies of the crn-like TPR motif

ociated with the U1 snRNP\; no counterpart in mammalian U1 snRNP. Serine-rich.

polymerase II\; BTF3 homolog
no acid metabolism, highly homologous to Met31p
be required for kinetochore function
A3

ng proteins

and Wilsons genes

f 3 ->5 exonucleases

hypothetical protein SPAC12G12.14

osphate lyase)

associated with polyadenylation factor 1 (PF I)

on
on

ine auxilin

ysteine rich regions of amino acids are essential for function
epeat containing proteins

3, a multiprotein complex which binds to the CDE III element of centromeres. In addition, Skp1p is a subu

PI) anchors to proteins
licase MSS116 / YDR194c

MR010w

nodulin, and a 35 kDa protein

y to signal transducing adaptor from mouse and man roteins

equired for expression of functional Rieske iron-sulfur protein

larity to Rga1p. Has some similarity to all known Rho-GAPs.

a complex from whole-cell extracts

e

complex
overexpressed
EC18 family of ATPases

lase (EC 3.2.2.1)
to N,N-bisformyl dityrosine in vitro

ll pathway converting L-tyrosine to N-formyl-L-tyrosine, expressed late (10-16 hr) in sporulation

r to L23 family of ribosomal proteins

e\; member of yeast Jun-family of transcription factors related to mammalian c-jun

adaptor\/HAT (histone acetyltransferase)complexes

r to RSP5\; contains motifs typical of protein kinases

n CAK subunit

or stability of the actin cytoskeleton

de chain release factor 1 and YJL149w

chore
plement 3 precursor

plexes on the cell surface in cells cultured in medium containing copper salts

activity

eVlate meiosis

MR322c

region

acids
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gy to known HATs and NATs

f mitotic spindle

ction of the Imp1 peptidase and\/or the protein sorting machinery

AU)

tion of glycosyltransferases in the Golgi, also involved in osmotic sensitivity and resistance to aminonitro

; protein

dicyclohexylcarbodiimide binding subunit

lex

)
)

nbrane

ıs

esistance
prised of six subunits

tor Cin8p\; required for normal microtubule stability

mplex\; the 91 kD component is a C-terminal proteolytic breakdown product of full length Sec3p
disassociation reactions of nuclear import\; human homologue complements yeast mutants

ine-rich proteins

ogous to human p58 subunit

all spliceosomal snRNPs

d for full chromosome pairing seen by in situ hybridization, heteroduplex DNA, synaptonemal complexes

d for full chromosome pairing seen by in situ hybridization, heteroduplex DNA, synaptonemal complexes

served 25 residue motif, called the GVNK motif, also found in GAC1, PIG1, PIG2, and RGI, the mamma

ression (O)

kinase

sequence), which was identified in a genetic screen by its ability to reverse the Cdc42p suppression of a se (also called N5-methyltetrahydrofolate homocysteine methyltransferase or 5-methyltetrahydropteroyl t

to synapsis (independently of ZIP1 and DMC1), and interacts with Rad52p and Rad55p by two-hybrid an

es an interaction with Srp1p and Rip1p\; copurifies with Nup116p

n SH3 domain, and a pleckstrin homology domain

dominant nuclear mutation that is inositol-dependent in the presence of choline

des a ubiquitin-protein ligase (E3 enzyme) thetical proteins

ATP synthase complex

the general transcription machinery in vivo

alizes with Rad51p to discrete subnuclear sites in nuclear spreads during mid prophase, briefly colocalize
alizes with Rad51p to discrete subnuclear sites in nuclear spreads during mid prophase, briefly colocalize

ndrial protein import

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otein

protein

otein

ncer of Polycomb
ESA) that binds human erythrocyte protein 4.1.

tif
AU)

3 component of alpha-ketoacid dehydrogenase complexes)

ans B0024.12 protein
ng

es on meiotic chromosomes

protein kinase

ty to other myosin class I heavy chains

olved in the the control of peptide transport

14 (S. pombe)\; involved in chromosome segregation and condensation, interacts with Smc1p and Trf4p

and Sbp1p

n remodeling complex and related to the Swi\/snf Complex.

L001w and YDR282c

ing activity

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991 and 182221 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the
with 100% identity.
with 100% identity.
with 100% identity.
cluding Cos2p, Cos4p, Cos8p, YIR040c, Cos5p, Cos9p, and Cos6p

dria, peroxisomes, and nucleus
o\; Probable 119 kD DNA\/RNA helicase family member

ne synapsis

nplex and are involved in the degradation of Clb2p

ase
products encoded by SEC3, SEC5, SEC6, SEC8, SEC10, SEC15 and EXO70.

ociate with the SIT4 protein phosphatase
overexpressed

hy

eract with Snf1p and Snf4p and are involved in the response to glucose starvation

on
rived transport vesicles

e expression

se to starvation

al signals and thereby regulate meiosis
TP

protein

ion of hybrid DNA in vitro\; has 5 -to-3 exonuclease activity on DNA and RNA\; binds to G4 tetraplex DN

ent RNA helicases\; high-copy suppressor of kem1 null mutant

eiotic recombination. mRNA increases in meiosis.

se

inoadipate reductase)

rt of peroxisomal matrix proteins

sport from the endoplasmic reticulum to the golgi apparatus

of the third mannose onto the GPI core structure.

ty to RNA polymerases. The Soh1 protein interacts with a DNA repair protein, Rad5p, in a two-hybrid sys

es after the release of mature mRNA
ssential for the electron transfer in the bc1 complex

for quadruplex nucleic acids

otein (Lig4p)

nology with UGA4

CCPu

e
act with Ubr1 (an E3 ubiquitin ligase needed for multiubiquitination), and Rad18p (a single-stranded DN

28w, YAR033w and YCR007c

in pre-mRNA 3 -end processing

ilms tumour proteins

somes

omain type

mine cytidylyltransferase or phosphocholine cytidylyltransferase)

P. Contains few SR-, RE- and RD-dipeptides.

notransferase)
sector

cal protein MTH972

enzae dihydrolipoamide acetyltransferase

stic for a wide variety of phosphatases, including lipid phosphatases and a protein phosphatase.
endozepine (EP)

tion
selection\; likely involvement in positioning the proximal pole signal

by a1-a2 regulator

ll surface

ly of bud neck microfilament genes and is regulated by ABFI

g Protein

s\; acts with Nmd2p and Nam7p

uration

g of a component of the bovine NABC complex

al repressor of GCN4 protein

f 3 ->5 exonucleases

latory system
from the chromatin of the cohesin Scc1. The anaphase-promoting complex promotes anaphase by me

cadillo

e

3, possesses nucleosome assembly activity

erminal half

nb2p

32 homolog
32 homolog

Kre6p
rsor of thiamine

tion

ous to Tif4632p, homologs of mammalian p220

eductase

plex

onse to loss of microtubule function

plex

m1p
ase
2 and to hypothetical protein YPR200c
nthase

ypothetical protein SGC3

the first intermediate in synthesis of glycosylphosphatidylinositol (GPI) anchors

MRL3)

AP37 and S. cerevisiae Phb1p

s Pan1p and clathrin

ırifies with transcription factor, TFIIH, mRNA is cell cycle regulated and induced by DNA damage and by

ı assembly complex

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;8818 and 1058976 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of th

Similarity to SLG1 (WSC1), WSC2 and WSC3

;.

otein S2, component of the 37 S subunit of mitochondrial ribosomes ex

other related essential mitochondrial processes

catalytic subunit of N-a-acetyltransferase (Nat1)

ught to be a meiosis-specific negative regulator of M-phase during meiosis I, coordinating sister-chromat

RNA-dependent ATPase possessing helicase activity which is not specific for RNA

se complex with Rrp41p, Rrp42p, Rrp43p and Dis3p (Rrp44p).

se and endoribonuclease activities
se and endoribonuclease activities
se and endoribonuclease activities

the REC107 transcripts in cooperation with the Mer1 protein

4 regulatory element which is a multicopy suppressor of glucose transport defects\; probable non-functi

e of mitochondria

. Suppression is very specific to this allele. It has no affect on the analogous YPT1 allele. No homology c ion\; thought to be a positive regulator of exit from M-phase in mitosis and meiosis. Spo12p interacts wit

s Pan1p and clathrin

c domains\; homologous to Sol2p and Sol1p

and Tub4p perhaps as part of the microtubule attachment site of the SBP

on

e nascent-polypeptide-associated complex ome

ion factors

ian ECA39, which is regulated by the oncogene myc

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skeleton, potential target of Rho4p

ase cascade and is similar to bacterial two-component regulators

function appears to be translesion synthesis ical of nucleoporins

rs involved in ER to Golgi transport

ing region hypothetical protein CS314

sis and chiasmata formation

products encoded by SEC3, SEC5, SEC6, SEC8, SEC10, SEC15 and EXO70

ngation
d

gulates Met4p

e

rase II transcription machinery

isomerase

from Golgi

ankyrin

ted in the cytosol

a sec23 mutation

PI-anchored cell wall proteins

ntains a Zn[2]-Cys[6] fungal-type binuclear cluster domain in the N-terminal region rge subunit

558 and 197818 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the

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74804 with 99.677419% identity.
74804 with 99.677419% identity.
74804 with 99.677419% identity.
forward in NC_001224 between 74755 and 75949 with 97.154812% identity.

between 75041 and 75472 with 64.392324% identity.
between 75041 and 75472 with 64.392324% identity.
between 75041 and 75472 with 64.392324% identity.
aturase-related hypothetical protein RF2
ain 5 Found forward in NC_001224 between 3940 and 4167 with 99.122807% identity.
ith 84.489796% identity.
en 13818 and 13988 with 100% identity.
14122 with 100% identity.
and 16322 with 99.92016% identity.
and 18830 with 99.872774% identity.
and 19996 with 98.308458% identity.
en 20508 and 20984 with 99.790356% identity.
0985 and 21935 with 99.684543% identity.
en 21995 and 22246 with 97.222222% identity.
etween 21995 and 23167 with 99.40324% identity.
en 23612 and 23746 with 100% identity.
24120 and 25151 with 96.317829% identity.
en 26228 and 26530 with 99.339934% identity.
en 26627 and 26701 with 100% identity.
between 27666 and 27812 with 99.319728% identity.
between 27666 and 27812 with 99.319728% identity.
122 and 28444 with 88.588589% identity.
4 between 28487 and 29266 with 97.564103% identity.
etween 46046 and 46361 with 69.393939% identity.
etween 8238 and 8509 with 72.463768% identity.
etween 8238 and 8509 with 72.463768% identity.
etween 11057 and 11551 with 65.530303% identity.
etween 77067 and 77606 with 61.663653% identity.
100% identity.
NC_001224 between 34032 and 34430 with 88.279302% identity.
NC_001224 between 34032 and 34430 with 88.279302% identity.
rward in NC_001224 between 36540 and 36954 with 100% identity.
nd 38579 with 99.883314% identity.
rward in NC_001224 between 39141 and 39217 with 100% identity.
nd 40265 with 98.577778% identity.

rward in NC_001224 between 40841 and 41093 with 100% identity.
ınd 42251 with 99.860821% identity.
rward in NC_001224 between 42508 and 42561 with 100% identity.
rward in NC_001224 between 43297 and 43647 with 100% identity.
between 46723 and 46953 with 100% identity.
(SGC4) Found reverse in NC_001224 between 48858 and 49169 with 99.679487% identity.
(SGC4) Found reverse in NC_001224 between 48858 and 49169 with 99.679487% identity.
en 48901 and 50097 with 98.436214% identity.
en 48901 and 50097 with 98.436214% identity.
001224 between 61193 and 61729 with 100% identity.

AL genes

C-terminal

equence. Found reverse in NC_001133 between 160593 and 164183 with 100% identity.
equence. Found reverse in NC_001133 between 160593 and 164183 with 100% identity.
equence. Found reverse in NC_001133 between 164540 and 165862 with 100% identity.

with 100% identity.

sequence. Found forward in NC_001142 between 197614 and 198699 with 100% identity.
sequence. Found forward in NC_001142 between 197614 and 198699 with 100% identity.
sequence. Found forward in NC_001142 between 197614 and 198858 with 100% identity.
sequence. Found forward in NC_001142 between 198701 and 203026 with 100% identity.
sequence. Found forward in NC_001142 between 198701 and 203026 with 100% identity.
sequence. Found forward in NC_001142 between 198701 and 203026 with 100% identity.
sequence. Found forward in NC_001142 between 198701 and 203026 with 100% identity.
sequence. Found forward in NC_001142 between 198701 and 203026 with 100% identity.

sequence. Found forward in NC_001142 between 473751 and 477716 with 100% identity.

sequence. Found forward in NC_001142 between 479334 and 483300 with 100% identity.

/Cos9p family, coded from subtelomeric region
/Cos9p family, coded from subtelomeric region

ed proteins

sequence. Found reverse in NC_001144 between 215441 and 219403 with 100% identity.

sequence. Found reverse in NC_001144 between 476334 and 480296 with 100% identity.

sequence. Found forward in NC_001144 between 594749 and 598706 with 100% identity.

3385 with 100% identity.
sequence. Found forward in NC_001144 between 654177 and 656387 with 100% identity.
sequence. Found forward in NC_001144 between 654177 and 656387 with 100% identity.

sequence. Found forward in NC_001144 between 941478 and 942778 with 100% identity.
sequence. Found forward in NC_001144 between 941478 and 942778 with 100% identity.
sequence. Found forward in NC_001144 between 942777 and 946791 with 100% identity.
sequence. Found forward in NC_001144 between 942777 and 946791 with 100% identity.
sequence. Found forward in NC_001144 between 942777 and 946791 with 100% identity.
sequence. Found forward in NC_001144 between 942777 and 946791 with 100% identity.

sequence. Found reverse in NC_001144 between 976606 and 980109 with 100% identity.

uch as Cos5p, Ybr302p, Cos3p, Cos1p, Cos4p, Cos8p, Cos6p, Cos9p (COS3 and YBR302C code for id
uch as Cos5p, Ybr302p, Cos3p, Cos1p, Cos4p, Cos8p, Cos6p, Cos9p (COS3 and YBR302C code for id

e sequence. Found forward in NC_001145 between 197939 and 201896 with 100% identity.

Cos5p, Ybr302p, Cos3p, Cos1p, Cos4p, Cos8p, Cos6p, Cos9p

e sequence. Found forward in NC_001146 between 520758 and 524702 with 100% identity.

e sequence. Found reverse in NC_001146 between 562383 and 566402 with 100% identity.

uch as Cos5p, Ybr302p, Cos3p, Cos1p, Cos4p, Cos8p, Cos6p, Cos9p
uch as Cos5p, Ybr302p, Cos3p, Cos1p, Cos4p, Cos8p, Cos6p, Cos9p
uch as Cos5p, Ybr302p, Cos3p, Cos1p, Cos4p, Cos8p, Cos6p, Cos9p
uch as Cos5p, Ybr302p, Cos3p, Cos1p, Cos4p, Cos8p, Cos6p, Cos9p

e sequence. Found forward in NC_001147 between 119305 and 123267 with 100% identity.

sequence. Found reverse in NC_001147 between 704417 and 708436 with 100% identity.

sequence. Found forward in NC_001147 between 971863 and 975882 with 100% identity.

sequence. Found forward in NC_001148 between 58054 and 62016 with 100% identity.

sequence. Found reverse in NC_001148 between 437328 and 439490 with 100% identity.
sequence. Found reverse in NC_001148 between 437328 and 439490 with 100% identity.
sequence. Found reverse in NC_001148 between 439423 and 442737 with 100% identity.

e sequence. Found reverse in NC_001148 between 804996 and 808958 with 100% identity.

sequence. Found forward in NC_001134 between 31221 and 35240 with 100% identity.

Cos8\/Cos6\/Cos9 family, coded from subtelomeric region

sequence. Found forward in NC_001135 between 86005 and 90030 with 100% identity.

eins such as Cos5p, Ybr302p, Cos3p, Cos1p, Cos4p, Cos8p, Cos6p, Cos9p
eins such as Cos5p, Ybr302p, Cos3p, Cos1p, Cos4p, Cos8p, Cos6p, Cos9p

sequence. Found reverse in NC_001136 between 514037 and 518056 with 100% identity.

sequence. Found reverse in NC_001136 between 645851 and 649813 with 100% identity.

sequence. Found forward in NC_001136 between 804494 and 805681 with 100% identity.

sequence. Found forward in NC_001136 between 873398 and 877417 with 100% identity.

sequence. Found reverse in NC_001136 between 878651 and 882613 with 100% identity.

sequence. Found forward in NC_001136 between 982747 and 986766 with 100% identity.

sequence. Found reverse in NC_001136 between 987525 and 991034 with 100% identity.

sequence. Found forward in NC_001136 between 1208292 and 1212254 with 100% identity.

ıch as Cos5p, Ybr302p, Cos3p, Cos1p, Cos4p, Cos8p, Cos6p, Cos9p

sequence. Found forward in NC_001138 between 139492 and 143511 with 100% identity.

8461 with 100% identity.
sequence. Found forward in NC_001139 between 708460 and 712248 with 100% identity.
sequence. Found forward in NC_001139 between 708460 and 712248 with 100% identity.
sequence. Found forward in NC_001139 between 708460 and 712248 with 100% identity.

eins such as Cos5p, Ybr302p, Cos3p, Cos1p, Cos4p, Cos8p, Cos6p, Cos9p

Cos5p, Ybr302p, Cos3p, Cos1p, Cos4p, Cos8p, Cos6p, Cos9p
Cos5p, Ybr302p, Cos3p, Cos1p, Cos4p, Cos8p, Cos6p, Cos9p
Cos5p, Ybr302p, Cos3p, Cos1p, Cos4p, Cos8p, Cos6p, Cos9p

sequence. Found forward in NC_001141 between 206488 and 210129 with 100% identity.

equence. Found forward in NC_001133 between 13744 and 14743 with 100% identity.
equence. Found forward in NC_001133 between 14744 and 15743 with 100% identity.
equence. Found forward in NC_001133 between 14744 and 15743 with 100% identity.
equence. Found forward in NC_001133 between 15744 and 16743 with 100% identity.
equence. Found forward in NC_001133 between 16744 and 17743 with 100% identity.
equence. Found forward in NC_001133 between 17744 and 18743 with 100% identity.

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equence. Found forward in NC_001133 between 18744 and 19729 with 100% identity.
equence. Found forward in NC_001133 between 88357 and 89356 with 100% identity.
equence. Found forward in NC_001133 between 89357 and 90356 with 100% identity.
equence. Found forward in NC_001133 between 90357 and 91356 with 100% identity.
equence. Found forward in NC_001133 between 91357 and 92356 with 100% identity.
equence. Found forward in NC_001133 between 92357 and 93356 with 100% identity.
equence. Found forward in NC_001133 between 92357 and 93356 with 100% identity.
equence. Found forward in NC_001133 between 93357 and 93988 with 100% identity.
equence. Found forward in NC_001133 between 159789 and 160788 with 100% identity.
equence. Found forward in NC_001133 between 160789 and 161788 with 100% identity.
equence. Found forward in NC_001133 between 161789 and 162788 with 100% identity.
equence. Found forward in NC_001133 between 164789 and 165788 with 100% identity.
equence. Found forward in NC_001133 between 165789 and 166468 with 100% identity.
equence. Found forward in NC_001133 between 208649 and 209648 with 100% identity.
equence. Found forward in NC_001133 between 209649 and 210648 with 100% identity.
equence. Found forward in NC_001133 between 210649 and 211648 with 100% identity.
equence. Found forward in NC_001133 between 211649 and 212648 with 100% identity.
equence. Found forward in NC_001133 between 212649 and 213648 with 100% identity.
equence. Found forward in NC_001133 between 213649 and 214648 with 100% identity.
equence. Found forward in NC_001133 between 214649 and 215648 with 100% identity.
equence. Found forward in NC_001133 between 214649 and 215648 with 100% identity.
equence. Found forward in NC_001133 between 215649 and 216648 with 100% identity.
equence. Found forward in NC_001133 between 216649 and 217143 with 100% identity.
sequence. Found forward in NC_001142 between 9138 and 10137 with 100% identity.
sequence. Found forward in NC_001142 between 10138 and 11137 with 100% identity.
sequence. Found forward in NC_001142 between 11138 and 12137 with 100% identity.
sequence. Found forward in NC_001142 between 12138 and 13137 with 100% identity.
sequence. Found forward in NC_001142 between 13138 and 14137 with 100% identity.
sequence. Found forward in NC_001142 between 14138 and 15137 with 100% identity.
sequence. Found forward in NC_001142 between 15138 and 15624 with 100% identity.
sequence. Found forward in NC_001142 between 41889 and 42888 with 100% identity.
sequence. Found forward in NC_001142 between 42889 and 43888 with 100% identity.
sequence. Found forward in NC_001142 between 43889 and 44888 with 100% identity.
sequence. Found forward in NC_001142 between 44889 and 45888 with 100% identity.
sequence. Found forward in NC_001142 between 45889 and 46888 with 100% identity.
sequence. Found forward in NC_001142 between 46889 and 47659 with 100% identity.
sequence. Found forward in NC_001142 between 165921 and 166920 with 100% identity.
sequence. Found forward in NC_001142 between 166921 and 167920 with 100% identity.
sequence. Found forward in NC_001142 between 167921 and 168920 with 100% identity.
sequence. Found forward in NC_001142 between 168921 and 169920 with 100% identity.
sequence. Found forward in NC_001142 between 169921 and 170920 with 100% identity.
sequence. Found forward in NC_001142 between 170921 and 171920 with 100% identity.
sequence. Found forward in NC_001142 between 171921 and 172694 with 100% identity.
sequence. Found forward in NC_001142 between 196825 and 197824 with 100% identity.
sequence. Found forward in NC_001142 between 203825 and 204824 with 100% identity.
sequence. Found forward in NC_001142 between 204825 and 205824 with 100% identity.
sequence. Found forward in NC_001142 between 204825 and 205824 with 100% identity.
sequence. Found forward in NC_001142 between 205825 and 206646 with 100% identity.
sequence. Found forward in NC_001142 between 212197 and 213196 with 100% identity.
sequence. Found forward in NC_001142 between 213197 and 214196 with 100% identity.
sequence. Found forward in NC_001142 between 214197 and 215196 with 100% identity.
sequence. Found forward in NC_001142 between 215197 and 216196 with 100% identity.
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sequence. Found forward in NC_001142 between 216197 and 217196 with 100% identity.
sequence. Found forward in NC_001142 between 217197 and 217402 with 100% identity.
sequence. Found forward in NC_001142 between 254933 and 255932 with 100% identity.
sequence. Found forward in NC_001142 between 255933 and 256932 with 100% identity.
sequence. Found forward in NC_001142 between 256933 and 257932 with 100% identity.
sequence. Found forward in NC_001142 between 256933 and 257932 with 100% identity.
sequence. Found forward in NC_001142 between 257933 and 258932 with 100% identity.
sequence. Found forward in NC_001142 between 258933 and 259932 with 100% identity.
sequence. Found forward in NC_001142 between 259933 and 260143 with 100% identity.
sequence. Found forward in NC_001142 between 368944 and 369943 with 100% identity.
sequence. Found forward in NC_001142 between 369944 and 370943 with 100% identity.
sequence. Found forward in NC_001142 between 370944 and 371943 with 100% identity.
sequence. Found forward in NC_001142 between 371944 and 372943 with 100% identity.
sequence. Found forward in NC_001142 between 372944 and 373943 with 100% identity.
sequence. Found forward in NC_001142 between 373944 and 374811 with 100% identity.
sequence. Found forward in NC_001142 between 373944 and 374811 with 100% identity.
sequence. Found forward in NC_001142 between 424301 and 425300 with 100% identity.
sequence. Found forward in NC_001142 between 424301 and 425300 with 100% identity.
sequence. Found forward in NC_001142 between 425301 and 426300 with 100% identity.
sequence. Found forward in NC_001142 between 426301 and 427300 with 100% identity.
sequence. Found forward in NC_001142 between 427301 and 428300 with 100% identity.
sequence. Found forward in NC_001142 between 428301 and 429300 with 100% identity.
sequence. Found forward in NC_001142 between 429301 and 430300 with 100% identity.
sequence. Found forward in NC_001142 between 430301 and 430425 with 100% identity.
sequence. Found forward in NC_001142 between 510427 and 511426 with 100% identity.
sequence. Found forward in NC_001142 between 511427 and 512426 with 100% identity.
sequence. Found forward in NC_001142 between 512427 and 513426 with 100% identity.
sequence. Found forward in NC_001142 between 513427 and 514426 with 100% identity.
sequence. Found forward in NC_001142 between 513427 and 514426 with 100% identity.
sequence. Found forward in NC_001142 between 514427 and 515426 with 100% identity.
sequence. Found forward in NC_001142 between 515427 and 515477 with 100% identity.
sequence. Found forward in NC_001142 between 557997 and 558996 with 100% identity.
sequence. Found forward in NC_001142 between 558997 and 559996 with 100% identity.
sequence. Found forward in NC_001142 between 558997 and 559996 with 100% identity.
sequence. Found forward in NC_001142 between 559997 and 560996 with 100% identity.
sequence. Found forward in NC_001142 between 560997 and 561996 with 100% identity.
sequence. Found forward in NC_001142 between 561997 and 562996 with 100% identity.
sequence. Found forward in NC_001142 between 562997 and 563996 with 100% identity.
sequence. Found forward in NC_001142 between 563997 and 564996 with 100% identity.
sequence. Found forward in NC_001142 between 564997 and 565996 with 100% identity.
sequence. Found forward in NC_001142 between 595249 and 596248 with 100% identity.
sequence. Found forward in NC_001142 between 596249 and 597248 with 100% identity.
sequence. Found forward in NC_001142 between 597249 and 598248 with 100% identity.
sequence. Found forward in NC_001142 between 598249 and 599248 with 100% identity.
sequence. Found forward in NC_001142 between 598249 and 599248 with 100% identity.
sequence. Found forward in NC_001142 between 599249 and 600248 with 100% identity.
sequence. Found forward in NC_001142 between 600249 and 601248 with 100% identity.
sequence. Found forward in NC_001142 between 601249 and 602248 with 100% identity.
sequence. Found forward in NC_001142 between 629774 and 630773 with 100% identity.
sequence. Found forward in NC_001142 between 630774 and 631773 with 100% identity.
sequence. Found forward in NC_001142 between 631774 and 632773 with 100% identity.
sequence. Found forward in NC_001142 between 632774 and 633773 with 100% identity.
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sequence. Found forward in NC_001142 between 632774 and 633773 with 100% identity.
sequence. Found forward in NC_001142 between 633774 and 634773 with 100% identity.
sequence. Found forward in NC_001142 between 690939 and 691938 with 100% identity.
sequence. Found forward in NC_001142 between 691939 and 692938 with 100% identity.
sequence. Found forward in NC_001142 between 692939 and 693938 with 100% identity.
sequence. Found forward in NC_001142 between 693939 and 694938 with 100% identity.
sequence. Found forward in NC_001142 between 694939 and 695938 with 100% identity.
sequence. Found forward in NC_001142 between 694939 and 695938 with 100% identity.
sequence. Found forward in NC_001142 between 695939 and 696138 with 100% identity.
sequence. Found forward in NC_001142 between 712444 and 713443 with 100% identity.
sequence. Found forward in NC_001142 between 713444 and 714443 with 100% identity.
sequence. Found forward in NC_001142 between 714444 and 715443 with 100% identity.
sequence. Found forward in NC_001142 between 715444 and 716443 with 100% identity.
sequence. Found forward in NC_001142 between 716444 and 717443 with 100% identity.
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sequence. Found forward in NC_001142 between 718444 and 719443 with 100% identity.
sequence. Found forward in NC_001142 between 719444 and 720443 with 100% identity.
sequence. Found forward in NC_001143 between 9592 and 10591 with 100% identity.
sequence. Found forward in NC_001143 between 10592 and 11591 with 100% identity.
sequence. Found forward in NC_001143 between 11592 and 12591 with 100% identity.
sequence. Found forward in NC_001143 between 12592 and 13591 with 100% identity.
sequence. Found forward in NC_001143 between 13592 and 14591 with 100% identity.
sequence. Found forward in NC_001143 between 14592 and 15208 with 100% identity.
sequence. Found forward in NC_001143 between 56435 and 57434 with 100% identity.
sequence. Found forward in NC_001143 between 57435 and 58434 with 100% identity.
sequence. Found forward in NC_001143 between 58435 and 59434 with 100% identity.
sequence. Found forward in NC_001143 between 59435 and 60434 with 100% identity.
sequence. Found forward in NC_001143 between 60435 and 61434 with 100% identity.
sequence. Found forward in NC_001143 between 61435 and 62434 with 100% identity.
sequence. Found forward in NC_001143 between 62435 and 63434 with 100% identity.
sequence. Found forward in NC_001143 between 63435 and 63899 with 100% identity.
sequence. Found forward in NC_001143 between 99643 and 100642 with 100% identity.
sequence. Found forward in NC_001143 between 100643 and 101642 with 100% identity.
sequence. Found forward in NC_001143 between 100643 and 101642 with 100% identity.
sequence. Found forward in NC_001143 between 101643 and 102642 with 100% identity.
sequence. Found forward in NC_001143 between 102643 and 103642 with 100% identity.
sequence. Found forward in NC_001143 between 103643 and 104642 with 100% identity.
sequence. Found forward in NC_001143 between 104643 and 105642 with 100% identity.
sequence. Found forward in NC_001143 between 105643 and 106328 with 100% identity.
sequence. Found forward in NC_001143 between 411757 and 412756 with 100% identity.
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sequence. Found forward in NC_001143 between 413757 and 414756 with 100% identity.
sequence. Found forward in NC_001143 between 414757 and 415756 with 100% identity.
sequence. Found forward in NC_001143 between 415757 and 416756 with 100% identity.
sequence. Found forward in NC_001143 between 416757 and 417146 with 100% identity.
sequence. Found forward in NC_001143 between 535784 and 536783 with 100% identity.
sequence. Found forward in NC_001143 between 536784 and 537783 with 100% identity.
sequence. Found forward in NC_001143 between 537784 and 538783 with 100% identity.
sequence. Found forward in NC_001143 between 538784 and 539783 with 100% identity.
sequence. Found forward in NC_001143 between 539784 and 540783 with 100% identity.
sequence. Found forward in NC_001143 between 540784 and 541783 with 100% identity.
sequence. Found forward in NC_001143 between 541784 and 542783 with 100% identity.
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sequence. Found forward in NC_001143 between 542784 and 543783 with 100% identity.
sequence. Found forward in NC_001143 between 543784 and 544783 with 100% identity.
sequence. Found forward in NC_001143 between 544784 and 545783 with 100% identity.
sequence. Found forward in NC_001143 between 545784 and 546783 with 100% identity.
sequence. Found forward in NC_001143 between 546784 and 547783 with 100% identity.
sequence. Found forward in NC_001143 between 547784 and 548228 with 100% identity.
sequence. Found forward in NC_001143 between 547784 and 548228 with 100% identity.
sequence. Found forward in NC_001143 between 619375 and 620374 with 100% identity.
sequence. Found forward in NC_001143 between 619375 and 620374 with 100% identity.
sequence. Found forward in NC_001143 between 620375 and 621374 with 100% identity.
sequence. Found forward in NC_001143 between 621375 and 622374 with 100% identity.
sequence. Found forward in NC_001143 between 622375 and 623374 with 100% identity.
sequence. Found forward in NC_001143 between 623375 and 624374 with 100% identity.
sequence. Found forward in NC_001143 between 624375 and 624566 with 100% identity.
sequence. Found forward in NC_001143 between 642133 and 643132 with 100% identity.
sequence. Found forward in NC_001143 between 643133 and 644132 with 100% identity.
sequence. Found forward in NC_001143 between 644133 and 645132 with 100% identity.
sequence. Found forward in NC_001143 between 645133 and 646132 with 100% identity.
sequence. Found forward in NC_001143 between 645133 and 646132 with 100% identity.
sequence. Found forward in NC_001143 between 646133 and 647132 with 100% identity.
sequence. Found forward in NC_001143 between 647133 and 648132 with 100% identity.
sequence. Found forward in NC_001143 between 648133 and 648994 with 100% identity.
sequence. Found forward in NC_001143 between 649494 and 650493 with 100% identity.
sequence. Found forward in NC_001143 between 650494 and 651493 with 100% identity.
sequence. Found forward in NC_001143 between 651494 and 652493 with 100% identity.
sequence. Found forward in NC_001143 between 652494 and 653493 with 100% identity.
sequence. Found forward in NC_001143 between 652494 and 653493 with 100% identity.
sequence. Found forward in NC_001143 between 653494 and 654493 with 100% identity.
sequence. Found forward in NC_001143 between 654494 and 655493 with 100% identity.
sequence. Found forward in NC_001143 between 655494 and 655865 with 100% identity.
sequence. Found forward in NC_001143 between 662918 and 663917 with 100% identity.
sequence. Found forward in NC_001143 between 663918 and 664917 with 100% identity.
sequence. Found forward in NC_001143 between 664918 and 665917 with 100% identity.
sequence. Found forward in NC_001143 between 665918 and 666445 with 100% identity.
sequence. Found forward in NC_001144 between 54710 and 55709 with 100% identity.
sequence. Found forward in NC_001144 between 55710 and 56709 with 100% identity.
sequence. Found forward in NC_001144 between 56710 and 57709 with 100% identity.
sequence. Found forward in NC_001144 between 57710 and 58709 with 100% identity.
sequence. Found forward in NC_001144 between 58710 and 59709 with 100% identity.
sequence. Found forward in NC_001144 between 59710 and 60709 with 100% identity.
sequence. Found forward in NC_001144 between 60710 and 61709 with 100% identity.
sequence. Found forward in NC_001144 between 61710 and 62709 with 100% identity.
sequence. Found forward in NC_001144 between 62710 and 63709 with 100% identity.
sequence. Found forward in NC_001144 between 63710 and 64061 with 100% identity.
sequence. Found forward in NC_001144 between 99543 and 100542 with 100% identity.
sequence. Found forward in NC_001144 between 100543 and 101542 with 100% identity.
sequence. Found forward in NC_001144 between 100543 and 101542 with 100% identity.
sequence. Found forward in NC_001144 between 101543 and 102542 with 100% identity.
sequence. Found forward in NC_001144 between 102543 and 103542 with 100% identity.
sequence. Found forward in NC_001144 between 103543 and 104542 with 100% identity.
sequence. Found forward in NC_001144 between 104543 and 104846 with 100% identity.
sequence. Found forward in NC_001144 between 188164 and 189163 with 100% identity.
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sequence. Found forward in NC_001144 between 189164 and 190163 with 100% identity.
sequence. Found forward in NC_001144 between 190164 and 191163 with 100% identity.
sequence. Found forward in NC_001144 between 191164 and 192163 with 100% identity.
sequence. Found forward in NC_001144 between 192164 and 193163 with 100% identity.
sequence. Found forward in NC_001144 between 193164 and 194163 with 100% identity.
sequence. Found forward in NC_001144 between 194164 and 194675 with 100% identity.
sequence. Found forward in NC_001144 between 194164 and 194675 with 100% identity.
sequence. Found forward in NC_001144 between 307356 and 308355 with 100% identity.
sequence. Found forward in NC_001144 between 308356 and 309355 with 100% identity.
sequence. Found forward in NC_001144 between 309356 and 310355 with 100% identity.
sequence. Found forward in NC_001144 between 310356 and 311355 with 100% identity.
sequence. Found forward in NC_001144 between 311356 and 312355 with 100% identity.
sequence. Found forward in NC_001144 between 312356 and 313355 with 100% identity.
sequence. Found forward in NC_001144 between 313356 and 314355 with 100% identity.
sequence. Found forward in NC_001144 between 314356 and 315355 with 100% identity.
sequence. Found forward in NC_001144 between 315356 and 315877 with 100% identity.
sequence. Found forward in NC_001144 between 330178 and 331177 with 100% identity.
sequence. Found forward in NC_001144 between 331178 and 332177 with 100% identity.
sequence. Found forward in NC_001144 between 332178 and 333177 with 100% identity.
sequence. Found forward in NC_001144 between 332178 and 333177 with 100% identity.
sequence. Found forward in NC_001144 between 333178 and 334177 with 100% identity.
sequence. Found forward in NC_001144 between 334178 and 335177 with 100% identity.
sequence. Found forward in NC_001144 between 335178 and 335534 with 100% identity.
sequence. Found forward in NC_001144 between 349507 and 350506 with 100% identity.
sequence. Found forward in NC_001144 between 350507 and 351506 with 100% identity.
sequence. Found forward in NC_001144 between 351507 and 352506 with 100% identity.
sequence. Found forward in NC_001144 between 352507 and 353506 with 100% identity.
sequence. Found forward in NC_001144 between 353507 and 354506 with 100% identity.
sequence. Found forward in NC_001144 between 354507 and 355506 with 100% identity.
sequence. Found forward in NC_001144 between 355507 and 356506 with 100% identity.
sequence. Found forward in NC_001144 between 356507 and 357506 with 100% identity.
sequence. Found forward in NC_001144 between 357507 and 358506 with 100% identity.
sequence. Found forward in NC_001144 between 358507 and 359506 with 100% identity.
sequence. Found forward in NC_001144 between 359507 and 360506 with 100% identity.
sequence. Found forward in NC_001144 between 360507 and 361506 with 100% identity.
sequence. Found forward in NC_001144 between 361507 and 362506 with 100% identity.
sequence. Found forward in NC_001144 between 362507 and 363506 with 100% identity.
sequence. Found forward in NC_001144 between 363507 and 364506 with 100% identity.
sequence. Found forward in NC_001144 between 363507 and 364506 with 100% identity.
sequence. Found forward in NC_001144 between 364507 and 364831 with 100% identity.
sequence. Found forward in NC_001144 between 629184 and 630183 with 100% identity.
sequence. Found forward in NC_001144 between 630184 and 631183 with 100% identity.
sequence. Found forward in NC_001144 between 631184 and 632183 with 100% identity.
sequence. Found forward in NC_001144 between 632184 and 633183 with 100% identity.
sequence. Found forward in NC_001144 between 633184 and 634183 with 100% identity.
sequence. Found forward in NC_001144 between 634184 and 635183 with 100% identity.
sequence. Found forward in NC_001144 between 635184 and 635584 with 100% identity.
sequence. Found forward in NC_001144 between 769817 and 770816 with 100% identity.
sequence. Found forward in NC_001144 between 770817 and 771816 with 100% identity.
sequence. Found forward in NC_001144 between 771817 and 772816 with 100% identity.
sequence. Found forward in NC_001144 between 771817 and 772816 with 100% identity.
sequence. Found forward in NC_001144 between 772817 and 773816 with 100% identity.
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sequence. Found forward in NC_001144 between 773817 and 774816 with 100% identity.
sequence. Found forward in NC_001144 between 774817 and 775803 with 100% identity.
sequence. Found forward in NC_001144 between 808817 and 809816 with 100% identity.
sequence. Found forward in NC_001144 between 809817 and 810816 with 100% identity.
sequence. Found forward in NC_001144 between 809817 and 810816 with 100% identity.
sequence. Found forward in NC_001144 between 810817 and 811816 with 100% identity.
sequence. Found forward in NC_001144 between 811817 and 812816 with 100% identity.
sequence. Found forward in NC_001144 between 812817 and 813816 with 100% identity.
sequence. Found forward in NC_001144 between 813817 and 814816 with 100% identity.
sequence. Found forward in NC_001144 between 814817 and 815126 with 100% identity.
sequence. Found forward in NC_001144 between 934909 and 935908 with 100% identity.
sequence. Found forward in NC_001144 between 935909 and 936908 with 100% identity.
sequence. Found forward in NC_001144 between 936909 and 937908 with 100% identity.
sequence. Found forward in NC_001144 between 936909 and 937908 with 100% identity.
sequence. Found forward in NC_001144 between 937909 and 938908 with 100% identity.
sequence. Found forward in NC_001144 between 938909 and 939908 with 100% identity.
sequence. Found forward in NC_001144 between 939909 and 940476 with 100% identity.
sequence. Found forward in NC_001144 between 965554 and 966553 with 100% identity.
sequence. Found forward in NC_001144 between 965554 and 966553 with 100% identity.
sequence. Found forward in NC_001144 between 966554 and 967553 with 100% identity.
sequence. Found forward in NC_001144 between 967554 and 968553 with 100% identity.
sequence. Found forward in NC_001144 between 968554 and 969553 with 100% identity.
sequence. Found forward in NC_001144 between 969554 and 970553 with 100% identity.
sequence. Found forward in NC_001144 between 970554 and 971189 with 100% identity.
sequence. Found forward in NC_001144 between 979430 and 980429 with 100% identity.
sequence. Found forward in NC_001144 between 980430 and 981429 with 100% identity.
sequence. Found forward in NC_001144 between 981430 and 982429 with 100% identity.
sequence. Found forward in NC_001144 between 982430 and 983429 with 100% identity.
sequence. Found forward in NC_001144 between 982430 and 983429 with 100% identity.
sequence. Found forward in NC_001144 between 983430 and 984429 with 100% identity.
sequence. Found forward in NC_001144 between 984430 and 985429 with 100% identity.
sequence. Found forward in NC_001144 between 985430 and 986311 with 100% identity.
sequence. Found forward in NC_001144 between 992726 and 993725 with 100% identity.
sequence. Found forward in NC_001144 between 992726 and 993725 with 100% identity.
sequence. Found forward in NC_001144 between 993726 and 994725 with 100% identity.
sequence. Found forward in NC_001144 between 994726 and 995725 with 100% identity.
sequence. Found forward in NC_001144 between 995726 and 996725 with 100% identity.
sequence. Found forward in NC_001144 between 996726 and 997725 with 100% identity.
sequence. Found forward in NC_001144 between 997726 and 998725 with 100% identity.
sequence. Found forward in NC_001144 between 998726 and 999623 with 100% identity.
sequence. Found forward in NC_001144 between 1042294 and 1043293 with 100% identity.
sequence. Found forward in NC_001144 between 1043294 and 1044293 with 100% identity.
sequence. Found forward in NC_001144 between 1043294 and 1044293 with 100% identity.
sequence. Found forward in NC_001144 between 1044294 and 1045293 with 100% identity.
sequence. Found forward in NC_001144 between 1045294 and 1046293 with 100% identity.
sequence. Found forward in NC_001144 between 1046294 and 1047293 with 100% identity.
sequence. Found forward in NC_001144 between 1047294 and 1048293 with 100% identity.
sequence. Found forward in NC_001144 between 1048294 and 1049293 with 100% identity.
sequence. Found forward in NC_001144 between 1049294 and 1050293 with 100% identity.
sequence. Found forward in NC_001144 between 1050294 and 1051293 with 100% identity.
sequence. Found forward in NC_001144 between 1051294 and 1051379 with 100% identity.
sequence. Found forward in NC_001144 between 1071425 and 1072424 with 100% identity.
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sequence. Found forward in NC_001144 between 1071425 and 1072424 with 100% identity.
sequence. Found forward in NC_001145 between 63082 and 64081 with 100% identity.
sequence. Found forward in NC_001145 between 64082 and 65081 with 100% identity.
sequence. Found forward in NC_001145 between 65082 and 66081 with 100% identity.
sequence. Found forward in NC_001145 between 66082 and 67081 with 100% identity.
sequence. Found forward in NC_001145 between 67082 and 68081 with 100% identity.
sequence. Found forward in NC_001145 between 68082 and 69081 with 100% identity.
sequence. Found forward in NC_001145 between 68082 and 69081 with 100% identity.
sequence. Found forward in NC_001145 between 69082 and 69200 with 100% identity.
sequence. Found forward in NC_001145 between 153719 and 154718 with 100% identity.
sequence. Found forward in NC_001145 between 154719 and 155718 with 100% identity.
sequence. Found forward in NC_001145 between 155719 and 156718 with 100% identity.
sequence. Found forward in NC_001145 between 156719 and 157718 with 100% identity.
sequence. Found forward in NC_001145 between 157719 and 158718 with 100% identity.
sequence. Found forward in NC_001145 between 183363 and 184362 with 100% identity.
sequence. Found forward in NC_001145 between 189363 and 190244 with 100% identity.
sequence. Found forward in NC_001145 between 195413 and 196412 with 100% identity.
sequence. Found forward in NC_001145 between 201413 and 202412 with 100% identity.
sequence. Found forward in NC_001145 between 202413 and 202775 with 100% identity.
sequence. Found forward in NC_001145 between 356810 and 357809 with 100% identity.
sequence. Found forward in NC_001145 between 357810 and 358809 with 100% identity.
sequence. Found forward in NC_001145 between 358810 and 359809 with 100% identity.
sequence. Found forward in NC_001145 between 360810 and 361809 with 100% identity.
sequence. Found forward in NC_001145 between 361810 and 362701 with 100% identity.
sequence. Found forward in NC_001145 between 368593 and 369592 with 100% identity.
sequence. Found forward in NC_001145 between 369593 and 370592 with 100% identity.
sequence. Found forward in NC_001145 between 370593 and 371592 with 100% identity.
sequence. Found forward in NC_001145 between 371593 and 372592 with 100% identity.
sequence. Found forward in NC_001145 between 371593 and 372592 with 100% identity.
sequence. Found forward in NC_001145 between 372593 and 373592 with 100% identity.
sequence. Found forward in NC_001145 between 373593 and 374592 with 100% identity.
sequence. Found forward in NC_001145 between 378593 and 379592 with 100% identity.
sequence. Found forward in NC_001145 between 379593 and 379699 with 100% identity.
sequence. Found forward in NC_001145 between 677692 and 678691 with 100% identity.
sequence. Found forward in NC_001145 between 678692 and 679691 with 100% identity.
sequence. Found forward in NC_001145 between 679692 and 680691 with 100% identity.
sequence. Found forward in NC_001145 between 680692 and 681691 with 100% identity.
sequence. Found forward in NC_001145 between 681692 and 682691 with 100% identity.
sequence. Found forward in NC_001145 between 682692 and 683691 with 100% identity.
sequence. Found forward in NC_001145 between 683692 and 684691 with 100% identity.
sequence. Found forward in NC_001145 between 683692 and 684691 with 100% identity.
sequence. Found forward in NC_001145 between 684692 and 685297 with 100% identity.
sequence. Found forward in NC_001145 between 704078 and 705077 with 100% identity.
sequence. Found forward in NC_001145 between 705078 and 706077 with 100% identity.
sequence. Found forward in NC_001145 between 706078 and 707077 with 100% identity.
sequence. Found forward in NC_001145 between 707078 and 708077 with 100% identity.
sequence. Found forward in NC_001145 between 708078 and 709077 with 100% identity.
sequence. Found forward in NC_001145 between 709078 and 710077 with 100% identity.
sequence. Found forward in NC_001145 between 710078 and 711077 with 100% identity.
sequence. Found forward in NC_001145 between 711078 and 711608 with 100% identity.
sequence. Found forward in NC_001145 between 726433 and 727432 with 100% identity.
sequence. Found forward in NC_001145 between 727433 and 728432 with 100% identity.
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sequence. Found forward in NC_001145 between 728433 and 729432 with 100% identity.
sequence. Found forward in NC_001145 between 729433 and 730432 with 100% identity.
sequence. Found forward in NC_001145 between 730433 and 731432 with 100% identity.
sequence. Found forward in NC_001145 between 731433 and 731964 with 100% identity.
sequence. Found forward in NC_001145 between 827528 and 828527 with 100% identity.
sequence. Found forward in NC_001145 between 828528 and 829527 with 100% identity.
sequence. Found forward in NC_001145 between 829528 and 830527 with 100% identity.
sequence. Found forward in NC_001145 between 830528 and 831527 with 100% identity.
sequence. Found forward in NC_001145 between 831528 and 832527 with 100% identity.
sequence. Found forward in NC_001145 between 831528 and 832527 with 100% identity.
sequence. Found forward in NC_001145 between 832528 and 832753 with 100% identity.
sequence. Found forward in NC_001145 between 842936 and 843935 with 100% identity.
sequence. Found forward in NC_001145 between 843936 and 844935 with 100% identity.
sequence. Found forward in NC_001145 between 844936 and 845935 with 100% identity.
sequence. Found forward in NC_001145 between 844936 and 845935 with 100% identity.
sequence. Found forward in NC_001145 between 845936 and 846935 with 100% identity.
sequence. Found forward in NC_001145 between 846936 and 847935 with 100% identity.
sequence. Found forward in NC_001145 between 847936 and 847986 with 100% identity.
sequence. Found forward in NC_001145 between 879563 and 880562 with 100% identity.
sequence. Found forward in NC_001145 between 880563 and 881562 with 100% identity.
sequence. Found forward in NC_001145 between 880563 and 881562 with 100% identity.
sequence. Found forward in NC_001145 between 881563 and 882562 with 100% identity.
sequence. Found forward in NC_001145 between 882563 and 883562 with 100% identity.
sequence. Found forward in NC_001145 between 883563 and 884562 with 100% identity.
sequence. Found forward in NC_001145 between 884563 and 885562 with 100% identity.
sequence. Found forward in NC_001145 between 885563 and 886016 with 100% identity.
sequence. Found forward in NC_001146 between 871 and 1870 with 100% identity.
sequence. Found forward in NC_001146 between 1871 and 2870 with 100% identity.
sequence. Found forward in NC_001146 between 2871 and 3870 with 100% identity.
sequence. Found forward in NC_001146 between 3871 and 4870 with 100% identity.
sequence. Found forward in NC_001146 between 4871 and 5870 with 100% identity.
sequence. Found forward in NC_001146 between 5871 and 6080 with 100% identity.
sequence. Found forward in NC_001146 between 130021 and 131020 with 100% identity.
sequence. Found forward in NC_001146 between 131021 and 132020 with 100% identity.
sequence. Found forward in NC_001146 between 132021 and 133020 with 100% identity.
sequence. Found forward in NC_001146 between 133021 and 134020 with 100% identity.
sequence. Found forward in NC_001146 between 134021 and 135020 with 100% identity.
sequence. Found forward in NC_001146 between 135021 and 135939 with 100% identity.
sequence. Found forward in NC_001146 between 147395 and 148394 with 100% identity.
sequence. Found forward in NC_001146 between 147395 and 148394 with 100% identity.
sequence. Found forward in NC_001146 between 148395 and 149394 with 100% identity.
sequence. Found forward in NC_001146 between 149395 and 150394 with 100% identity.
sequence. Found forward in NC_001146 between 150395 and 151394 with 100% identity.
sequence. Found forward in NC_001146 between 151395 and 152394 with 100% identity.
sequence. Found forward in NC_001146 between 152395 and 153394 with 100% identity.
sequence. Found forward in NC_001146 between 153395 and 154379 with 100% identity.
sequence. Found forward in NC_001146 between 161130 and 162129 with 100% identity.
sequence. Found forward in NC_001146 between 162130 and 163129 with 100% identity.
sequence. Found forward in NC_001146 between 163130 and 164129 with 100% identity.
sequence. Found forward in NC_001146 between 164130 and 165129 with 100% identity.
sequence. Found forward in NC_001146 between 164130 and 165129 with 100% identity.
sequence. Found forward in NC_001146 between 165130 and 166129 with 100% identity.
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e sequence. Found forward in NC_001146 between 166130 and 166596 with 100% identity.
e sequence. Found forward in NC_001146 between 173087 and 174086 with 100% identity.
e sequence. Found forward in NC_001146 between 174087 and 175086 with 100% identity.
e sequence. Found forward in NC_001146 between 175087 and 176086 with 100% identity.
e sequence. Found forward in NC_001146 between 175087 and 176086 with 100% identity.
e sequence. Found forward in NC_001146 between 176087 and 177086 with 100% identity.
e sequence. Found forward in NC_001146 between 177087 and 178086 with 100% identity.
e sequence. Found forward in NC_001146 between 178087 and 178847 with 100% identity.
e sequence. Found forward in NC_001146 between 309454 and 310453 with 100% identity.
e sequence. Found forward in NC_001146 between 310454 and 311453 with 100% identity.
e sequence. Found forward in NC_001146 between 310454 and 311453 with 100% identity.
e sequence. Found forward in NC_001146 between 311454 and 312453 with 100% identity.
e sequence. Found forward in NC_001146 between 312454 and 313453 with 100% identity.
e sequence. Found forward in NC_001146 between 313454 and 314453 with 100% identity.
e sequence. Found forward in NC_001146 between 314454 and 315379 with 100% identity.
e sequence. Found forward in NC_001146 between 524084 and 525083 with 100% identity.
e sequence. Found forward in NC_001146 between 525084 and 526083 with 100% identity.
e sequence. Found forward in NC_001146 between 526084 and 527083 with 100% identity.
e sequence. Found forward in NC_001146 between 527084 and 528083 with 100% identity.
e sequence. Found forward in NC_001146 between 528084 and 529079 with 100% identity.
e sequence. Found forward in NC_001146 between 655170 and 656169 with 100% identity.
e sequence. Found forward in NC_001146 between 656170 and 657169 with 100% identity.
e sequence. Found forward in NC_001146 between 657170 and 658169 with 100% identity.
e sequence. Found forward in NC_001146 between 658170 and 659169 with 100% identity.
e sequence. Found forward in NC_001146 between 659170 and 660169 with 100% identity.
e sequence. Found forward in NC_001146 between 660170 and 661169 with 100% identity.
e sequence. Found forward in NC_001146 between 661170 and 661997 with 100% identity.
e sequence. Found forward in NC_001146 between 681191 and 682190 with 100% identity.
e sequence. Found forward in NC_001146 between 682191 and 683190 with 100% identity.
e sequence. Found forward in NC_001146 between 683191 and 684190 with 100% identity.
e sequence. Found forward in NC_001146 between 684191 and 685190 with 100% identity.
e sequence. Found forward in NC_001146 between 685191 and 686190 with 100% identity.
e sequence. Found forward in NC_001146 between 685191 and 686190 with 100% identity.
e sequence. Found forward in NC_001146 between 686191 and 686613 with 100% identity.
e sequence. Found forward in NC_001146 between 761618 and 762617 with 100% identity.
e sequence. Found forward in NC_001146 between 762618 and 763617 with 100% identity.
e sequence. Found forward in NC_001146 between 763618 and 764617 with 100% identity.
e sequence. Found forward in NC_001146 between 764618 and 765617 with 100% identity.
e sequence. Found forward in NC_001146 between 764618 and 765617 with 100% identity.
e sequence. Found forward in NC_001146 between 765618 and 766617 with 100% identity.
e sequence. Found forward in NC_001146 between 766618 and 767617 with 100% identity.
e sequence. Found forward in NC_001146 between 767618 and 768617 with 100% identity.
e sequence. Found forward in NC_001146 between 768618 and 768871 with 100% identity.
sequence. Found forward in NC_001147 between 2078 and 3077 with 100% identity.
sequence. Found forward in NC_001147 between 3078 and 4077 with 100% identity.
sequence. Found forward in NC_001147 between 4078 and 5077 with 100% identity.
sequence. Found forward in NC_001147 between 5078 and 6077 with 100% identity.
sequence. Found forward in NC_001147 between 6078 and 7077 with 100% identity.
sequence. Found forward in NC_001147 between 6078 and 7077 with 100% identity.
sequence. Found forward in NC_001147 between 7078 and 7615 with 100% identity.
sequence. Found forward in NC_001147 between 169973 and 170972 with 100% identity.
sequence. Found forward in NC_001147 between 170973 and 171972 with 100% identity.
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sequence. Found forward in NC_001147 between 170973 and 171972 with 100% identity.
sequence. Found forward in NC_001147 between 171973 and 172972 with 100% identity.
sequence. Found forward in NC_001147 between 172973 and 173972 with 100% identity.
sequence. Found forward in NC_001147 between 173973 and 174972 with 100% identity.
sequence. Found forward in NC_001147 between 174973 and 175972 with 100% identity.
sequence. Found forward in NC_001147 between 175973 and 176972 with 100% identity.
sequence. Found forward in NC_001147 between 176973 and 177972 with 100% identity.
sequence. Found forward in NC_001147 between 177973 and 178972 with 100% identity.
sequence. Found forward in NC_001147 between 178973 and 179808 with 100% identity.
sequence. Found forward in NC_001147 between 346694 and 347693 with 100% identity.
sequence. Found forward in NC_001147 between 347694 and 348693 with 100% identity.
sequence. Found forward in NC_001147 between 348694 and 349693 with 100% identity.
sequence. Found forward in NC_001147 between 349694 and 350693 with 100% identity.
sequence. Found forward in NC_001147 between 350694 and 351693 with 100% identity.
sequence. Found forward in NC_001147 between 351694 and 352693 with 100% identity.
sequence. Found forward in NC_001147 between 352694 and 353362 with 100% identity.
sequence. Found forward in NC_001147 between 540261 and 541260 with 100% identity.
sequence. Found forward in NC_001147 between 541261 and 542260 with 100% identity.
sequence. Found forward in NC_001147 between 542261 and 543260 with 100% identity.
sequence. Found forward in NC_001147 between 543261 and 544260 with 100% identity.
sequence. Found forward in NC_001147 between 544261 and 545260 with 100% identity.
sequence. Found forward in NC_001147 between 544261 and 545260 with 100% identity.
sequence. Found forward in NC_001147 between 545261 and 545831 with 100% identity.
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sequence. Found forward in NC_001147 between 619016 and 620015 with 100% identity.
sequence. Found forward in NC_001147 between 620016 and 621015 with 100% identity.
sequence. Found forward in NC_001147 between 621016 and 622015 with 100% identity.
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sequence. Found forward in NC_001147 between 623016 and 623873 with 100% identity.
sequence. Found forward in NC_001147 between 730506 and 731505 with 100% identity.
sequence. Found forward in NC_001147 between 731506 and 732505 with 100% identity.
sequence. Found forward in NC_001147 between 732506 and 733505 with 100% identity.
sequence. Found forward in NC_001147 between 733506 and 734505 with 100% identity.
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sequence. Found forward in NC_001147 between 735506 and 735675 with 100% identity.
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sequence. Found forward in NC_001147 between 858642 and 859641 with 100% identity.
sequence. Found forward in NC_001147 between 859642 and 860641 with 100% identity.
sequence. Found forward in NC_001147 between 860642 and 861641 with 100% identity.
sequence. Found forward in NC_001147 between 860642 and 861641 with 100% identity.
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sequence. Found forward in NC_001147 between 863642 and 864641 with 100% identity.
sequence. Found forward in NC_001147 between 864642 and 865088 with 100% identity.
sequence. Found forward in NC_001147 between 946724 and 947723 with 100% identity.
sequence. Found forward in NC_001147 between 947724 and 948723 with 100% identity.
sequence. Found forward in NC_001147 between 948724 and 949723 with 100% identity.
sequence. Found forward in NC_001147 between 949724 and 950723 with 100% identity.
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sequence. Found forward in NC_001147 between 949724 and 950723 with 100% identity.
sequence. Found forward in NC_001147 between 950724 and 951723 with 100% identity.
sequence. Found forward in NC_001147 between 951724 and 952723 with 100% identity.
sequence. Found forward in NC_001147 between 952724 and 953361 with 100% identity.
sequence. Found forward in NC_001147 between 959693 and 960692 with 100% identity.
sequence. Found forward in NC_001147 between 960693 and 961692 with 100% identity.
sequence. Found forward in NC_001147 between 960693 and 961692 with 100% identity.
sequence. Found forward in NC_001147 between 961693 and 962692 with 100% identity.
sequence. Found forward in NC_001147 between 962693 and 963692 with 100% identity.
sequence. Found forward in NC_001147 between 963693 and 964692 with 100% identity.
sequence. Found forward in NC_001147 between 964693 and 965472 with 100% identity.
e sequence. Found forward in NC_001148 between 19079 and 20078 with 100% identity.
e sequence. Found forward in NC_001148 between 20079 and 21078 with 100% identity.
e sequence. Found forward in NC_001148 between 21079 and 22078 with 100% identity.
e sequence. Found forward in NC_001148 between 22079 and 23078 with 100% identity.
e sequence. Found forward in NC_001148 between 22079 and 23078 with 100% identity.
e sequence. Found forward in NC_001148 between 23079 and 24078 with 100% identity.
e sequence. Found forward in NC_001148 between 24079 and 24201 with 100% identity.
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e sequence. Found forward in NC_001148 between 108147 and 109146 with 100% identity.
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e sequence. Found forward in NC_001148 between 110147 and 111146 with 100% identity.
e sequence. Found forward in NC_001148 between 111147 and 112146 with 100% identity.
e sequence. Found forward in NC_001148 between 112147 and 113146 with 100% identity.
e sequence. Found forward in NC_001148 between 113147 and 113815 with 100% identity.
e sequence. Found forward in NC_001148 between 140119 and 141118 with 100% identity.
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e sequence. Found forward in NC_001148 between 142119 and 143118 with 100% identity.
e sequence. Found forward in NC_001148 between 143119 and 144118 with 100% identity.
e sequence. Found forward in NC_001148 between 143119 and 144118 with 100% identity.
e sequence. Found forward in NC_001148 between 144119 and 145118 with 100% identity.
e sequence. Found forward in NC_001148 between 145119 and 146118 with 100% identity.
e sequence. Found forward in NC_001148 between 146119 and 146628 with 100% identity.
e sequence. Found forward in NC_001148 between 385268 and 386267 with 100% identity.
e sequence. Found forward in NC_001148 between 386268 and 387267 with 100% identity.
e sequence. Found forward in NC_001148 between 386268 and 387267 with 100% identity.
e sequence. Found forward in NC_001148 between 387268 and 388267 with 100% identity.
e sequence. Found forward in NC_001148 between 388268 and 389267 with 100% identity.
e sequence. Found forward in NC_001148 between 389268 and 390267 with 100% identity.
e sequence. Found forward in NC_001148 between 390268 and 391267 with 100% identity.
e sequence. Found forward in NC_001148 between 391268 and 392267 with 100% identity.
e sequence. Found forward in NC_001148 between 392268 and 393149 with 100% identity.
e sequence. Found forward in NC_001148 between 398975 and 399974 with 100% identity.
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e sequence. Found forward in NC_001148 between 400975 and 401974 with 100% identity.
e sequence. Found forward in NC_001148 between 401975 and 402974 with 100% identity.
e sequence. Found forward in NC_001148 between 402975 and 403974 with 100% identity.
e sequence. Found forward in NC_001148 between 403975 and 404451 with 100% identity.
e sequence. Found forward in NC_001148 between 435759 and 436758 with 100% identity.
e sequence. Found forward in NC_001148 between 436759 and 437758 with 100% identity.
e sequence. Found forward in NC_001148 between 437759 and 438758 with 100% identity.
e sequence. Found forward in NC_001148 between 438759 and 439758 with 100% identity.
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sequence. Found forward in NC_001148 between 440759 and 441758 with 100% identity.
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sequence. Found forward in NC_001148 between 442759 and 443758 with 100% identity.
sequence. Found forward in NC_001148 between 443759 and 444574 with 100% identity.
sequence. Found forward in NC_001148 between 446337 and 447336 with 100% identity.
sequence. Found forward in NC_001148 between 447337 and 448336 with 100% identity.
sequence. Found forward in NC_001148 between 448337 and 449336 with 100% identity.
sequence. Found forward in NC_001148 between 449337 and 450336 with 100% identity.
sequence. Found forward in NC_001148 between 450337 and 451336 with 100% identity.
sequence. Found forward in NC_001148 between 451337 and 451904 with 100% identity.
sequence. Found forward in NC_001148 between 519230 and 520229 with 100% identity.
sequence. Found forward in NC_001148 between 520230 and 521229 with 100% identity.
sequence. Found forward in NC_001148 between 520230 and 521229 with 100% identity.
sequence. Found forward in NC_001148 between 521230 and 522229 with 100% identity.
sequence. Found forward in NC_001148 between 522230 and 523229 with 100% identity.
sequence. Found forward in NC_001148 between 523230 and 524229 with 100% identity.
sequence. Found forward in NC_001148 between 524230 and 524453 with 100% identity.
sequence. Found forward in NC_001148 between 536315 and 537314 with 100% identity.
sequence. Found forward in NC_001148 between 537315 and 538314 with 100% identity.
sequence. Found forward in NC_001148 between 538315 and 539314 with 100% identity.
sequence. Found forward in NC_001148 between 539315 and 540314 with 100% identity.
sequence. Found forward in NC_001148 between 540315 and 541314 with 100% identity.
sequence. Found forward in NC_001148 between 541315 and 541465 with 100% identity.
sequence. Found forward in NC_001148 between 542577 and 543576 with 100% identity.
sequence. Found forward in NC_001148 between 543577 and 544576 with 100% identity.
sequence. Found forward in NC_001148 between 544577 and 545576 with 100% identity.
sequence. Found forward in NC_001148 between 545577 and 546576 with 100% identity.
sequence. Found forward in NC_001148 between 546577 and 547576 with 100% identity.
sequence. Found forward in NC_001148 between 547577 and 547638 with 100% identity.
sequence. Found forward in NC_001148 between 624964 and 625963 with 100% identity.
sequence. Found forward in NC_001148 between 625964 and 626963 with 100% identity.
sequence. Found forward in NC_001148 between 626964 and 627963 with 100% identity.
sequence. Found forward in NC_001148 between 626964 and 627963 with 100% identity.
sequence. Found forward in NC_001148 between 627964 and 628963 with 100% identity.
sequence. Found forward in NC_001148 between 628964 and 629963 with 100% identity.
sequence. Found forward in NC_001148 between 629964 and 630740 with 100% identity.
sequence. Found forward in NC_001148 between 759478 and 760477 with 100% identity.
sequence. Found forward in NC_001148 between 759478 and 760477 with 100% identity.
sequence. Found forward in NC_001148 between 760478 and 761477 with 100% identity.
sequence. Found forward in NC_001148 between 761478 and 762477 with 100% identity.
sequence. Found forward in NC_001148 between 762478 and 763477 with 100% identity.
sequence. Found forward in NC_001148 between 763478 and 764477 with 100% identity.
sequence. Found forward in NC_001148 between 764478 and 765477 with 100% identity.
sequence. Found forward in NC_001148 between 765478 and 766477 with 100% identity.
sequence. Found forward in NC_001148 between 766478 and 766991 with 100% identity.
sequence. Found forward in NC_001148 between 869140 and 870139 with 100% identity.
sequence. Found forward in NC_001148 between 870140 and 871139 with 100% identity.
sequence. Found forward in NC_001148 between 870140 and 871139 with 100% identity.
sequence. Found forward in NC_001148 between 871140 and 872139 with 100% identity.
sequence. Found forward in NC_001148 between 872140 and 873139 with 100% identity.
sequence. Found forward in NC_001148 between 873140 and 874139 with 100% identity.
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e sequence. Found forward in NC_001148 between 874140 and 874421 with 100% identity.
equence. Found forward in NC_001134 between 25441 and 26440 with 100% identity.
equence. Found forward in NC_001134 between 26441 and 27440 with 100% identity.
equence. Found forward in NC_001134 between 27441 and 28440 with 100% identity.
equence. Found forward in NC_001134 between 28441 and 29440 with 100% identity.
equence. Found forward in NC_001134 between 29441 and 30440 with 100% identity.
equence. Found forward in NC_001134 between 35441 and 35606 with 100% identity.
equence. Found forward in NC_001134 between 51513 and 52512 with 100% identity.
equence. Found forward in NC_001134 between 52513 and 53512 with 100% identity.
equence. Found forward in NC_001134 between 53513 and 54512 with 100% identity.
equence. Found forward in NC_001134 between 54513 and 55512 with 100% identity.
equence. Found forward in NC_001134 between 55513 and 56512 with 100% identity.
equence. Found forward in NC_001134 between 56513 and 57512 with 100% identity.
equence. Found forward in NC_001134 between 57513 and 58512 with 100% identity.
equence. Found forward in NC_001134 between 58513 and 59512 with 100% identity.
equence. Found forward in NC_001134 between 59513 and 59815 with 100% identity.
equence. Found forward in NC_001134 between 73564 and 74563 with 100% identity.
equence. Found forward in NC_001134 between 74564 and 75563 with 100% identity.
equence. Found forward in NC_001134 between 74564 and 75563 with 100% identity.
equence. Found forward in NC_001134 between 75564 and 76563 with 100% identity.
equence. Found forward in NC_001134 between 76564 and 77563 with 100% identity.
equence. Found forward in NC_001134 between 77564 and 78563 with 100% identity.
equence. Found forward in NC_001134 between 78564 and 79261 with 100% identity.
equence. Found forward in NC_001134 between 187307 and 188306 with 100% identity.
equence. Found forward in NC_001134 between 188307 and 189306 with 100% identity.
equence. Found forward in NC_001134 between 189307 and 190306 with 100% identity.
equence. Found forward in NC_001134 between 190307 and 191306 with 100% identity.
equence. Found forward in NC_001134 between 191307 and 192306 with 100% identity.
equence. Found forward in NC_001134 between 192307 and 192975 with 100% identity.
equence. Found forward in NC_001134 between 192307 and 192975 with 100% identity.
equence. Found forward in NC_001134 between 220363 and 221362 with 100% identity.
equence. Found forward in NC_001134 between 226363 and 227362 with 100% identity.
equence. Found forward in NC_001134 between 227363 and 228362 with 100% identity.
equence. Found forward in NC_001134 between 227363 and 228362 with 100% identity.
equence. Found forward in NC_001134 between 228363 and 229362 with 100% identity.
equence. Found forward in NC_001134 between 229363 and 230362 with 100% identity.
equence. Found forward in NC_001134 between 230363 and 231362 with 100% identity.
equence. Found forward in NC_001134 between 231363 and 232362 with 100% identity.
equence. Found forward in NC_001134 between 232363 and 233362 with 100% identity.
equence. Found forward in NC_001134 between 233363 and 234362 with 100% identity.
equence. Found forward in NC_001134 between 234363 and 234580 with 100% identity.
equence. Found forward in NC_001134 between 505265 and 506264 with 100% identity.
equence. Found forward in NC_001134 between 505265 and 506264 with 100% identity.
equence. Found forward in NC_001134 between 506265 and 507264 with 100% identity.
equence. Found forward in NC_001134 between 507265 and 508264 with 100% identity.
equence. Found forward in NC_001134 between 508265 and 509264 with 100% identity.
equence. Found forward in NC_001134 between 509265 and 510264 with 100% identity.
equence. Found forward in NC_001134 between 510265 and 511264 with 100% identity.
equence. Found forward in NC_001134 between 511265 and 512233 with 100% identity.
equence. Found forward in NC_001134 between 517809 and 518808 with 100% identity.
equence. Found forward in NC_001134 between 518809 and 519808 with 100% identity.
equence. Found forward in NC_001134 between 519809 and 520808 with 100% identity.
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sequence. Found forward in NC_001134 between 520809 and 521808 with 100% identity.
sequence. Found forward in NC_001134 between 521809 and 522808 with 100% identity.
sequence. Found forward in NC_001134 between 522809 and 523808 with 100% identity.
sequence. Found forward in NC_001134 between 523809 and 524808 with 100% identity.
sequence. Found forward in NC_001134 between 524809 and 525808 with 100% identity.
sequence. Found forward in NC_001134 between 525809 and 526808 with 100% identity.
sequence. Found forward in NC_001134 between 526809 and 526984 with 100% identity.
sequence. Found forward in NC_001134 between 637162 and 638161 with 100% identity.
sequence. Found forward in NC_001134 between 638162 and 639161 with 100% identity.
sequence. Found forward in NC_001134 between 639162 and 640161 with 100% identity.
sequence. Found forward in NC_001134 between 640162 and 641161 with 100% identity.
sequence. Found forward in NC_001134 between 641162 and 642161 with 100% identity.
sequence. Found forward in NC_001134 between 642162 and 642542 with 100% identity.
sequence. Found forward in NC_001134 between 751813 and 752812 with 100% identity.
sequence. Found forward in NC_001134 between 752813 and 753812 with 100% identity.
sequence. Found forward in NC_001134 between 753813 and 754812 with 100% identity.
sequence. Found forward in NC_001134 between 754813 and 755812 with 100% identity.
sequence. Found forward in NC_001134 between 755813 and 756812 with 100% identity.
sequence. Found forward in NC_001134 between 756813 and 757578 with 100% identity.
sequence. Found forward in NC_001135 between 82220 and 83219 with 100% identity.
sequence. Found forward in NC_001135 between 83220 and 84219 with 100% identity.
sequence. Found forward in NC_001135 between 84220 and 85219 with 100% identity.
sequence. Found forward in NC_001135 between 90220 and 91219 with 100% identity.
sequence. Found forward in NC_001135 between 90220 and 91219 with 100% identity.
sequence. Found forward in NC_001135 between 91220 and 91533 with 100% identity.
sequence. Found forward in NC_001135 between 177526 and 178525 with 100% identity.
sequence. Found forward in NC_001135 between 177526 and 178525 with 100% identity.
sequence. Found forward in NC_001135 between 178526 and 179525 with 100% identity.
sequence. Found forward in NC_001135 between 179526 and 180525 with 100% identity.
sequence. Found forward in NC_001135 between 180526 and 181525 with 100% identity.
sequence. Found forward in NC_001135 between 181526 and 182525 with 100% identity.
sequence. Found forward in NC_001135 between 182526 and 183525 with 100% identity.
sequence. Found forward in NC_001135 between 183526 and 184252 with 100% identity.
sequence. Found forward in NC_001135 between 275986 and 276985 with 100% identity.
sequence. Found forward in NC_001135 between 276986 and 277985 with 100% identity.
sequence. Found forward in NC_001135 between 277986 and 278985 with 100% identity.
sequence. Found forward in NC_001135 between 277986 and 278985 with 100% identity.
sequence. Found forward in NC_001135 between 278986 and 279985 with 100% identity.
sequence. Found forward in NC_001135 between 279986 and 280985 with 100% identity.
sequence. Found forward in NC_001135 between 280986 and 281985 with 100% identity.
sequence. Found forward in NC_001135 between 281986 and 282985 with 100% identity.
sequence. Found forward in NC_001135 between 282986 and 283985 with 100% identity.
sequence. Found forward in NC_001135 between 283986 and 284665 with 100% identity.
sequence. Found forward in NC_001136 between 79795 and 80794 with 100% identity.
sequence. Found forward in NC_001136 between 80795 and 81794 with 100% identity.
sequence. Found forward in NC_001136 between 81795 and 82794 with 100% identity.
sequence. Found forward in NC_001136 between 82795 and 83794 with 100% identity.
sequence. Found forward in NC_001136 between 83795 and 84794 with 100% identity.
sequence. Found forward in NC_001136 between 83795 and 84794 with 100% identity.
sequence. Found forward in NC_001136 between 84795 and 85486 with 100% identity.
sequence. Found forward in NC_001136 between 149704 and 150703 with 100% identity.
sequence. Found forward in NC_001136 between 150704 and 151703 with 100% identity.
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sequence. Found forward in NC_001136 between 151704 and 152703 with 100% identity.
sequence. Found forward in NC_001136 between 152704 and 153703 with 100% identity.
sequence. Found forward in NC_001136 between 153704 and 154703 with 100% identity.
sequence. Found forward in NC_001136 between 154704 and 155703 with 100% identity.
sequence. Found forward in NC_001136 between 155704 and 156703 with 100% identity.
sequence. Found forward in NC_001136 between 155704 and 156703 with 100% identity.
sequence. Found forward in NC_001136 between 156704 and 157405 with 100% identity.
sequence. Found forward in NC_001136 between 205861 and 206860 with 100% identity.
sequence. Found forward in NC_001136 between 206861 and 207860 with 100% identity.
sequence. Found forward in NC_001136 between 207861 and 208860 with 100% identity.
sequence. Found forward in NC_001136 between 208861 and 209860 with 100% identity.
sequence. Found forward in NC_001136 between 209861 and 210860 with 100% identity.
sequence. Found forward in NC_001136 between 210861 and 211376 with 100% identity.
sequence. Found forward in NC_001136 between 257132 and 258131 with 100% identity.
sequence. Found forward in NC_001136 between 258132 and 259131 with 100% identity.
sequence. Found forward in NC_001136 between 258132 and 259131 with 100% identity.
sequence. Found forward in NC_001136 between 259132 and 260131 with 100% identity.
sequence. Found forward in NC_001136 between 260132 and 261131 with 100% identity.
sequence. Found forward in NC_001136 between 261132 and 262131 with 100% identity.
sequence. Found forward in NC_001136 between 262132 and 262724 with 100% identity.
sequence. Found forward in NC_001136 between 344736 and 345735 with 100% identity.
sequence. Found forward in NC_001136 between 345736 and 346735 with 100% identity.
sequence. Found forward in NC_001136 between 346736 and 347735 with 100% identity.
sequence. Found forward in NC_001136 between 347736 and 348735 with 100% identity.
sequence. Found forward in NC_001136 between 348736 and 349735 with 100% identity.
sequence. Found forward in NC_001136 between 349736 and 350536 with 100% identity.
sequence. Found forward in NC_001136 between 618990 and 619989 with 100% identity.
sequence. Found forward in NC_001136 between 619990 and 620989 with 100% identity.
sequence. Found forward in NC_001136 between 620990 and 621989 with 100% identity.
sequence. Found forward in NC_001136 between 621990 and 622989 with 100% identity.
sequence. Found forward in NC_001136 between 622990 and 623989 with 100% identity.
sequence. Found forward in NC_001136 between 623990 and 624214 with 100% identity.
sequence. Found forward in NC_001136 between 630598 and 631597 with 100% identity.
sequence. Found forward in NC_001136 between 630598 and 631597 with 100% identity.
sequence. Found forward in NC_001136 between 631598 and 632597 with 100% identity.
sequence. Found forward in NC_001136 between 632598 and 633597 with 100% identity.
sequence. Found forward in NC_001136 between 633598 and 634597 with 100% identity.
sequence. Found forward in NC_001136 between 634598 and 635597 with 100% identity.
sequence. Found forward in NC_001136 between 735394 and 736393 with 100% identity.
sequence. Found forward in NC_001136 between 736394 and 737393 with 100% identity.
sequence. Found forward in NC_001136 between 737394 and 738393 with 100% identity.
sequence. Found forward in NC_001136 between 738394 and 739393 with 100% identity.
sequence. Found forward in NC_001136 between 739394 and 740393 with 100% identity.
sequence. Found forward in NC_001136 between 756048 and 757047 with 100% identity.
sequence. Found forward in NC_001136 between 757048 and 758047 with 100% identity.
sequence. Found forward in NC_001136 between 759048 and 760047 with 100% identity.
sequence. Found forward in NC_001136 between 760048 and 761047 with 100% identity.
sequence. Found forward in NC_001136 between 761048 and 762047 with 100% identity.
sequence. Found forward in NC_001136 between 762048 and 763047 with 100% identity.
sequence. Found forward in NC_001136 between 763048 and 763367 with 100% identity.
sequence. Found forward in NC_001136 between 796686 and 797685 with 100% identity.
sequence. Found forward in NC_001136 between 797686 and 798685 with 100% identity.
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sequence. Found forward in NC_001136 between 798686 and 799685 with 100% identity.
sequence. Found forward in NC_001136 between 799686 and 800685 with 100% identity.
sequence. Found forward in NC_001136 between 800686 and 801685 with 100% identity.
sequence. Found forward in NC_001136 between 801686 and 802685 with 100% identity.
sequence. Found forward in NC_001136 between 802686 and 803685 with 100% identity.
sequence. Found forward in NC_001136 between 877250 and 878249 with 100% identity.
sequence. Found forward in NC_001136 between 878250 and 879249 with 100% identity.
sequence. Found forward in NC_001136 between 647450 and 647656 with 100% identity.
sequence. Found forward in NC_001136 between 1133751 and 1134750 with 100% identity.
sequence. Found forward in NC_001136 between 1134751 and 1135750 with 100% identity.
sequence. Found forward in NC_001136 between 1135751 and 1136750 with 100% identity.
sequence. Found forward in NC_001136 between 1135751 and 1136750 with 100% identity.
sequence. Found forward in NC_001136 between 1136751 and 1137750 with 100% identity.
sequence. Found forward in NC_001136 between 1137751 and 1138750 with 100% identity.
sequence. Found forward in NC_001136 between 1138751 and 1139750 with 100% identity.
sequence. Found forward in NC_001136 between 1139751 and 1139967 with 100% identity.
sequence. Found forward in NC_001136 between 1305061 and 1306060 with 100% identity.
sequence. Found forward in NC_001136 between 1306061 and 1307060 with 100% identity.
sequence. Found forward in NC_001136 between 1306061 and 1307060 with 100% identity.
sequence. Found forward in NC_001136 between 1307061 and 1308060 with 100% identity.
sequence. Found forward in NC_001136 between 1308061 and 1309060 with 100% identity.
sequence. Found forward in NC_001136 between 1309061 and 1310060 with 100% identity.
sequence. Found forward in NC_001136 between 1310061 and 1311060 with 100% identity.
sequence. Found forward in NC_001136 between 1311061 and 1311164 with 100% identity.
sequence. Found forward in NC_001136 between 1346165 and 1347164 with 100% identity.
sequence. Found forward in NC_001136 between 1347165 and 1348164 with 100% identity.
sequence. Found forward in NC_001136 between 1348165 and 1349164 with 100% identity.
sequence. Found forward in NC_001136 between 1349165 and 1350164 with 100% identity.
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sequence. Found forward in NC_001136 between 1369375 and 1370374 with 100% identity.
sequence. Found forward in NC_001136 between 1370375 and 1371374 with 100% identity.
sequence. Found forward in NC_001136 between 1371375 and 1372374 with 100% identity.
sequence. Found forward in NC_001136 between 1372375 and 1373374 with 100% identity.
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sequence. Found forward in NC_001136 between 1374375 and 1375374 with 100% identity.
sequence. Found forward in NC_001136 between 1375375 and 1376374 with 100% identity.
sequence. Found forward in NC_001136 between 1376375 and 1377374 with 100% identity.
sequence. Found forward in NC_001136 between 1377375 and 1378374 with 100% identity.
sequence. Found forward in NC_001136 between 1378375 and 1379085 with 100% identity.
sequence. Found forward in NC_001137 between 7553 and 8552 with 100% identity.
sequence. Found forward in NC_001137 between 8553 and 9552 with 100% identity.
sequence. Found forward in NC_001137 between 9553 and 10552 with 100% identity.
sequence. Found forward in NC_001137 between 10553 and 11552 with 100% identity.
sequence. Found forward in NC_001137 between 11553 and 12552 with 100% identity.
sequence. Found forward in NC_001137 between 12553 and 13552 with 100% identity.
sequence. Found forward in NC_001137 between 13553 and 13915 with 100% identity.
sequence. Found forward in NC_001137 between 13553 and 13915 with 100% identity.
sequence. Found forward in NC_001137 between 109004 and 110003 with 100% identity.
sequence. Found forward in NC_001137 between 110004 and 111003 with 100% identity.
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sequence. Found forward in NC_001137 between 111004 and 112003 with 100% identity.
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sequence. Found forward in NC_001137 between 112004 and 113003 with 100% identity.
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sequence. Found forward in NC_001137 between 115004 and 115300 with 100% identity.
sequence. Found forward in NC_001137 between 425685 and 426684 with 100% identity.
sequence. Found forward in NC_001137 between 426685 and 427684 with 100% identity.
sequence. Found forward in NC_001137 between 427685 and 428684 with 100% identity.
sequence. Found forward in NC_001137 between 428685 and 429684 with 100% identity.
sequence. Found forward in NC_001137 between 429685 and 430684 with 100% identity.
sequence. Found forward in NC_001137 between 430685 and 431126 with 100% identity.
sequence. Found forward in NC_001137 between 442412 and 443411 with 100% identity.
sequence. Found forward in NC_001137 between 442412 and 443411 with 100% identity.
sequence. Found forward in NC_001137 between 446412 and 447411 with 100% identity.
sequence. Found forward in NC_001137 between 476841 and 477840 with 100% identity.
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sequence. Found forward in NC_001137 between 478841 and 479840 with 100% identity.
sequence. Found forward in NC_001137 between 479841 and 480840 with 100% identity.
sequence. Found forward in NC_001137 between 480841 and 481840 with 100% identity.
sequence. Found forward in NC_001137 between 481841 and 482840 with 100% identity.
sequence. Found forward in NC_001137 between 482841 and 483321 with 100% identity.
sequence. Found forward in NC_001137 between 491954 and 492953 with 100% identity.
sequence. Found forward in NC_001137 between 492954 and 493953 with 100% identity.
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sequence. Found forward in NC_001137 between 498954 and 499172 with 100% identity.
sequence. Found forward in NC_001137 between 530026 and 531025 with 100% identity.
sequence. Found forward in NC_001137 between 531026 and 532025 with 100% identity.
sequence. Found forward in NC_001137 between 532026 and 533025 with 100% identity.
sequence. Found forward in NC_001137 between 533026 and 534025 with 100% identity.
sequence. Found forward in NC_001137 between 534026 and 535025 with 100% identity.
sequence. Found forward in NC_001137 between 535026 and 536025 with 100% identity.
sequence. Found forward in NC_001137 between 536026 and 536271 with 100% identity.
sequence. Found forward in NC_001138 between 69614 and 70613 with 100% identity.
sequence. Found forward in NC_001138 between 70614 and 71613 with 100% identity.
sequence. Found forward in NC_001138 between 71614 and 72613 with 100% identity.
sequence. Found forward in NC_001138 between 72614 and 73613 with 100% identity.
sequence. Found forward in NC_001138 between 73614 and 74613 with 100% identity.
sequence. Found forward in NC_001138 between 74614 and 74871 with 100% identity.
sequence. Found forward in NC_001138 between 136029 and 137028 with 100% identity.
sequence. Found forward in NC_001138 between 137029 and 138028 with 100% identity.
sequence. Found forward in NC_001138 between 143029 and 144028 with 100% identity.
sequence. Found forward in NC_001138 between 144029 and 145028 with 100% identity.
sequence. Found forward in NC_001138 between 145029 and 145108 with 100% identity.
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sequence. Found forward in NC_001138 between 186470 and 187469 with 100% identity.
sequence. Found forward in NC_001138 between 187470 and 188469 with 100% identity.
sequence. Found forward in NC_001138 between 188470 and 189469 with 100% identity.
sequence. Found forward in NC_001138 between 189470 and 190469 with 100% identity.
sequence. Found forward in NC_001138 between 190470 and 190825 with 100% identity.
sequence. Found forward in NC_001139 between 16307 and 17306 with 100% identity.
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sequence. Found forward in NC_001139 between 17307 and 18306 with 100% identity.
sequence. Found forward in NC_001139 between 18307 and 19306 with 100% identity.
sequence. Found forward in NC_001139 between 19307 and 20306 with 100% identity.
sequence. Found forward in NC_001139 between 20307 and 21306 with 100% identity.
sequence. Found forward in NC_001139 between 20307 and 21306 with 100% identity.
sequence. Found forward in NC_001139 between 21307 and 21608 with 100% identity.
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sequence. Found forward in NC_001139 between 105045 and 106044 with 100% identity.
sequence. Found forward in NC_001139 between 106045 and 107044 with 100% identity.
sequence. Found forward in NC_001139 between 107045 and 108044 with 100% identity.
sequence. Found forward in NC_001139 between 108045 and 109044 with 100% identity.
sequence. Found forward in NC_001139 between 108045 and 109044 with 100% identity.
sequence. Found forward in NC_001139 between 109045 and 109906 with 100% identity.
sequence. Found forward in NC_001139 between 131050 and 132049 with 100% identity.
sequence. Found forward in NC_001139 between 131050 and 132049 with 100% identity.
sequence. Found forward in NC_001139 between 132050 and 133049 with 100% identity.
sequence. Found forward in NC_001139 between 133050 and 134049 with 100% identity.
sequence. Found forward in NC_001139 between 134050 and 135049 with 100% identity.
sequence. Found forward in NC_001139 between 135050 and 136049 with 100% identity.
sequence. Found forward in NC_001139 between 136050 and 137049 with 100% identity.
sequence. Found forward in NC_001139 between 137050 and 138049 with 100% identity.
sequence. Found forward in NC_001139 between 138050 and 139047 with 100% identity.
sequence. Found forward in NC_001139 between 176031 and 177030 with 100% identity.
sequence. Found forward in NC_001139 between 177031 and 178030 with 100% identity.
sequence. Found forward in NC_001139 between 178031 and 179030 with 100% identity.
sequence. Found forward in NC_001139 between 179031 and 180030 with 100% identity.
sequence. Found forward in NC_001139 between 180031 and 181030 with 100% identity.
sequence. Found forward in NC_001139 between 180031 and 181030 with 100% identity.
sequence. Found forward in NC_001139 between 181031 and 181622 with 100% identity.
sequence. Found forward in NC_001139 between 241856 and 242855 with 100% identity.
sequence. Found forward in NC_001139 between 242856 and 243855 with 100% identity.
sequence. Found forward in NC_001139 between 243856 and 244855 with 100% identity.
sequence. Found forward in NC_001139 between 244856 and 245855 with 100% identity.
sequence. Found forward in NC_001139 between 245856 and 246855 with 100% identity.
sequence. Found forward in NC_001139 between 246856 and 247627 with 100% identity.
sequence. Found forward in NC_001139 between 331616 and 332615 with 100% identity.
sequence. Found forward in NC_001139 between 332616 and 333615 with 100% identity.
sequence. Found forward in NC_001139 between 333616 and 334615 with 100% identity.
sequence. Found forward in NC_001139 between 334616 and 335615 with 100% identity.
sequence. Found forward in NC_001139 between 334616 and 335615 with 100% identity.
sequence. Found forward in NC_001139 between 335616 and 336615 with 100% identity.
sequence. Found forward in NC_001139 between 336616 and 337137 with 100% identity.
sequence. Found forward in NC_001139 between 547463 and 548462 with 100% identity.
sequence. Found forward in NC_001139 between 547463 and 548462 with 100% identity.
sequence. Found forward in NC_001139 between 548463 and 549462 with 100% identity.
sequence. Found forward in NC_001139 between 549463 and 550462 with 100% identity.
sequence. Found forward in NC_001139 between 550463 and 551462 with 100% identity.
sequence. Found forward in NC_001139 between 551463 and 552462 with 100% identity.
sequence. Found forward in NC_001139 between 552463 and 553445 with 100% identity.
sequence. Found forward in NC_001139 between 659764 and 660763 with 100% identity.
sequence. Found forward in NC_001139 between 660764 and 661763 with 100% identity.
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sequence. Found forward in NC_001139 between 661764 and 662763 with 100% identity.
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sequence. Found forward in NC_001139 between 664764 and 665565 with 100% identity.
sequence. Found forward in NC_001139 between 683060 and 684059 with 100% identity.
sequence. Found forward in NC_001139 between 684060 and 685059 with 100% identity.
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sequence. Found forward in NC_001139 between 686060 and 687059 with 100% identity.
sequence. Found forward in NC_001139 between 687060 and 688059 with 100% identity.
sequence. Found forward in NC_001139 between 687060 and 688059 with 100% identity.
sequence. Found forward in NC_001139 between 688060 and 689059 with 100% identity.
sequence. Found forward in NC_001139 between 689060 and 689459 with 100% identity.
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sequence. Found forward in NC_001139 between 863395 and 864394 with 100% identity.
sequence. Found forward in NC_001139 between 864395 and 865394 with 100% identity.
sequence. Found forward in NC_001139 between 865395 and 866330 with 100% identity.
sequence. Found forward in NC_001139 between 923127 and 924126 with 100% identity.
sequence. Found forward in NC_001139 between 924127 and 925126 with 100% identity.
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sequence. Found forward in NC_001139 between 1036505 and 1037190 with 100% identity.
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sequence. Found forward in NC_001139 between 1053406 and 1054405 with 100% identity.
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sequence. Found forward in NC_001139 between 1056406 and 1056753 with 100% identity.
sequence. Found forward in NC_001139 between 1084878 and 1085877 with 100% identity.
sequence. Found forward in NC_001140 between 39533 and 40532 with 100% identity.
sequence. Found forward in NC_001140 between 39533 and 40532 with 100% identity.

e sequence. Found forward in NC_001140 between 40533 and 41532 with 100% identity.
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e sequence. Found forward in NC_001140 between 150066 and 151065 with 100% identity.
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e sequence. Found forward in NC_001140 between 312647 and 313497 with 100% identity.
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e sequence. Found forward in NC_001140 between 434206 and 435205 with 100% identity.
e sequence. Found forward in NC_001140 between 435206 and 436205 with 100% identity.
e sequence. Found forward in NC_001140 between 436206 and 437169 with 100% identity.
e sequence. Found forward in NC_001140 between 522872 and 523871 with 100% identity.
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e sequence. Found forward in NC_001140 between 526872 and 527871 with 100% identity.
e sequence. Found forward in NC_001140 between 527872 and 528114 with 100% identity.
e sequence. Found forward in NC_001140 between 532177 and 533176 with 100% identity.
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e sequence. Found forward in NC_001140 between 534177 and 535176 with 100% identity.
e sequence. Found forward in NC_001140 between 535177 and 536176 with 100% identity.
e sequence. Found forward in NC_001140 between 537177 and 537754 with 100% identity.
e sequence. Found forward in NC_001140 between 543488 and 544487 with 100% identity.
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e sequence. Found forward in NC_001140 between 547488 and 548487 with 100% identity.

sequence. Found forward in NC_001140 between 548488 and 549487 with 100% identity.
sequence. Found forward in NC_001140 between 549488 and 549898 with 100% identity.
sequence. Found forward in NC_001141 between 9696 and 10695 with 100% identity.
sequence. Found forward in NC_001141 between 10696 and 11695 with 100% identity.
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sequence. Found forward in NC_001141 between 12696 and 13695 with 100% identity.
sequence. Found forward in NC_001141 between 13696 and 14695 with 100% identity.
sequence. Found forward in NC_001141 between 106607 and 107606 with 100% identity.
sequence. Found forward in NC_001141 between 107607 and 108606 with 100% identity.
sequence. Found forward in NC_001141 between 108607 and 109606 with 100% identity.
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sequence. Found forward in NC_001141 between 114607 and 115606 with 100% identity.
sequence. Found forward in NC_001141 between 115607 and 116404 with 100% identity.
sequence. Found forward in NC_001141 between 204053 and 205052 with 100% identity.
sequence. Found forward in NC_001141 between 205053 and 206052 with 100% identity.
sequence. Found forward in NC_001141 between 365963 and 366962 with 100% identity.
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sequence. Found forward in NC_001141 between 369963 and 370962 with 100% identity.
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sequence. Found forward in NC_001141 between 370963 and 371962 with 100% identity.
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solated Syf1p, Prp39p and YPL213p (a homologue of U2A) suggesting an involvement in pre-mRNA sp

s PTP (PiC), a mitochondrial phosphate transport protein. Mir1p localizes between the inner and outer m

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of Aspergillus nidulans. Microbiol. 142:3211-3218.

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C15 and EXO70.

NA is induced in meiosis

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s when expressed from high copy plasmid

aperones

genes have similar phenotypes. mRNA is induced in meiosis

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ses\; it co-localizes to spots with Mre11p and Xrs2p in a rad50s background

ing a G-T mismatch

n

chemical features

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ssociated with telomeres

p to repair single-base and insertion-deletion mispairs, or Msh3p to repair only insertion-deletion mispai ae

amount associates with membranes), and shows diffuse cytosolic labeling when immunolocalized in wil

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o other proteins. Required for modification of CDC53\/cullin with RUB1

, and EXO70

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t. AUT7 was identified as a suppressor of mutant phenotypes of aut2-1 cells. Uptake of precursor Amino

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ease named VDE (PI-SceI) that is homologous to HO. Cleavage is meiosis-specific and induces gene cc xpression

rad52 for its repair and recombination defects. The RAD59 gene product has homology to the Rad52 pr ates in vitro protein kinase activity, but also behaves like a null mutation in vivo, suggesting that kinase a eptonate aldolase\; 3-deoxy-D-arabine-heptulosonate-7-phosphate synthase eletion mispairs

and epsp synthase)

x is a variable amino acid (aa)]

ADA complex and the 1.8 MD SAGA complex

s Ume4 for mitotic repression and interacts with and requires Ime1p and Rim11p for induction of meiosi

unit of the SculCdc4 (also termed SCFCdc4p) complex, which also contains the ubiquitin ligase Cdc34p

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phenyl propanediol

, meiotic intra- and interchromosomal gene conversion, reciprocal recombination and viable spores. me

, meiotic intra- and interchromosomal gene conversion, reciprocal recombination and viable spores. me

lian type 1 phosphatase targeting subunit.

cdc24-4ts mutant

triglutamate homocysteine methyltransferase)

nalysis\; human Rad51p homolog interacts with Brca2 protein which has been implicated in causing brea es with Zip1p, and then disappears by pachytene

es with Zip1p, and then disappears by pachytene

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IA and cuts in a single-stranded region 5 to the G4 structure\; protein increases several-fold in meiotic c stem assay.

A-binding protein). The C-terminal 23 residues are critical for sporulation and histone polyubiquitinating

diating destruction of Pds1 which binds to Esp1 and inhibits its activity

meiosis (different cis-sites utilized in damage and meiotic induction

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tid\/centromere cohesion with nuclear division. Spo13p has transcriptional activation activity in one-hybri onal ORF

or known function.

h Dbf2p and Dbf20p protein kinases.

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lentical proteins)

licing. Immunoprecipitation experiments demonstrated that Isy1p interacts with the spliceosome before

itochondrial membranes

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d-type yeast\; however, in vps27 mutant cells (a class E vps mutant, which accumulates a prevaculoar co

peptidase I into the vacuole depends on Aut2p and Aut7p.

onversion at the TFP1 locus.

otein.

activity contributes to the essential function of the protein.

s-specific transcription

, the cullin Cdc53p, and Cdc4p. SculCdc4 complexes transfer ubiquitin to phosphorylated Sic1p, and su

ei4 has near wild-type chromosome condensation, executes both divisions with a delay in meiosis II, is re

ei4 has near wild-type chromosome condensation, executes both divisions with a delay in meiosis II, is re

ast cancer

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activity, but not UV repair or induced mutagenesis.

id analysis.

step 1 of splicing, prior to the dissociation of Prp2p, and remains associated throughout both steps of sp

ompartment), Grd19p-HA co-localizes with the vacuolar H+-ATPase in the prevaculoar compartment\; G

bstrate recognition is thought to involve the Cdc4p and Skp1p subunits. Following the SculCdc4-mediat

escued by spo13 and is epiststic to rad52, and is classified and an early recombination function. mRNA i

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olicing.

Grd19p contains PX domain, which is found in proteins such as human SNX1 (Sorting Nexin-1) (Ponting,

ed monoubiquitination of Sic1p, a polyubiquitin chain is added, andubiquitinated Sic1p is then degraded

is meiosis-specific and has 88 bp intron at 5 end spliced independently of MER1.

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, C.P. 1996. Protein Science 5:2353-2357)

by the 26S proteosome.