	1511 SCP_	1511 SCP_	Descriptions
AFFX-MurI	178.8	A	M16762 Mouse interleukin 2 (IL-2) gene, exon 4
AFFX-MurI	76.7	A	M37897 Mouse interleukin 10 mRNA, complete cds
AFFX-MurI	146.9	A	M25892 Mus musculus interleukin 4 (Il-4) mRNA, complete cds
AFFX-Mur	196.3	A	M83649 Mus musculus Fas antigen mRNA, complete cds
AFFX-BioB	6357.9	P	J04423 E coli bioB gene biotin synthetase (-5, -M, -3 represent trans
AFFX-BioB	7081.5	P	J04423 E coli bioB gene biotin synthetase (-5, -M, -3 represent trans
AFFX-BioB	8076.9	P	J04423 E coli bioB gene biotin synthetase (-5, -M, -3 represent trans
AFFX-BioC	14295.3	P	J04423 E coli bioC protein (-5 and -3 represent transcript regions 5
AFFX-BioC	13649.3	P	J04423 E coli bioC protein (-5 and -3 represent transcript regions 5
AFFX-BioD	4817.5	P	J04423 E coli bioD gene dethiobiotin synthetase (-5 and -3 represen
AFFX-BioD	19911.3	P	J04423 E coli bioD gene dethiobiotin synthetase (-5 and -3 represen
AFFX-Cre	9962	P	X03453 Bacteriophage P1 cre recombinase protein (-5 and -3 repre
AFFX-Cre	16112.8	P	X03453 Bacteriophage P1 cre recombinase protein (-5 and -3 repre
AFFX-BioB	363.1	A	J04423 E coli bioB gene biotin synthetase (-5, -M, -3 represent trans
AFFX-BioB	313.7	A	J04423 E coli bioB gene biotin synthetase (-5, -M, -3 represent trans
AFFX-BioB	183.5	A	J04423 E coli bioB gene biotin synthetase (-5, -M, -3 represent trans
AFFX-BioC	232.6	A	J04423 E coli bioC protein (-5 and -3 represent transcript regions 5
AFFX-BioC	94.1	A	J04423 E coli bioC protein (-5 and -3 represent transcript regions 5
AFFX-BioD	352.3	A	J04423 E coli bioD gene dethiobiotin synthetase (-5 and -3 represen
AFFX-BioD	1072.4	A	J04423 E coli bioD gene dethiobiotin synthetase (-5 and -3 represen
AFFX-Cre	317.3	A	X03453 Bacteriophage P1 cre recombinase protein (-5 and -3 repre
AFFX-Cre	82.9	A	X03453 Bacteriophage P1 cre recombinase protein (-5 and -3 repre
AFFX-Dap	216.8	A	L38424 B subtilis dapB, jojF, jojG genes corresponding to nucleotide
AFFX-Dap	176	A	L38424 B subtilis dapB, jojF, jojG genes corresponding to nucleotide
AFFX-Dap	36.6	A	L38424 B subtilis dapB, jojF, jojG genes corresponding to nucleotide
AFFX-Lys	20.1	A	X17013 B subtilis lys gene for diaminopimelate decarboxylase corres
AFFX-Lys	400	A	X17013 B subtilis lys gene for diaminopimelate decarboxylase corres
AFFX-Lys	111.9	A	X17013 B subtilis lys gene for diaminopimelate decarboxylase corres
AFFX-Phe	64.3	A	M24537B subtilis pheB, pheA genes corresponding to nucleotides 2
AFFX-Phe	79.7	A	M24537B subtilis pheB, pheA genes corresponding to nucleotides 2
AFFX-Phe	519.2	A	M24537B subtilis pheB, pheA genes corresponding to nucleotides 2
AFFX-Thr	109.1	A	X04603 B subtilis thrC, thrB genes corresponding to nucleotides 248
AFFX-Thr	248.4	A	X04603 B subtilis thrC, thrB genes corresponding to nucleotides 248
AFFX-Thr	159.6	A	X04603 B subtilis thrC, thrB genes corresponding to nucleotides 248
AFFX-Trpn	80.2	A	K01391 B subtilis TrpE protein, TrpD protein, TrpC protein correspon
AFFX-Trpn	47.4	A	K01391 B subtilis TrpE protein, TrpD protein, TrpC protein correspon
AFFX-Trpn	208.3	A	K01391 B subtilis TrpE protein, TrpD protein, TrpC protein correspon
AFFX-YFL	36255.6	P	V01288 SGD:YFL039C Yeast S. cerevisiae gene for actin (5, M, 3 re
AFFX-YFL	30538.7	P	V01288 SGD:YFL039C Yeast S. cerevisiae gene for actin (5, M, 3 re
AFFX-YFL	13925.3	P	V01288 SGD:YFL039C Yeast S. cerevisiae gene for actin (5, M, 3 re
AFFX-YER	8657	P	X16860 SGD:YER148W Yeast S. cervisiae TATA-binding protein (tfI
AFFX-YER	11853.1	P	X16860 SGD:YER148W Yeast S. cervisiae TATA-binding protein (tfI
AFFX-YER	18859.7	P	X16860 SGD:YER148W Yeast S. cervisiae TATA-binding protein (tfI
AFFX-YER	386.1	A	L12026 SGD:YER022W Yeast S. cerevisiae subunit of RNA polymer
AFFX-YER	1171.8	P	L12026 SGD:YER022W Yeast S. cerevisiae subunit of RNA polymer
AFFX-YER	1614.8	P	L12026 SGD:YER022W Yeast S. cerevisiae subunit of RNA polymer
AFFX-18sr	6332.1	P	Z75578 SGD:YLR154C Yeast S. cerevisiae 18S ribosomal RNA corr
AFFX-18sr	2983.3	P	Z75578 SGD:YLR154C Yeast S. cerevisiae 18S ribosomal RNA corr
AFFX-18sr	983.1	P	Z75578 SGD:YLR154C Yeast S. cerevisiae 18S ribosomal RNA corr
AFFX-18sr	1474	P	Z75578 SGD:YLR154C Yeast S. cerevisiae 18S ribosomal RNA corr
AFFX-18sr	1754.5	P	Z75578 SGD:YLR154C Yeast S. cerevisiae 18S ribosomal RNA corr

AFFX-25sr	23356.1	P	Z73326 SGD:YLR154C Yeast S.cerevisiae 25S ribosomal RNA corre
AFFX-25sr	5012.1	P	Z73326 SGD:YLR154C Yeast S.cerevisiae 25S ribosomal RNA corre
AFFX-25sr	2635.1	P	Z73326 SGD:YLR154C Yeast S.cerevisiae 25S ribosomal RNA corre
AFFX-25sr	3489.6	P	Z73326 SGD:YLR154C Yeast S.cerevisiae 25S ribosomal RNA corre
AFFX-25sr	22058	P	Z73326 SGD:YLR154C Yeast S.cerevisiae 25S ribosomal RNA corre
AFFX-YEL	10362.9	P	X61388 SGD: YEL002C Yeast S.cerevisiae WBP1 Oligosaccharyltra
AFFX-YEL	8128.9	P	U18530 SGD:YEL018W Yeast S. cerevisiae Protein of unknown func
AFFX-YEL	11183.5	P	M23316 SGD:YEL024C Yeast S.cerevisiae RIP1 Rieske iron-sulfur p
AFFX-YEL	1617.3	P	K02207 SGD:YEL021W Yeast S.cerevisiae URA3 gene coding for O
11378_at	19.9	A	Aldehyde dehydrogenase 1, mitochondrial
11379_at	1513.9	P	Suppressor of Sulfoxyde Ethionine resistance
11380_at	313	P	hypothetical protein
11381_at	691.7	A	putative pseudogene
11382_at	182.7	A	putative pseudogene
11383_at	24.7	A	putative pseudogene
11384_at	203.2	A	hypothetical protein
11385_s_a	2950.1	P	putative Flo1p homolog
11386_at	696.5	A	NADP-linked glutamate dehydrogenase
11387_at	622.8	A	similarity to alcohol/sorbitol dehydrogenase
11388_at	7537	P	similarity to alcohol/sorbitol dehydrogenase
11389_at	13265.3	P	ExtraCellular Mutant
11390_at	1824.2	M	Calnexin and calreticulin homolog
11391_at	920.7	A	questionable ORF
11392_at	955.8	P	similarity to hypothetical protein YOR371c
11393_at	4878.3	P	hypothetical protein
11356_at	3144.1	P	inducible acetyl-coenzyme A synthetase
11357_at	7841.3	P	strong similarity to hypothetical proteins YOR365c,YGL139w,YPL22
11358_at	1955.3	P	peroxisome proliferating transcription factor
11359_at	5973.9	P	weak similarity to Legionella small basic protein sbpA
11360_at	353.9	P	weak similarity to GTP-binding proteins
11361_at	469.9	P	Spc72p interacts with Stu2p in the two-hybrid assay\; Spc72p localize
11362_at	1636.2	P	hypothetical protein
11363_at	1064.9	A	hypothetical protein
11364_at	6816.5	P	H-protein subunit of the glycine cleavage system
11365_at	4002.3	P	pre-tRNA processing
11366_at	105.8	A	questionable ORF
11367_at	21759.4	P	Function unknown now
11368_at	3566.8	P	Guanine nucleotide exchange factor (a.k.a. GDP-release factor) for c
11369_at	21194	P	G(sub)1 cyclin
11370_at	9459.1	P	cytochrome c heme lyase (CCHL)
11371_at	2569.7	P	Pyruvate kinase
11372_at	1355.3	A	strong similarity to GTP-binding proteins
11373_at	15395.3	P	Function unknown now
11374_at	21662.4	P	97 kDa protein
11375_at	132.7	A	questionable ORF
11376_at	2440.3	P	hypothetical protein
11377_at	5130.2	P	Function unknown now
11333_at	4092.9	P	An integral subunit of RNase P and apparent subunit of RNase MRP
11334_at	312.6	A	Function unknown now
11335_at	3610	P	FUN21
11336_at	1689	P	homolog of Snc2p, vesicle-associated membrane protein (synaptobr
11337_at	7933.4	P	homolog of Snc2p, vesicle-associated membrane protein (synaptobr

11338_at	5416.3	P	myosin
11339_at	213.6	A	similarity to hypothetical protein YOR324c
11340_at	904.6	P	hypothetical protein
11341_at	2013.1	P	Membrane-spanning Ca-ATPase (P-type),member of the cation tran
11342_at	2458.1	P	putative nuclear protein
11343_at	618.1	P	putative GTP-exchange protein
11344_at	20544	P	dolichyl phosphate-D-mannose:protein O-D-mannosyltransferase
11345_at	9065.8	P	predicted membrane protein
11346_at	23778.8	P	95 kDa containg leucine rich tandem repeats
11347_at	2722.6	A	Protein with similarity to human RCC1 protein
11348_at	2872.8	P	Shows homology to SNF2 transcriptional regulator
11349_at	934.6	P	3 transmembrane domains
11350_at	4580.3	P	Serine\/threonine kinase
11351_at	19975.1	P	protein phosphatase 2A regulatory subunit A
11352_at	2066.6	P	DNA glycosylase
11353_at	4592.3	P	protein of unknown function
11354_at	4217.5	P	regulation of phospholipid metabolism
11355_at	32590.8	P	cystathionine gamma-lyase
11310_at	842.6	P	possible mitochondrial transit peptide
11311_at	443.3	A	Mitochondrial outer membrane protein involved in mitochondrial mor
11312_at	1611.9	P	sporulation protein
11313_at	4861.3	P	protein of unknown function
11314_at	11125.9	P	p24 protein involved in membrane trafficking
11315_i_a	0.4	A	Heat shock protein of HSP70 family, cytoplasmic
11316_r_a	0.4	P	Heat shock protein of HSP70 family, cytoplasmic
11317_s_a	33567.9	P	Heat shock protein of HSP70 family, cytoplasmic
11318_at	2225.3	P	strong similarity to A.klebsiana glutamate dehydrogenase
11319_at	16400.8	P	Translation elongation factor EF-1beta, GDP\/GTP exchange factor
11320_at	25595.6	P	Translation elongation factor EF-1beta, GDP\/GTP exchange factor
11321_at	1233	P	Vps8p is a membrane-associated hydrophilic protein which contains
11322_at	4150.8	P	transcription factor tau (TFIIIC) subunit 138
11323_at	237.4	A	transcription factor tau (TFIIIC) subunit 138
11324_at	3451.2	P	protein of unknown function
11325_at	24433.3	P	p24 protein involved in membrane trafficking
11326_at	3099.1	P	beta transducin domain
11327_at	10773.8	P	69 kDa subunit of the heterotrimeric RPA (RF-A) single-stranded D
11328_at	2877	P	34kDa subunit of the tetrameric tRNA splicing endonuclease
11329_at	4382.1	P	maximal growth
11330_at	6464.6	P	phosphoribosyl amino imidazolesuccinocarbozamide synthetase
11331_at	742.5	P	protein kinase
11332_at	735.9	M	protein kinase domain
11287_f_a	1741.9	P	strong similarity to members of the srp1p/Tip1p family
11288_at	361.8	A	membrane protein
11289_at	258.7	A	membrane protein
11290_at	1563.9	P	membrane protein
11291_at	239.2	A	membrane protein
11292_at	89.1	A	hypothetical protein
11293_at	764.6	A	membrane protein
11294_g_a	2695	P	membrane protein
11295_r_a	1170.3	P	membrane protein
11296_s_a	1142.7	P	membrane protein
11297_at	4208.2	P	Outer carnitine acetyltransferase, mitochondrial

11298_at	2768.5	A	ankyrin repeat
11299_at	1431.4	P	Shows homology to the human oxysterol binding protein (OSBP)
11300_at	208.3	A	predicted nuclear targeting signal
11301_i_at	31.3	A	FLO1 putative cell wall glycoprotein
11302_at	704	A	predicted membrane protein
11303_s_a	492.8	P	strong similarity to hypothetical protein YHR212c
11304_at	1679.6	A	putative pseudogene
11305_s_a	56.4	A	putative pseudogene
11306_at	1150.5	P	Potential membrane protein
11307_s_a	1618.3	P	identical to YHR214w hypothetical protein, similarity to Sta1p
11308_s_a	6962.9	P	Potential membrane protein
11309_at	1210.3	A	Potential membrane protein
11261_at	74.5	A	potential mitochondrial transit peptide
11262_s_a	34845.3	P	Acid phosphatase, secreted
11263_f_at	12361.7	P	strong similarity to IMP dehydrogenases
11264_f_at	19775.3	P	strong similarity to IMP dehydrogenases
11265_i_at	5986.4	M	hypothetical protein
11266_f_at	26298.7	P	hypothetical protein
11267_at	359.4	P	identified by SAGE
11268_at	302.7	A	hypothetical protein
11269_at	1292.9	A	non-annotated SAGE orf Found forward in NC_001133 between 101
11270_at	155.6	M	non-annotated SAGE orf Found forward in NC_001133 between 237
11271_at	114.3	A	non-annotated SAGE orf Found reverse in NC_001133 between 312
11272_at	683.5	P	non-annotated SAGE orf Found reverse in NC_001133 between 222
11273_at	629.9	P	non-annotated SAGE orf Found forward in NC_001133 between 734
11274_at	1577.9	P	non-annotated SAGE orf Found reverse in NC_001133 between 139
11275_at	1947.2	P	non-annotated SAGE orf Found reverse in NC_001133 between 166
11276_at	79.2	A	non-annotated SAGE orf Found reverse in NC_001133 between 317
11277_at	5	A	non-annotated SAGE orf Found forward in NC_001133 between 197
11278_f_at	1963.5	P	non-annotated SAGE orf Found reverse in NC_001133 between 199
11279_s_a	156.3	A	non-annotated SAGE orf Found reverse in NC_001133 between 223
11280_at	42.6	A	non-annotated SAGE orf Found reverse in NC_001133 between 290
11281_at	102.4	A	non-annotated SAGE orf Found forward in NC_001133 between 299
11282_i_at	0.5	A	non-annotated SAGE orf Found reverse in NC_001133 between 182
11283_r_a	247.5	P	non-annotated SAGE orf Found reverse in NC_001133 between 182
11284_f_at	13213.1	A	non-annotated SAGE orf Found reverse in NC_001133 between 182
11285_at	23.3	A	non-annotated SAGE orf Found forward in NC_001133 between 198
11286_at	112.5	A	non-annotated SAGE orf Found reverse in NC_001133 between 199
11238_at	18.7	A	non-annotated SAGE orf Found forward in NC_001133 between 200
11239_at	218.9	A	non-annotated SAGE orf Found reverse in NC_001133 between 203
11240_s_a	219.4	A	non-annotated SAGE orf Found reverse in NC_001133 between 219
11241_at	901.8	P	non-annotated SAGE orf Found reverse in NC_001133 between 138
11242_f_at	273.2	A	non-annotated SAGE orf Found forward in NC_001133 between 223
11243_s_a	600.3	M	non-annotated SAGE orf Found forward in NC_001133 between 223
11244_s_a	457.4	P	non-annotated SAGE orf Found forward in NC_001133 between 223
11245_i_at	10.2	A	Centromere
11246_r_a	137.2	A	Centromere
11247_s_a	29115.5	P	strong similarity to members of the Sir1p/Tip1p family
11248_s_a	38.4	A	strong similarity to members of the Sir1p/Tip1p family
11249_f_at	3742.3	P	strong similarity to members of the Srp1p/Tip1p family
11250_s_a	1070.9	A	strong similarity to Pep1p
11251_s_a	517.4	P	homology to maltase(alpha-D-glucosidase)

11252_s_a	44.7	A	questionable ORF
11253_s_a	407.4	A	High-affinity hexose transporter
11254_at	502.9	A	strong similarity to E.coli galactoside O-acetyltransferase
11255_at	382.7	A	hypothetical protein
11256_at	6.5	A	strong similarity to Mal62p
11257_at	73.9	A	hypothetical protein
11258_at	240.8	A	High-affinity hexose transporter
11259_at	3974.5	P	similarity to Methanobacterium aryldialkylphosphatase related protei
11260_at	6376	P	strong similarity to S.pombe isp4 protein
11215_at	186.3	A	questionable ORF
11216_at	7570.5	P	CH3HC4 zinc-binding integral peroxisomal membrane protein
11217_at	2086.5	P	Protein required for COB mRNA stability or 5 processing
11218_at	4067.6	P	mitochondrial nuclease
11219_at	1259.1	P	weak similarity to rat omega-conotoxin-sensitive calcium channel alp
11220_at	1718.9	P	similarity to YIL130p and Put3p
11221_at	3727.9	P	involved in secretion of proteins that lack classical secretory signal s
11222_at	3536.1	P	weak similarity to Tor2p
11223_at	1314.2	P	RNA splicing factor
11224_at	99.9	A	questionable ORF
11225_at	1405.9	P	ExtraCellular Mutant
11226_at	18088.2	P	strong similarity to aconitate hydratase
11227_at	4197.7	P	hypothetical protein
11228_at	24382.3	P	strong similarity to Pho87p
11229_at	3161.5	P	ubiquitin carboxyl-terminal hydrolase
11230_at	21861.3	P	Elongation enzyme 1, required for the elongation of the saturated fat
11231_at	119.4	A	questionable ORF
11232_at	2448.8	P	Protein involved in initiation of DNA replication
11233_at	7269.9	P	similarity to Sly41p
11234_at	2505.5	P	hypothetical protein
11235_at	8240.4	P	Ribosomal protein S14B (rp59B)
11236_at	10327.8	P	Ribosomal protein S22A (S24A) (rp50) (YS22)
11237_at	26548	P	Ribosomal protein L39 (L46) (YL40)
11192_at	1030.6	P	questionable ORF
11193_at	1734.6	P	protein kinase homolog
11194_at	2805.8	P	putative mannosyltransferase
11195_at	403.1	A	hypothetical protein
11196_at	2603.6	P	hypothetical protein
11197_at	6871.4	P	A new gene encoding a protein that is related to Mnn10p, and that is
11198_at	458	A	questionable ORF
11199_at	2795	P	similarity to hypothetical protein YJR030c
11200_at	947.7	P	essential for assembly of a functional F1-ATPase
11201_at	717.3	P	Putative homolog of subunit 1 of bovine prefoldin, a chaperone com
11202_at	4658.6	P	hypothetical protein
11203_i_at	24924.3	P	Ribosomal protein L17B (L20B) (YL17)
11204_s_a	27402.5	P	Ribosomal protein L17B (L20B) (YL17)
11205_i_at	923.5	P	Ribosomal protein L17B (L20B) (YL17)
11206_f_at	22858.8	P	Ribosomal protein L17B (L20B) (YL17)
11207_at	730.3	P	transcription factor
11208_at	297.7	A	questionable ORF
11209_at	15867.9	P	Cell wall beta-glucan assembly
11210_at	6151.2	P	subunit 3 of replication factor-A
11211_at	6005.4	P	carboxypeptidase yscS

11212_at	17946.1	P	similarity to YBR162c
11213_at	19.5	A	An a-specific gene that is induced to a higher expression level by alp
11214_at	300.1	A	questionable ORF
11170_at	568.3	A	transcription factor containing a SET domain
11171_at	22392.4	P	Farnesyl diphosphate synthetase (FPP synthetase)
11172_at	11978.5	P	Ubiquinol cytochrome-c reductase subunit 8 (11 kDa protein)
11173_at	3498	P	Protein kinase homolog, mutant is salt and pH sensitive
11174_at	4572.6	P	putative catalytic subunit of cAMP-dependent protein kinase
11175_at	1127	A	hypothetical protein
11176_at	112.1	A	weak similarity to dnaJ proteins
11177_at	67.5	A	hypothetical protein
11178_at	598.7	A	member of the Pir1p/Hsp150p/Pir3p family
11179_at	7358.3	P	Heat shock protein, secretory glycoprotein
11180_at	22715.8	P	Protein with homology to Hsp150p and Pir1p, Pir2p, and Pir3p
11181_at	21350.5	P	Factor arrest protein
11182_at	1593.3	P	sensitive to sulfonylurea herbicides on complex media (YPD)
11183_at	1927.5	P	Fructose-2,6-bisphosphatase
11184_at	2261.5	P	Protein involved in vacuolar sorting
11185_at	806.4	A	L-myo-inositol-1-phosphate synthase
11186_at	881.9	A	questionable ORF
11187_at	7644.3	P	similarity to hypothetical protein YDL123w
11188_at	299.6	M	questionable ORF
11189_at	2325.5	P	similarity to hypothetical protein YDR131c
11190_at	23591.7	P	RNA polymerase I subunit, not shared (A34.5)
11191_at	1143.3	P	weak similarity to C.elegans hypothetical protein C43G2.4
11147_at	1637.1	P	IME2-Dependent Signalling
11148_at	4233.6	P	weak similarity to T.pacificus retinal-binding protein
11149_at	594.6	A	hypothetical protein
11150_at	14533.1	P	16.5 kDa inner membrane protein required for import of mitochondria
11151_at	1569.7	P	questionable ORF
11152_g_a	2667	P	questionable ORF
11153_at	1935.1	P	Serine-threonine protein kinase
11154_at	3460.2	P	fourth-largest subunit of RNA polymerase II
11155_at	3562.6	P	Probable glycosyltransferase of KRE2\/KTR1\/YUR1 family\; located
11156_s_a	32975	P	translation initiation factor eIF4A
11157_at	1269.7	P	self-glucosylating initiator of glycogen synthesis\; similar to mammalia
11158_i_at	16560	P	Ribosomal protein S21B (S26B) (YS25)
11159_s_a	14251.1	P	Ribosomal protein S21B (S26B) (YS25)
11160_at	280.6	A	questionable ORF
11161_at	7123.1	P	putative plasma membrane transporter capable of transporting sphin
11162_at	2526.8	P	mitochondrial carrier protein
11163_at	370.4	P	weak similarity to human phospholipase D
11164_at	3669.7	P	weak similarity to nonepidermal Xenopus keratin, type I
11165_at	23832.8	P	carbamoyl-phophate synthetase, aspartate transcarbamylase, and g
11166_at	2442.6	P	180 kDa high affinity potassium transporter
11167_at	3540.9	P	MAP kinase kinase (MEK), may act as a scaffolding protein for Sho1
11168_at	435.6	P	negative transcriptional regulator
11169_at	1816.5	P	Nit2 nitrilase
11124_at	8819.8	P	translational repressor of GCN4
11125_at	3112.4	P	Like Sm-B protein\; contains the Sm consensus motifs and most clo
11126_at	13021.2	P	weak similarity to D.melanogaster troponin T and human nucleolin
11127_at	6376.7	P	weak similarity to dog-fish transition protein S2

11128_at	32546	P	D-ribulose-5-Phosphate 3-epimerase
11129_at	906.6	M	questionable ORF
11130_at	588.2	A	questionable ORF
11131_at	11575.2	P	hypothetical protein
11132_at	13324.4	P	Putative inorganic phosphate transporter
11133_at	13685.3	P	With NCA2, regulates proper expression of subunits 6 (Atp6p) and
11134_at	19525.7	P	Anti-silencing protein that causes depression of silent loci when over
11135_at	1743.8	P	similarity to Met30p and N.crassa sulfur controller-2
11136_at	7996.8	P	Component of Chaperonin Containing T-complex subunit seven
11137_at	1937.4	P	GATA zinc finger protein 3 homologous to Dal80 in structure and fun
11138_at	9853.3	P	weak similarity to ATPase Drs2p
11139_at	11572.5	P	strong similarity to hypothetical S. pombe protein
11140_at	438	P	similarity to hypothetical S. pombe protein
11141_at	207	A	Serine\/Threonine protein kinase, positively regulated by IME1
11142_at	151.5	A	similarity to hypothetical protein YKR029c
11143_at	1839	P	weak similarity to C.elegans hypothetical protein F45G2.c
11144_at	517.5	P	putative regulatory protein
11145_at	3203.3	P	mitochondrial elongation factor G-like protein
11146_at	3550.3	P	gamma-glutamylcysteine synthetase
11102_at	5087.6	P	similarity to hypothetical C. elegans protein C56A3.8
11103_at	2542.3	P	Involved in chitin biosynthesis and\/or its regulation
11104_at	3291.3	P	SIT4 associated protein, MW of 185 kDa
11105_at	20077.5	P	similarity to hypothetical C. elegans protein T15B7.2
11106_at	2019.6	P	ribosomal protein YmL49, mitochondrial
11107_at	1169.7	P	putative 163 kDa protein kinase
11108_at	6322.2	P	similarity to E.hirae NaH-antiporter NapA
11109_at	1414.9	P	outward-rectifier potassium channel
11110_at	1530.4	P	DNA helicase
11111_at	7769.1	P	weak similarity to human G protein-coupled receptor
11112_at	1612.4	P	Part of the DNA polymerase II complex, acts in a checkpoiint pathw
11113_at	212	A	shows homology to DNA binding domain of Gal4p, has a leucine zip
11114_at	1800.7	P	Ornithine carbamoyltransferase
11115_at	1360.5	P	tRNA ligase
11116_at	56	A	questionable ORF
11117_at	463.4	P	70 kD component of the Exocyst complex\; required for exocytosis
11118_at	1350.3	P	similarity to hypothetical protein YKR021w
11119_at	1830.8	P	similarity to hypothetical protein YKR019c
11120_at	3634.6	P	strong similarity to hypothetical protein YKR018c
11121_at	5659.3	P	54.8 kDa actin-related protein
11122_at	12155.6	P	May be required during cell division for faithful partitioning of the ER
11123_at	19919	P	Similar to plant PR-1 class of pathogen related proteins
11079_at	11391.2	P	Similar to plant PR-1 class of pathogen related proteins
11080_at	387.1	A	hypothetical protein
11081_at	9266.1	P	Establishes Silent omatin\; homolog of TOF2
11082_at	1253.6	A	questionable ORF
11083_at	2478.8	P	required for structural maintenance of chromosomes
11084_at	1333	P	DnaJ-like protein of the endoplasmic reticulum membrane
11085_at	1082.5	P	hypothetical protein
11086_at	895.5	P	Acetylglutamate Synthase
11087_at	1014.4	P	similarity to AMP deaminases
11088_at	5245.3	P	similarity to C.elegans hypothetical protein
11089_at	7118.6	P	strong similarity to human esterase D

11090_at	1047.3	A	questionable ORF
11091_at	913.6	A	hypothetical protein
11092_at	5088.3	P	weak similarity to DNA-directed DNA polymerase II chain C
11093_at	444	A	hypothetical protein
11094_at	9595.9	P	Mitochondrial ribosomal protein MRPL8 (YmL8) (E. coli L17)
11095_at	10338	P	similarity to S.pombe SPAC13G6.3 protein
11096_at	1085.6	P	82-kDa protein, with putative coiled-coil domain, has carboxy-termin
11097_at	1754.7	P	similarity to kynurenine aminotransferase and glutamine-phenylpyruv
11098_at	656.3	P	Homolog of human CLN3
11099_at	105.9	A	strong similarity to hypothetical protein YBR270c
11100_at	566.2	P	probable serine\/threonine kinase
11101_at	1371.9	P	Metalloregulatory protein involved in zinc-responsive transcriptional
11057_at	15427.8	P	similarity to R.fascians hypothetical protein 6
11058_at	5426.6	P	Translocase for the insertion of proteins into the mitochondrial inner
11059_at	534.8	P	Vacuolar protein similar to mouse gene H<beta>58
11060_at	13888.5	P	Glyceraldehyde-3-phosphate dehydrogenase 1
11061_g_	2311.5	P	Glyceraldehyde-3-phosphate dehydrogenase 1
11062_at	1277.5	P	hypothetical protein
11063_at	3966.4	P	DEAD-box family helicase required for mRNA export from nucleus
11064_at	5058.1	P	hypothetical protein
11065_at	8038.3	P	similarity to hypothetical protein YBR273c
11066_at	608.4	P	Regulator of Ty1 Transposition
11067_at	700.5	P	similarity to E.coli lipoate-protein ligase A
11068_at	162.7	A	strong similarity to succinate dehydrogenase flavoprotein
11069_at	3260.6	P	GTPase-activating protein for Ypt6
11070_at	128.9	A	similarity to hypothetical protein YKR015c
11071_at	9014.5	P	Putative microtubule-associated protein (MAP)
11072_at	7906.4	P	Nucleoskeletal protein found in nuclear pores and spindle pole body
11073_at	2533.8	P	similarity to human protein interacting with human nuclearpore protei
11074_at	93.4	A	strong similarity to hypothetical protein YJL037w
11075_at	234	A	strong similarity to hypothetical protein YJL038c
11076_at	643.2	P	weak similarity to Mvp1p
11077_at	2037.2	P	weak similarity to P.gingivalis PgaA and B.japonicum nitrogen fixatio
11078_at	18752.5	P	Homologue of mammalian BiP (GPR78) protein\; member of the HS
11034_at	2343.1	P	putative RNA helicase
11035_at	3205.7	P	questionable ORF
11036_at	1719.5	P	Geranylgeranyltransferase Type II alpha subunit (PGGTase-II, alph
11037_at	1549.1	P	spindle-assembly checkpoint protein
11038_at	2259.7	P	similarity to C.elegans hypothetical protein T05G5.8
11039_at	62.2	A	hypothetical protein
11040_at	1661.9	P	hypothetical protein
11041_at	22926.4	P	small subunit of ribonucleotide reductase
11042_at	3025.6	P	member of yeast Pol I core factor (CF) also composed of Rrn11p, R
11043_at	610.3	P	similar to Aps1p and mammalian small subunit (sigma-2 adaptin) of
11044_at	344.6	A	Nuclear gene encoding mitochondrial protein
11045_at	46	A	questionable ORF
11046_at	3500	P	weak similarity to S.pombe hypothetical protein SPAC23A1.16
11047_at	2301.1	P	similarity to P.falciparum glutamic acid-rich protein
11048_at	356.8	A	hypothetical protein
11049_g_	850.3	P	hypothetical protein
11050_at	2008.7	P	questionable ORF
11051_at	835	P	hypothetical protein

11052_at	3286.8	P	weak similarity to hypothetical protein YNL278w and YLR187w
11053_at	252.4	P	questionable ORF
11054_at	12487.8	P	Cytoplasmic chaperonin subunit gamma
11055_at	242.7	P	Checkpoint protein required for cell cycle arrest in response to loss o
11056_at	20663	P	weak similarity to regulatory protein PHO81
11010_at	4969.1	P	weak similarity to chicken hypothetical protein
11011_at	8442.4	P	weak similarity to C.elegans hypothetical protei ZK792.5
11012_at	2885.2	P	questionable ORF
11013_at	24281.8	P	Component of Chaperonin Containing T-complex subunit eight
11014_at	158.1	A	hypothetical protein
11015_at	1702.6	P	cyclin-related subunit of the kinase complex that phosphorylates the
11016_at	1234.9	P	adenylate cyclase
11017_at	1967.5	P	Multicopy suppressor of ypt6 null mutation
11018_at	2287	P	hypothetical protein
11019_at	28892.7	P	64-kDa, alpha subunit of oligosaccharyltransferase complex\; homol
11020_i_a	6708.5	P	Subunit of 20S proteasome
11021_f_a	10163.6	A	Subunit of 20S proteasome
11022_at	22981.9	P	Subunit of 20S proteasome
11023_at	23158.7	P	weak similarity to A.thaliana aminoacid permease AAP4
11024_at	4158.4	P	Protein component of the U3 small nucleolar ribonucleoprotein (sno
11025_at	2298.3	P	hypothetical protein
11026_at	25431.2	P	alpha-agglutinin
11027_at	2750.8	P	beta-adaptin, large subunit of the clathrin-associated protein comple
11028_at	2789.1	P	DNA-directed DNA polymerase delta, 55 KD subunit
11029_at	6130.6	P	Translation initiation factor eIF-2 alpha subunit
11030_at	277	A	similarity to S.pombe hypothetical protein
11031_s_a	31227.8	P	glyceraldehyde 3-phosphate dehydrogenase
11032_at	1936.9	P	ATP sulfurylase
11033_at	1070.5	P	Homologue of the SPC12 subunit of mammalian signal peptidase co
10988_at	717.5	P	hypothetical protein
10989_at	513.1	P	hypothetical protein
10990_at	6350.3	P	similarity to C.elegans B0491.1 protein
10991_at	5160.9	P	strong similarity to S.pombe hypothetical protein SPBC16C6.05
10992_at	5497.1	P	strong similarity to Sng1p
10993_at	32712.8	P	dihydroxyacid dehydratase
10994_at	6763.8	P	Peptidyl-prolyl cis\/trans isomerase (PPIase)
10995_at	1224.7	A	questionable ORF
10996_at	2135.4	P	peroxisomal acyl-CoA thioesterase
10997_at	195.6	A	questionable ORF
10998_at	315.6	A	meiotic recombination protein
10999_at	13	A	meiotic recombination protein
11000_at	1534.2	P	Sm-like protein
11001_at	208.6	A	hypothetical protein
11002_at	11326.8	P	weak similarity to C.elegans Z49131_E ZC373.5 protein
11003_at	8784.4	P	3-hydroxyanthranilic acid dioxygenase
11004_at	848.8	P	similarity to hypothetical protein YJL181w
11005_at	3533.1	P	Component of a complex guanine nucleotide exchange activity for th
11006_at	3613	P	a cyclophilin related to the mammalian CyP-40\; physically interacts
11007_at	2498.6	P	similarity to Drosophila DmX gene
11008_at	528.4	P	Required for assembly of active cytochrome c oxidase
11009_at	601.2	P	DNA-dependent ATPase, homologous to human Cockayne syndrom
10965_at	1401.6	P	similarity to human E6-associated protein

10966_at	226.8	A	questionable ORF
10967_at	1778	A	questionable ORF
10968_at	1113.4	P	hypothetical protein
10969_at	1727.9	P	putative transport protein involved in intracellular iron metabolism
10970_at	3377.6	P	hypothetical protein
10971_at	10797.5	P	Protein in nuclear pore complex\; may function in nuclear envelope ir
10972_at	101.3	A	third (55 kDa) subunit of DNA polymerase delta
10973_at	21706.9	P	weak similarity to putative transport protein YKR103w
10974_at	4723.5	P	Mitochondrial matrix protein involved in protein import\; subunit of Sc
10975_at	3576.7	P	weak similarity to Xenopus vimentin 4
10976_at	2033.7	P	anaerobically expressed form of translation initiation factor eIF-5A
10977_at	24745	P	iso-1-cytochrome c
10978_at	2105.8	P	Associated with ferric reductase
10979_at	367.8	A	Interacts with Syf1p: Isy1p was identified through a two-hybrid scree
10980_at	3684.9	P	osmotic growth protein
10981_at	6337.4	P	Nucleotide excision repair protein involved in G(sub)2 repair of inacti
10982_at	467.7	A	hypothetical protein
10983_at	2820.3	P	similarity to hypothetical protein YML047c
10984_at	609.4	P	Protein required for growth at high temperature
10985_at	1135.4	P	hypothetical protein
10986_at	3023.3	P	thymidylate kinase
10987_at	7259.5	P	Clathrin-associated protein, small subunit
10943_at	3121.1	P	Putative serine\/threonine protein kinase that enhances spermine up
10944_at	304.4	A	basic helix-loop-helix protein
10945_at	146.7	A	similarity to Mnn4p
10946_at	1211.4	P	52-kDa amidase specific for N-terminal asparagine and glutamine
10947_at	4222.9	P	A12.2 subunit of RNA polymerase I
10948_at	24921.4	P	subunit of chaperonin subunit epsilon
10949_at	22022.1	P	actin-related gene
10950_at	2415.1	P	phosphatidylinositol kinase homolog
10951_at	1504.4	P	Essential protein of unknown function
10952_at	2503.8	P	Subunit 2 of Replication Factor C\; homologous to human RFC 37 k
10953_at	12661.5	P	controls 6-N-hydroxylaminopurine sensitivity and mutagenesis
10954_at	22676.8	P	similarity to C.elegans hypothetical protein C14A4.1
10955_at	44.2	A	questionable ORF
10956_at	3796.1	P	strong similarity to C.elegans hypothetical protein and similarity to YL
10957_at	6425	P	Methylene-fatty-acyl-phospholipid synthase (unsaturated phospholipi
10958_at	3393.6	P	Protein interacts with Gsp1p
10959_at	3422.3	P	putative mannosyltransferase
10960_at	10151.1	P	Component of 10 nm filaments of mother-bud neck
10961_at	15272.8	P	Mir1p has been purified as a mitochondrial import receptor (p32) wh
10962_at	3759	P	similarity to mammalian indoleamine 2,3-dioxygenase
10963_at	5277.5	P	questionable ORF
10964_at	6404.8	P	hypothetical protein
10920_at	316.6	A	questionable ORF
10921_at	770.8	P	hypothetical protein
10922_at	811.2	P	hypothetical protein
10923_at	2048.8	P	weak similarity to S.pombe hypothetical protein SPAC1B3.08
10924_at	14587.1	P	hypothetical protein
10925_at	896.1	P	gamma subunit of G protein coupled to mating factor receptors
10926_at	929.1	P	questionable ORF
10927_at	3946.2	P	weak similarity to S.pombe hypothetical protein SPBC14C8.18c

10928_at	1209.9	P	hypothetical protein
10929_at	3819.6	P	F box protein with several leucine rich repeats
10930_at	4602.6	P	Benomyl dependent tubulin mutant
10931_at	2824.3	P	Component of a pre-mRNA polyadenylation factor that interacts with
10932_at	2347.7	P	meiotic gene expression\; meiosis inducing protein
10933_at	16582.2	P	Ribosomal protein L43B
10934_at	423.3	A	protein related to mitochondrial carriers
10935_at	820.7	P	similarity to Corynebacterium 2,5-diketo-D-gluconic acid reductase
10936_at	1012.9	P	weak similarity to Caj1p
10937_at	1286.3	P	weak similarity to Bacillus licheniformis esterase
10938_at	643.2	P	ubiquitin hydrolase
10939_at	2167.2	P	weak similarity to Bud3p
10940_at	3615.4	P	weak similarity to superoxide dismutases
10941_at	2346.2	P	hypothetical protein
10942_at	23537.1	P	CTP synthase
10897_at	21856.2	P	Cu, Zn superoxide dismutase
10898_at	27294.4	P	strong similarity to human adenosine kinase
10899_at	930	P	ExtraCellular Mutant
10900_at	3968.1	P	weak similarity to acylglycerol lipase
10901_at	445.1	A	similarity to hypothetical protein YIL014c-a
10902_at	11327.7	P	carbamyl phosphate synthetase
10903_at	1208.8	P	similarity to human myotubularin
10904_at	2990.4	P	weak similarity to E.coli colanic acid biosynthesis positive regulator R
10905_at	1890.3	P	involved in nuclear function
10906_at	5551.8	P	similarity to bacterial, chloroplast and mitochondrial ribosomal protei
10907_at	699.7	A	questionable ORF
10908_at	3697.7	A	similarity to hypothetical protein YBL043w
10909_at	9789.8	P	similarity to hypothetical protein YPR114w
10910_at	16050	P	zinc metallo-protease that catalyzes the first step of N-terminal proce
10911_at	3637.5	P	weak similarity to Helicobacter pylori UreD protein
10912_at	681.2	P	similarity to human retinoblastoma binding protein 2
10913_at	322.3	A	hypothetical protein
10914_at	15972	P	F(1)F(0)-ATPase complex beta subunit, mitochondrial
10915_at	1285.6	P	CCR4 associated factor
10916_at	22852.9	P	Ribosomal protein S5 (S2) (rp14) (YS8)
10917_at	4422.2	P	weak similarity to Staphylococcus multidrug resistance protein
10918_at	3640.1	P	similarity to human KIAA0171 protein
10919_at	2860.8	P	similarity to human prostate-specific membrane antigen and transfe
10875_at	3862.8	P	similarity to regulatory protein Ard1p
10876_at	76.3	A	questionable ORF
10877_at	3712.3	P	weak similarity to hypothetical protein YNL024c
10878_at	2459.6	P	similarity to O-succinylhomoserine (thiol)-lyase
10879_at	1940.3	P	specific alpha-mannosidase
10880_at	3827.1	P	Putative Upf1p interacting protein
10881_at	10659.2	P	strong similarity to hypothetical protein YDR399w
10882_at	1041.9	P	similarity to paramyosin, myosin
10883_at	134.2	A	Required for maintenance of chromosomes and minichromosomes
10884_at	1443.8	P	weak similarity to human 3 ,5 -cyclic-GMP phosphodiesterase
10885_at	8235.2	P	ExtraCellular Mutant
10886_at	1219.6	P	similarity to C.elegans hypothetical protein T08A11.1
10887_at	26534.9	P	Homoserine dehydrogenase (L-homoserine:NADP oxidoreductase)
10888_at	1876.7	P	involved in cell-cycle regulation of histone transcription

10889_at	1003.7	P	hypothetical protein
10890_at	1139.2	P	similarity to thiamin pyrophosphokinase
10891_at	22566.3	P	dolichyl phosphate-D-mannose:protein O-D-mannosyltransferase
10892_at	2478.5	P	involved in mitochondrial genome maintenance
10893_s_a	28983.3	P	Ribosomal protein S4A (YS6) (rp5) (S7A)
10894_at	592.3	A	questionable ORF
10895_at	5917.3	P	heat shock transcription factor homolog
10896_at	12736.8	P	Branched-Chain Amino Acid Transaminase
10851_at	939.9	P	similarity to 2-nitropropane dioxygenase
10852_at	1098.9	A	Protein induced during anaerobic growth
10853_at	7138.9	P	similarity to mucin proteins, YKL224c, Sta1p
10854_at	1200.6	P	allantoate permease
10855_at	830.8	A	Endo-polygalacturonase
10856_at	241.5	A	hypothetical protein
10857_at	2330.5	P	Hypothetical aryl-alcohol dehydrogenase (AAD)
10858_s_a	1648.9	P	Thiamine biosynthetic enzyme
10859_at	28.4	A	hypothetical protein
10860_s_a	857.7	P	hexose transporter
10861_s_a	1682.9	P	sorbitol-induced sorbitol dehydrogenase
10862_s_a	139.9	A	strong similarity to Mal31p
10863_i_at	3224.2	P	identified by SAGE
10864_r_a	1832.7	P	identified by SAGE
10865_at	1689.7	P	C-terminal part of YJR030c
10866_at	6160.6	P	similarity to human DDP gene, hypothetical protein of S.pombe (YA
10867_s_a	3014.5	P	Co-assembles with Bud3p at bud sites
10868_at	9407	P	non-annotated SAGE orf Found reverse in NC_001142 between 159
10869_at	1689.6	P	non-annotated SAGE orf Found reverse in NC_001142 between 181
10870_i_at	58.9	A	non-annotated SAGE orf Found reverse in NC_001142 between 227
10871_s_a	1996.1	P	non-annotated SAGE orf Found reverse in NC_001142 between 227
10872_at	3737.4	A	non-annotated SAGE orf Found reverse in NC_001142 between 227
10873_at	454.6	A	non-annotated SAGE orf Found reverse in NC_001142 between 471
10874_at	8047.5	P	non-annotated SAGE orf Found forward in NC_001142 between 316
10828_at	218.2	A	non-annotated SAGE orf Found forward in NC_001142 between 444
10829_at	552.9	P	non-annotated SAGE orf Found forward in NC_001142 between 445
10830_at	311.8	A	non-annotated SAGE orf Found reverse in NC_001142 between 451
10831_s_a	2467.6	M	non-annotated SAGE orf Found reverse in NC_001142 between 731
10832_s_a	670.2	P	non-annotated SAGE orf Found reverse in NC_001142 between 740
10833_at	892.5	P	non-annotated SAGE orf Found forward in NC_001142 between 106
10834_at	648	P	non-annotated SAGE orf Found reverse in NC_001142 between 121
10835_at	836.5	A	non-annotated SAGE orf Found reverse in NC_001142 between 187
10836_at	21896.8	P	non-annotated SAGE orf Found reverse in NC_001142 between 289
10837_at	522.5	P	non-annotated SAGE orf Found reverse in NC_001142 between 312
10838_at	28379.7	P	non-annotated SAGE orf Found reverse in NC_001142 between 410
10839_at	552	M	non-annotated SAGE orf Found reverse in NC_001142 between 518
10840_at	538.4	A	non-annotated SAGE orf Found forward in NC_001142 between 548
10841_at	852.4	A	non-annotated SAGE orf Found forward in NC_001142 between 622
10842_at	4002.5	P	non-annotated SAGE orf Found forward in NC_001142 between 637
10843_at	10.5	A	non-annotated SAGE orf Found reverse in NC_001142 between 136
10844_at	412.9	A	non-annotated SAGE orf Found forward in NC_001142 between 900
10845_at	73.2	A	non-annotated SAGE orf Found reverse in NC_001142 between 116
10846_at	651.6	A	non-annotated SAGE orf Found forward in NC_001142 between 142
10847_at	2687.1	P	non-annotated SAGE orf Found forward in NC_001142 between 180

10848_at	3269.7	P	non-annotated SAGE orf Found forward in NC_001142 between 236
10849_at	1109.4	A	non-annotated SAGE orf Found forward in NC_001142 between 337
10850_at	408.8	A	non-annotated SAGE orf Found reverse in NC_001142 between 416
10806_at	19.1	A	non-annotated SAGE orf Found reverse in NC_001142 between 424
10807_at	1523.3	A	non-annotated SAGE orf Found reverse in NC_001142 between 448
10808_at	51.3	A	non-annotated SAGE orf Found forward in NC_001142 between 471
10809_g_a	576.6	M	non-annotated SAGE orf Found forward in NC_001142 between 471
10810_i_at	279	P	non-annotated SAGE orf Found forward in NC_001142 between 471
10811_at	55.5	A	non-annotated SAGE orf Found reverse in NC_001142 between 626
10812_s_a	423.9	P	non-annotated SAGE orf Found reverse in NC_001142 between 731
10813_s_a	369.1	A	non-annotated SAGE orf Found reverse in NC_001142 between 734
10814_s_a	2117.9	P	non-annotated SAGE orf Found forward in NC_001142 between 741
10815_at	731.4	P	non-annotated SAGE orf Found reverse in NC_001142 between 104
10816_at	6.8	A	non-annotated SAGE orf Found reverse in NC_001142 between 172
10817_at	4060.9	P	non-annotated SAGE orf Found forward in NC_001142 between 283
10818_at	1178.1	P	non-annotated SAGE orf Found forward in NC_001142 between 322
10819_at	2164.9	P	non-annotated SAGE orf Found reverse in NC_001142 between 396
10820_at	5526.1	P	non-annotated SAGE orf Found forward in NC_001142 between 447
10821_g_a	584.3	P	non-annotated SAGE orf Found forward in NC_001142 between 447
10822_at	101	A	non-annotated SAGE orf Found forward in NC_001142 between 447
10823_at	1509.4	P	non-annotated SAGE orf Found forward in NC_001142 between 549
10824_at	715.3	A	non-annotated SAGE orf Found forward in NC_001142 between 578
10825_at	1369	P	non-annotated SAGE orf Found reverse in NC_001142 between 637
10826_at	111.5	A	non-annotated SAGE orf Found reverse in NC_001142 between 727
10827_s_a	299.3	A	non-annotated SAGE orf Found reverse in NC_001142 between 737
10782_at	3786.7	P	small nuclear RNA128
10783_at	35.8	A	small nuclear RNA190
10784_at	1115.8	P	small nuclear RNA37
10785_at	705	P	snRNA
10786_i_at	3.3	A	Centromere
10787_at	937.2	P	small nuclear RNA3
10788_at	282.9	A	ARS121 Found forward in NC_001142 between 683650 and 683699
10789_f_at	2802	P	strong similarity to members of the Srp1p/Tip1p family
10790_at	686.1	A	weak similarity to transcription factors, similarity to finger proteins YC
10791_at	143.8	A	weak similarity to human X-linked PEST-containing transporter
10792_at	656.5	A	Ferric reductase, similar to Fre1p
10793_at	1556.5	P	Protein with similarity to subtelomerically-encoded proteins such as
10794_at	1604.8	A	threonine dehydratase
10795_at	79.2	A	carboxylic acid transporter protein homolog
10796_at	33888.9	P	dihydroorotate dehydrogenase
10797_at	3498.3	P	similarity to P. aeruginosa hyuA and hyuB
10798_at	2643.1	P	weak similarity to mouse transcriptional coactivator ALY
10799_at	8005.3	P	phospholipase A2-activating protein
10800_at	21623.5	P	integral membrane protein localizing to the ER and Golgi
10801_at	4408.6	P	anthranilate synthase Component II and indole-3-phosphate (multifur
10802_at	22266.4	P	ubiquitin activating enzyme, similar to Uba2p
10803_at	311.4	P	ABC transporter, glycoprotein, component of a-factor secretory path
10804_at	1192.6	P	Subunit of complex involved in processing of the 3 end of cytochrom
10805_at	2780	P	hypothetical protein
10760_at	1870.6	P	hypothetical protein
10761_at	5248.1	P	nuclear protein LOS1
10762_at	7750.1	P	probable purine nucleotide-binding protein

10763_at	2647.8	P	phosphatidylinositol kinase homolg
10764_at	798.6	A	questionable ORF
10765_at	3124.7	P	member of the AAA-protein family
10766_at	15254.7	P	v-SNARE
10767_at	8550.3	P	similarity to rabbit histidine-rich calcium-binding protein
10768_at	2125.1	P	mitochondrial threonine-tRNA synthetase
10769_at	3179.7	P	Interacts with and may be a positive regulator of GLC7 which encode
10770_at	14185.7	P	acyl carrier protein
10771_at	13577.8	P	diphthamide synthesis protein
10772_at	3439.1	P	Type 2B protein phosphatase\; regulatory B subunit of calcineurin
10773_at	9388.9	P	Type 2B protein phosphatase\; regulatory B subunit of calcineurin
10774_at	2355.9	P	The homologue in Aspergillus nidulans, hymA, is involved in develop
10775_at	226.3	A	peroxisomal ABC transporter 2
10776_at	1086.1	P	strong similarity to hypothetical protein YLR413w
10777_at	1921.1	P	mRNA transport regulator
10778_at	227	A	probable purine nucleotide-binding protein
10779_at	5638.9	P	Ornithine decarboxylase
10780_at	2254.2	P	hypothetical protein
10781_at	13834.4	P	pentafunctional enzyme consisting of the following domains : acetyl
10737_at	23611.5	P	ribose-phosphate pyrophosphokinase
10738_i_at	0	A	Ribosomal protein L17A (L20A) (YL17)
10739_f_at	25972.4	P	Ribosomal protein L17A (L20A) (YL17)
10740_at	6816.3	P	kinesin-like protein
10741_at	12871.2	P	a factor recptor
10742_at	1074.4	A	questionable ORF
10743_at	2817.1	P	hypothetical protein
10744_at	14055.1	P	weak similarity to E.coli hypothetical protein
10745_at	1650.4	P	probable transport protein
10746_at	6568.3	P	U5 snRNP-specific protein related to EF-2
10747_at	6989.4	P	Nucleolar protein
10748_at	2289.2	M	probable serine\/threonine-specific protein kinase (EC 2.7.1.-)
10749_at	3900.8	P	mitochondrial ribosomal protein L14
10750_at	1211.3	P	questionable ORF
10751_at	854.4	P	probable serine\/threonine-specific protein kinase (EC 2.7.1.-)
10752_at	2478.2	P	16 kDa mitochondrial ribosomal large subunit protein
10753_at	3028.1	P	cAMP-dependent protein kinase catalytic subunit
10754_at	19224.6	P	Morphogenesis Checkpoint Dependent
10755_at	28216.1	P	Protein containing tandem internal repeats
10756_at	3603	P	Protein containing tandem internal repeats
10757_at	530	P	hypothetical protein
10758_at	408.1	A	probable serine\/threonine-specific protein kinase (EC 2.7.1.-)
10759_at	6306.8	P	similarity to hypothetical S. pombe protein
10714_at	823.7	P	hypothetical protein
10715_at	1280.5	A	hypothetical protein
10716_at	13374.6	P	aminopeptidase yscII
10717_at	17232.9	P	40S ribosomal protein S27A (rp61) (YS20)
10718_at	2296.2	P	hypothetical protein
10719_at	1845.8	P	signal recognition particle receptor, beta chain
10720_at	1168.4	P	questionable ORF
10721_at	33632.2	P	Phosphoglycerate mutase
10722_at	2022.5	P	similarity to C.elegans hypothetical protein R107.2
10723_at	6078.1	P	NADH-cytochrome b5 reductase

10724_at	1637.7	P	debranching enzyme
10725_at	11782.8	P	flavoprotein subunit of succinate dehydrogenase
10726_at	1234.1	A	questionable ORF
10727_at	18716.1	P	strong similarity to S.pombe hypothetical protein C3H1.09C
10728_at	18256.6	P	putative ATPase, 26S protease subunit component
10729_at	2144.4	P	Subunit of RNA polymerase III
10730_at	5964.1	P	low temperature viability protein
10731_at	2857.3	M	mitochondrial ribosomal protein
10732_at	12808.1	P	succinate dehydrogenase cytochrome b
10733_at	2575.8	P	triglyceride lipase-cholesterol esterase
10734_at	1363.7	P	alpha subunit of the kinase which phosphorylates the RNA polymeras
10735_at	1930.4	P	15.5 kDa mitochondrial ribosomal protein YmL31
10736_at	799.5	P	hypothetical protein
10692_at	1019.5	P	questionable ORF
10693_at	3440.3	P	Beta-adaptin, large subunit of the clathrin-associated protein (AP-1)
10694_at	794.6	P	probable neutral zinc metalloproteinase
10695_at	349.6	A	probable purine nucleotide-binding protein
10696_at	1588.4	P	probable folyl-polyglutamate synthetase
10697_at	459	A	questionable ORF
10698_at	5760.5	P	Required for mother cell-specific HO expression
10699_at	1346.9	P	myosin I
10700_at	6163.6	P	Phospo-mutase homolog
10701_at	9657	P	phosphoglucomutase, minor isoform
10702_at	5768.9	P	76.5 kDa Serine\/threonine protein kinase with similarity to protein ki
10703_at	4893.6	P	DNA-independent RNA Polymerase I transcription factor
10704_at	118.2	A	suppressor of SHR3\; confers leflunomide resistance when overexpr
10705_g_a	41.9	A	suppressor of SHR3\; confers leflunomide resistance when overexpr
10706_at	855.3	P	questionable ORF
10707_at	5362.9	P	component of signal recognition particle
10708_at	1403.6	P	strong similarity to YMR102c
10709_at	17083.8	P	similarity to mitochondrial uncoupling proteins (MCF)
10710_at	2359.5	P	25.2 kDa protein involved in assembly of vacuolar H(+) ATPase
10711_at	327.4	A	questionable ORF
10712_at	26439.4	P	Hsp90 (Ninety) Associated Co-chaperone
10713_at	2964.1	P	probable serine\/threonine-specific protein kinase (EC 2.7.1.-)
10669_at	255.7	A	questionable ORF
10670_at	7863.2	P	major apurinic\/apyrimidinic endonuclease\/3 -repair diesterase
10671_at	5766.1	P	42 kDa 5 to 3 exonuclease required for Okazaki fragment processir
10672_at	2404.7	P	transcriptional activator and ARS1 binding protein
10673_at	1532.8	P	questionable ORF
10674_at	8859.7	P	Protein involved in resistance to K. lactis killer toxin
10675_at	6091	P	transcriptional activator protein of CYC1 (component of HAP2\/HAP3
10676_at	53.8	A	DNA replication and checkpoint protein 1
10677_at	7.5	A	weak similarity to S.antibioticus probable oxidoreductase
10678_at	5514.4	P	aspartate aminotransferase, mitochondrial
10679_at	522.9	A	similarity to YMR086w
10680_at	13045.9	P	Glutamine_fructose-6-phosphate amidotransferase (glucoseamine-6
10681_at	7149.1	P	vacuolar aminopeptidase ysc1
10682_at	34	A	hypothetical protein
10683_at	462.5	P	Putative protein kinase homologous to S. pombe cdr1\/nim1
10684_at	17155	P	similarity to C.elegans hypothetical protein
10685_at	745.4	P	similarity to C.elegans hypothetical proteins C18G6.06 and C16C10.

10686_at	3423.6	P	hypothetical protein
10687_at	298.8	A	hypothetical protein
10688_at	17246.5	P	cell wall mannoprotein
10689_at	9130.6	P	cell wall mannoprotein
10690_at	183.7	A	similarity to C.elegans hypothetical proteins
10691_at	4573.3	P	weak similarity to E.coli hypothetical protein
10646_at	496.3	A	MBR1 protein precursor
10647_at	815.5	P	GTPase-activating protein (GAP) for Rsr1p\/Bud1p
10648_at	925.8	P	strong similarity to Sec14p
10649_at	863.4	P	hypothetical protein
10650_at	3125.7	P	Centromere protein required for normal chromosome segregation an
10651_at	3447.8	P	similarity to C.tropicalis hal3 protein, to C-term. of Sis2p and to hypo
10652_at	6902.5	P	cytochrome c1 heme lyase
10653_at	1144.6	A	hypothetical protein
10654_at	18161.8	P	mitochondrial malate dehydrogenase
10655_at	3903.6	P	strong similarity to S.pombe hypothetical protein SPAC29B12
10656_at	6339.1	P	weak similarity to C.elegans hypothetical protein
10657_at	2611.9	P	questionable ORF
10658_at	8203.7	P	Translation elongation factor EF-1gamma
10659_at	30338.5	P	Translation elongation factor EF-1gamma
10660_at	12565.4	P	Vacuolar H-ATPas hydrophilic subunit C of V1 sector
10661_at	1159.5	P	kinesin heavy chain homolog, but is not believed to act as a kinesin,
10662_at	5999.8	P	probable ATP-dependent RNA helicase
10663_at	12020.7	P	hypothetical protein
10664_at	2220.8	P	questionable ORF
10665_g_a	1964.3	P	questionable ORF
10666_at	1925.8	P	hypothetical protein
10667_at	2954.3	P	involved in early pre-mRNA splicing
10668_at	2565	P	novel member of the Hsp70 family of molecular chaperones that loca
10624_at	703.9	P	Binds Sin3p in two-hybrid assay
10625_at	310.8	A	weak similarity to A.parasiticus nor-1 protein
10626_at	408.2	P	similarity to B.subtilis transcriptional regulatory protein
10627_at	3374.6	P	strong similarity to hypothetical E.coli protein b1832
10628_at	9308.6	P	Nuclear pore complex protein homologous to Nup116p
10629_at	7741.3	P	Nucleoside diphosphate kinase
10630_at	3101.6	P	hypothetical protein
10631_at	4977.1	P	Yeast endoplasmic reticulum 25 kDa transmembrane protein
10632_at	9691.6	P	overexpression overcomes manganese toxicity
10633_at	2227.6	P	weak similarity to mammalian microtubule-associated protein MAP 1
10634_at	7193	P	zinc finger protein
10635_at	564.7	P	hypothetical protein
10636_at	20044.7	P	aldolase
10637_at	7078.1	P	similarity to C.elegans hypothetical protein
10638_at	12941.2	P	Transcription factor IIA, small chain
10639_at	3234.3	P	100-kDa protein (predicted molecular weight is 120 kDa) with two leu
10640_at	28108.1	P	strong similarity to human IgE-dependent histamine-releasing factor
10641_at	447.3	A	probable acetoacetyl-CoA reductase
10642_at	24828.9	P	similarity to glutenin, high molecular weight chain proteins and Snf5p
10643_at	21237	P	similarity to C.elegans hypothetical protein T09A5.7 (12.5 kD)
10644_at	2906.4	M	questionable ORF
10645_at	2096.6	P	hypothetical protein
10601_at	8168.5	P	hypothetical protein

10602_at	429.4	P	similarity to YMR031c
10603_at	1329.2	P	high similarity to histone H3 and to human centromere protein CENP
10604_at	863	P	protein kinase
10605_at	2218.9	P	hypothetical protein
10606_at	7933.2	P	strong similarity to YMR238w
10607_at	1831.1	P	p58 polypeptide of DNA primase
10608_at	6327.4	P	hypothetical protein
10609_at	13835.1	P	putative transcription factor
10610_at	1028.1	P	component of the spindle pole body
10611_at	3167.4	P	endosomal Vps protein complex subunit
10612_at	3846.1	P	NifU-like protein B
10613_at	11819.2	P	Putative membrane protein
10614_at	3164.3	P	transcriptional repressor and activator
10615_at	1710.7	A	weak similarity to C.elegans ubc-2 protein
10616_at	27.8	A	questionable ORF
10617_at	20648.6	P	Uridinephosphoglucose pyrophosphorylase
10618_at	2952.4	P	weak similarity to YOL013c
10619_at	1624.3	P	hypothetical protein
10620_at	15232.2	P	intrastrand crosslink recognition protein
10621_at	3745	P	hypothetical protein
10622_at	587.2	A	questionable ORF
10623_at	23838.6	P	mitochondrial malic enzyme
10579_at	3944.7	P	Large subunit of transcription factor tfIIE
10580_at	2309.7	P	similarity to E.coli molybdopterin-converting factor chlN
10581_at	1244.7	P	strong similarity to glutathione peroxidase
10582_at	10035.2	P	76-kDa subunit of Pab1p-dependent poly(A) ribonuclease (PAN)
10583_at	9182.7	P	uridine-monophosphate kinase (uridylate kinase)
10584_at	1134.9	P	weak similarity to human cylicin II
10585_at	1686.1	P	putative metal-binding nucleic acid-binding protein, interacts with Cd
10586_at	5901.8	P	contains four beta-transducin repeats
10587_at	3425.1	P	suppressor protein
10588_at	3104	P	CAAX farnesyltransferase alpha subunit
10589_at	5876.6	P	similarity to C.elegans hypothetical protein
10590_at	1648.1	P	DNA helicase A
10591_at	4946.5	P	ATP synthase d subunit
10592_at	2901.4	P	zinc-finger transcription factor of the Zn(2)-Cys(6) binuclear cluster d
10593_at	12170.3	P	hypothetical protein
10594_at	4981.2	P	Arp Complex Subunit
10595_at	1625.6	P	Splicing component that associates with the yeast U1 small nuclear r
10596_at	1116.2	P	cruciform cutting endonuclease
10597_at	4480	P	Ubiquitin Fusion Degradation
10598_at	8787.4	P	mRNA turnover 4
10599_at	7807	P	strong similarity to Lag1p
10600_at	2395	P	alpha subunit of capping protein
10555_at	1570.3	P	required for transport of proteins between an early and a later golgi c
10556_i_at	36983	P	Ribosomal protein L14A
10557_f_at	20961.6	P	Ribosomal protein L14A
10558_s_a	31673.2	P	Ribosomal protein L14A
10559_at	2093.4	P	weak similarity to YKR029c and D.melanogaster transcription elonga
10560_at	18146.8	P	aureobasidin-resistance protein
10561_at	7433.8	P	Mitochondrial ribosomal protein MRP17
10562_at	3402.4	P	similarity to hypothetical protein YKL041w

10563_at	1897.5	P	adenylylsulfate kinase
10564_at	4510.1	P	putative GTP-binding protein\; similar to mammalian Mx proteins
10565_at	3377.9	P	poly(A) polymerase
10566_at	2045.9	P	similarity to Kes1p, Hes1p and Osh1p
10567_at	2071.1	P	ExtraCellular Mutant
10568_at	756.1	P	hypothetical protein
10569_at	6320.6	P	mitochondrial ribosomal protein YmL13
10570_at	2513.6	P	weak similarity to Streptococcus protein M5 precursor
10571_at	2067.4	P	Member of RSC complex.
10572_at	423.9	A	peroxisomal multifunctional beta-oxidation protein
10573_at	1538.3	A	topoisomerase I interacting factor 2
10574_at	1632.7	P	hypothetical protein
10575_at	34.6	A	questionable ORF
10576_at	33313.3	P	Similar to plant PR-1 class of pathogen related proteins
10577_at	6276.8	P	probable purine nucleotide-binding protein
10578_at	6.8	A	similarity to hypothetical protein YJL043w
10533_at	1384.3	P	weak similarity to mysoin heavy chain proteins
10534_at	481.3	A	similarity to human hypothetical KIAA0161 protein
10535_at	6238.3	P	strong similarity to hypothetical protein YJL082w
10536_at	330.5	A	Increased rDNA silencing
10537_at	222.5	A	hypothetical protein
10538_at	886.2	P	strong similarity to hypothetical protein YJL084c
10539_at	639.4	P	hypothetical protein
10540_at	888.7	P	similarity to S.pombe hypothetical protein SPAC23C4
10541_at	6967	P	putative RNA helicase
10542_at	2403.1	P	hypothetical protein
10543_at	5457.2	P	translation initiation factor eIF2B, 34 KD, alpha subunit\; negative re
10544_at	3093	P	strong similarity to Chs6p
10545_at	9879.3	P	Type 2A-related protein phosphatase
10546_at	1005.9	P	similarity to YJL105w and Lentinula MFBA protein
10547_at	5874.1	P	weak similarity to NADH dehydrogenases
10548_at	2586	P	Phospholipase D
10549_at	85.2	A	hypothetical protein
10550_at	307.8	A	questionable ORF
10551_at	26.4	A	negative regulator of multiple nitrogen catabolic genes
10552_at	1038.9	P	RAD52 Inhibitor (Fifty Two Inhibitor)
10553_at	3022.2	P	CCR4 associated factor
10554_at	1512.4	P	component of spindle pole
10510_at	3837.1	P	probable calcium-binding protein
10511_at	1298.1	P	general amino acid permease
10512_at	1353.9	P	questionable ORF
10513_at	249.6	A	hypothetical protein
10514_at	23858	P	YOUTH, involved in determining yeast longevity
10515_at	15079.4	P	weak similarity to phosphoglycerate mutase
10516_at	1162	P	hypothetical protein
10517_at	689.6	A	hypothetical protein
10518_at	28962.4	P	hypothetical protein
10519_at	3512.2	P	questionable ORF
10520_at	11504.4	P	nucleosome assembly protein I
10521_at	4754.6	P	hypothetical protein
10522_at	2350.9	P	membrane protein\; low affinity potassium transport
10523_at	893.8	P	similarity to C.elegans hypothetical protein

10524_at	1545.2	P	mitochondrial carrier protein, highly homologous to Mrs3p
10525_at	892.8	P	DHS-1-P phosphatase
10526_at	3366	P	heavy chain of cytoplasmic dynein
10527_at	5195	P	ras homolog--GTP binding protein
10528_at	4040.7	P	endo-exonuclease yNucR
10529_i_at	18932.1	P	Ribosomal protein S21A (S26A) (YS25)
10530_at	290.8	P	self-glucosylating initiator of glycogen synthesis\; similar to mammali
10531_at	1765.6	P	hypothetical protein
10532_at	1544.2	P	putative mannosyltransferase\; type 2 membrane protein
10487_at	1169.1	P	Small subunit of TFIIE transcription factor
10488_at	3632.2	P	May regulate expression of genes involved in bud formation and mor
10489_at	1611.4	P	weak similarity to transcription factors
10490_at	8982.3	P	hypothetical protein
10491_at	13796.2	P	Cytochrome-c peroxidase
10492_at	6858	P	strong similarity to Sct1p
10493_at	17860	P	Hydrophilic protein that acts in conjunction with SNARE proteins in ta
10494_at	5117.1	P	siroheme synthase
10495_at	3733.3	P	strong similarity to S. pombe phosphatidyl synthase
10496_at	5076.1	P	weak similarity to C.elegans hypothetical protein
10497_at	7329.8	P	sit4 suppressor
10498_at	1658.9	A	hypothetical protein
10499_at	2109	P	strong similarity to hypothetical S. pombe protein
10500_at	8154.6	P	weak similarity to negative regulator Reg1p
10501_at	1856.4	P	ExtraCellular Mutant
10502_at	3406.9	P	hypothetical protein
10503_at	541.5	P	similarity to Vps5p
10504_at	1963.2	P	similarity to S.pombe hypothetical protein SPAC1D4.10
10505_at	12086.7	P	NAD-dependent 5,10-methylenetetrahydrafolate dehydrogenase
10506_at	17749.8	P	hypothetical protein
10507_at	5720.4	P	Nuclear pore complex protein involved in poly(A)+ RNA transport, nu
10508_at	860.4	P	weak similarity to S.japonicum paramyosin
10509_at	4680.9	P	Protein related to translation elongation factor EF-1alpha and to Suf1
10464_at	3783.1	P	22.3 kDa mitochondrial ribosomal large subunit protein YmL20\; hom
10465_at	4703.6	P	putative ATP-binding protein
10466_at	5448.7	P	similarity to hypothetical Myxococcus xanthus protein
10467_at	2309.3	P	weak similarity to b.subtilis spore germination protein II
10468_at	2126.1	P	strong similarity to YOR081c
10469_at	1991.6	P	similarity to chicken Lim protein kinase and Islet proteins
10470_at	2586	P	Suppressor of rad53 lethality
10471_at	29909.6	P	nucleolar protein that is immunologically and structurally related to ra
10472_at	19611.1	P	Peptide transporter
10473_i_at	26000.7	P	Ribosomal protein L40B
10474_s_a	13010.4	P	Ribosomal protein L40B
10475_at	1733.3	P	myosin-like protein
10476_at	2922.2	P	similarity to mitochondrial aldehyde dehydrogenase Ald1p
10477_g_a	633.5	P	similarity to mitochondrial aldehyde dehydrogenase Ald1p
10478_at	783.7	P	phosphoenolpyruvate carboxylkinase
10479_at	2027.9	P	Ubiquitin-specific protease
10480_at	1074.5	P	Transcription factor regulating basal and induced activity of histidine
10481_at	2290.1	P	cause growth inhibition when overexpressed
10482_at	474.5	P	repressor of silent mating loci
10483_at	1092	P	Protein with similarity to flocculation protein Flo1p

10484_at	337.5	A	similarity to multidrug resistance proteins
10485_at	576.2	P	similarity to multidrug resistance proteins
10486_s_a	183.1	A	strong similarity to Sge1p and hypothetical protein YCL069w
10442_s_a	577.8	P	regulates the mannosylphosphorylation
10443_at	32.1	A	hypothetical protein identified by SAGE
10444_at	1788.4	P	hypothetical protein
10445_s_a	10385.9	P	regulates the mannosylphosphorylation
10446_s_a	3375	P	Protein of unknown function
10447_s_a	3325.4	P	probable serine\/threonine-specific protein kinase (EC 2.7.1.-)
10448_s_a	3221.5	P	strong similarity to holacid-halidohydrolase
10449_at	38.6	A	non-annotated SAGE orf Found forward in NC_001143 between 916
10450_at	160.7	A	non-annotated SAGE orf Found forward in NC_001143 between 940
10451_at	279.2	A	non-annotated SAGE orf Found forward in NC_001143 between 146
10452_at	1434.5	P	non-annotated SAGE orf Found reverse in NC_001143 between 403
10453_at	143	P	non-annotated SAGE orf Found forward in NC_001143 between 618
10454_at	420	A	non-annotated SAGE orf Found forward in NC_001143 between 618
10455_at	368.7	A	non-annotated SAGE orf Found reverse in NC_001143 between 168
10456_at	7972.4	P	non-annotated SAGE orf Found forward in NC_001143 between 982
10457_at	25.2	A	non-annotated SAGE orf Found forward in NC_001143 between 145
10458_at	1051.7	M	non-annotated SAGE orf Found reverse in NC_001143 between 145
10459_at	1192.2	A	non-annotated SAGE orf Found reverse in NC_001143 between 164
10460_at	2068.4	P	non-annotated SAGE orf Found forward in NC_001143 between 178
10461_at	929.6	P	non-annotated SAGE orf Found reverse in NC_001143 between 195
10462_at	15319.3	P	non-annotated SAGE orf Found forward in NC_001143 between 233
10463_at	474.1	A	non-annotated SAGE orf Found reverse in NC_001143 between 261
10419_at	1375.6	P	non-annotated SAGE orf Found forward in NC_001143 between 320
10420_at	4711.6	P	non-annotated SAGE orf Found forward in NC_001143 between 612
10421_at	2196.2	P	non-annotated SAGE orf Found reverse in NC_001143 between 638
10422_at	1210.3	P	non-annotated SAGE orf Found forward in NC_001143 between 219
10423_at	386.2	A	non-annotated SAGE orf Found forward in NC_001143 between 298
10424_at	68.2	A	non-annotated SAGE orf Found reverse in NC_001143 between 379
10425_at	6671	P	non-annotated SAGE orf Found reverse in NC_001143 between 464
10426_at	145.9	A	non-annotated SAGE orf Found reverse in NC_001143 between 189
10427_at	281.6	A	non-annotated SAGE orf Found reverse in NC_001143 between 389
10428_at	6.7	A	non-annotated SAGE orf Found forward in NC_001143 between 465
10429_at	88.8	A	non-annotated SAGE orf Found reverse in NC_001143 between 939
10430_at	1071.2	P	non-annotated SAGE orf Found reverse in NC_001143 between 983
10431_at	240.1	A	non-annotated SAGE orf Found reverse in NC_001143 between 108
10432_at	684.6	P	non-annotated SAGE orf Found reverse in NC_001143 between 136
10433_at	163.2	A	non-annotated SAGE orf Found reverse in NC_001143 between 136
10434_at	1368.4	P	non-annotated SAGE orf Found reverse in NC_001143 between 142
10435_at	529	P	non-annotated SAGE orf Found reverse in NC_001143 between 184
10436_at	139.2	A	non-annotated SAGE orf Found reverse in NC_001143 between 219
10437_at	2236.6	P	non-annotated SAGE orf Found reverse in NC_001143 between 264
10438_at	118.6	A	non-annotated SAGE orf Found reverse in NC_001143 between 308
10439_at	8888.6	P	non-annotated SAGE orf Found forward in NC_001143 between 308
10440_at	706.3	M	non-annotated SAGE orf Found reverse in NC_001143 between 340
10441_at	91.5	A	non-annotated SAGE orf Found reverse in NC_001143 between 468
10396_at	558.1	A	non-annotated SAGE orf Found reverse in NC_001143 between 468
10397_at	568	A	non-annotated SAGE orf Found reverse in NC_001143 between 527
10398_at	74.4	A	non-annotated SAGE orf Found forward in NC_001143 between 533
10399_at	214.7	A	non-annotated SAGE orf Found reverse in NC_001143 between 137

10400_at	90.1	A	non-annotated SAGE orf Found forward in NC_001143 between 173
10401_at	591.3	A	non-annotated SAGE orf Found reverse in NC_001143 between 185
10402_at	363	P	non-annotated SAGE orf Found forward in NC_001143 between 219
10403_at	679.6	A	non-annotated SAGE orf Found reverse in NC_001143 between 442
10404_at	697.8	P	non-annotated SAGE orf Found reverse in NC_001143 between 447
10405_at	2253.6	P	non-annotated SAGE orf Found forward in NC_001143 between 456
10406_at	1866.3	P	non-annotated SAGE orf Found forward in NC_001143 between 619
10407_at	300.2	A	snRNA
10408_at	3092.1	P	snRNA
10409_at	3312.2	P	snRNA
10410_at	151.8	A	snRNA
10411_f_a	2476.9	P	Growth INhibitory protein
10412_f_a	5028.4	P	strong similarity to members of the Srp1/Tip1p family
10413_at	704.8	A	transacetylase
10414_at	492.7	P	weak similarity to M.leprae metH2 protein
10415_at	575.7	M	strong similarity to amino acid transport protein Gap1p
10416_at	532.7	P	Glutathione transferase
10417_at	9.7	A	hypothetical protein
10418_at	1627.4	P	similarity to N.crassa O-succinylhomoserine (thiol)-lyase
10373_at	22.6	A	similarity to E.coli dioxygenase
10374_at	1631.6	M	weak similarity to Y.pseudotuberculosis CDP-3,6-dideoxy-D-glycero-
10375_at	1812.8	P	similarity to Dal5p
10376_at	2325.7	P	similarity to transcription factor Pip2p
10377_at	11073.3	P	similarity to water channel proteins
10378_at	2833.7	P	member of mip family transmembrane channels
10379_at	523.9	P	similar to FRE2
10380_at	15434	P	Cofilin, actin binding and severing protein
10381_at	522.3	P	hypothetical protein
10382_at	18260.7	P	yeast bile transporter, similar to mammalian bile transporter
10383_at	553.2	P	questionable ORF
10384_at	539.3	A	ribonucleoprotein 1
10385_i_at	38014.4	P	Ribosomal protein L8B (L4B) (rp6) (YL5)
10386_s_a	29510.3	P	Ribosomal protein L8B (L4B) (rp6) (YL5)
10387_at	1743.1	P	questionable ORF
10388_at	8422.2	P	Suppressor of tps1\/fdp1 and member of the MIP family of transmem
10389_at	324.3	A	hypothetical protein
10390_at	15223	P	Succinate dehydrogenase (ubiquinone) iron-sulfur protein subunit
10391_at	3699.8	P	involved in regulating membrane traffic
10392_at	3284	P	ubiquitin
10393_at	1275.8	A	weak similarity to YJR125c and YDL161w
10394_at	446	A	weak similarity to human platelet-activating factor receptor
10395_at	3738.2	P	RNA splicing factor
10351_at	830.8	A	hypothetical protein
10352_at	14227.6	P	similarity to mammalian valosin
10353_at	394.3	P	hypothetical protein
10354_at	1318	P	hypothetical protein
10355_at	11429.5	P	similarity to hypothetical protein YJL062w
10356_at	167.6	A	hypothetical protein
10357_at	5135.1	P	similarity to M.jannaschii X-Pro dipeptidase and S.pombe hypothetica
10358_at	20223.6	P	similarity to multidrug resistance proteins
10359_at	8354.6	P	similarity to H.influenzae and E.coli hypothetical proteins
10360_at	5196.4	P	heat shock protein 104

10361_f_a	1517.2	A	strong similarity to members of the Srp1p/Tip1p family
10362_at	1106.1	P	member of 70 kDa heat shock protein family
10363_at	14660.9	P	similarity to hypothetical protein YLR064w
10364_at	8090.7	P	Hat1 Interacting Factor 1
10365_at	3078.9	P	spindle pole antigen
10366_i_a	7587.6	P	questionable ORF
10367_r_a	3453.6	P	questionable ORF
10368_s_a	13384.7	P	questionable ORF
10369_at	1665.6	P	protein kinase homolog
10370_at	23855.6	P	Aspartyl-tRNA synthetase, cytosolic
10371_at	69.3	A	maybe part of SCD25
10372_at	155	A	homologous to cdc25
10328_at	2353.7	P	similarity to metal resistance proteins
10329_at	6935.1	P	hypothetical protein
10330_at	4298.4	P	similarity to Drosophila pumilio protein
10331_at	12672	P	similarity to triacylglycerol lipases
10332_at	10580.5	P	56 kDa nucleolar snRNP protein that shows homology to beta subuni
10333_at	5331.2	P	strong similarity to hypothetical protein YLR019w
10334_at	2954.5	P	cysteine-rich cytoplasmic protein
10335_at	6471.6	P	putative ATP dependent RNA helicase
10336_at	322	M	hypothetical protein
10337_at	1178.9	P	mitochondrial outer membrane protein
10338_at	20	A	similarity to A.thaliana hyp1 protein
10339_at	4106.4	P	Third subunit of the origin recognition complex
10340_at	1726.3	P	protein of unknown function
10341_at	1121.5	M	Killed in Mutagen, sensitive to diepoxybutane and\/or mitomycin C
10342_at	1238.7	P	Dynamin-related protein
10343_at	2451.7	P	hypothetical protein
10344_at	2177.8	P	similarity to hypothetical C. elegans protein
10345_at	2348.4	P	hypothetical protein
10346_at	1081.4	P	similarity to allantoate transport protein
10347_at	8718	P	Component of RNA polymerase transcription factor TFIIH
10348_at	2991.7	P	Two-component signal transducer that with Sln1p regulates osmoser
10349_at	3079.7	P	hypothetical protein
10350_at	3329.1	P	similarity to hypothetical protein YNL328c
10305_at	8224.1	P	similarity to ribosomal protein L24.e.B
10306_at	289.8	A	weak similarity to Aquifex aeolicus adenylosuccinate synthetase
10307_at	295.2	A	weak similarity to E.coli hypothetical 20.4 kDa protein
10308_at	40	A	hypothetical protein
10309_at	44.1	A	weak similarity to nitrogen regulatory proteins
10310_at	1389.2	P	zinc-finger transcription factor of the Zn(2)-Cys(6) binuclear cluster d
10311_at	1353.6	P	weak similarity to S.pombe hypothetical protein SPBC13G1
10312_at	482.1	P	hypothetical protein
10313_at	1885.2	A	Protein that regulates ADH2 gene expression
10314_at	2100.3	P	hypothetical protein
10315_at	6619.9	P	strong similarity to YLL010c
10316_at	2258.1	P	similarity to triacylglycerol lipase
10317_at	1746.3	P	hypothetical protein
10318_at	5002	P	similarity to C.elegans and M.jannaschii hypothetical proteins
10319_at	16366.4	P	similarity to S.pombe hypothetical protein SPAC30D11.11
10320_at	1248.4	P	similarity to ubiquitin--protein ligase Ubr1p
10321_at	4347.9	P	involved in derepression of SUC2 in response to glucose limitation

10322_at	698.2	P	Sed5p is a t-SNARE (soluble NSF attachment protein receptor) requi
10323_at	29107.2	P	aspartate aminotransferase, cytosolic
10324_at	7488.9	P	5-aminoimidazole-4-carboxamide ribonucleotide (AICAR) transformy
10325_at	36488.3	P	Ribosomal protein L15A (YL10) (rp15R) (L13A)
10326_g_a	25225.4	P	Ribosomal protein L15A (YL10) (rp15R) (L13A)
10327_at	29.7	A	hypothetical protein
10283_at	245.3	A	similarity to hypothetical protein YMR124w
10284_at	1398.3	P	putative ATPase\/DNA helicase
10285_at	5238	P	hypothetical protein
10286_at	20282.9	P	strong similarity to SMF2 protein
10287_at	985	P	similarity to human mutL protein homolog
10288_at	2686.2	P	similarity to YIL089w
10289_f_at	3392.6	P	strong similarity to members of the Srp1p/Tip1p family
10290_at	13642.8	P	subunit VIb of cytochrome c oxidase
10291_at	1454.7	P	involved in transcription of ribosomal proteins and ribosomal RNA
10292_at	24590.5	P	weak similartity to hypothetical protein YIL011w
10293_at	902.3	P	questionable ORF
10294_at	3012.5	P	hypothetical protein
10295_at	15666.9	P	thioredoxin
10296_at	26745.4	P	pyruvate decarboxylase
10297_at	5174.7	P	May play a role in attachment, organization, and\/or dynamics of mic
10298_at	1235.2	P	strong similarity to Rta1p and Rtm1p protein
10299_at	533.3	A	similarity to hypothetical protein YGL160w
10300_f_at	24419.9	P	Ribosomal protein S0B
10301_at	5173.4	P	Ribosomal protein S0B
10302_g_a	21670.9	P	Ribosomal protein S0B
10303_at	1780.8	P	hypothetical protein
10304_at	18863.4	P	weak similarity to human MAC30 C-terminus
10260_at	5984.5	P	similarity to human acidic 82 kDa protein
10261_at	3046.2	P	hypothetical protein
10262_at	224.2	A	hypothetical protein
10263_at	832.2	P	hypothetical protein
10264_at	7058.6	P	transcription factor, probable member of histone acetyltransferase S
10265_at	29459.2	P	C-5 sterol desaturase
10266_at	1844	P	weak similarity to mouse alpha-mannosidase
10267_at	22162.9	P	serine hydroxymethyltransferase
10268_at	4776.3	P	suppressor of rna12/yme2
10269_at	24242.8	P	Phenylalanyl-tRNA synthetase, alpha subunit, cytoplasmic
10270_at	18626.1	P	Ribosomal protein L22A (L1c) (rp4) (YL31)
10271_at	1221.2	P	questionable ORF
10272_at	1840.2	P	ser/thr protein kinase
10273_at	12516.8	P	weak similarity to Anopheles NADH-ubiquinone oxidoreductase, cha
10274_at	21496	P	hypothetical protein
10275_at	13419.4	P	signal peptidase subunit
10276_at	854.2	P	Involved in expression of mitochondrial COX1 by regulating translatic
10277_at	2395.9	A	hypothetical protein
10278_at	6978.8	P	mitochondrial elongation factor G-like protein
10279_at	520.2	P	strong similarity to sugar dehydrogenases
10280_at	4464.3	P	component of RNA polymerase II holoenzyme\/mediator complex, in
10281_at	1273.6	P	similarity to YFL042c, YFL043c, YDR326c and YHR080c
10282_at	5283	P	hypothetical protein
10238_at	4511.7	P	weak similarity to human zinc finger protein

10239_at	1330.5	P	Ribosomal protein L10\; Ubiquinol-cytochrome C reductase complex
10240_at	2625.4	P	questionable ORF
10241_at	2270.7	P	weak similarity to Xenopus RCC1 protein
10242_at	3562.6	P	necessary for vesicular transport from the ER to the Golgi complex
10243_at	4235.9	P	P40 inhibitor of Cdc28p-Clb5 protein kinase complex
10244_at	427.1	P	strong similarity to Emp47p
10245_at	686.1	A	galactose permease
10246_at	1544.3	P	Suppressor of rad53 lethality
10247_at	25944.3	P	integral membrane protein\; p24a protein
10248_at	14679.7	P	weak similarity to S.pombe hypothetical protein SPAC6F6
10249_at	3701.7	P	Actin-related protein
10250_at	812.5	P	Smc4 protein, member of SMC family
10251_at	873.7	P	hypothetical protein
10252_at	8454.3	P	Possible component of GPI:protein transamidase
10253_at	21462.3	P	strong similarity to alanine transaminases
10254_at	3766.5	P	Homolog of E. coli DnaJ, closely related to Ydj1p
10255_at	643.6	A	hypothetical protein
10256_at	2437	P	high affinity sulfate permease
10257_at	1220.3	P	vacuolar v-SNARE
10258_at	2571.4	P	hypothetical protein
10259_at	3546.2	P	hypothetical protein
10215_at	3848.2	P	Serine\/threonine protein kinase
10216_at	1366.3	P	hypothetical protein
10217_at	1344	P	DNA-binding transcriptional activator or CHA1
10218_at	4123.5	P	similarity to YDR125c
10219_at	18421.5	P	similarity to rat ovarian specific protein
10220_at	949.6	M	questionable ORF
10221_at	434.3	P	subunit of the anaphase promoting complex (APC)
10222_at	2224.3	P	omosomal DNA replication initiation protein
10223_at	1774.5	P	hypothetical protein
10224_at	7089.2	P	tRNA splicing endonuclease subunit
10225_at	3076.4	P	similarity to Kaposi s sarcoma-associated herpes-like virus ORF73 h
10226_at	2781	P	similarity to Pan troglodytes prot GOR
10227_at	1301.4	P	strong similarity to YDR132c
10228_at	27926.3	P	similarity to C.boidinii peroxisomal membrane protein 20K A
10229_at	0.1	P	strong similarity to Flo1p
10230_at	989.9	A	hypothetical protein
10231_at	3811.2	P	hypothetical protein
10232_at	23878.8	P	mitogen-activated protein kinase (MAP kinase)
10233_at	2563	P	similarity to C.elegans hypothetical protein and YOR054c
10234_at	1293.4	P	Component of cleavage factor II (CF II)\; 105-kDa protein associated
10235_at	5637.7	P	Branchpoint bridging protein -- component of the splicing commitmen
10236_at	780.2	P	SYnthetic lethal with cdc40 (Forty)
10237_at	1792.9	P	similarity to several esterases
10192_at	1172.7	P	suppressor of rna1-1 mutation
10193_at	19102.6	P	GPI-anchored aspartic protease
10194_at	9674.7	P	GPI-anchored aspartic protease
10195_at	16.1	A	hypothetical protein
10196_g_a	1296	M	hypothetical protein
10197_at	349.5	P	questionable ORF
10198_at	463.1	P	hypothetical protein
10199_at	19.9	A	hypothetical protein

10200_at	667	A	weak similarity to P.aeruginosa anthranilate synthase component II
10201_at	281.5	P	subunit of the anaphase promoting complex (APC)
10202_at	826.5	P	similarity to S.pombe hypothetical protein SPBC24E9
10203_at	5504.9	P	DOM34 Interacting Protein
10204_at	20153.3	P	Low-affinity zinc transport protein
10205_at	1778.4	P	zinc finger transcription factor
10206_at	1193.4	P	hypothetical protein
10207_at	4891.4	P	choline kinase
10208_at	4789.3	P	pyruvate decarboxylase
10209_at	410.6	A	hypothetical protein
10210_at	615.2	P	zinc finger containing homolog of mammalian TIS11, glucose repres
10211_at	1800.5	P	hypothetical protein
10212_at	2909.4	P	Putative Na+\/H+ antiporter
10213_at	2242.8	P	73 kDa mitochondrial integral membrane protein
10214_at	429.8	A	questionable ORF
10170_g_a	10229.1	P	questionable ORF
10171_at	1100.8	P	transcription factor, member of UAF (upstream activation factor) alo
10172_at	466.7	A	proline oxidase
10173_at	1275.3	P	weak similarity to Pyrococcus horikoshii hypothetical protein PHBJ01
10174_at	4097.8	P	Identified as an activity necessary for actin polymerization in permea
10175_at	2115	P	hypothetical protein
10176_at	4265.5	P	Spermine Synthase
10177_at	1782.7	P	encodes a core snRNP protein
10178_at	107.2	A	vacuolar membrane protein
10179_at	502	A	hypothetical protein
10180_at	25567	P	specific affinity for guanine-rich quadruplex nucleic acids
10181_at	1168.9	P	weak similarity to A.thaliana hypothetical protein ATU78721
10182_at	1443.5	P	similarity to YOR3165w and YNL095c
10183_at	22987.2	P	acetyl-coenzyme A synthetase
10184_at	3191.7	P	hypothetical protein
10185_s_a	5578.9	P	nitrogen catabolite-regulated cell-wall L-asparaginase II
10186_s_a	239.5	A	identical to hypothetical proteins YLR161w and YLR159w
10187_at	5860.4	P	hypothetical protein
10188_at	2121.9	P	mitochondrial processing protease subunit
10189_at	159.2	A	strong similarity to Sdh4p
10190_at	1152.1	P	weak similarity to H.influenzae hypothetical protein HI0176
10191_at	1993.2	P	100 kD component of the Exocyst complex\; required for exocytosis.
10147_at	35615.4	P	Ribosomal protein S31 (S37) (YS24)
10148_at	1809.9	P	probably involved in intramitochondrial protein sorting
10149_at	2487	P	questionable ORF
10150_at	15912.7	P	clathrin-associated protein complex, small subunit
10151_at	2373	P	questionable ORF
10152_at	12194.3	P	S-adenosylmethionine (AdoMet)-dependent methyltransferase of dip
10153_at	490.9	A	hypothetical protein
10154_at	167.8	A	Cytosolic form of NADP-dependent isocitrate dehydrogenase
10155_at	24422.9	P	major low affinity 55 kDa Centromere\/microtubule binding protein
10156_at	1374	P	DNA binding protein, homologous to a family of mammalian RFX1-4
10157_at	1940.3	P	similarity to suppressor protein Psp5p
10158_at	1361.7	P	suppressor of cdc25
10159_at	18765	P	similarity to Tfs1p
10160_at	16787.2	P	S-adenosylmethionine synthetase
10161_g_a	0.1	P	S-adenosylmethionine synthetase

10162_at	3712.3	P	hypothetical protein
10163_at	2627	P	regulatory protein
10164_at	980.6	P	similarity to YDR501w
10165_at	330.8	A	weak similarity to ribulose-bisphosphate carboxylase
10166_at	45.9	P	60S ribosomal protein L37A (L43) (YL35)
10167_at	9778.2	P	strong similarity to S.pombe hypothetical protein C18G6.07C
10168_at	3333.2	P	similarity to hypothetical protein YNL278w
10169_at	13211.4	P	ATP-binding cassette (ABC) transporter family member
10124_at	2969.1	P	similarity to P.aeruginosa rhamnosyltransferase 1 chain B
10125_at	4333	P	hypothetical protein
10126_at	987.6	P	Peroxisomal membrane protein that contains Src homology 3 (SH3)
10127_at	18710.7	P	weak similarity to fruit fly transcription factor 5 large chain
10128_at	1194	P	similarity to G.gallus px19 and Msf1p
10129_at	8813	P	hypothetical protein
10130_at	4259.9	P	N-myristoyl transferase
10131_at	14774.4	P	Protein with periodic trytophan residues that resembles members of
10132_at	29284.6	P	homology to microtubule binding proteins and to X90565_5.cds
10133_at	3953.2	P	questionable ORF
10134_at	4173.5	P	hypothetical protein
10135_at	1638.4	P	Polypeptide 6 of a Yeast Non-native Actin Binding Complex, homolo
10136_at	3629.6	P	similarity to hypothetical S. pombe protein
10137_at	1232.1	A	questionable ORF
10138_g_a	738.1	A	questionable ORF
10139_i_at	31307.7	A	questionable ORF
10140_r_a	14785.6	P	questionable ORF
10141_at	5629.2	P	Protein involved in maturation of COX1 and COB mRNA
10142_at	4392.6	P	protein of unknown function
10143_at	6245	P	hypothetical protein
10144_at	9066.4	P	similarity to human tricohyalin and protein KIAA0171
10145_at	945.4	P	HMG-CoA Reductase Degradation
10146_at	28207.5	P	cytoplasmic protein involved in release of transport vesicles from the
10101_at	2282.9	P	strong similarity to purine-nucleoside phosphorylases
10102_at	2647	P	G(sub)2-specific B-type cyclin
10103_at	1970.5	P	hypothetical protein
10104_at	2851.2	P	gamma tubulin-like protein, interacts with Spc98p and Spc97p, the
10105_at	458.1	P	similarity to UTR2 protein
10106_at	22414.5	P	Ferric (and cupric) reductase
10107_at	3608.5	P	strong similarity to rat cell cycle progression related D123 protein
10108_at	14077	P	a cyclophilin related to the mammalian CyP-40\; physically interacts
10109_at	26.1	A	questionable ORF
10110_at	1882.5	P	hypothetical protein
10111_at	2178.2	P	hypothetical protein
10112_at	5426.3	P	Possible transmembrane Ca2+ transporter
10113_at	3721.9	P	hypothetical protein
10114_at	9791.4	P	similarity to Dip2p
10115_at	3483.9	P	has a weak RNA-dependent ATPase activity which is not specific for
10116_at	3005.6	P	hypothetical protein
10117_at	3749.4	P	strong similarity to YDR222w
10118_at	1910.6	P	hypothetical protein
10119_at	178.3	A	hypothetical protein
10120_at	3117.6	P	strong similarity to YDR213w, weak similarity to Lys14p
10121_at	24363.2	P	member of the Rho subfamily of Ras-like proteins

10122_at	366.7	A	questionable ORF
10123_at	2998.2	P	strong similarity to rat kynureninase
10079_at	485.9	A	questionable ORF
10080_at	311	A	Telomere elongation protein (ever shorter telomeres)
10081_at	1015.2	A	DNA Topoisomerase III
10082_at	1267.2	P	questionable ORF
10083_g_a	589.5	A	questionable ORF
10084_at	1311.4	A	hypothetical protein
10085_at	9609.7	P	thiamine transporter
10086_at	1011.9	P	similarity to YDR200c
10087_at	3232.6	P	weak similarity to H.influenzae lipoate biosynthesis protein B
10088_at	2069.6	P	phosphatidylinositol 3-kinase
10089_at	2641.9	P	similarity to hypothetical S.pombe protein SPAC2G11.09
10090_at	424	P	weak similarity to C.elegans R05H5.5 protein and Nup120p
10091_at	4563.6	P	strong similarity to YOR262w
10092_at	4581.2	P	methionine aminopeptidase
10093_at	2077.5	P	strong similarity to B.subtilis cytidine deaminase
10094_at	3637.5	P	similarity to human DHHC-domain-containing cysteine-rich protein
10095_at	1608.9	P	similarity to S.pombe rad8 protein and Rdh54p
10096_at	7131.4	P	Serine\/threonine protein kinase
10097_at	5875	P	EF-3 (translational elongation factor 3)
10098_at	2444.9	P	secretory protein
10099_at	1165.3	A	similarity to peroxisomal rat membrane protein PMP22
10100_at	603.2	P	questionable ORF
10055_at	1265.8	P	weak similarity to bacterial aminoglycoside acetyltransferase regulat
10056_at	1336.3	P	hypothetical protein
10057_at	1134	A	hypothetical protein
10058_at	2115.2	P	zinc-finger transcription factor of the Zn(2)-Cys(6) binuclear cluster d
10059_at	4606.4	P	hypothetical protein
10060_at	728.9	P	Glycogen synthase (UDP-gluocse--starch glucosyltransferase)
10061_at	20385.9	P	heat shock protein 60\; chaperonin protein
10062_at	2928.6	P	sphingoid long chain base (LCB) kinase
10063_i_at	2285.3	P	questionable ORF
10064_s_a	2578	P	questionable ORF
10065_at	992.6	P	highly homologous to the human GTPase, Rab6
10066_s_a	1622.4	P	strong similarity to F49C12.11 (Z68227_K) from C. elegans
10067_at	359.6	A	Meiosis-specific protein involved in homologous chromosome synaps
10068_i_at	11353.6	P	Ribosomal protein S28B (S33B) (YS27)
10069_f_at	3877.2	P	Ribosomal protein S28B (S33B) (YS27)
10070_at	193.4	A	hypothetical protein
10071_at	1087.2	P	weak similarity to transcription factors
10072_at	253.1	A	Bypass of PAM1
10073_at	2298	P	Synaptobrevin (v-SNARE) homolog present on ER to Golgi vesicles
10074_at	53.8	A	questionable ORF
10075_at	2891.5	P	strong similarity to YOR173w
10076_at	725.6	A	hypothetical protein
10077_at	777.1	P	similarity to human hypothetical ORF
10078_at	697.3	A	Protein similar to Gac1p, a putative type 1 protein phosphatase targe
10032_at	787.2	P	Member of complex that acts at ARS s to initiate replication
10033_at	1085.6	P	U1 snRNP protein of the Sm class
10034_at	6963	P	DEAD-Box Protein 9
10035_at	3403.8	P	subunit of Polyadenylation factor I (PF I)

10036_at	2247.8	P	weak similarity to regulatory proteins
10037_at	1623.5	A	questionable ORF
10038_i_a	11871.2	A	questionable ORF
10039_s_a	248.7	A	questionable ORF
10040_at	667	P	similarity to polypeptide chain release factors
10041_at	425.2	A	questionable ORF
10042_at	1030.3	P	weak similarity to Smc2p
10043_at	82.6	A	Peroxisomal enoyl-CoA hydratase
10044_at	10323.4	P	hypothetical protein
10045_at	35033.8	P	Endochitinase
10046_at	671.8	P	weak similarity to S.pombe hypothetical protein SPAC22E12
10047_f_a	24481.6	P	Ribosomal protein S30A
10048_at	1138.7	P	involved in checkpoint control and DNA repair
10049_at	1119.5	P	GTPase
10050_at	2584.6	P	hypothetical protein
10051_at	7993.9	P	translation initiation factor eIF2b, 43 kDa subunit\; negative regulato
10052_at	2665.6	P	protein involved in membrane protein insertion into the ER
10053_at	35465.3	P	GTP-binding protein
10054_at	16397.6	P	questionable ORF
10010_at	10936	P	ATP synthase subunit h
10011_at	381.3	A	hypothetical protein
10012_at	889.3	P	weak similarity to Vibrio vulnificus VvpC protein
10013_at	1062.4	P	U1 snRNP protein required for pre-mRNA splicing
10014_at	2482.3	P	gamma-glutamyltransferase homolog
10015_at	16887.2	P	Exo-1,3-beta-glucanase
10016_at	17873.2	P	hypothetical protein
10017_at	100.2	A	questionable ORF
10018_at	25294.1	P	O-Acetylhomoserine-O-Acetylserine Sulfhydralase
10019_at	25985.5	P	Aconitase, mitochondrial
10020_at	3902.2	P	encodes a phosphatidylinositol-4-kinase, homologous to VPC34
10021_at	510.7	M	Ubiquitin-conjugating enzyme
10022_at	28.3	A	Chitin Deacetylase
10023_at	99.1	A	Chitin Deacetylase
10024_at	4814.8	P	similarity to human centromere protein E
10025_at	618.3	M	regulatory protein of adenylate cyclase
10026_at	51.3	A	weak similarity to S.tarentolae cryptogene protein G4
10027_at	44.2	A	hypothetical protein
10028_at	627.7	A	homologous to Spa2p, localizes to sites of polarized growth
10029_at	2670.7	P	Component of 10 nm filaments of mother-bud neck
10030_at	702.7	A	weak similarity to rat apolipoprotein A-IV
10031_at	7005	P	weak similarity to H.influenzae hypothetical protein HI0906
9986_at	6082.9	P	questionable ORF
9987_at	290	P	103 kD basic protein, catalytic subunit of telomerase
9988_at	4076.5	P	Actin Interacting Protein
9989_at	1050.7	P	hypothetical protein
9990_at	6641.7	P	homolog of Snf5p, member of the chromatin remodeling complex, R
9991_at	21.6	A	questionable ORF
9992_at	748.2	P	weak similarity to N.crassa uvs2 protein
9993_at	426.7	A	strong similarity to YGR004w
9994_at	20395.7	P	Ribosomal protein L38
9995_at	3341.9	P	hypothetical protein
9996_at	657.6	P	strong similarity to Stf2p

9997_at	9223.3	P	strong similarity to YGR010w
9998_at	65.7	A	23 kDa protein containing a putative leucine zipper\; meiosis specific
9999_at	4090.4	P	Involved in chitin synthase III activity, also required for homozygosis
10000_at	304	P	questionable ORF
10001_at	9100.5	P	Protein required for mating
10002_i_at	28232	A	Ribosomal protein S25B (S31B) (rp45) (YS23)
10003_f_at	37189.1	P	Ribosomal protein S25B (S31B) (rp45) (YS23)
10004_at	200.1	A	questionable ORF
10005_at	5216	P	nuclear pore complex protein with central repetitive domain similar to
10006_at	10475.8	P	Suppressor of Glycerol Defect
10007_at	6355.6	P	Proline-rich protein verprolin
10008_at	74.7	A	questionable ORF
10009_at	518.6	A	questionable ORF
9964_at	0.1	P	60S ribosomal protein P0 (A0) (L10E)
9965_at	92.4	A	hypothetical protein
9966_at	23429.1	P	1,3-beta-D-glucan synthase
9967_at	694.5	P	strong similarity to Gas1p and C.albicans pH responsive protein
9968_s_at	7759.1	P	Ribosomal protein L26A (L33A) (YL33)
9969_at	2585.3	P	similarity to Pfk26p and other 6-phosphofructo-2-kinases
9970_at	1155.1	P	weak similarity to YGR035c
9971_at	10235.2	P	95 kDa structural and functional homolog of vertebrate karyopherin b
9972_at	24086	P	mitochondrial dicarboxylate transport protein
9973_at	3378.2	P	questionable ORF
9974_at	18389	P	strong similarity to YGR038w
9975_at	13420	P	Nit3 nitrilase
9976_at	1921.4	P	hypothetical protein
9977_at	3333.4	P	budding protein
9978_at	14469.9	P	Transaldolase, enzyme in the pentose phosphate pathway
9979_at	33077.6	P	acetohydroxyacid reductoisomerase
9980_at	1680	P	similarity to SCM4 protein
9981_at	1147	M	questionable ORF
9982_at	4026.3	P	Member of RSC complex.
9983_at	17698.2	P	Adenylosuccinate Lyase
9984_at	309.6	A	protein involved in vacuolar sorting
9985_at	4600.5	P	similarity to YOR3329c
9941_at	1949.7	P	Ser\/Thr protein kinase\; MEKK homolog
9942_at	393.6	P	putative Upf1p-interacting protein
9943_at	744.3	P	hypothetical protein
9944_at	300.4	P	weak similarity to Udf2p
9945_at	261.9	A	hypothetical protein
9946_at	4840.2	P	Ribosomal protein S22B (S24B) (rp50) (YS22)
9947_i_at	33206.7	P	Ribosomal protein S22B (S24B) (rp50) (YS22)
9948_f_at	14463.6	P	Ribosomal protein S22B (S24B) (rp50) (YS22)
9949_at	2252.6	P	hypothetical protein
9950_at	491.9	P	Hsp70 protein
9951_at	7766.4	P	Arp2\/3 Complex Subunit
9952_at	2939.5	P	GDP-GTP Exchange Protein (GEP) for the Rho1p Small GTP-bindin
9953_at	32715.8	P	required for conversion of 24-carbon fatty acids to 26-carbon species
9954_at	3494.5	P	similarity to hypothetical protein YGR071c
9955_at	475.5	A	questionable ORF
9956_at	19341.7	P	Involved in pre-tRNA splicing and in uptake of branched-chain amino
9957_at	1010.5	P	hypothetical protein

9958_at	345.6	A	fructose-1,6-bisphosphatase
9959_at	24106.8	P	membrane component of ER protein translocation apparatus
9960_at	66.1	A	questionable ORF
9961_at	8343.1	P	weak similarity to SEC14 protein
9962_at	588.6	P	hypothetical protein
9963_at	2048.9	P	mitochondrial leucyl tRNA synthetase
9918_at	2604.6	P	Protein involved in recombination repair, homologous to S. pombe ra
9919_at	7049.4	P	confers sensitivity to killer toxin
9920_at	199.1	A	hypothetical protein
9921_at	5271.7	P	similarity to hypothetical S. pombe protein
9922_at	5509.1	P	similarity to YBR267w
9923_f_at	16998	P	Ribosomal protein S29A (S36A) (YS29)
9924_at	2569.9	P	protease involved in a-factor processing
9925_at	3352.6	P	ExtraCellular Mutant
9926_at	8325.1	P	Secretory Stress Response protein 1
9927_at	458.8	A	hypothetical protein
9928_at	353.6	P	essential for assembly of a functional mitochondrial ATPase complex
9929_at	732.9	A	weak similarity to chicken RING zinc finger protein
9930_at	7173.4	P	Cytochrome-c oxidase chain VIII
9931_at	1922.6	P	Vacuolar sorting protein essential for vacuolar morphogenesis and fu
9932_at	2812.8	P	homology to the CDC48 gene product
9933_at	7634.9	P	antiviral protein, putative helicase
9934_at	6707.7	P	Bdf1p contains two bromodomains, localizes to the nucleus and to c
9935_at	488.2	A	hypothetical protein
9936_at	3139.5	P	similarity to A.brasilense nifR3 protein
9937_at	1910.2	P	hypothetical protein
9938_at	3987.2	P	split zinc finger protein
9939_at	1012.4	A	hypothetical protein
9940_at	3187.1	P	similarity to A.brasilense nifR3 protein
9895_i_at	12328.2	P	Ribosomal protein L31B (L34B) (YL28)
9896_f_at	18076.8	P	Ribosomal protein L31B (L34B) (YL28)
9897_f_at	35129.2	P	Ribosomal protein L31B (L34B) (YL28)
9898_at	1989.6	P	hypothetical protein
9899_at	1779.1	P	hypothetical protein
9900_at	9728.5	P	strong similarity to S. pombe beta-transducin
9901_at	7921	P	Homologous to S. pombe asp1+
9902_at	11382.8	P	Copper Transporter
9903_at	2095.6	P	weak similarity to Candida maltosa cytochrome P450
9904_at	10704.9	P	strong similarity to YKL187c
9905_at	12570.6	P	weak similarity to YLR413w
9906_at	229	A	questionable ORF
9907_at	589	P	hypothetical protein
9908_at	1000.8	A	defective in vacuolar protein sorting
9909_at	9609.6	P	Accessory factor associated with RNA polymerase II by affinity chrom
9910_at	4460.8	P	similarity to helicases
9911_at	21087.8	P	dihydroorotase
9912_at	18494.5	P	weak similarity to human 42K membrane glycoprotein
9913_at	4180.6	P	similarity to human DOCK180 protein
9914_at	555	P	hypothetical protein
9915_at	417.7	A	weak similarity to Stu1p
9916_at	1483.1	P	hypothetical protein
9917_at	6594.4	P	weak similarity to 3-oxoacyl-[acyl-carrier-protein] reductase from E. c

9873_at	1232.9	M	weak similarity to 3-oxoacyl-[acyl-carrier-protein] reductase from E. c
9874_at	3511.3	P	weak similarity to human transcription regulator Staf-5
9875_at	485.2	A	questionable ORF
9876_at	6626.1	P	has homology to the Dictyostelium and human actin-binding protein c
9877_at	3733.7	P	component of a nuclear-localized tRNA splicing complex
9878_at	587.6	A	weak similarity to rabbit trichohyalin
9879_f_at	29494	P	strong similarity to IMP dehydrogenases, Pur5p and YML056c
9880_at	2730.5	P	Calcineurin subunit A\; type 2B protein serine\/threonine phosphatase
9881_at	2420.8	P	questionable ORF
9882_at	2616.8	P	hypothetical protein
9883_at	3011.8	P	ExtraCellular Mutant
9884_at	4819	P	hypothetical protein
9885_at	23352.3	P	ornithine aminotransferase
9886_at	7942.2	P	Putative snRNP protein containing Sm-like domain\; coprecipitates w
9887_at	5409.2	P	Mitochondrial 60S ribosomal protein L4
9888_at	3619.8	P	hypothetical protein
9889_i_at	12411.5	P	Ribosomal protein S1A (rp10A)
9890_s_at	16460.2	P	Ribosomal protein S1A (rp10A)
9891_at	1864.6	P	regulator of silent mating loci
9892_at	2433.2	P	ExtraCellular Mutant
9893_at	482.5	A	questionable ORF
9894_at	21.6	A	hypothetical protein
9850_at	1551.9	P	weak similarity to hexokinases
9851_at	12772.7	P	36 kDa subunit (D subunit of VO sector) of the vacuolar H(+) ATPase
9852_at	24806.8	P	60S ribosomal subunit protein L6B (L17B) (rp18) (YL16)
9853_at	5961.6	P	60 kDa nuclear FK506 binding protein
9854_at	11395.5	P	3-hydroxy-3-methylglutaryl-coenzyme A (HMG-CoA) reductase isozy
9855_at	1293.7	A	zinc-finger transcription factor of the Zn(2)-Cys(6) binuclear cluster d
9856_at	9156.4	P	Protein involved in desensitization to alpha-factor pheromone
9857_at	59.5	A	Nuclear protein
9858_at	4626.4	P	similarity to YPR117w
9859_at	2595.9	P	weak similarity to human G/T mismatch binding protein
9860_at	1166.9	P	strong similarity to YPR172w
9861_at	286	P	Nap1p-binding protein
9862_at	312.9	A	questionable ORF
9863_at	15901.4	P	cell division control protein
9864_at	495.7	A	similarity to C.carbonum toxD protein
9865_f_at	4402.9	P	member of the seripauperin protein\/gene family (see Gene_class PA
9866_i_at	383.3	A	questionable ORF
9867_s_at	357.9	P	questionable ORF
9868_at	1486.1	P	hypothetical protein identified by SAGE
9869_at	4889.6	P	identified by SAGE
9870_s_at	1400.1	P	Mitochondrial ribosomal protein MRPL15 (YmL15)
9871_at	483.1	P	non-annotated SAGE orf Found forward in NC_001144 between 230
9872_at	4731.5	M	non-annotated SAGE orf Found forward in NC_001144 between 320
9826_at	1027.2	A	non-annotated SAGE orf Found forward in NC_001144 between 341
9827_at	1908.4	P	non-annotated SAGE orf Found forward in NC_001144 between 433
9828_at	1157.1	A	non-annotated SAGE orf Found forward in NC_001144 between 449
9829_at	880.4	P	non-annotated SAGE orf Found forward in NC_001144 between 449
9830_at	212.5	A	non-annotated SAGE orf Found forward in NC_001144 between 449
9831_at	1048.1	P	non-annotated SAGE orf Found forward in NC_001144 between 603
9832_at	82.8	A	non-annotated SAGE orf Found reverse in NC_001144 between 789

9833_at	533.5	P	non-annotated SAGE orf Found reverse in NC_001144 between 867
9834_at	16.3	A	non-annotated SAGE orf Found forward in NC_001144 between 925
9835_at	2389.5	A	non-annotated SAGE orf Found forward in NC_001144 between 198
9836_at	10005.4	P	non-annotated SAGE orf Found forward in NC_001144 between 199
9837_s_at	6110.5	P	non-annotated SAGE orf Found forward in NC_001144 between 451
9838_s_at	24104.5	P	non-annotated SAGE orf Found forward in NC_001144 between 453
9839_s_at	21057.9	P	non-annotated SAGE orf Found forward in NC_001144 between 455
9840_f_at	327.2	A	non-annotated SAGE orf Found reverse in NC_001144 between 596
9841_at	526.2	A	non-annotated SAGE orf Found forward in NC_001144 between 687
9842_at	2765.1	P	non-annotated SAGE orf Found reverse in NC_001144 between 849
9843_at	202.3	A	non-annotated SAGE orf Found reverse in NC_001144 between 906
9844_at	21566.1	P	non-annotated SAGE orf Found reverse in NC_001144 between 529
9845_at	16954.2	P	non-annotated SAGE orf Found reverse in NC_001144 between 121
9846_at	24.6	A	non-annotated SAGE orf Found reverse in NC_001144 between 228
9847_at	2034.9	P	non-annotated SAGE orf Found forward in NC_001144 between 371
9848_at	379.3	P	non-annotated SAGE orf Found forward in NC_001144 between 373
9849_at	1909.3	P	non-annotated SAGE orf Found forward in NC_001144 between 390
9804_at	739.4	P	non-annotated SAGE orf Found forward in NC_001144 between 441
9805_at	358	P	non-annotated SAGE orf Found reverse in NC_001144 between 576
9806_at	17978.7	P	non-annotated SAGE orf Found reverse in NC_001144 between 578
9807_at	1330.9	A	non-annotated SAGE orf Found reverse in NC_001144 between 669
9808_at	2595.4	P	non-annotated SAGE orf Found reverse in NC_001144 between 708
9809_at	104.2	A	non-annotated SAGE orf Found forward in NC_001144 between 787
9810_at	92.3	A	non-annotated SAGE orf Found forward in NC_001144 between 789
9811_at	516.2	A	non-annotated SAGE orf Found reverse in NC_001144 between 315
9812_at	474.7	P	non-annotated SAGE orf Found reverse in NC_001144 between 136
9813_at	814.7	P	non-annotated SAGE orf Found reverse in NC_001144 between 223
9814_at	543.5	P	non-annotated SAGE orf Found forward in NC_001144 between 293
9815_at	1308.1	P	non-annotated SAGE orf Found reverse in NC_001144 between 368
9816_s_at	6545.6	P	non-annotated SAGE orf Found forward in NC_001144 between 458
9817_at	466.7	A	non-annotated SAGE orf Found reverse in NC_001144 between 460
9818_at	89	A	non-annotated SAGE orf Found forward in NC_001144 between 677
9819_at	155.6	A	non-annotated SAGE orf Found reverse in NC_001144 between 884
9820_s_at	883.4	P	non-annotated SAGE orf Found forward in NC_001144 between 288
9821_at	18.8	A	non-annotated SAGE orf Found reverse in NC_001144 between 156
9822_at	106.2	A	non-annotated SAGE orf Found forward in NC_001144 between 171
9823_at	26806.5	P	non-annotated SAGE orf Found reverse in NC_001144 between 185
9824_at	2971.5	P	non-annotated SAGE orf Found reverse in NC_001144 between 388
9825_s_at	1121.9	P	non-annotated SAGE orf Found reverse in NC_001144 between 468
9779_at	3946.8	A	non-annotated SAGE orf Found forward in NC_001144 between 514
9780_at	490.5	P	non-annotated SAGE orf Found forward in NC_001144 between 573
9781_at	168.7	A	non-annotated SAGE orf Found reverse in NC_001144 between 658
9782_at	25.1	A	non-annotated SAGE orf Found forward in NC_001144 between 672
9783_at	2343.3	P	non-annotated SAGE orf Found forward in NC_001144 between 710
9784_at	1179.6	M	non-annotated SAGE orf Found reverse in NC_001144 between 712
9785_at	842	A	non-annotated SAGE orf Found forward in NC_001144 between 949
9786_at	1039.6	P	non-annotated SAGE orf Found forward in NC_001144 between 949
9787_at	4306.4	P	non-annotated SAGE orf Found forward in NC_001144 between 964
9788_at	2237.5	P	non-annotated SAGE orf Found forward in NC_001144 between 988
9789_at	3298.1	P	non-annotated SAGE orf Found forward in NC_001144 between 103
9790_i_at	8.8	A	Centromere
9791_f_at	73.9	A	Centromere

9792_s_at	3968.8	P	CEN12-associated
9793_at	300.1	P	snRNA
9794_at	5122.7	P	snRNA
9795_at	10265	P	snRNA
9796_at	2733.4	P	snRNA
9797_i_at	597.4	P	snRNA
9798_at	13955.3	P	snRNA
9799_at	851.5	P	snRNA
9800_s_at	213	A	hypothetical protein Y .2
9801_at	616.1	P	similarity to human leukotriene b4 12-hydroxydehydrogenase
9802_at	2238.3	P	required for protein disulfide bond formation in the ER
9803_at	2875.9	P	mitochondrial membrane protein
9757_at	1357.8	P	C-terminal part starting with aa 262 cause growth inhibition when ove
9758_at	18889.4	P	weak similarity to Los1p
9759_at	27571.2	P	Hydroxymethylglutaryl-CoA Synthase
9760_at	6554.7	P	strong similarity to cytochrome-b5- and nitrate reductases
9761_at	14271	P	alpha-tubulin
9762_at	15842.1	P	inorganic phosphate transporter, transmembrane protein
9763_at	196.2	A	hypothetical protein
9764_at	8554.7	P	Putative small GTPase
9765_at	13077.7	P	mitochondrial NADH ubiquinone 6 oxidoreductase
9766_at	864.9	P	hypothetical protein
9767_at	343.7	A	similarity to YMR285c
9768_at	1598.4	P	similarity to YPL184c
9769_g_at	3025.4	P	similarity to YPL184c
9770_at	4202	P	questionable ORF
9771_at	4199.3	P	predicted protein is very hydrophobic, has many membrane-spannin
9772_at	18042	P	Vanadate resistance protein
9773_at	3279.4	P	hypothetical protein
9774_at	9364.9	P	datin, an oligo(dA).oligo(dT)-binding protein
9775_at	2190.5	P	CTD kinase-I gamma subunit
9776_at	1938.1	P	strong similarity to ubiquitination protein Bul1p
9777_at	25876.2	P	DBF2 Interacting Protein
9778_at	1835.9	P	multicopy suppressor of a sin4 defect
9734_at	1453.9	P	hypothetical protein
9735_at	3508.3	P	hypothetical protein
9736_at	18155.5	P	Orotate phosphoribosyltransferase 1
9737_at	2144.6	P	signal recognition particle subunit, homologue of mammalian SRP1
9738_at	2050	P	Intermediate filament protein involved in organelle inheritance
9739_at	2826.8	P	Nucleoporin
9740_at	4461.7	P	p60 subunit of the yeast omatin Assembly Factor-I (CAF-I)
9741_at	129.5	A	questionable ORF
9742_at	11751.9	P	weak similarity to YMR264w
9743_at	2946.3	P	123 kD regulatory subunit of trehalose-6-phosphate synthase\/phosp
9744_at	1209.6	A	questionable ORF
9745_at	989.4	P	zinc-finger transcription factor of the Zn(2)-Cys(6) binuclear cluster d
9746_at	2030.8	P	TFIID subunit
9747_at	2912.2	P	required for Golgi to vacuole trafficking, shares similarity to mammal
9748_at	1222.5	P	similarity to asparagine synthases
9749_at	549.5	P	Endonuclease (with Rad1p) that degrades single-stranded DNA for r
9750_at	72.2	A	questionable ORF
9751_at	2963.5	P	Putative homolog of subunit 5 of bovine prefoldin, a chaperone com

9752_at	7565.8	P	similarity to P.falciparum liver stage antigen LSA-1
9753_at	27430	P	proteasome component Y7
9754_at	2784.9	P	subunit of mitochondrial RNase P
9755_at	171	A	hypothetical protein
9756_at	309.2	A	questionable ORF
9711_at	1911.7	P	hypothetical protein
9712_at	74.1	A	strong similarity to YML125c, similarity to cytochrome-b5- and nitrat
9713_at	15536.7	P	D-arabinono-1,4-lactone oxidase
9714_at	25119.3	P	alpha-tubulin
9715_at	36.4	A	hypothetical protein
9716_at	26.3	A	hypothetical protein
9717_at	2465.6	P	similarity to N.crassa O-succinylhomoserine (thiol)-lyase
9718_at	2883.5	P	strong similarity to ZMS1 protein
9719_at	2333.9	P	similarity to A.brasilense nifR3 protein
9720_at	723.7	P	weak similarity to Synechocystis sp. hypothetical protein sll1188
9721_at	19958.9	P	cyclophilin-3 (cyclosporin-sensitive proline rotamase-3)
9722_at	4161.5	P	Bet5p\/18kD component of TRAPP
9723_at	2715.2	P	weak similarity to transcription factor
9724_at	17288.7	P	3-hydroxy-3-methylglutaryl-coenzyme A (HMG-CoA) reductase isozy
9725_at	24704.1	P	Prolyl cis-trans isomerase, also called proline rotamase or peptidylp
9726_at	30223.5	P	Ribosomal protein L6A (L17A) (rp18) (YL16)
9727_at	8282.7	P	similarity to YOR3141c and YNL087w
9728_at	8594.9	P	hypothetical protein
9729_at	13734.3	P	putative dihydroxyacetone kinase
9730_at	7714.3	P	Binds to catalytic subunit of DNA polymerase alpha (Pol1p)
9731_at	1774.1	P	similarity to C.elegans hypothetical protein
9732_at	17401.2	P	weak similarity to YAL042w
9733_at	173.2	A	hypothetical protein
9689_at	2028.9	P	120-kDa (largest) subunit of origin recognition complex (ORC)\; sho
9690_at	695.9	A	GTP-binding protein of the ras superfamily involved in termination of
9691_i_at	35914.6	P	Ribosomal protein S1B (rp10B)
9692_at	5953.2	P	Protein involved in mitochondrial import of fusion proteins
9693_at	1704.4	P	5 to 3 DNA helicase
9694_at	2791.4	P	43-kDa 8-oxo-guanine DNA glycosylase
9695_at	3340.6	P	similarity to C.elegans ZK370.4 protein
9696_at	31483.4	P	Suppressor of mec lethality
9697_at	586.7	A	questionable ORF
9698_at	1621	P	Catalytic A subunit of calcineurin, type 2B protein serine\/threonine
9699_at	29766.1	P	strong similarity to IMP dehydrogenases
9700_at	17820.1	P	strong similarity to IMP dehydrogenases
9701_at	7396.5	P	subunit of signal peptidase complex, homologous to mammalian pr
9702_at	732.1	P	Cytochrome b2 [L--lactate cytochrome-c oxidoreductase]
9703_at	8466.6	P	hypothetical protein
9704_at	19960	P	putative integral membrane protein
9705_at	10916.8	P	regulatory protein
9706_at	494	P	weak similarity to potato sucrose cleavage protein
9707_at	3711	P	RNA splicing and ER to Golgi transport
9708_at	13544.4	P	Glucose Signaling Factor
9709_at	515.4	A	questionable ORF
9710_at	1095.8	M	strong similarity to YJR054w
9666_at	3813.8	P	RNA splicing factor associated with U1 snRNP
9667_at	472.7	P	Component of rDNA transcription factor CF, which also contains Rr

9668_at	759.3	P	Carnitine O-acetyltransferase, peroxisomal and mitochondrial
9669_at	3380.6	P	hypothetical protein
9670_at	2441.7	P	hypothetical protein
9671_at	513.1	A	hypothetical protein
9672_at	3458.7	P	weak similarity to C.elegans hypothetical protein CELW03F8
9673_at	3833.9	P	putative alpha-mannosidase
9674_at	166.1	A	questionable ORF
9675_at	1417.8	P	similarity to YDR458c
9676_at	2006.5	P	similarity to YDR458c
9677_at	6728.2	P	Interacts with Rad51p by two hybrid analysis. mRNA is induced in me
9678_at	970.5	P	questionable ORF
9679_at	12920.8	P	Nuclear envelope protein with multiple putative transmembrane doma
9680_at	8559.9	P	hypothetical protein
9681_at	3518.4	P	hypothetical protein
9682_at	17496.1	P	Thiol-specific antioxidant
9683_at	10856.1	P	Homeobox-domain containing protein
9684_s_at	34980.1	P	Ribosomal protein S18B
9685_at	2042.9	P	ribosomal protein, mitochondrial
9686_s_at	21981.5	P	Ribosomal protein S17A (rp51A)
9687_at	2487.6	P	weak similarity to Nmd2p
9688_at	22626.5	P	Adenine phosphoribosyltransferase
9643_at	6559.8	P	uracil DNA glycosylase
9644_at	1137.6	P	hypothetical protein
9645_at	13422.9	P	Putative new 37kDa subunit of N-oligosaccharyltransferase complex
9646_at	5584.4	P	similarity to YDR438w
9647_at	620.4	P	Polymerase suppressor 2\; Suppressors of group II intron-splicing de
9648_at	4602.3	P	serine-threonine phosphatase Z
9649_at	7796.4	P	TFIID subunit
9650_at	5730.6	P	similarity to C.elegans hypothetical protein C14B1.5
9651_at	2465.3	P	hypothetical protein
9652_at	57.7	A	questionable ORF
9653_at	20798.7	P	Component of the COPII coat of certain ER-derived vesicles
9654_at	1580.2	P	hypothetical protein
9655_at	2466.6	P	transcription factor
9656_g_at	12279.4	P	transcription factor
9657_i_at	1221.3	P	questionable ORF
9658_r_at	976.8	P	questionable ORF
9659_at	3054.2	P	questionable ORF
9660_at	4595.6	P	Mitochondrial ribosomal protein MRPL39 (YmL39)
9661_at	16962.9	P	S-adenoslymethionine: delta 24-methyltransferase
9662_at	1729.6	P	jun-like transcription factor
9663_at	5775.9	P	hypothetical protein
9664_at	642.3	P	similarity to hypothetical S.pombe protein
9665_at	8373.2	P	lactoylglutathione lyase (glyoxalase I)
9620_at	379.6	P	hypothetical protein
9621_at	989.6	P	hypothetical protein
9622_at	6050.9	P	GTP-binding protein of the rab family\; required for homotypic fusion
9623_at	4740.8	P	protein kinase which functions at the G(sub)2\/M boundary
9624_at	11071.9	P	similarity to hypothetical S.pombe and C.elegans proteins
9625_at	1166.9	P	hypothetical protein
9626_at	4508.4	P	Protein required for sorting proteins to the vacuole
9627_at	4361.2	P	Protein required for protein synthesis

9628_at	20466.2	P	strong similarity to Plb1p
9629_at	579.8	P	hypothetical protein
9630_at	23076.8	P	Phospholipase B (lypophospholipase)
9631_at	5415	P	weak similarity to P.aeruginosa regulatory protein mmsR
9632_at	3372.7	P	weak similarity to hypothetical protein YDR352w
9633_at	20780.1	P	high affinity hexose transporter-2
9634_at	11875.3	P	CLU1 is similar to the Dictyostelium cluA gene
9635_at	2308.3	P	membrane protein required for core glycosylation
9636_at	5970.3	P	weak similarity to S.pombe hypothetical protein SPAC4F10
9637_at	12417.4	P	cytochrome P450 involved in C-22 denaturation of the ergosterol side
9638_at	3141.3	P	displays homologies to several transcription factors
9639_at	23.1	A	DBF2 Interacting Protein\; SNAP 25 homolog
9640_at	151.1	A	similarity to tetratricopeptide-repeat protein PAS10
9641_at	1861.6	P	Binds Sin3p in two-hybrid assay
9642_at	2935.4	P	Multicopy suppressor of fenpropimorph resistance (fen2 mutant), sh
9598_at	741.3	P	metal-binding transcriptional activator
9599_at	8384.3	P	ubiquitin conjugating enzyme
9600_at	572	M	putative mitochondrial GTPase
9601_at	12247	P	Mitochondrial ribosomal protein MRPL3 (YmL3)
9602_at	752.1	A	hypothetical protein
9603_at	1201	P	C3HC4 zinc-binding integral peroxisomal membrane protein
9604_at	6947.7	P	High level expression reduced Ty3 Transposition
9605_at	592.3	P	42 kDa protein that pysically associates with the PP2A and SIT4 prot
9606_at	949.1	P	weak similarity to human nuclear autoantigen
9607_at	593.8	P	hypothetical protein
9608_at	4011.8	P	similarity to YKL050c and human restin
9609_at	379.2	A	questionable ORF
9610_at	3690.5	P	Cytokinesis
9611_at	4768.2	P	Actin-related protein
9612_at	331.8	A	weak similarity to YPR201w
9613_at	641.4	P	Inner membrane protease (mitochondrial protein)
9614_at	1272.1	P	homolog of S. pombe cdc25
9615_at	6212.3	P	zinc finger protein
9616_at	7398.4	P	Homocitrate
9617_at	9198.8	P	suppressor of TFIIB mutations
9618_at	999.7	P	strong similarity to Yet1p
9619_at	635.7	A	weak similarity to Pseudomonas L-fucose dehydrogenase
9575_at	3427.1	P	Regulator of arginine-responsive genes with ARG81 and ARG82
9576_at	6155.2	P	putative transcriptional activator of alpha-specific genes
9577_at	9335.7	P	hypothetical protein
9578_at	6815.9	P	Nuclear pore complex protein that is member of GLFG repeat-contai
9579_at	1336.6	P	hypothetical protein
9580_at	18743.5	P	weak similarity to A.thaliana PRL1 protein
9581_at	219.8	A	Required for arrest in G1 in response to pheromone
9582_at	458.5	A	questionable ORF
9583_at	97.2	A	Binds Sin3p in two-hybrid assay and is part of large protein complex
9584_at	9741.8	P	vacuolar proton pumping ATPase, 110-kDa subunit\; not in vacuole
9585_at	8478.8	P	Protein required for cell cycle arrest in response to loss of microtubul
9586_at	2162.3	P	mitochondrial ADP\/ATP translocator
9587_at	552.8	A	hypothetical protein
9588_at	14063.3	P	multicopper oxidase
9589_at	898.4	P	15kDa subunit of the tetrameric tRNA splicing endonuclease

9590_at	1503.4	P	mitochondrial import receptor, heterodimerizes with Tom70p, prefere
9591_at	1542.9	P	component of the cleavage and polyadenylation factor CF I involved
9592_at	6709.3	P	acetylornithine acetyltransferase
9593_at	56.8	A	Regulator of Rim1p, required for IME1 expression
9594_at	1117.6	P	basic, hydrophilic protein of 59 kDa
9595_at	1104.2	A	appears to be required for the completion of nuclear membrane fusio
9596_at	181.7	A	Synthesis Of Var
9597_at	5082.7	P	hypothetical protein
9553_at	442.2	M	weak similarity to mouse transcription factor NF-kappaB
9554_at	735.3	P	hypothetical protein
9555_at	1965.8	P	2 Cys2-His2 zinc fingers at c-terminus, glutamine and asparagine ric
9556_at	8894.6	P	hypothetical protein
9557_at	11606.7	P	HMG-1 homolog, mitochondrial
9558_at	5636.8	P	weak similarity to C-terminal part of cytochrome b5 and b2
9559_at	1951	P	strong similarity to hypothetical S. pombe protein
9560_at	707	P	weak similarity to human Mi-2 protein
9561_at	391.2	P	questionable ORF
9562_at	3359.9	P	Precocious Dissociation of Sister chromatids
9563_at	1229.5	P	similarity to SNF7 protein
9564_at	958.7	P	chromosome transmission
9565_at	12627.5	P	phosphatidylinositol transfer protein
9566_at	3578.2	P	putative helicase
9567_at	790.1	A	May regulate NAM7 function, possibly at level of mRNA turnover
9568_at	264.6	A	hypothetical protein
9569_at	25738.2	P	alcohol dehydrogenase isoenzyme III
9570_at	257	A	putative pseudogene
9571_at	41.5	A	putative pseudogene
9572_at	3069	P	similarity to YKL105c
9573_at	681.4	A	questionable ORF
9574_at	801.3	A	hypothetical protein
9530_at	4107.7	P	similarity to multidrug resistance proteins
9531_at	8959.5	P	mitochondrial membrane ATPase of the CDC48\/PAS1\/SEC18 (AA
9532_at	1115.4	P	strong similarity to B. subtilis conserved hypothetical protein yhfK
9533_at	9876.2	P	nuclear protein localization factor
9534_at	4800.4	P	Protein localizes to actin cortical patches. Probable binding site on ac
9535_at	4084.1	P	weak similarity to Pwp2p
9536_at	220	A	58 kd component (Cbf3c) of the multisubunit Cbf3 kinetochore prot
9537_at	844.4	P	SNZ1 proximal ORF, stationary phase induced gene
9538_at	1596.3	P	encodes highly conserved 35 kDa protein that shows increased expr
9539_at	1659.5	P	weak similarity to M.genitalium hypothetical protein homolog MG442
9540_at	1274.3	P	hypothetical protein
9541_at	12028.8	P	similarity to P.ciliare possible apospory-associated protein
9542_at	3035.1	P	Homolog of samB gene of Aspergillus nidulans (deletion of samB res
9543_at	899.8	P	similarity to YBR002c
9544_at	1979.4	P	strong similarity to YKL121w
9545_at	2601.3	P	hypothetical protein
9546_at	753.7	A	protein kinase
9547_at	1167.4	P	Phosphoglucomutase
9548_at	790.5	A	Ku80 homolog, exhibits DNA binding activity on its own, associates
9549_at	60.2	A	hypothetical protein
9550_at	16521.5	P	acetolactate synthase
9551_at	8092.5	P	myosin I

9552_at	9945.5	P	similarity to aldehyde dehydrogenase
9507_at	664.9	P	weak similarity to MSN1 protein
9508_at	2672.3	P	hypothetical protein
9509_at	4647.4	P	similarity to folylpolyglutamate synthetases and strong similarity to YK
9510_at	424.6	A	similarity to B. subtilis conserved hypothetical proteins yoqW and yoa
9511_at	2394.5	P	similarity to YKL133c
9512_at	561	P	WD repeat protein (G-beta like protein) that interacts with the transla
9513_at	2342	P	WD repeat protein (G-beta like protein) that interacts with the transla
9514_at	207.3	A	component of spindle pole
9515_at	291.9	A	strong similarity to succinate dehydrogenase
9516_at	2174.6	P	similarity to YNL008c
9517_g_at	8610.4	P	similarity to YNL008c
9518_at	3398.6	P	questionable ORF
9519_at	7005.2	P	5-aminoimidazole-4-carboxamide ribonucleotide (AICAR) transformy
9520_at	6820.6	P	Ribosomal protein L15B (YL10) (L13B) (rp15R)
9521_at	740	A	hypothetical protein
9522_at	14558.6	P	resistance against Pichia farinosa killer toxin (SMK toxin) when expre
9523_at	732.9	P	weak similarity to YLR031w
9524_at	5557.7	P	transcriptional activator of glycolytic genes
9525_at	1522.2	P	hypothetical protein
9526_at	1178.5	P	Protein involved in silencing HMR, homologous to acetyltransferase
9527_at	7271.9	P	ExtraCellular Mutant
9528_at	5039	P	Nuclear pore membrane glycoprotein
9529_at	589.8	P	similarity to D.melanogaster Dreg-2 protein
9484_at	9854.1	P	similarity to human retinoblastoma-binding protein
9485_at	648.6	P	similarity to hypothetical S. pombe protein
9486_at	15.4	A	mRNA is induced early in sporulation
9487_at	1753.4	P	hypothetical protein
9488_at	2033.7	P	hypothetical protein
9489_at	259	A	questionable ORF
9490_at	3594.6	P	weak similarity to YIR013c and YLR013w
9491_at	202.6	A	interstrand crosslink repair protein
9492_at	853.3	A	GTP-binding protein
9493_at	1889.6	P	Serine\/threonine protein kinase, phosphorylates the mitotic activato
9494_at	1871.6	P	hypothetical protein
9495_at	420.3	A	hypothetical protein
9496_at	30121.1	P	Ribosomal protein L13B
9497_i_at	2241.2	P	Ribosomal protein S16A (rp61R)
9498_f_at	14148.7	P	Ribosomal protein S16A (rp61R)
9499_at	754.9	A	weak similarity to Mlp1p
9500_at	12513.6	P	mitochondrial cytosolically directed NADH dehydrogenase
9501_at	15516.5	P	p39 subunit of translation initiation factor eIF3
9502_at	3293.7	P	hypothetical protein
9503_at	8281	P	hypothetical protein
9504_at	17413	P	oligosaccharyl transferase glycoprotein complex, delta subunit
9505_at	2040.9	P	Inner membrane protease (mitochondrial protein)
9506_at	171.5	A	hypothetical protein
9462_at	1474.4	P	mitochondrial inner membrane protease
9463_at	9540.2	P	similarity to Asm4p
9464_at	559	A	questionable ORF
9465_at	509	A	Involved in proteolytic processing of Rim1p
9466_at	1692.5	P	weak similarity to E.coli hypothetical protein f402

9467_at	985.7	P	weak similarity to S.pombe hypothetical protein SPAC23C11
9468_at	4057.7	P	hypothetical protein
9469_at	854.9	P	weak similarity to E.coli ribosomal S8 protein
9470_at	78	A	questionable ORF
9471_at	54.3	A	Protein homologous to human Sin3 complex component SAP18, po
9472_at	2020.2	P	weak similarity to fruit fly ecdysone-inducible protein
9473_at	4056.8	P	Homologous to E coli dnaJ protein
9474_at	707.6	P	similarity to ATPases
9475_at	949.2	P	hypothetical protein
9476_at	2320.9	P	Predicted 758 amino acid polypeptide with poly-glutamine and poly-a
9477_at	2488.3	P	involved in plasmid maintenance
9478_at	3064.1	P	similarity to members of the mitochondrial carrier protein family
9479_at	159.7	A	MutL homolog, forms a complex with Pms1p and Msh2p to repair m
9480_at	447.3	P	contains an N-terminal Zn2Cys6 type zinc finger domain, a C-termin
9481_at	315.4	A	Aldehyde Dehydrogenase (NAD(P)+)
9482_g_at	1759	P	Aldehyde Dehydrogenase (NAD(P)+)
9483_at	1150.1	P	aldehyde dehydrogenase, (NAD(P)+), likely cytosolic
9439_at	507.4	P	similarity to YKL124w
9440_at	975.8	P	similarity to MSN1 protein
9441_at	337.9	A	questionable ORF
9442_s_at	23614.3	P	flocculent specific protein\; contains >35 repeats of the amino acid s
9443_at	16427.3	P	questionable ORF
9444_at	521.5	P	Cytoplasmic inhibitor of proteinase Pep4p
9445_at	24.4	A	protein of unknown function
9446_at	428.9	P	ExtraCellular Mutant
9447_at	2022	P	Protein involved in mitochondrial iron accumulation
9448_at	608.8	P	similarity to C.elegans hypothetical protein
9449_at	755.9	P	non-specific DNA binding protein
9450_at	668.9	P	similarity to YPL228w
9451_at	1588.2	P	similarity to YPL229w
9452_at	2118.9	M	Putative transcriptional repressor with proline-rich zinc fingers
9453_at	4265.7	P	SSO1 and SSO2 encode syntaxin homologs\; act in late stages of se
9454_at	2403.6	P	hypothetical protein
9455_at	1356.2	P	hypothetical protein
9456_at	29844.2	P	constitutively expressed heat shock protein
9457_g_at	21816.8	P	constitutively expressed heat shock protein
9458_at	2463.4	P	hypothetical protein
9459_at	3269.3	P	weak similarity to bacterial ribosomal protein S17
9460_at	6279.1	P	Glycine decarboxylase complex (P-subunit), glycine synthase (P-su
9461_at	933.7	P	has DNA helicase signature motifs
9416_at	6229.4	P	hypothetical protein
9417_at	388.9	A	similarity to mouse Tbc1 protein
9418_at	1736	P	Mitochondrial ribosomal protein MRPL24 (YmL24)
9419_at	510.4	A	questionable ORF
9420_i_at	17120.9	P	Ribosomal protein L36A (L39) (YL39)
9421_s_at	26123.1	P	Ribosomal protein L36A (L39) (YL39)
9422_at	3607.1	P	similarity to YPL250c
9423_at	587.1	P	hypothetical protein
9424_at	1372.8	P	Vti1p is a v-SNARE that interacts with two t-SNARES, Sed5p and P
9425_at	1904.9	P	spindle pole body associated protein
9426_at	6675.2	P	G(sub)1 cyclin
9427_at	6559.7	P	putative membrane protein

9428_at	2217.9	P	human xeroderma pigmentosum group A DNA repair gene homolog
9429_at	28601.5	P	C-8 sterol isomerase
9430_at	24552.8	P	Mitochondrial outer membrane protein\; forms the outer membrane i
9431_at	1956.8	P	weak similarity to D.melanogaster hypothetical protein DMC39E1
9432_at	23860.8	P	phosphofructokinase beta subunit
9433_at	286.6	A	weak similarity to hypothetical protein YNR014w
9434_at	1166.3	P	Similar to acetyl-coenzyme A carboxylase
9435_at	7701.4	P	mevalonate kinase
9436_at	2899.9	P	hypothetical protein
9437_at	3395.5	P	similarity to P.glauca late embryogenesis abundant protein and YBR
9438_at	1491.9	P	weak similarity to beta tubulins
9394_at	9653.1	P	weak similarity to myosins
9395_at	680.9	P	S. cerevisiae homologue of S. pombe cdc5+
9396_at	5319.2	P	dnaJ homolog
9397_at	27687.2	P	similarity to GAS1 protein
9398_at	14848.2	P	Serine Protein Kinase
9399_at	30373.1	P	GMP synthase
9400_at	2664.7	P	hypothetical protein
9401_at	1806.3	P	Establishes Silent omatin
9402_at	29847.2	P	48 kDa Phosphomevalonate kinase
9403_at	20745.5	P	weak similarity to photosystem II protein D2
9404_at	4672	P	similarity to S.pombe dihydrofolate reductase
9405_at	1716.4	P	encodes putative deubiquitinating enzyme
9406_at	722.2	P	localizes to discrete sites in rad50s mutants. Mre11p, Rad50p, Mer2
9407_at	1576.2	P	Mitochondrial ribosomal protein MRPL44 (YmL44)
9408_at	250	P	Mitochondrial ribosomal protein MRPL44 (YmL44)
9409_at	20830	P	similarity to ketoreductases
9410_at	1395	P	TFIID subunit
9411_at	3039.5	P	Mitochondrial RNA polymerase specificity factor
9412_at	17969.6	P	Protein required for processing of pre-rRNA
9413_f_at	426.2	P	Ribosomal protein S10B
9414_f_at	17269.7	P	Ribosomal protein S10B
9415_at	502.2	P	peripheral vaculor membrane protein\; putative Zn-finger protein
9371_at	286.3	A	involved in cell fusion during mating, also required for the alignment
9372_at	4692.4	P	strong similarity to YOR295w
9373_at	598.8	P	ribonuclease H
9374_at	23878.9	P	Protein involved in RNA processing and export from nucleus
9375_at	5426.8	P	TFIID subunit
9376_at	5956	P	similarity to CHS6 protein
9377_at	16825.2	P	Protein required for filamentous growth, cell polarity, and cellular elo
9378_at	2571.2	P	Ribonuclease III
9379_at	2162.3	P	U2 snRNP protein
9380_at	28261.2	P	DNA-binding protein, mtDNA stabilizing protein, mitochondrial inner
9381_s_at	29858	P	Ribosomal protein L20A (L18A)
9382_at	20115.4	P	Zinc- and cadmium-resistance protein
9383_at	356.4	A	similarity to Uth1p, Nca3p, YIL123w and Sun4p
9384_at	5196.1	P	questionable ORF
9385_at	1864.9	P	weak similarity to mouse thyrotropin-releasing hormone receptor
9386_at	10951.3	P	long-chain fatty acid--CoA ligase and synthetase 4
9387_at	12758.4	P	hypothetical protein
9388_at	1976.4	A	similarity to glutamate decarboxylases
9389_at	322.6	A	strong similarity to YKR076w and YGR154c

9390_at	25637.7	P	hyperosmolarity-responsive gene
9391_at	3748.7	P	hypothetical protein
9392_at	2101.4	P	strong similarity to YPL264c
9393_at	347.9	A	hypothetical protein
9349_at	1382.6	P	hypothetical protein
9350_at	15724.6	P	subunit VII of cytochrome c oxidase
9351_at	965.1	P	translational activator of cytochrome c oxidase subunit II
9352_at	769.5	P	hypothetical protein
9353_at	2819.3	P	hypothetical protein
9354_at	10758.5	P	Translation initiation factor eIF1A
9355_at	9056	P	115 kD regulatory subunit of trehalose-6-phosphate synthase\/phosp
9356_at	1103.7	P	similarity to S.pombe scn1 protein
9357_at	577.7	A	subunit of the histone deacetylase B complex
9358_at	4952.3	P	Cue1p assembles with Ubc7p. Cue1p recruits Ubc7p to the cytosolic
9359_at	522.1	M	hypothetical protein
9360_at	15765.1	P	similarity to A.thaliana hyp1 protein
9361_at	2233.3	P	mitochondrial inorganic pyrophosphatase
9362_at	625.3	P	U4\/U6 snRNA-associated splicing factor
9363_at	6500.6	P	weak similarity to C.elegans hypothetical protein CELT23B3
9364_at	1494.2	P	Upstream activation factor subunit
9365_at	304.7	A	Orotate phosphoribosyltransferase 2
9366_at	20057	P	desaturase\/hydroxylase enzyme
9367_at	4040.9	P	Negative regulator of cell polarity
9368_at	6394.1	P	Protease involved in ras and a-factor terminal proteolysis
9369_at	4180.1	P	Involved in the ubiquination pathway, possibly by functioning with Rs
9370_at	23641.8	P	ubiquitin-like protein
9326_at	2503.1	P	TFIIF interacting Component of CTD Phosphatase
9327_at	2898.8	P	similarity to phosphomannomutases
9328_at	221.6	A	strong similarity to aminotriazole resistance protein
9329_at	79.7	A	Zinc-cluster protein involved in activating gluconeogenic genes\; relat
9330_at	1654.6	P	hypothetical protein
9331_at	2504.1	P	basic, hydrophilic 67.5 kDa protein
9332_at	908.4	P	Initiator methionine tRNA 2 -O-ribosyl phosphate transferase
9333_at	1923.7	P	DNA binding protein
9334_at	1641.7	P	similarity to Ccr4p
9335_at	3040	P	Mitochondrial ribosomal protein MRPL33 (YmL33) (E. coli L30)
9336_at	844.1	P	Protein essential for mitochondrial biogenesis
9337_at	1768.6	P	strong similarity to hypothetical S.pombe and C.elegans proteins
9338_at	2193.2	P	hypothetical protein
9339_at	8889	P	Putative RNA-dependent helicase
9340_at	77.5	A	questionable ORF
9341_at	2754.2	P	similarity to ser/thr protein kinase
9342_at	17825.4	P	strong similarity to C.elegans hypothetical protein
9343_at	346.1	A	similarity to amidases
9344_at	363.9	P	Coiled-coil domain protein required for proper nuclear migration durir
9345_at	2386.8	A	questionable ORF
9346_at	30280.4	P	similarity to YGR273c
9347_at	13597.8	P	Probable component of serine palmitoyltransferase, which catalyzes
9348_at	27605.3	P	carboxypeptidase Y (proteinase C)
9304_at	6389.1	P	hypothetical protein
9305_at	393.2	P	weak similarity to hypothetical protein YJL062w
9306_at	2196.4	P	phosphoribosylpyrophosphate amidotransferase

9307_at	3414.4	P	mitochondrial ABC transporter protein
9308_at	3497.2	P	Integral membrane mitochondrial protein
9309_at	3978.5	P	alcohol dehydrogenase II
9310_at	1773.4	P	encodes putative deubiquitinating enzyme
9311_at	7430.8	P	questionable ORF
9312_at	26172.9	P	member of the glucanase gene family
9313_at	755.9	A	Protein with similarity to Gls1p and Gls2p (GB:Z49212)
9314_at	193.5	A	questionable ORF
9315_at	20844.8	P	cell surface glycoprotein 115-120 kDa
9316_at	28294.3	P	Karyopherin
9317_at	9233.7	P	~100 kDa cytoplasmic protein
9318_at	12151	P	similarity to YGR283c
9319_at	2265.6	P	Regulates activity of protein phosphatase 1, Glc7p, which is involvec
9320_at	11903.9	P	hypothetical protein
9321_at	1731.6	P	similarity to YKR089c and YOR081c
9322_at	10477.1	P	alpha-type of subunit of 20S proteasome
9323_at	19091.2	P	similarity to hypothetical S. pombe protein
9324_at	2866.1	P	similarity to YOR385w and YNL165w
9325_at	1688.8	A	questionable ORF
9281_at	1575.7	P	questionable ORF
9282_at	114.5	A	similarity to mucins, glucan 1,4-alpha-glucosidase and exo-alpha-sia
9283_at	16998.7	P	strong similarity to alcohol-dehydrogenase
9284_at	3751.3	P	Low-affinity Fe(II) transport protein
9285_at	1039.2	M	hypothetical protein
9286_s_at	18142.3	P	strong similarity to hypothetical proteins YPL273w and YLL062c
9287_s_at	628.6	A	strong similarity to YPL280w, YOR391c and YDR533c
9288_s_at	871.6	P	strong similarity to phosphopyruvate hydratases
9289_at	483.1	A	strong similarity to YBL108w, YCR103c and YKL223w
9290_f_at	3067.5	P	strong similarity to members of the Srp1p/Tip1p family
9291_at	20510.7	P	protein associated to the ATP synthase
9292_at	736.6	P	hypothetical protein identified by SAGE
9293_at	969.2	A	identified by SAGE
9294_at	10026.7	P	hypothetical protein
9295_g_at	12615.6	P	hypothetical protein
9296_at	654.1	P	non-annotated SAGE orf Found reverse in NC_001145 between 159
9297_at	1242.1	P	non-annotated SAGE orf Found reverse in NC_001145 between 390
9298_at	438.8	P	non-annotated SAGE orf Found forward in NC_001145 between 318
9299_at	556	A	non-annotated SAGE orf Found reverse in NC_001145 between 122
9300_at	169.5	A	non-annotated SAGE orf Found reverse in NC_001145 between 503
9301_at	523.8	A	non-annotated SAGE orf Found reverse in NC_001145 between 503
9302_at	109.7	A	non-annotated SAGE orf Found reverse in NC_001145 between 768
9303_at	663.6	M	non-annotated SAGE orf Found forward in NC_001145 between 769
9258_at	42.4	A	non-annotated SAGE orf Found forward in NC_001145 between 460
9259_at	1416.6	P	non-annotated SAGE orf Found forward in NC_001145 between 171
9260_at	1263.1	A	non-annotated SAGE orf Found reverse in NC_001145 between 347
9261_at	186.4	A	non-annotated SAGE orf Found forward in NC_001145 between 363
9262_at	517.6	P	non-annotated SAGE orf Found forward in NC_001145 between 390
9263_at	945.3	P	non-annotated SAGE orf Found reverse in NC_001145 between 492
9264_at	1976.1	A	non-annotated SAGE orf Found forward in NC_001145 between 632
9265_at	2336.2	P	non-annotated SAGE orf Found forward in NC_001145 between 752
9266_at	497.4	A	non-annotated SAGE orf Found forward in NC_001145 between 762
9267_at	12395.2	P	non-annotated SAGE orf Found reverse in NC_001145 between 849

9268_at	764.2	P	non-annotated SAGE orf Found forward in NC_001145 between 863
9269_at	2989.7	A	non-annotated SAGE orf Found reverse in NC_001145 between 910
9270_at	43.2	A	non-annotated SAGE orf Found forward in NC_001145 between 272
9271_at	11047.6	P	non-annotated SAGE orf Found reverse in NC_001145 between 426
9272_at	364.5	A	non-annotated SAGE orf Found forward in NC_001145 between 486
9273_at	45	A	non-annotated SAGE orf Found reverse in NC_001145 between 501
9274_at	283.9	A	non-annotated SAGE orf Found reverse in NC_001145 between 299
9275_g_at	172.9	A	non-annotated SAGE orf Found reverse in NC_001145 between 299
9276_at	121	A	non-annotated SAGE orf Found reverse in NC_001145 between 300
9277_at	251	M	non-annotated SAGE orf Found forward in NC_001145 between 115
9278_at	151	A	non-annotated SAGE orf Found forward in NC_001145 between 286
9279_at	372.5	P	non-annotated SAGE orf Found reverse in NC_001145 between 297
9280_at	476.9	A	non-annotated SAGE orf Found reverse in NC_001145 between 433
9234_at	394	A	non-annotated SAGE orf Found reverse in NC_001145 between 433
9235_at	1770.6	P	non-annotated SAGE orf Found forward in NC_001145 between 433
9236_at	2711.5	A	non-annotated SAGE orf Found forward in NC_001145 between 434
9237_at	865.3	P	non-annotated SAGE orf Found forward in NC_001145 between 465
9238_at	612	M	non-annotated SAGE orf Found reverse in NC_001145 between 465
9239_at	20.8	A	non-annotated SAGE orf Found forward in NC_001145 between 478
9240_at	164.4	A	non-annotated SAGE orf Found forward in NC_001145 between 480
9241_at	804.9	P	non-annotated SAGE orf Found forward in NC_001145 between 480
9242_i_at	8	A	non-annotated SAGE orf Found forward in NC_001145 between 481
9243_at	40.5	A	non-annotated SAGE orf Found forward in NC_001145 between 481
9244_at	109	A	non-annotated SAGE orf Found forward in NC_001145 between 482
9245_at	1546.9	P	non-annotated SAGE orf Found reverse in NC_001145 between 511
9246_at	1733.5	A	non-annotated SAGE orf Found reverse in NC_001145 between 556
9247_g_at	1612.7	A	non-annotated SAGE orf Found reverse in NC_001145 between 556
9248_at	957.6	P	non-annotated SAGE orf Found reverse in NC_001145 between 556
9249_i_at	0	A	non-annotated SAGE orf Found forward in NC_001145 between 625
9250_f_at	0.1	A	non-annotated SAGE orf Found forward in NC_001145 between 625
9251_at	784.2	P	non-annotated SAGE orf Found reverse in NC_001145 between 646
9252_at	16780.1	P	non-annotated SAGE orf Found reverse in NC_001145 between 762
9253_at	10871.9	P	non-annotated SAGE orf Found reverse in NC_001145 between 762
9254_at	399.9	A	non-annotated SAGE orf Found forward in NC_001145 between 837
9255_at	116.2	A	non-annotated SAGE orf Found reverse in NC_001145 between 915
9256_at	24.2	A	non-annotated SAGE orf Found reverse in NC_001145 between 982
9257_at	13	A	non-annotated SAGE orf Found reverse in NC_001145 between 133
9209_at	14928.7	P	non-annotated SAGE orf Found reverse in NC_001145 between 279
9210_at	4208	P	non-annotated SAGE orf Found forward in NC_001145 between 498
9211_at	14174.7	P	non-annotated SAGE orf Found reverse in NC_001145 between 624
9212_at	140.9	A	non-annotated SAGE orf Found reverse in NC_001145 between 797
9213_at	4.7	A	non-annotated SAGE orf Found reverse in NC_001145 between 151
9214_at	104.4	A	non-annotated SAGE orf Found reverse in NC_001145 between 234
9215_at	372.4	A	non-annotated SAGE orf Found forward in NC_001145 between 271
9216_at	324.5	P	non-annotated SAGE orf Found reverse in NC_001145 between 302
9217_at	313.6	A	non-annotated SAGE orf Found forward in NC_001145 between 337
9218_at	567.2	P	non-annotated SAGE orf Found forward in NC_001145 between 426
9219_i_at	166.9	A	non-annotated SAGE orf Found forward in NC_001145 between 483
9220_r_at	51	A	non-annotated SAGE orf Found forward in NC_001145 between 483
9221_f_at	4	A	non-annotated SAGE orf Found forward in NC_001145 between 483
9222_at	44.1	A	non-annotated SAGE orf Found reverse in NC_001145 between 509
9223_at	52.5	A	non-annotated SAGE orf Found forward in NC_001145 between 611

9224_at	4989.7	P	non-annotated SAGE orf Found reverse in NC_001145 between 623
9225_at	1145.6	P	non-annotated SAGE orf Found forward in NC_001145 between 652
9226_at	463.7	M	non-annotated SAGE orf Found forward in NC_001145 between 667
9227_i_at	25107.9	P	non-annotated SAGE orf Found reverse in NC_001145 between 671
9228_r_at	6798.1	P	non-annotated SAGE orf Found reverse in NC_001145 between 671
9229_i_at	2327.8	P	non-annotated SAGE orf Found forward in NC_001145 between 733
9230_r_at	904.3	P	non-annotated SAGE orf Found forward in NC_001145 between 733
9231_s_at	4489.7	P	non-annotated SAGE orf Found forward in NC_001145 between 733
9232_at	440.3	A	non-annotated SAGE orf Found forward in NC_001145 between 733
9233_at	3633.8	P	non-annotated SAGE orf Found forward in NC_001145 between 774
9186_at	3178.3	P	snRNA
9187_i_at	541.7	A	Centromere
9188_at	217.8	P	snRNA
9189_at	18201	P	snRNA
9190_at	707.4	P	snRNA
9191_at	3289.9	P	snRNA
9192_at	617.8	M	snRNA
9193_at	3060.9	P	snRNA
9194_at	1359.7	P	snRNA
9195_at	3124.4	P	snRNA
9196_s_at	59.9	A	similarity to M.verrucaria cyanamide hydratase, identical to hypotheti
9197_s_at	4928.6	P	SNZ2 proximal ORF, stationary phase induced gene
9198_s_at	1242.2	P	Snooze: stationary phase-induced gene family
9199_at	6781.1	P	Hypothetical aryl-alcohol dehydrogenase
9200_at	8315.8	P	histone deacetylase
9201_at	1686	P	Member of the AAA-protein family that includes NSFp and PEX1p
9202_at	427.5	A	Protein of the mitochondrial inner membrane with similarity to E. coli
9203_at	20088.6	P	Cell-cycle regulation protein, may be involved in the correct timing o
9204_at	2337.3	P	similarity to YOL003c, YLR246w and C.elegans hypothetical protein
9205_at	916.8	P	FIG4 expression is induced by mating factor.
9206_at	122.4	A	hypothetical protein
9207_at	14070.6	P	strong similarity to YCR094w and YNR048w
9208_at	24563.9	P	Cell wall beta-glucan assembly
9163_at	14051.7	P	weak similarity to Vcx1p
9164_at	3100.1	P	strong similarity to S.pombe Bem46 protein
9165_at	220.1	A	questionable ORF
9166_at	16.3	A	hexose transport protein
9167_at	2062.1	P	similarity to A.thaliana PRL1/2 protein
9168_at	1469.2	P	prephenate dehydratase
9169_at	8083.5	P	essential for assembly of a functional F1-ATPase
9170_at	1637.1	P	positive regulator of allophanate inducible genes
9171_at	4252.7	P	similarity to C.elegans hypothetical protein
9172_at	6247.5	P	subunit 2 of replication factor RF-A\; 29\% identical to the human p34
9173_at	960.1	P	hypothetical protein
9174_at	1612.4	P	similarity to S.pombe hypothetical protein SPAC24H6.02c
9175_at	1896.6	A	Binds Sin3p in two-hybrid assay and is present in a large protein com
9176_at	16549	P	similarity to S.pombe and C.elegans hypothetical proteins
9177_at	24393.1	P	43.1 kDa Serine\/threonine\/tyrosine protein kinase
9178_at	4527.3	P	ribosomal protein of the small subunit, mitochondrial
9179_at	13925.8	P	similarity to C-term. of A.nidulans regulatory protein (qutR)
9180_at	1153.6	P	similarity to Ypt1p and rab GTP-binding proteins
9181_at	2213.2	P	hypothetical protein

9182_s_at	15002	P	Ribosomal protein S19B (rp55B) (S16aB) (YS16B)
9183_s_at	12563.8	P	Ribosomal protein L18B (rp28B)
9184_at	13015.9	P	Ribosomal protein L18B (rp28B)
9185_at	29125.1	P	hypothetical protein
9140_at	1184	P	exhibits homology to Trf4p and Top1p
9141_at	3353.9	P	protein kinase, homologous to Ste20p, interacts with CDC42
9142_at	3716.3	P	similarity to S.pombe hypothetical protein SPAC23D3.13c
9143_at	457.1	A	questionable ORF
9144_at	419.4	P	hypothetical protein
9145_at	1044.7	P	hypothetical protein
9146_at	1089.3	P	Multicopy Suppressor of Bud Emergence
9147_at	6405.5	P	Pseudouridine synthase
9148_at	6610.9	P	N-glycosylated integral plasma membrane protein
9149_at	3451.3	P	Subunit 3 of Replication Factor C\; homologous to human RFC 36 kD
9150_at	2686.5	P	G(sub)1 cyclin that associates with PHO85
9151_at	17155	P	strong similarity to C.elegans hypothetical protein
9152_at	18561.3	P	non-clathrin coat protein involved in transport between ER and Golgi
9153_at	2232.1	P	Cold sensitive U2 snRNA Supressor
9154_at	506.5	A	hypothetical protein
9155_at	6787.2	P	Mitochondrial ribosomal protein MRPL10 (YmL10)
9156_at	11966.2	P	Putative integral membrane protein containing novel cysteine motif.
9157_at	1023.1	M	involved in processsing of tRNAs and rRNAs
9158_at	5510.5	P	strong similarity to YDR214w
9159_at	14419.4	P	sterol C-14 reductase
9160_at	753	P	hypothetical protein
9161_at	3471.6	P	similarity to YLR187w
9162_at	176	A	homoserine O-trans-acetylase
9118_at	101.9	A	questionable ORF
9119_at	1371.2	P	similarity to human band 3 anion transport protein
9120_at	3231.9	P	similarity to glycerate- and formate-dehydrogenases
9121_at	2958.2	P	topoisomerase I interacting factor 1
9122_at	656.3	P	Protein with coiled-coil domain essential for vesicular transport
9123_at	4609.6	P	contains formin homology domains\; homologous to BNR1 (BNI1 rela
9124_at	1076.8	P	Protein highly homologous to permeases Can1p and Lyp1p for basic
9125_at	1189.1	A	hypothetical protein
9126_at	15454.1	P	lysine permease
9127_at	4707.2	P	Phosphatidylinositol 4-kinase
9128_at	118.2	A	questionable ORF
9129_at	530.8	A	similarity to human protein KIAA0174
9130_at	2334.4	P	weak similarity to Sec14p
9131_at	18879.4	P	YIP1-Interacting Factor, shows similarity to NADH dehydrogenases
9132_at	4118.3	P	DNA polymerase II
9133_at	3421.3	P	Fifth largest subunit of origin recognition complex\; contains possible
9134_at	225.4	A	hypothetical protein
9135_at	4163.2	P	Antioxidant protein and metal homeostasis factor, protects against o
9136_at	3407.5	P	hypothetical protein
9137_at	586.9	P	Interacts with SNF1 protein kinase
9138_at	6410.8	P	similarity to bacterial dihydropteroate synthase
9139_at	15266.8	P	strong similarity to nucleic acid-binding proteins
9095_at	457.8	A	hypothetical protein
9096_at	1493.6	P	hypothetical protein
9097_at	4647.7	P	ribosomal protein of the large subunit (YmL30), mitochondrial

9098_at	6122	P	RNA recognition motif-containing protein that participates in sequenc
9099_at	735.6	P	protein contains a purine-binding domain, two heptad repeats and a
9100_at	239.3	P	similarity to YDR109c
9101_at	10686.9	P	49-kDa alpha subunit of RNA polymerase A
9102_at	5220.4	P	cysteinyl-tRNA synthetase
9103_at	4204.3	P	similarity to D.melanogaster SET protein
9104_at	839.4	P	hypothetical protein
9105_at	23127.1	P	translation initiation factor 3 (eIF3)
9106_at	11781	P	transmembrane protein
9107_at	1262.3	P	similarity to human hypothetical protein KIAA0404
9108_at	11618.6	P	Glucose-6-phosphate dehydrogenase
9109_at	2331.3	P	strong similarity to K.marxianus LET1 protein
9110_at	6723.9	P	Ca2+-dependent serine protease
9111_at	314.3	P	Yeast putative Transmembrane Protein
9112_at	4505.7	P	component of RNA polymerase II holoenzyme\/mediator complex
9113_at	393.3	A	questionable ORF
9114_at	517.7	P	weak similarity to mouse hemoglobin zeta chain
9115_at	3999.5	P	Is required to link Chs3p and Chs4p to the septins
9116_at	4633.4	P	hypothetical protein
9117_at	7935	P	weak similarity to Sec14p
9073_at	1823.2	P	weak similarity to mammalian transcription elongation factor elongin
9074_at	4185.7	P	transcriptional regulator, putative glutathione transferase
9075_at	1512.2	P	similarity to dnaJ-like proteins
9076_at	423.9	M	questionable ORF
9077_at	125	A	questionable ORF
9078_at	2354.8	P	chaotic nuclear migration\; predicted mass is 67kDa
9079_at	1009.3	P	hypothetical protein
9080_at	237.3	A	Aut2p interacts with Tub1p and Tub2p\; Aut2p forms a protein compl
9081_at	4473.1	P	functionally related to TFIIB, affects start site selection in vivo
9082_at	4412.2	P	Component of nuclear RNase P and RNase MRP
9083_at	16716.1	P	adenylosuccinate synthetase
9084_at	15076.1	P	mannosyltransferase
9085_at	91.7	A	similarity to E.coli hypothetical protein in serS 5 region
9086_at	3655.8	P	weak similarity to E.coli bis(5 -nucleosyl)-tetraphosphatase
9087_at	5625.8	P	repressor activator protein
9088_at	1352.7	P	similarity to hypothetical S. pombe protein
9089_at	313.5	A	23 kDa peroxisome associated protein, binds Pex14p
9090_at	1929.4	P	hypothetical protein
9091_at	8771.8	P	weak simlarity to C.cardunculus cypro4 protein
9092_at	1119.1	P	hypothetical protein
9093_at	225.3	A	encodes protein with RNA-binding motifs required for MRE2-depend
9094_s_at	29750.4	P	Heat shock protein of HSP70 family, homolog of SSB1
9050_at	26250.1	P	weak similarity to Colletotrichum gloeosporioides nitrogen starvation-
9051_at	5341.1	P	similarity to M.jannaschii hypothetical protein MJ1073
9052_at	878	P	similarity to structure-specific recognition proteins
9053_at	25.5	A	questionable ORF
9054_g_at	217.7	A	questionable ORF
9055_at	427.6	A	sporulation-specific protein
9056_at	304.5	A	weak similarity to B.subtilis CDP-diacylglycerol--serine O-phosphatid
9057_at	430.6	P	peroxisomal 2,4-dienoyl-CoA reductase
9058_at	1673.4	P	involved in regulation of carbon metabolism
9059_at	1022.2	M	strong similarity to human TGR-CL10C

9060_at	1896.4	P	Activates transcription of glycolytic genes\; homologous to GCR1\; m
9061_at	66.8	A	questionable ORF
9062_at	2302.4	P	Protein involved in regulation of cell size
9063_at	21.9	A	sporulation-specific protein with a leucine zipper motif, regulated by
9064_at	1769.9	P	hypothetical protein
9065_at	30.7	A	strong similarity to YDL222c and similarity to Sur7p
9066_at	1139.2	P	hypothetical protein
9067_at	6883.3	P	chitin synthase 1
9068_at	1389.5	P	similarity to Synechocystis hypothetical protein
9069_at	31241.3	P	hypothetical protein
9070_at	8808.2	P	karyopherin alpha homolog of 60 kDa
9071_at	1921.6	P	involved in spindle pole body duplication and karyogamy, interacts w
9072_at	628.6	A	hypothetical protein
9028_at	23671.5	P	a deubiquitinating enzyme
9029_at	2685.4	P	ribosomal protein of the large subunit, mitochondrial
9030_at	795.4	P	questionable ORF
9031_at	3133.6	P	protein kinase homolog
9032_at	2640.3	P	weak similarity to S.pombe hypothetical protein
9033_at	5239.9	P	similarity to hypothetical S. pombe protein
9034_at	708.6	P	hypothetical protein
9035_at	27816.7	P	Ribosomal protein S3 (rp13) (YS3)
9036_at	2255.7	P	hypothetical protein
9037_at	4908.6	P	weak similarity to Hkr1p
9038_at	19285.4	P	similarity to S.pombe Rnp24p
9039_at	2452.1	P	hypothetical protein
9040_at	2695.5	P	multicopy suppressor of bem1 mutation, may be involved in G-protei
9041_at	2536.8	P	Component of the anaphase-promoting complex
9042_at	324.3	A	questionable ORF
9043_at	1050.9	P	questionable ORF
9044_at	22843	P	Phosphatidylserine Decarboxylase 1
9045_at	3104.6	P	similarity to C.elegans ZK688.3 protein and E.coli hpcEp
9046_at	3455.4	P	CREB like repressor, bZIP protein that binds to CRE motifs, interact
9047_at	1680	P	hypothetical protein
9048_at	2694.1	P	similarity to YOR385w and YMR316w
9049_at	2569.7	P	hypothetical protein
9005_at	3931.6	P	translation elongation factor eEF4
9006_s_at	22355.1	P	Ribosomal protein L42A (YL27) (L41A)
9007_at	3090.9	P	Protein kinase
9008_at	8450.5	P	YGP1 encodes gp37, a glycoprotein synthesized in response to nutr
9009_at	1206.3	P	hypothetical protein
9010_at	930.8	P	hypothetical protein
9011_at	4778	P	weak similarity to S.pombe hypothetical protein SPAC10F6
9012_at	12777.3	P	similarity to YHR133c
9013_at	574.9	P	hypothetical protein
9014_at	3618.5	P	membrane-bound casein kinase I homolog
9015_at	9895.1	P	Putative homolog of subunit 4 of bovine prefoldin, a chaperone com
9016_at	2462.1	P	hypothetical protein
9017_at	8967.3	P	31-kDa subunit of RNA polymerase III (C)\; HMG1 like protein
9018_at	1657.3	P	hypothetical protein
9019_at	3405	P	weak similarity to S.pombe hypothetical protein
9020_at	2025.9	P	cofactor B
9021_at	2020.3	P	Sm-like protein

9022_at	549.5	P	hypothetical protein
9023_at	1979.8	A	mating a-factor pheromone precursor
9024_at	476.4	P	similarity to YHR131c
9025_at	193.8	A	hypothetical protein
9026_at	2079.4	P	Ammonia transport protein
9027_at	4143.5	P	Adenosine deaminase\/adenine aminohydrolase
8982_i_at	199.6	A	questionable ORF
8983_s_at	1959.5	A	questionable ORF
8984_at	32826.9	P	70-kDa adenylyl cyclase-associated protein
8985_at	10460.9	P	putative mitochondrial S4 ribosomal protein
8986_at	2639.4	P	similarity to neurofilament triplet M protein
8987_at	18839.7	P	peptidylprolyl cis-trans isomerase
8988_at	14793.4	P	similarity to C.carbonum toxD gene
8989_at	1969.7	P	hypothetical protein
8990_at	2257.2	P	similarity to A.ambisexualis antheridiol steroid receptor
8991_at	3944.8	P	Mitochondrial import receptor complex protein
8992_at	21134.2	P	sn-1,2-diacylglycerol cholinephosphotransferase
8993_at	1129.6	P	weak similarity to M.pneumoniae uridine kinase udk
8994_at	335.4	A	Similar to human tumor suppressor gene known as TEP1, MMAC1
8995_at	2207.9	P	similarity to C.elegans hypothetical protein
8996_at	397	P	spindle pole body component, associates in a complex with Spc97p
8997_at	10149.1	P	Protein with similarity to mammalian monocarboxylate transporters
8998_at	2998.9	P	similarity to hypothetical S. pombe protein
8999_at	11825.8	P	weak similarity to C.jejuni serine protease
9000_at	197.9	A	hypothetical protein
9001_at	7231.3	P	70 kDa mitochondrial specialized import receptor of the outer membr
9002_at	64.9	A	questionable ORF
9003_at	5177.8	P	weak similarity to M.jannaschii hypothetical protein MJ1257
9004_at	999.3	P	essential suppressor of the respiratory deficiency of a pet mutant
8959_at	64.5	A	carbon-catabolite sensitive malate synthase
8960_at	1547.1	P	weak similarity to RING zinc finger protein from Gallus gallus
8961_at	1761.2	P	weak similarity to S.pombe hypothetical protein SPAC23C11
8962_at	2903.7	P	questionable ORF
8963_at	28535.6	P	subunit common to RNA polymerases I (A) and III (C)
8964_at	20342.7	P	ATP-dependent RNA helicase of DEAD box family
8965_at	21255.5	P	ATP-dependent RNA helicase of DEAD box family
8966_at	20023.7	P	cytochrome b5
8967_at	10016.6	P	weak similarity to fruit fly RNA-binding protein
8968_at	451.2	A	weak similarity to cytochrome-c oxidase
8969_at	4289	P	strong similarity to YOR110w
8970_at	3083.5	P	similarity to human AF-9 protein
8971_at	2837.4	P	inositol polyphosphate 5-phosphatase
8972_at	54.6	A	questionable ORF
8973_at	22182.7	P	alpha-isopropylmalate synthase (2-Isopropylmalate Synthase)
8974_at	2247.3	P	member of the leucine zipper family of transcriptional activators
8975_at	7319.8	P	DNA polymerase I alpha subunit, p180
8976_at	5674.6	P	similarity to YKL146w
8977_at	5856.3	P	hypothetical protein
8978_at	8719.9	P	similarity to YNL032w, YNL056w and YDR067c
8979_at	6284.1	P	Ras proto-oncogene homolog
8980_at	2104.3	P	involved in transcriptional regulation of PHO5
8981_at	21149	P	Ribosomal protein S7B (rp30)

8936_at	26407.5	P	Ribosomal protein S7B (rp30)
8937_at	1558.4	M	strong similarity to YOR092w
8938_at	1266.8	P	similarity to S.pombe hypothetical protein
8939_at	41.3	A	rab5-like GTPase involved in vacuolar protein sorting and endocytosi
8940_at	64.8	A	similarity to hypothetical C. elegans proteins Y48E1C.2 and Y48E1C.
8941_at	3044.9	P	similarity to chicken h-caldesmon, Uso1p and YKL201c
8942_at	5068.4	P	GTP-binding protein of the rho subfamily of ras-like proteins
8943_at	43.4	A	questionable ORF
8944_at	5110.2	P	topoisomerase II, Top2p localizes to axial cores in meiosis
8945_at	2183.7	P	weak similarity to synaptogamines
8946_at	1944.2	P	hypothetical protein
8947_at	14636.6	P	Protein involved in propagation of M2 dsRNA satellite of L-A virus
8948_at	3095.2	P	Required for endocytosis and organization of the cytoskeleton
8949_at	2807.6	P	weak similarity to rabbit peroxisomal Ca-dependent solute carrier
8950_at	1733.6	P	MutL homolog, similar to Mlh1p, associates with Mlh1p, possibly for
8951_at	2186.6	P	similarity to ribosomal protein S13
8952_at	4975.3	P	hypothetical protein
8953_at	12649.1	P	tropomyosin I
8954_at	4140	P	hypothetical protein
8955_at	1299.1	P	similarity to dnaJ protein homolog YDJ1
8956_at	1913	P	negative regulator of Ras cAMP pathway, shares weak homology wi
8957_at	9203.5	P	similarity to YHR088w and C.elegans hypothetical protein F44G4.1
8958_at	3452.4	P	Protein of unknown function
8914_at	4238.4	P	mitochondrial lysine-tRNA synthetase
8915_at	1770.7	P	RNase H(35), a 35 kDa ribonuclease H
8916_at	13910.6	P	Dihydrolipoamide acetyltransferase component (E2) of pyruvate deh
8917_at	6738.1	P	translocase of the outer mito. membrane
8918_at	22667.6	P	Ribosomal protein L16B (L21B) (rp23) (YL15)
8919_at	1211.9	P	Fork Head homolog two
8920_i_at	22978.9	P	Ribosomal protein L9B (L8B) (rp24) (YL11)
8921_s_at	12941.1	P	Ribosomal protein L9B (L8B) (rp24) (YL11)
8922_at	35268.1	P	Protein involved in the aging process
8923_at	5788	P	similarity to resistance proteins
8924_at	9925.5	P	yeast dnaJ homolog (nuclear envelope protein)\; heat shock protein
8925_at	2198.4	P	weak similarity to Mycoplasma protoporphyrinogen oxidase
8926_at	7899.7	P	RNA-binding (zeta) subunit of translation initiation factor 3 (eIF-3)
8927_at	18134.8	P	90-kDa protein, located in nucleolus, that is homologous to a human
8928_at	1910.6	P	Actin-related protein
8929_at	4302.9	P	similarity to YIL117c
8930_at	781.1	A	questionable ORF
8931_at	7685.2	P	similarity to YNL032w and YNL099c
8932_at	33118.9	P	Outer mitochondrial membrane porin (voltage-dependent anion cha
8933_at	2796.8	P	vacuolar protein
8934_at	1353.6	P	Tyrosine protein phosphatase involved in adaptation response to ph
8935_at	17634.8	P	Cytochrome-c oxidase chain Va
8891_at	1574.3	P	hypothetical protein
8892_at	536.2	A	hypothetical protein
8893_at	3402.2	P	putative zinc finger protein
8894_at	5423.8	P	Required for aspargine-linked glycosylation
8895_at	974.9	P	similarity to probable transcription factor Ask10p and hypothetical p
8896_at	4802.1	P	hypothetical protein
8897_at	8193.1	P	strong similarity to human leukotriene-A4 hydrolase

8898_at	869	P	questionable ORF
8899_at	949.2	P	Bypass of PAM1
8900_at	2094.5	P	weak similarity to Mlp1
8901_at	1042	P	weak similarity to M.genitalium alanine--tRNA ligase
8902_at	2843.1	P	90 kd subunit of TFIIIB, also called TFIIIB90 or B or B 90 compone
8903_at	1228.9	P	hypothetical protein
8904_at	8506.3	P	alpha-4-beta-4 subunit of mitochondrial isocitrate dehydrogenase 1
8905_at	4493.8	P	involved in secretion of proteins that lack classical secretory signal se
8906_at	1815.4	P	hypothetical protein
8907_s_at	564.8	A	nearly identical to YNL018c
8908_s_at	170.4	A	nearly identical to YNL019c
8909_at	5299.5	P	Tyrosine phosphatase
8910_at	25422.8	P	Histone H3 (HHT1 and HHT2 code for identical proteins)
8911_s_at	26173.7	P	Histone H4 (HHF1 and HHF2 code for identical proteins)
8912_at	3942.1	P	Putative mannosyltransferase of the KRE2 family
8913_at	606.2	A	questionable ORF
8868_at	4620.9	P	putative transcription factor
8869_at	4971.2	P	similarity to S.pombe hypothetical protein
8870_at	937.3	P	C-type cyclin associated with the Ssn3p cyclin-dependent kinase
8871_at	1277.9	P	weak similarity to YBR271w and YJR129c
8872_at	3288.8	P	Transcription factor homolog\; similarity to Drosophila melanogaster s
8873_at	6349.3	P	weak similarity to C.burnetii FMU protein
8874_at	2655.4	P	histone deacetylase, shares sequence similarity with Rpd3p, Hos1p,
8875_at	473.2	A	Predicted Ser\/thr kinase
8876_i_at	6020.2	A	hypothetical protein
8877_r_at	163.8	A	hypothetical protein
8878_s_at	74	A	hypothetical protein
8879_at	18229.2	P	poly(A)+ RNA-binding protein
8880_at	5518.8	P	Proteinase inhibitor I2B (PBI2), that inhibits protease Prb1p (yscB)
8881_at	1863.3	A	translation elongation factor eEF3 homolog
8882_at	584.2	P	questionable ORF
8883_at	258.8	A	encodes a protein with high similarity to phospholipase B
8884_at	2330.7	P	similarity to hypothetical A. thaliana protein T14G11.21
8885_at	9611.7	P	weak similarity to B.subtilis hypothetical protein ykrX
8886_at	370	A	peroxisomal NADP-dependent isocitrate dehydrogenase
8887_at	5479.3	P	similarity to YMR119w
8888_at	23855.6	P	sit4 suppressor, dnaJ homolog
8889_at	4932.1	P	Required for amino acid permease transport from the Golgi to the ce
8890_at	3921.9	P	Mitochondrial ribosomal protein MRP7 (YmL2) (E. coli L27)
8845_at	5025.9	P	hypothetical RNA-binding protein
8846_at	666.9	A	Member of family of mitochondrial carrier proteins
8847_at	11257.6	P	Significant sequence similarity to RPL7B, but neither can functionally
8848_at	2350.8	P	an ORF of unknown function located in a centromeric region duplicat
8849_at	23855.1	P	citrate synthase. Nuclear encoded mitochondrial protein.
8850_at	1044.1	M	Putative transmembrane protein
8851_at	2210.3	P	34-kDa subunit of RNA polymerase III (C)
8852_at	147.7	P	weak similarity to bovine interferon gamma precursor
8853_at	48.5	A	questionable ORF
8854_at	2013.3	P	hydrophilic protein\; has cysteine rich putative zinc finger esential for
8855_at	1589.9	P	Protein involved in autophagocytosis during starvation
8856_at	5052.4	P	weak similarity to human phosphatidylcholine--sterol O-acyltransfera
8857_at	8116.2	P	hypothetical protein

8858_at	1087.6	P	Protein required for accurate mitotic chromosome segregation
8859_at	550.7	P	putative RNA-dependent ATPase
8860_at	2707.7	P	Uridine kinase
8861_at	14233.3	P	similarity to Pho87p and YJL198w
8862_at	841.2	A	weak similarity to hypothetical protein YMR206w
8863_at	3279.3	P	Suppressor of Mitochondrial Mutation in the tRNAasp gene
8864_at	28511.3	P	acetyl-CoA carboxylase
8865_at	10614	P	23 kDa mitochondrial inner membrane protein
8866_at	15478.1	P	hypothetical protein
8867_at	4979.1	P	Acyl-CoA cholesterol acyltransferase (sterol-ester synthetase)
8823_at	2828.3	P	hypothetical protein
8824_at	5125.6	P	hypothetical protein
8825_at	802.7	P	weak similarity to protein phosphatases
8826_at	1882.8	P	73 kDa subunit of the SWI\/SNF transcription activation complex, ho
8827_at	3462.2	P	weak similarity to Rpc31p
8828_at	3028.1	P	questionable ORF
8829_at	4273.3	P	Guanine nucleotide exchange factor for Sar1p.
8830_at	7419.7	P	similarity to human pyridoxal kinase
8831_at	1724.8	P	Cyclophilin
8832_at	5819.9	P	similarity to P.denitrificans cobW protein
8833_at	8985.3	P	ExtraCellular Mutant
8834_at	7519.8	P	A MAP kinase kinase kinase\; activator of Pbs2p
8835_at	3361.1	P	Serine\/threonine protein phosphatase involved in glycogen accumul
8836_at	2605.7	P	para-aminobenzoate synthase, PABA synthase
8837_at	1761.5	P	shows similarity to glucose-6-phosphate dehydrogenase non-catalyti
8838_at	2890.4	P	Arp Complex Subunit
8839_at	6113.9	P	strong similarity to ribosomal protein S12
8840_at	3036.9	P	strong similarity to Mycoplasma ribosomal protein S19
8841_at	16454.4	P	putative RNA helicase
8842_at	8073.4	P	weak similarity to Anopheles mitochondrial NADH dehydrogenase su
8843_at	2118.3	P	hypothetical protein
8844_at	5472.2	P	para hydroxybenzoate: polyprenyl transferase
8800_at	1543.1	A	hypothetical protein
8801_at	34183.4	P	mevalonate pyrophosphate decarboxylase
8802_at	28162.2	P	anchorage subunit of a-agglutinin
8803_at	1191	P	translational activator of cytochrome c oxidase
8804_at	6661.5	P	strong similarity to S.pombe hypothetical protein SPAC31A2.02
8805_at	704.1	P	similarity to ser/thr protein kinases
8806_at	1221.3	P	strong similarity to YCR094w and YNL323w
8807_at	1405.7	P	small hydrophilic protein, enriched in microsomal membrane fractio
8808_at	12713.1	P	Saccharopine dehydrogenase (NADP+, L-glutamate forming) (sacc
8809_at	2921.1	P	weak similarity to chicken nucleolin
8810_at	7766	P	Putative transcription factor
8811_at	14282.4	P	strong similarity to human breast tumor associated autoantigen
8812_at	15678.3	P	strong similarity to human breast tumor associated autoantigen
8813_at	4726.6	P	similarity to C.elegans hypothetical protein CEESL47F
8814_at	13188.1	P	Putative ion transporter similar to the major facilitator superfamily of
8815_at	415.8	A	transmembrane regulator of KAPA\/DAPA transport
8816_at	1338.7	M	dethiobiotin synthetase
8817_at	1152.6	P	7,8-diamino-pelargonic acid aminotransferase (DAPA) aminotransfe
8818_at	489.4	M	similarity to to alpha-1,3-mannosyltransferase
8819_at	1430.7	P	similar to FRE2

8820_at	2002.2	P	weak similarity to hypothetical protein YDL218w
8821_at	407.9	A	weak similarity to H.influenzae L-lactate permease (lctP) homolog
8822_at	26.5	A	weak similarity to CYC1/CYP3 transcription activator
8776_at	11.2	A	similarity to R.capsulatus 1-chloroalkane halidohydrolase
8777_at	5383.9	P	strong similarity to YJL222w, YIL173w and Pep1p
8778_at	928.3	P	strong similarity to Pep1p
8779_at	13398	P	similarity to beta-glucan-elicitor receptor - Glycine max
8780_at	664.8	A	similarity to Bul1p
8781_at	265.4	A	similarity to central part of Bul1p
8782_at	343.3	P	strong similarity to Snq2p
8783_at	524.9	P	strong similarity to UDP-glucose 4-epimerase Gal10p
8784_s_at	1229.3	A	strong similarity to E.coli D-mannonate oxidoreductase, identical to
8785_at	4061.7	P	weak similarity to B.subtilis nitrite reductase (nirB)
8786_f_at	3952.8	P	member of the seripauperin protein\/gene family
8787_at	2887.1	P	hypothetical protein identified by SAGE
8788_at	529.4	A	hypothetical protein
8789_s_at	8891.2	P	Aminopeptidase of cysteine protease family
8790_s_at	12821.2	P	protein of unknown function
8791_at	84.3	A	non-annotated SAGE orf Found reverse in NC_001146 between 600
8792_at	130.3	A	non-annotated SAGE orf Found reverse in NC_001146 between 601
8793_at	386.1	A	non-annotated SAGE orf Found reverse in NC_001146 between 118
8794_i_at	276.2	A	non-annotated SAGE orf Found forward in NC_001146 between 440
8795_r_at	1058.7	A	non-annotated SAGE orf Found forward in NC_001146 between 440
8796_at	2095.1	P	non-annotated SAGE orf Found forward in NC_001146 between 728
8797_f_at	3183.3	P	non-annotated SAGE orf Found forward in NC_001146 between 101
8798_at	307.9	A	non-annotated SAGE orf Found reverse in NC_001146 between 301
8799_at	896.3	M	non-annotated SAGE orf Found forward in NC_001146 between 499
8752_f_at	3570.2	P	non-annotated SAGE orf Found reverse in NC_001146 between 519
8753_at	293.6	A	non-annotated SAGE orf Found forward in NC_001146 between 547
8754_at	81.3	A	non-annotated SAGE orf Found forward in NC_001146 between 568
8755_at	8405.1	P	non-annotated SAGE orf Found forward in NC_001146 between 716
8756_i_at	31314.8	P	non-annotated SAGE orf Found forward in NC_001146 between 949
8757_at	170.7	A	non-annotated SAGE orf Found forward in NC_001146 between 281
8758_g_at	93.5	A	non-annotated SAGE orf Found forward in NC_001146 between 281
8759_at	27.7	A	non-annotated SAGE orf Found reverse in NC_001146 between 351
8760_at	32.8	A	non-annotated SAGE orf Found reverse in NC_001146 between 412
8761_at	163.3	A	non-annotated SAGE orf Found reverse in NC_001146 between 413
8762_at	939.8	A	non-annotated SAGE orf Found reverse in NC_001146 between 478
8763_at	664.1	A	non-annotated SAGE orf Found reverse in NC_001146 between 478
8764_at	2245.7	P	non-annotated SAGE orf Found forward in NC_001146 between 482
8765_at	3582	P	non-annotated SAGE orf Found forward in NC_001146 between 663
8766_at	1413.7	P	non-annotated SAGE orf Found reverse in NC_001146 between 177
8767_at	2350.7	P	non-annotated SAGE orf Found forward in NC_001146 between 140
8768_at	98.9	A	non-annotated SAGE orf Found reverse in NC_001146 between 254
8769_g_at	45.6	A	non-annotated SAGE orf Found reverse in NC_001146 between 254
8770_i_at	465.4	P	non-annotated SAGE orf Found reverse in NC_001146 between 254
8771_r_at	242.4	A	non-annotated SAGE orf Found reverse in NC_001146 between 254
8772_at	14239	P	non-annotated SAGE orf Found forward in NC_001146 between 283
8773_at	6708.5	P	non-annotated SAGE orf Found forward in NC_001146 between 465
8774_at	8369.6	P	non-annotated SAGE orf Found reverse in NC_001146 between 586
8775_at	1548.3	P	non-annotated SAGE orf Found forward in NC_001146 between 890
8729_at	2897.8	P	non-annotated SAGE orf Found forward in NC_001146 between 892

8730_g_at	10798.4	P	non-annotated SAGE orf Found forward in NC_001146 between 892
8731_at	56.4	A	non-annotated SAGE orf Found reverse in NC_001146 between 240
8732_at	48.1	A	non-annotated SAGE orf Found reverse in NC_001146 between 286
8733_at	588.3	P	non-annotated SAGE orf Found forward in NC_001146 between 330
8734_at	100.1	A	non-annotated SAGE orf Found reverse in NC_001146 between 335
8735_at	3411.2	P	non-annotated SAGE orf Found reverse in NC_001146 between 355
8736_at	58.1	A	non-annotated SAGE orf Found forward in NC_001146 between 366
8737_i_at	310.9	A	non-annotated SAGE orf Found reverse in NC_001146 between 546
8738_s_at	1404.3	A	non-annotated SAGE orf Found reverse in NC_001146 between 546
8739_at	201.6	P	non-annotated SAGE orf Found forward in NC_001146 between 553
8740_f_at	516.1	A	non-annotated SAGE orf Found forward in NC_001146 between 563
8741_at	745.3	A	non-annotated SAGE orf Found forward in NC_001146 between 586
8742_at	1642.6	P	non-annotated SAGE orf Found forward in NC_001146 between 591
8743_at	973.3	P	non-annotated SAGE orf Found reverse in NC_001146 between 604
8744_at	592.7	A	non-annotated SAGE orf Found reverse in NC_001146 between 661
8745_at	1454.6	P	non-annotated SAGE orf Found reverse in NC_001146 between 663
8746_at	29	A	non-annotated SAGE orf Found reverse in NC_001146 between 779
8747_at	1100.5	P	non-annotated SAGE orf Found forward in NC_001146 between 915
8748_at	88.9	A	non-annotated SAGE orf Found reverse in NC_001146 between 104
8749_at	115.4	A	non-annotated SAGE orf Found forward in NC_001146 between 116
8750_at	35.5	A	non-annotated SAGE orf Found forward in NC_001146 between 191
8751_at	3409.8	P	non-annotated SAGE orf Found reverse in NC_001146 between 267
8705_at	614	P	non-annotated SAGE orf Found reverse in NC_001146 between 342
8706_at	684.9	P	non-annotated SAGE orf Found forward in NC_001146 between 394
8707_at	1065	P	non-annotated SAGE orf Found forward in NC_001146 between 449
8708_at	593.9	P	non-annotated SAGE orf Found forward in NC_001146 between 452
8709_at	487.1	A	non-annotated SAGE orf Found reverse in NC_001146 between 614
8710_at	730	A	non-annotated SAGE orf Found forward in NC_001146 between 623
8711_i_at	35.3	A	non-annotated SAGE orf Found reverse in NC_001146 between 651
8712_r_at	341.6	A	non-annotated SAGE orf Found reverse in NC_001146 between 651
8713_at	1222.9	P	snRNA
8714_at	867.8	P	snRNA
8715_at	223.6	A	hypothetical protein
8716_s_at	3248.6	P	Hypothetical aryl-alcohol dehydrogenase (AAD)
8717_at	778.6	P	similarity to Pseudomonas alkyl sulfatase
8718_at	250.4	A	similarity to P.putida phthalate transporter
8719_at	308.9	A	strong similarity to hypothetical protein YIL166c
8720_f_at	532	A	strong similarity to members of the Srp1p/Tip1p family
8721_at	29.2	A	hypothetical protein
8722_at	769	P	hypothetical protein
8723_at	8799.1	P	similarity to subtelomeric encoded proteins
8724_at	15515.9	P	similarity to glucan 1,4-alpha-glucosidase Sta1p and YAR066w
8725_g_at	14285.2	P	similarity to glucan 1,4-alpha-glucosidase Sta1p and YAR066w
8726_at	3560.4	P	similarity to S.fumigata Asp FII
8727_at	14.3	A	strong similarity to Cps1p
8728_at	928.3	P	similar to FRE2
8683_at	1135.4	P	induced by osmotic stress\; similar to dihydroflavonol 4-reductase fro
8684_at	630.9	M	questionable ORF
8685_at	2399.9	P	Decapping protein involved in mRNA degradation
8686_at	1173.8	P	transcription factor, member of the histone acetyltransferase SAGA
8687_at	10876.1	P	Peroxisomal membrane protein
8688_at	1402.9	P	hypothetical protein

8689_at	1087.6	P	CTR9 is required for normal CLN1 and CLN2 G1 cyclin expression
8690_at	5796.4	P	hypothetical protein
8691_at	17959.3	P	6,7-dimethyl-8-ribityllumazine synthase (DMRL synthase)
8692_at	4449.3	P	strong similarity to hypothetical S. pombe protein
8693_at	354.1	A	similarity to YDR435c and C.elegans hypothetical protein
8694_at	1192.2	P	Acetylornithine aminotransferase
8695_at	15793.4	P	mRNA cap binding protein eIF-4E
8696_at	854.2	P	hypothetical protein
8697_at	4814.9	P	weak similarity to tetracycline resistance proteins
8698_at	5462.8	P	6-phosphofructo-2-kinase
8699_at	2098.4	P	Stoichiometric member of mediator complex
8700_at	56.9	A	questionable ORF
8701_at	2320.8	P	High level expression Reduces Ty3 Transposition
8702_at	535.5	A	similarity to glycophospholipid-anchored surface glycoprotein Gas1p
8703_at	8.7	A	hypothetical protein
8704_at	4075.8	P	ALuminium Resistance 1
8660_at	10976.2	P	similarity to hypothetical S. pombe protein
8661_at	1756.4	P	strong similarity to protein kinase Mck1p
8662_at	14624.3	P	Ribosomal protein L25 (rpl6L) (YL25)
8663_at	25573.7	P	cytosolic malate dehydrogenase
8664_at	2121.3	P	hypothetical protein
8665_at	11166.4	P	weak similarity to M.jannaschii hypothetical protein
8666_at	13973.5	P	Putative polyadenylated-RNA-binding protein located in nucleus\; sim
8667_at	6287.6	P	has been localized to both the plasma membrane and the mitochond
8668_at	31688.9	P	Ribosomal protein L18A (rp28A)
8669_at	7675.3	P	similarity to monocarboxylate transporter proteins
8670_at	361.7	A	hypothetical protein
8671_at	1081.6	P	weak similarity to human sodium channel alpha chain HBA
8672_at	1018.1	P	43 kDa protein, transcriptional activator
8673_at	2142.4	P	homologous to Trf5p and Top1p, associates with Smc1p and Smc2
8674_at	558.7	P	similarity to human DS-1 protein
8675_at	1033.4	P	Serine\/threonine protein kinase with similarity to Ste20p and Cla4p
8676_at	3563	P	Multicopy Suppressor of Bud Emergence
8677_at	6037	P	weak similarity to human ubiquitin-like protein GDX
8678_at	6334.7	P	Involved in RAS localization and palmitoylation
8679_at	36997.2	P	Overexpression yields resistance to Zeocin
8680_at	905.6	P	Transcription factor involved in activation of phospholipid synthetic g
8681_at	1883.2	A	weak similarity to human PL6 protein
8682_at	792.2	P	questionable ORF
8638_at	4961.1	P	Putative integral membrane protein containing novel cysteine motif.
8639_at	583.2	P	Involved in meiotic chromosome segregation\; may stabilize homolo
8640_at	12221.4	P	myo-inositol transporter
8641_at	1548.3	P	tRNA 2 -phosphotransferase
8642_at	3381.3	P	similarity to YOL002c and YDR492w
8643_at	203.4	P	Ser\/Thr protein kinase
8644_at	510.6	A	questionable ORF
8645_at	11898.3	P	similarity to hypothetical S.pombe protein
8646_at	18959.5	P	cytoplasmic tryptophanyl-tRNA synthetase
8647_at	3345.3	P	3,4-dihydroxy-5-hexaprenylbenzoate methyltransferase
8648_at	657.8	M	Helicase in MItochondria
8649_at	492.1	P	Subunit 4 of Replication Factor C\; homologous to human RFC 40 k
8650_at	1416.5	P	similarity to C.elegans hypothetical protein F25H8.1

8651_at	23059.1	P	strong similarity to YBR147w
8652_at	568.2	A	hypothetical protein
8653_at	10735.3	P	MutS homolog encoding major mismatch repair activity in mitosis an
8654_at	3705.5	P	putative transcription factor\; contains a zinc finger
8655_at	1492	P	protein disulfide isomerase related protein
8656_at	1004.8	P	similarity to S.pombe hypothetical protein
8657_at	1369.9	P	Alcohol dehydrogenase
8658_at	121.1	A	hypothetical protein
8659_at	647.1	P	similarity to A.thaliana hyp1 protein
8615_at	1629.9	A	similarity to YOL082w
8616_at	1539	P	similarity to YOL083w
8617_at	1142.1	P	encodes a GTPase activating protein, highly homologous to Ira1p, h
8618_at	3722.8	P	strong similarity to X.laevis XPMC2 protein
8619_at	371.6	A	similarity to NADH dehydrogenases
8620_at	825.6	P	hypothetical protein
8621_at	8921.3	P	strong similarity to C.elegans K12H4.3 protein
8622_at	1374.7	P	Dislikes Extra CIN8, (MDM) Mitochondrial distribution and morpholo
8623_at	2145.7	P	similarity to A.gambiae ATP-binding-cassette protein
8624_at	2319.9	P	hypothetical protein
8625_at	2424.4	P	hypothetical protein
8626_at	5659.8	P	similarity to hypothetical S. pombe protein
8627_at	3241.1	P	hypothetical protein
8628_at	253.1	P	53-kDa coiled-coil protein
8629_at	5759.5	P	Homolog of SIR2
8630_at	433.1	A	Transcription factor (bHLH) involved in interorganelle communicatio
8631_at	2155.1	P	DRAP deaminase
8632_at	1480.3	P	inositol polyphosphate 5-phosphatase
8633_at	8305.1	P	3 (2)5 -bisphosphate nucleotidase
8634_at	1545.4	P	hypothetical protein
8635_at	2035.5	P	Clathrin associated protein, medium subunit
8636_at	17188.8	P	Phosphoribosylpyrophosphate synthetase (ribose-phosphate pyropho
8637_at	3609.4	P	similarity to C.elegans hypothetical protein M02F4.4
8592_at	18521.2	P	Glycerol-3-phosphate dehydrogenase (NAD+)
8593_at	12890.8	P	arginosuccinate synthetase
8594_at	650.1	P	similarity to hypothetical C. elegans protein F02E9.6
8595_at	1477.9	P	phosphoglycerate mutase
8596_at	2961.4	P	similarity to B. subtilis transcriptional activator tenA
8597_at	9040.6	P	weak similarity to transcription factors
8598_at	3117.1	P	hypothetical protein
8599_at	6477.9	P	DNA Damage Responsive
8600_at	9819.9	P	S-adenosylmethionine decarboxylase
8601_at	7391.6	P	Component of the RNA polymerase II holoenzyme complex, positive
8602_at	806.4	P	questionable ORF
8603_at	8945.6	P	Glutathione Synthetase
8604_at	608.3	P	similarity to YAL018c and YOL047c
8605_at	465.7	A	weak similarity to hypothetical proteins YAL018c and YOL048c
8606_at	49.8	A	questionable ORF
8607_at	1873	P	similarity to ser/thr protein kinase
8608_at	2285.8	P	44 kDa phosphorylated integral peroxisomal membrane protein
8609_at	2670.8	P	Endonuclease III-like glycosylase 2
8610_at	3621	P	similarity to CCR4 protein
8611_at	1430.4	P	weak similarity to M.sativa nuM1, hnRNP protein from C. tentans an

8612_at	23449	P	40S ribosomal protein S15 (S21) (rp52) (RIG protein)
8613_at	30373.7	P	60S acidic ribosomal protein P2A (L44) (A2) (YP2alpha)
8614_at	22307.9	P	alpha-type of subunit of 20S proteasome
8570_at	192.8	A	questionable ORF
8571_at	4379.4	P	weak similarity to YMR317w
8572_at	868.7	A	questionable ORF
8573_at	788.8	P	similarity to S.pombe rad18 and rpgL29 genes and other members o
8574_at	1120.5	P	Mitochondrial glutamyl-tRNA synthetase
8575_at	570.9	A	hypothetical protein
8576_at	4392	P	weak similarity to Y.lipolytica Sls1 protein precursor
8577_at	19117.4	P	strong similarity to glycoprotein Gas1p
8578_at	5642.8	P	hypothetical protein
8579_at	2062.4	P	bZIP protein
8580_at	6869.9	P	similarity to YPR125w
8581_at	8197.4	P	hypothetical protein
8582_at	3734.3	P	Affects longevity
8583_at	69.1	A	hypothetical protein
8584_at	1010.9	P	mitochondrial initiation factor 2
8585_at	9283.6	P	weak similarity to rat apoptosis protein RP-8
8586_at	5285.1	P	possible component of RCC1-Ran pathway
8587_at	6141.2	P	Tryptophan permease, high affinity
8588_at	10875.9	P	similarity to Rim9p and YFR012w
8589_at	1625.7	P	tSNARE that affects a Late Golgi compartment
8590_at	373.4	P	similarity to YFR013w
8591_at	3631.3	P	Calmodulin-dependent protein kinase
8547_at	113.3	A	weak similarity to YKR015c
8548_at	1247.5	P	hypothetical protein
8549_at	1282	P	Hmg-coa Reductase Degradation
8550_at	10915.8	P	An evolutionarily conserved member of the histone H2A F\/Z family o
8551_at	7528.8	P	strong similarity to phospholipases
8552_at	4105.3	P	putative RNA 3 -terminal phosphate cyclase
8553_at	1514.3	P	Mdm12p is a mitochondrial outer membrane protein. An Mdm12p ho
8554_at	991.3	P	hypothetical protein
8555_at	3294.9	P	Appears to be a structural component of the chitin synthase 3 comple
8556_at	4726.7	P	topoisomerase I
8557_at	3336.7	P	RNA polymerase II subunit, homologous to S. pombe Rpb11p subur
8558_at	4711.6	P	DNA binding protein involved in transcriptional regulation
8559_at	4114.3	P	similarity to C.elegans hypothetical protein, YDR126w, YNL326c anc
8560_at	14853.3	P	strong similarity to YDR492w and S.pombe hypothetical protein
8561_at	2046.5	P	negative transcriptional regulator
8562_at	3921.7	P	Ribosomal RNA Processing
8563_at	13101.7	P	Required for glucosylation in the N-linked glycosylation pathway
8564_at	2647.8	P	subtilisin-like protease III
8565_at	7909.1	P	weak similarity to hypothetical protein YDR339c
8566_at	561.4	M	ATP dependent DNA ligase
8567_at	2683.6	P	similarity to M.jannaschii hypothetical protein MJ0708
8568_at	13408.2	P	small glutamine-rich tetratricopeptide repeat containing protein
8569_at	4015.5	P	Cell wall integrity and stress response component 1
8525_at	54.9	A	Killed In Mutagen, reduced growth in diepoxybutane and\/or mitomyc
8526_at	6948.3	P	similarity to Tir1p and Tir2p
8527_at	12763.7	P	Cold-shock induced protein of the Srp1p\/Tip1p family of serine-alani
8528_at	4690.2	P	strong similarity to ATP-dependent permeases

8529_at	450.4	A	similarity to YDR391c
8530_g_at	202.8	A	similarity to YDR391c
8531_at	1464.2	P	strong similarity to YDR391c
8532_at	2425.4	P	B-type regulatory subunit of protein phosphatase 2A (PP2A)
8533_at	8215.4	P	hypothetical protein
8534_at	1593.8	P	p24 protein involved in membrane trafficking
8535_at	11750.7	P	Mitochondrial membrane protein
8536_at	1543.2	P	Resistance to o-dinitrobenzene, calcium, and zinc
8537_at	671.1	P	similarity to YDR474c
8538_at	14245.9	P	10 kDa mitochondrial heat shock protein
8539_at	12524.1	P	similarity to Pyrococcus horikoshii hypothetical protein PHBQ041
8540_at	444.7	P	weak similarity to D.melanogaster probable Ca2+ transporter rdgB
8541_at	2247.6	P	hypothetical protein
8542_at	539.1	P	hypothetical protein
8543_at	642.9	P	Homolog of SIR2
8544_at	2362.3	P	Protein required for cell cycle arrest in response to loss of microtubul
8545_at	18570.9	P	Heat shock protein also induced by canavanine and entry into station
8546_at	1760.1	P	bZIP protein, can activate transcription from a promoter containing a
8502_at	157.8	A	hypothetical protein
8503_at	337.6	M	involved in invasive growth upon nitrogen starvation
8504_at	1976.4	P	Metallothionein-like protein
8505_at	2158.9	P	myc-family transcription factor homolog
8506_at	1659.5	P	Protein that complements a drug-hypersensitive mutation
8507_at	1632.8	P	Protein involved in constitutive endocytosis of Ste3p
8508_at	1039.4	P	Required for mother cell-specific HO expression
8509_at	641.7	P	integral membrane protein\; c-terminal TMD\; located in endosome
8510_at	1472.3	P	cytochrome c mitochondrial import factor
8511_at	4536	P	putative repressor protein\; contains nuclear targeting signal
8512_at	8687.7	P	Casein kinase II, beta subunit
8513_at	858.3	P	Mitochondrial glyoxylase-II
8514_at	810.8	A	questionable ORF
8515_at	3389.5	P	weak similarity to YDR273w
8516_at	3266.2	P	Protein involved in growth regulation
8517_at	5388.4	P	weak similarity to YDR275w
8518_at	20427.8	P	outer mitochondrial membrane protein, component of the mitochond
8519_at	26605.9	P	RNA helicase
8520_at	4888.9	P	homologous to MTH1\; interacts with the SNF1 protein kinase and T
8521_at	3900	P	RNA trafficking protein\; transcription activator
8522_at	14	A	similarity to YER185w, Rta1p
8523_at	232.1	A	hypothetical protein
8524_at	6177.2	P	weak similarity to myosin heavy chain proteins
8480_at	7582.3	P	hypothetical protein
8481_at	1866.4	P	similarity to protamines
8482_at	1987.1	P	similarity to Sis2p protein and C.tropicalis hal3 protein
8483_at	174.8	A	questionable ORF
8484_at	4347.7	P	weak similarity to human phosphorylation regulatory protein HP-10
8485_at	902.3	P	G2 allele of skp1 suppressor
8486_at	979.9	A	encodes component of the spindle midzone
8487_at	1631.4	P	weak similarity to YGL144c
8488_at	382.5	P	hypothetical protein
8489_at	5975.2	P	alpha subunit of casein kinase II
8490_at	1048.4	A	strong similarity to YKR075c

8491_at	22164	P	Ribosomal protein L3 (rp1) (YL1)
8492_at	2004.9	P	weak similarity to human retinoblastoma binding protein 2
8493_at	11090	P	Cytochrome c1
8494_at	1745.9	P	hypothetical protein
8495_at	23262	P	glycosyl transferase
8496_at	60	A	hypothetical protein
8497_at	929.8	A	GTPase activating protein
8498_at	3611.8	P	strong similarity to Thi10p
8499_at	1195	A	hypothetical protein
8500_at	1683.8	P	hypothetical protein
8501_at	1411	P	endoplasmic reticulum t-SNARE, coprecipitates with Sec20p, Tip1p.
8457_at	6200	P	similarity to Hbs1p, Sup2p and EF1-alpha
8458_at	936.7	A	similarity to mouse KIN17 protein
8459_at	7760.6	P	weak similarity to YMR172w
8460_at	9442.8	P	Multi-copy suppressor of SOD-linked defects
8461_at	2556.5	P	hypothetical protein
8462_at	5265	P	strong similarity to YKR089c
8463_at	3203.6	P	questionable ORF
8464_at	981	P	weak similarity to YKR091w
8465_at	6666.5	P	hypothetical protein
8466_at	24405.9	P	34-kDa, gamma subunit of oligosaccharyl transferase glycoprotein c
8467_at	5396.8	P	weak similarity to synaptogamines
8468_at	1133.1	P	hypothetical protein
8469_g_at	1731.7	P	hypothetical protein
8470_at	5519.9	P	weak similarity to human calcium influx channel
8471_at	10771.9	P	small GTP-binding protein\; geranylgeranylated\; geranylgeranylation
8472_at	2306.5	P	similarity to ser/thr protein phosphatases
8473_at	1451.3	P	similarity to hypothetical S.pombe protein D83992_G
8474_at	2505.3	P	ExtraCellular Mutant
8475_at	1850	P	similarity to S.pombe hypothetical protein SPAC22F3.04
8476_at	6710.2	P	GTP-binding ADP-ribosylation factor
8477_at	5767.6	P	Ribose-5-phosphate ketol-isomerase
8478_at	29412.4	P	Ribosomal protein S7A (rp30)
8479_at	12038.4	P	Ribosomal protein S7A (rp30)
8434_at	1445.7	P	hypothetical protein
8435_at	14601.5	P	nuclear pore complex protein
8436_at	18531.2	P	type 2 membrane protein\; probable secretory protein
8437_at	1156.1	P	similarity to mitochondrial carrier proteins
8438_at	7633.5	P	ras proto-oncogene homolog
8439_at	200.1	A	questionable ORF
8440_at	2791	P	16-kDa, epsilon subunit of oligosaccharyltransferase complex\; 40\
8441_at	835.5	P	hypothetical protein
8442_g_at	710.3	P	hypothetical protein
8443_at	440.6	P	member of the syntaxin family of proteins\; predicted C-terminal TM
8444_at	1448.9	P	weak similarity to human G-0/G-1 switch regulatory protein 8
8445_at	17253.7	P	putative isoform of Leu4p
8446_at	4148.3	P	inositol polyphosphate 5-phosphatase
8447_at	1835.9	P	TFIIIC (transcription initiation factor) subunit, 55 kDa
8448_at	218.4	A	weak similarity to B.subtilis maf protein
8449_at	2417.6	P	similarity to C.elegans hypothetical protein
8450_at	1353.3	P	probable transcription factor, asparagine-rich zinc-finger protein, su
8451_at	721.1	P	hypothetical protein

8452_at	1477.6	P	involved in targeting and fusion of ER to golgi transport vesicles
8453_at	13201	P	RNA polymerase III large subunit
8454_at	17301.1	P	Probable 26S protease subunit and member of the CDC48\/PAS1\/S
8455_at	1315.6	P	hypothetical protein
8456_at	4129.6	P	similarity to a C.elegans ZK632.3 protein
8412_at	2177.5	P	Similar to mammalian aldo\/keto reductases
8413_at	114.5	A	questionable ORF
8414_at	23988.4	P	profilin (actin-binding protein)
8415_at	2133.7	P	extremely hydrophilic protein
8416_at	2787.7	P	Ubiquitin-specific protease
8417_at	505.9	A	may encode a protein involved in one or more monoxygenase or hyd
8418_at	1090.1	P	isoamyl acetate hydrolytic enzyme
8419_at	2159.1	P	rho type GTPase activating protein
8420_at	8099.5	P	phosphoribosylamino-imidazole-carboxylase
8421_at	2459.5	P	hypothetical protein
8422_at	1859.9	P	mitochondrial integral membrane protein
8423_at	1834.9	P	weak similarity to E.coli hypothetical 27K protein
8424_at	4495.8	P	Peripheral membrane protein required for vacuolar protein sorting
8425_s_at	26387.3	P	translation elongation factor 2 (EF-2)
8426_at	84.2	A	GTPase activating protein (GAP)
8427_at	265.2	A	questionable ORF
8428_at	22640.5	P	NAD+-dependent isocitrate dehydrogenase
8429_at	1406.7	P	similarity to YLR361c
8430_at	1372.3	P	hypothetical protein
8431_at	647.2	A	questionable ORF
8432_at	4683.1	P	Transcription factor
8433_at	1415.8	P	Actin-related protein
8389_at	17593.5	P	Succinate-CoA Ligase (ADP-Forming)
8390_at	1487.7	P	Thiamin pyrophosphokinase
8391_at	3769.8	P	weak similarity to human DNA-binding protein PO-GA and to bacteri
8392_at	14844.3	P	strong similarity to hypothtical S. pombe protein and to hypothetical C
8393_at	312.8	A	questionable ORF
8394_at	385.2	P	similarity to YHR194w
8395_at	2089.5	P	required for final stages of splicesome maturation\; promotes step 1
8396_at	1640	P	Involved in plasmid maintenance
8397_at	2575	P	ribosomal protein of the large subunit, mitochondrial
8398_at	14514.1	P	second largest subunit of RNA polymerase II
8399_at	464.9	A	hypothetical protein
8400_at	20719.9	P	multidrug resistance transporter
8401_at	1288.6	P	similarity to hypothetical A. thaliana proteins F19G10.15 and T19F06
8402_at	9623.8	P	similarity to 5 -flanking region of the Pichia MOX gene
8403_at	957.8	P	Interacts with C-terminus of CDC12
8404_at	12158.5	P	putative proteasome subunit
8405_at	962.4	P	Mitochondrial ribosomal protein of small subunit
8406_at	3645.3	P	homologue of human E core protein
8407_at	2744.9	P	Protein involved in mRNA transport from nucleus to cytoplasm
8408_at	1943.3	P	similarity to C.elegans cosmid F35C8
8409_at	764.8	P	transcription factor
8410_at	2250.3	P	strong similarity to S.pombe SPAC13G6.14 protein
8411_at	7179.1	P	hypothetical protein
8366_at	7477.7	P	similarity to E.histolytica surface lectin
8367_at	1413.9	P	hypothetical protein

8368_i_at	13331.8	P	Ribosomal protein S28A (S33A) (YS27)
8369_f_at	16814.7	P	Ribosomal protein S28A (S33A) (YS27)
8370_at	7825.7	P	glutaminyl-tRNA synthetase
8371_at	1656.8	P	questionable ORF
8372_at	553.8	P	questionable ORF
8373_at	1425.3	P	sphingoid long chain base (LCB) kinase
8374_at	1085.9	P	similarity to finger protein YKL222c, YOR162c and YLR266c
8375_at	551.4	P	strong similarity to YLR270w
8376_at	3744.9	P	Stoichiometric member of mediator complex
8377_at	10379.5	P	similarity to human and murine C3f protein
8378_at	13081.7	P	ferrochelatase (protoheme ferrolyase)
8379_at	201.1	M	weak similarity to rat SCP1 protein
8380_at	192.3	A	Regulatory subunit for Glc7p
8381_at	1402	P	similarity to BRR5 protein
8382_at	263.2	P	Peroxisomal enoyl-CoA hydratase
8383_at	4434.4	P	Actin assembly factor
8384_f_at	22757	P	Ribosomal protein S30B
8385_at	50.7	A	hypothetical protein
8386_at	11302	P	phosphoserine transaminase
8387_at	986.6	P	GTP binding protein, almost identical to Gsp1p
8388_at	275.9	A	hypothetical protein
8343_at	15684.2	P	Translation elongation factor Tu, mitochondrial
8344_at	1837.3	P	Protein that may play a role in polarity establishment and bud formati
8345_at	1358.7	P	weak similarity to chicken nonhistone chromosomal protein HMG-2
8346_at	261.1	A	sporulation-specific exo-1,3-beta-glucanase
8347_at	605.9	P	contains motifs that are present in a family of DNA-dependent ATPa
8348_i_at	1072.3	P	strong similarity to Thi10p
8349_f_at	2908.8	P	strong similarity to Thi10p
8350_at	178.5	A	weak similarity to YPL112c
8351_at	2923.4	P	Transcription factor IIA, large chain
8352_at	618.1	P	possible leucine zipper
8353_at	11162.7	P	Involved in lipoic acid metabolism
8354_at	9787.3	P	hypothetical protein
8355_at	13766.1	P	Multicopy suppressor of BFA (Brefeldin A)-induced lethality\; implicat
8356_at	31.1	A	questionable ORF
8357_at	781.4	A	questionable ORF
8358_at	3083.5	P	Ribose methyltransferase for mitochondrial 21S rRNA
8359_at	3351.3	P	imidazoleglycerol-phosphate dehydratase
8360_at	1759.7	P	questionable ORF
8361_at	19431.7	P	ATP-dependent RNA helicase of DEAD box family\; suppressor of a
8362_at	2857.5	P	hypothetical protein
8363_at	3547.2	P	similarity to Brettanomyces RAD4 and to S.pombe hypothetical prote
8364_at	22590.3	P	second-largest subunit of RNA polymerase III
8365_at	2057.1	P	protein tyrosine phosphatase
8320_at	19051.6	P	homology to bacterial nicotinate phosphoribosyl transferase
8321_at	10839.7	P	RNA polymerase II subunit
8322_at	1162.2	P	encodes protein with GTP-binding domain related to dynamin
8323_at	11141.3	P	beta subunit of G protein coupled to mating factor receptor
8324_at	576	P	Involved in silencing at telomeres, HML and HMR
8325_at	33.4	A	hypothetical protein
8326_at	573.7	P	similarity to M.xanthus hypothetical protein
8327_at	1116.5	P	Relieves uso1-1 Transport Defect

8328_at	3127.4	P	Subunit 1 of Replication Factor C\; homologous to human RFC 140 k
8329_at	1266.7	P	questionable ORF
8330_at	6300.2	P	dipeptidyl aminopeptidase
8331_at	3079.4	P	hypothetical protein
8332_at	3203	P	malonyl-CoA:ACP transferase
8333_at	30.4	A	malonyl-CoA:ACP transferase
8334_at	868.7	P	similarity to ADP/ATP carrier proteins
8335_at	6122.9	P	protein of unknown function
8336_at	15912.4	P	16-kDa RNA polymerase subunit (common to polymerases I, II and
8337_at	695.4	A	questionable ORF
8338_at	19754.7	P	NifU-like protein A
8339_at	1938.5	P	similarity to microtubule-interacting protein Mhp1p
8340_at	3476	P	weak similarity to YNR013c
8341_at	9339.3	P	Transcriptional modulator
8342_at	30643.6	P	Transcriptional modulator
8297_at	4244.3	P	protein kinase involved in protein kinase C pathway
8298_at	2526.7	P	GrpE homolog, mitochondrial matrix protein
8299_at	3167.8	P	protein kinase
8300_f_at	14159.5	P	Ribosomal protein L33B (L37B) (rp47) (YL37)
8301_at	40.2	A	encodes snRNA U3, SNR17B also encodes snRNA U3
8302_at	4074.4	P	dihydrofolate reductase
8303_at	70.1	A	homology to human oxysterol binding protein
8304_at	1307.4	P	similarity to hypothetical S. pombe protein
8305_at	1550.3	P	hypothetical protein
8306_at	5867.9	P	similarity to C.elegans ZK1058.5 protein
8307_at	9798.2	P	tetrahydrofolylpolyglutamate synthase
8308_at	420.3	P	Sporulation Specific
8309_at	13246.5	P	similarity to M.jannaschii hypothetical protein MJ0588
8310_at	2452.5	P	Acetyltransferase in the SAS gene family
8311_at	5286.4	P	similarity to hypothetical C. elegans proteins
8312_at	9518.5	P	weak similarity to reductases
8313_at	932.6	P	Suppressor of rad53 lethality
8314_g_at	23722.1	P	Suppressor of rad53 lethality
8315_i_at	39947.3	A	questionable ORF
8316_at	649.7	P	subunit of the anaphase promoting complex
8317_at	1675.4	P	CLeavage\/Polyadenylation factor IA subunit\; interacts with Pcf11p i
8318_at	3921.8	P	similarity to thiosulfate sulfurtransferases
8319_at	2880	P	hypothetical protein
8274_at	3221	P	hypothetical protein
8275_at	2505.2	P	Protein involved in protein import into ER
8276_at	52.8	A	hypothetical protein
8277_at	4125.3	P	strong similarity to secretory protein Ssp134p
8278_at	5902.7	P	calcium-binding protein component of spindle pole bodies, localizes
8279_at	692	M	hypothetical protein
8280_at	13765.3	P	ATPase\; component of the 26S proteasome cap subunit
8281_at	12991.1	P	translation initiation factor eIF2b gamma subunit\; negative regulator
8282_at	15482.1	P	Subunit of the regulatory particle of the proteasome
8283_at	3955.4	P	similarity to YLR243w
8284_at	258.1	A	questionable ORF
8285_at	1097.6	P	hypothetical protein
8286_at	6007.7	P	Binds to beta-tubulin and may participate in microtubule morphogene
8287_at	633.3	P	Pentamidine resistance protein

8288_at	21008	P	similarity to ser/thr protein kinases
8289_at	1603	A	hypothetical protein
8290_at	2099.9	P	Required for viability in the absence of the kinesin-related Cin8p mito
8291_at	16365.8	P	Vacuolar H-ATPase 100 kDa subunit of membrane (V0) sector, ess
8292_at	23313.7	P	strong similarity to Rattus tricarboxylate carrier
8293_at	10103.8	P	microtubule-associated protein
8294_at	4171.1	P	similarity to resistance proteins
8295_at	2248.5	P	transfer RNA isopentenyl transferase
8296_at	686.7	P	similarity to A.nidulans palA protein
8252_at	13619.1	P	Binds to eIF4E, the mRNA cap-binding protein, and represses cap-d
8253_at	188	A	questionable ORF
8254_at	1610.7	P	uroporphyrinogen III synthase
8255_at	78.9	A	hypothetical protein
8256_at	1927.1	P	similarity to S.pombe dihydrofolate reductase
8257_at	8489.4	P	weak similarity to phosducins
8258_at	101.6	A	questionable ORF
8259_at	8620.8	P	weak similarity to phosphoglycerate mutases
8260_at	320.6	P	weak similarity to M.jannaschii hypothetical protein MJ0694
8261_at	7990.7	P	similarity to D.melanogaster heat shock protein 67B2
8262_at	7867.6	P	similarity to D.melanogaster heat shock protein 67B2
8263_at	4510.7	P	weak similarity to PITSLRE protein kinase isoforms
8264_at	2357.9	P	Disulfide isomerase related protein
8265_at	617.1	P	similarity to C.elegans hypothetical protein
8266_at	4924.3	P	transcriptional regulator
8267_at	5503.4	P	similarity to cation translocating ATPases
8268_at	1578.9	M	similarity to human and mouse glomerulosclerosis protein Mpv17
8269_f_at	6374.8	P	Ribosomal protein S10A
8270_f_at	31937	P	Ribosomal protein S10A
8271_at	4433.5	P	similarity to human hypothetical protein
8272_at	146.6	P	weak similarity to SWI/SNF complex 60 KDa subunit from man and r
8273_at	702.5	P	similarity to hypothetical S. pombe protein
8229_at	11419.9	P	similarity to Sdh4p
8230_at	167.8	A	required for meiosis
8231_at	9917.4	P	multiprotein bridging factor
8232_at	2887.5	P	BUD site selection
8233_g_at	3517.3	P	BUD site selection
8234_at	415.5	A	questionable ORF
8235_at	4978.5	P	hypothetical protein
8236_at	7700.9	P	CPA1 leader peptide
8237_at	14001.8	P	Carbamoyl phosphate synthetase, arginine specific
8238_at	1050.9	P	has strong homology to Drosophila ISWI
8239_at	1439	P	AIP3 binding protein
8240_at	1264.7	P	hypothetical protein
8241_at	7240	P	similarity to human X-linked PEST-containing transporter
8242_at	5089.5	P	homolog of chloroplast phosphate transporter
8243_at	831	P	weak similarity to YIL149c
8244_i_at	37700.3	P	questionable ORF
8245_r_at	4442.4	P	questionable ORF
8246_s_at	11877.4	P	questionable ORF
8247_at	31400.8	P	57 kDa nucleolar protein
8248_at	19962.8	P	similarity to hypothetical S. pombe protein
8249_at	409.5	M	sporulation-specific protein

8250_at	464.4	P	hypothetical protein
8251_at	3668.3	P	hypothetical protein
8206_at	2584.9	P	Protein involved in cobalt accumulation\; dosage dependent suppres
8207_at	13095.9	P	long chain fatty acyl:CoA synthetase
8208_at	261.6	A	hypothetical protein
8209_at	446.3	P	homolog of mammalian splicing factor\/U2 snRNP protein
8210_at	3238.8	P	hypothetical protein
8211_at	3468.2	P	dolichyl phosphate-D-mannose:protein O-D-mannosyltransferase
8212_at	5229.6	P	similarity to hypothetical S.pombe protein SPAC1F12.05
8213_at	24302	P	gamma-glutamyl phosphate reductase
8214_at	794.1	P	similarity to YAL028w
8215_at	1087.1	A	questionable ORF
8216_at	8276.2	P	myosin-1
8217_at	12569.6	P	vesicle-associated membrane protein (synaptobrevin) homolog
8218_at	2594.1	P	Putative ABC transporter highly similar to Pdr5p
8219_at	2186.5	P	Multicopy suppressor of clathrin deficiency and of ts mutants of IPL1
8220_at	656.9	P	catalytic subunit of mitochondrial DNA polymerase
8221_at	1147	P	questionable ORF
8222_at	7668.5	P	27-kDa subunit of the vacuolar ATPase\; E subunit of V1 sector
8223_at	345.2	A	questionable ORF
8224_at	1740	P	splicing factor
8225_at	16092.5	P	Cytoplasmic alanyl-tRNA synthetase gene
8226_at	4304.6	P	Appears to function early in (1,6)-beta-D-glucan synthesis pathway
8227_at	1823.8	P	Mutants are defective in Ty1 Enhancer-mediated Activation
8228_at	9576.4	P	similarity to YAL034c
8183_at	25.3	A	strong similarity to E2 ubiquitin-conjugating enzymes
8184_at	13978.3	P	DNA-dependent RNA polymerase I subunit A43
8185_at	32222.2	P	RNA polymerase I subunit 190 (alpha)
8186_at	14096.6	P	weak similarity to YAl037w
8187_at	2588.3	P	hypothetical protein
8188_at	2439.2	P	TYE7, a 33 kDa serine-rich protein, is a potential member of the bas
8189_at	123	A	questionable ORF
8190_at	1622.1	P	deoxycytidyl transferase
8191_at	2896	P	Pyruvate kinase, glucose-repressed isoform
8192_at	975.8	P	putative proline-specific permease
8193_at	115	A	Protein involved in chromosome segregation, required for microtubu
8194_at	184.6	A	weak similarity to Esp1p and mitochondrial L.illustris cytochrome oxic
8195_at	143.5	A	mRNA is induced in meiosis, encodes a meiosis-specific serine\/thre
8196_at	1659.9	P	hypothetical protein
8197_at	873.1	P	weak similarity to adenylate cyclases
8198_at	1182.1	P	hypothetical protein
8199_at	16829.8	P	nam9-1 suppressor
8200_at	12165.7	P	strong similarity to human electron transfer flavoprotein-ubiquinone o
8201_at	4086.4	P	Grd19p that is epitope tagged with the HA epitope at the C-terminus
8202_at	1063.8	P	Component, along with Hap2p and Hap3p, of CCAAT-binding transc
8203_at	10278.1	P	hypothetical protein
8204_at	6183.1	P	low-Km (high-affinity) cAMP phosphodiesterase
8205_at	21993.4	P	translation initiation factor eIF3 subunit
8161_at	12620.2	P	proteasome component YC1 (protease yscE subunit 1)
8162_at	1441.2	P	Activator of peroxisome proliferation
8163_at	544	P	hypothetical protein
8164_at	171	A	strong similarity to YAL053w

8165_at	190.3	A	questionable ORF
8166_at	916.2	P	Calponin homolog
8167_at	557.8	A	encodes a putative 3 ->5 exonuclease
8168_at	31287	P	40S ribosomal protein S12
8169_at	6271.3	P	protein of the TCD\/MRS6 family of GDP dissociation inhibitors (Rab
8170_at	561.8	A	similarity to YAL056w
8171_at	7343.1	P	hypothetical protein
8172_at	3304.6	P	nucleosome assembly protein I
8173_at	10576.9	P	aldehyde dehydrogenase (E.C. 1.2.1.5) (sold by SIGMA under the ca
8174_at	17770.3	P	NADP-specific glutamate dehydrogenase
8175_at	147.1	A	hypothetical protein
8176_at	1124.9	P	Alcohol acetyltransferase
8177_at	72.3	A	strong similarity to aminotriazole resistance protein
8178_at	65.9	A	questionable ORF
8179_at	1235.3	P	weak similarity to Pdr3p
8180_at	204.7	A	similar to FRE2
8181_at	2978.3	P	hypothetical protein
8182_at	12288.8	P	weak similarity to L.mexicana secreted acid phosphatase 2
8138_at	5.6	A	similar to FRE2
8139_at	3365	P	strong similarity to hypothetical protein YMR316w
8140_at	485.1	M	photolyase
8141_at	8.9	A	strong similarity to YGL258w
8142_s_at	56.7	A	Protein with similarity to formate dehydrogenases
8143_at	966.2	P	strong similarity to putative pseudogenes YPL277c and YPL278c
8144_g_at	1914.4	P	strong similarity to putative pseudogenes YPL277c and YPL278c
8145_s_at	7296.9	P	nearly identical to YPL279c
8146_at	548.8	A	hypothetical protein
8147_s_at	24.3	A	strong similarity to members of the Srp1p/Tip1p family
8148_at	414.3	A	hypothetical protein identified by SAGE
8149_at	1595.7	A	identified by SAGE
8150_s_at	431	P	Sorting nexin I homologue
8151_s_at	2765.9	P	Thymidylate synthase
8152_f_at	656	P	Thymidylate synthase
8153_at	683	P	non-annotated SAGE orf Found forward in NC_001147 between 331
8154_at	68.6	A	non-annotated SAGE orf Found reverse in NC_001147 between 359
8155_at	442	A	non-annotated SAGE orf Found forward in NC_001147 between 242
8156_g_at	14.1	A	non-annotated SAGE orf Found forward in NC_001147 between 242
8157_at	153.3	A	non-annotated SAGE orf Found forward in NC_001147 between 571
8158_g_at	1570.2	P	non-annotated SAGE orf Found forward in NC_001147 between 571
8159_at	339.3	M	non-annotated SAGE orf Found forward in NC_001147 between 571
8160_at	1107.8	A	non-annotated SAGE orf Found reverse in NC_001147 between 882
8112_at	1358.8	P	non-annotated SAGE orf Found reverse in NC_001147 between 147
8113_at	420.3	A	non-annotated SAGE orf Found reverse in NC_001147 between 241
8114_i_at	17.6	A	non-annotated SAGE orf Found forward in NC_001147 between 464
8115_f_at	1863.1	P	non-annotated SAGE orf Found forward in NC_001147 between 464
8116_f_at	3910.3	A	non-annotated SAGE orf Found reverse in NC_001147 between 599
8117_i_at	261.1	M	non-annotated SAGE orf Found forward in NC_001147 between 703
8118_i_at	663.3	A	non-annotated SAGE orf Found reverse in NC_001147 between 703
8119_f_at	1422.3	A	non-annotated SAGE orf Found reverse in NC_001147 between 703
8120_at	3255	P	non-annotated SAGE orf Found forward in NC_001147 between 600
8121_at	1496.8	P	non-annotated SAGE orf Found reverse in NC_001147 between 852
8122_at	12.9	A	non-annotated SAGE orf Found forward in NC_001147 between 106

8123_at	1217.1	A	non-annotated SAGE orf Found reverse in NC_001147 between 136
8124_at	3982.7	P	non-annotated SAGE orf Found forward in NC_001147 between 185
8125_at	3229.7	A	non-annotated SAGE orf Found forward in NC_001147 between 254
8126_at	2155.9	P	non-annotated SAGE orf Found reverse in NC_001147 between 290
8127_at	70.8	A	non-annotated SAGE orf Found reverse in NC_001147 between 316
8128_at	305.9	A	non-annotated SAGE orf Found reverse in NC_001147 between 372
8129_at	1922.2	P	non-annotated SAGE orf Found reverse in NC_001147 between 397
8130_at	605.9	A	non-annotated SAGE orf Found reverse in NC_001147 between 414
8131_at	761.5	A	non-annotated SAGE orf Found forward in NC_001147 between 423
8132_at	6447.2	P	non-annotated SAGE orf Found forward in NC_001147 between 646
8133_at	649.7	A	non-annotated SAGE orf Found forward in NC_001147 between 658
8134_at	194.6	A	non-annotated SAGE orf Found reverse in NC_001147 between 671
8135_at	667.9	A	non-annotated SAGE orf Found forward in NC_001147 between 680
8136_at	1918.3	P	non-annotated SAGE orf Found reverse in NC_001147 between 715
8137_at	11413.4	P	non-annotated SAGE orf Found forward in NC_001147 between 738
8088_i_at	22	A	non-annotated SAGE orf Found forward in NC_001147 between 792
8089_at	2159.2	P	non-annotated SAGE orf Found forward in NC_001147 between 850
8090_at	1000.2	P	non-annotated SAGE orf Found forward in NC_001147 between 918
8091_at	249.3	A	non-annotated SAGE orf Found reverse in NC_001147 between 922
8092_i_at	16364.2	P	non-annotated SAGE orf Found forward in NC_001147 between 100
8093_r_at	10670.6	P	non-annotated SAGE orf Found forward in NC_001147 between 100
8094_f_at	15710.5	A	non-annotated SAGE orf Found forward in NC_001147 between 100
8095_at	340.5	M	non-annotated SAGE orf Found forward in NC_001147 between 301
8096_at	1265.2	P	non-annotated SAGE orf Found forward in NC_001147 between 413
8097_i_at	75.5	A	non-annotated SAGE orf Found reverse in NC_001147 between 798
8098_at	15.4	A	non-annotated SAGE orf Found forward in NC_001147 between 980
8099_at	34.6	A	non-annotated SAGE orf Found reverse in NC_001147 between 178
8100_at	45.7	A	non-annotated SAGE orf Found forward in NC_001147 between 187
8101_at	241.6	A	non-annotated SAGE orf Found forward in NC_001147 between 278
8102_at	1351	P	non-annotated SAGE orf Found forward in NC_001147 between 136
8103_at	6.5	A	non-annotated SAGE orf Found forward in NC_001147 between 158
8104_at	2068.6	P	non-annotated SAGE orf Found forward in NC_001147 between 159
8105_at	9.6	A	non-annotated SAGE orf Found forward in NC_001147 between 226
8106_at	1160.8	A	non-annotated SAGE orf Found forward in NC_001147 between 418
8107_at	1498.3	P	non-annotated SAGE orf Found forward in NC_001147 between 438
8108_at	79.2	A	non-annotated SAGE orf Found reverse in NC_001147 between 682
8109_at	42	A	non-annotated SAGE orf Found reverse in NC_001147 between 682
8110_at	277.8	A	non-annotated SAGE orf Found reverse in NC_001147 between 759
8111_g_at	287.1	A	non-annotated SAGE orf Found reverse in NC_001147 between 759
8063_at	4540	P	non-annotated SAGE orf Found reverse in NC_001147 between 775
8064_at	938.6	A	non-annotated SAGE orf Found reverse in NC_001147 between 836
8065_at	254.1	P	non-annotated SAGE orf Found reverse in NC_001147 between 854
8066_at	1489	P	non-annotated SAGE orf Found reverse in NC_001147 between 969
8067_i_at	1839.1	P	non-annotated SAGE orf Found reverse in NC_001147 between 974
8068_at	188.7	A	non-annotated SAGE orf Found reverse in NC_001147 between 978
8069_at	988.8	A	non-annotated SAGE orf Found reverse in NC_001147 between 978
8070_at	338.3	P	non-annotated SAGE orf Found reverse in NC_001147 between 979
8071_f_at	613.4	M	non-annotated SAGE orf Found reverse in NC_001147 between 108
8072_i_at	296	A	non-annotated SAGE orf Found reverse in NC_001147 between 108
8073_f_at	44.4	A	non-annotated SAGE orf Found reverse in NC_001147 between 108
8074_s_at	2578	P	non-annotated SAGE orf Found reverse in NC_001147 between 108
8075_s_at	1993.1	P	non-annotated SAGE orf Found reverse in NC_001147 between 109

8076_at	196.5	A	non-annotated SAGE orf Found reverse in NC_001147 between 165
8077_at	42.9	A	non-annotated SAGE orf Found reverse in NC_001147 between 166
8078_at	46.9	A	non-annotated SAGE orf Found reverse in NC_001147 between 167
8079_s_at	308.7	A	non-annotated SAGE orf Found forward in NC_001147 between 270
8080_at	546.1	P	non-annotated SAGE orf Found forward in NC_001147 between 271
8081_at	293	A	non-annotated SAGE orf Found forward in NC_001147 between 427
8082_at	233.7	A	non-annotated SAGE orf Found forward in NC_001147 between 430
8083_at	30	A	non-annotated SAGE orf Found forward in NC_001147 between 431
8084_at	451.3	A	non-annotated SAGE orf Found forward in NC_001147 between 108
8085_at	1757.4	P	non-annotated SAGE orf Found forward in NC_001147 between 180
8086_at	289.9	A	non-annotated SAGE orf Found forward in NC_001147 between 193
8087_at	65.4	A	non-annotated SAGE orf Found reverse in NC_001147 between 271
8039_at	662.3	P	non-annotated SAGE orf Found reverse in NC_001147 between 301
8040_at	8667.5	P	non-annotated SAGE orf Found forward in NC_001147 between 524
8041_at	6958.7	P	non-annotated SAGE orf Found reverse in NC_001147 between 609
8042_at	110.2	A	non-annotated SAGE orf Found forward in NC_001147 between 690
8043_at	72.7	A	non-annotated SAGE orf Found forward in NC_001147 between 692
8044_at	4375.1	P	non-annotated SAGE orf Found forward in NC_001147 between 758
8045_at	777.3	A	non-annotated SAGE orf Found forward in NC_001147 between 778
8046_at	404.9	M	non-annotated SAGE orf Found forward in NC_001147 between 825
8047_at	2795	P	non-annotated SAGE orf Found forward in NC_001147 between 877
8048_at	12781.7	P	non-annotated SAGE orf Found forward in NC_001147 between 100
8049_at	41.4	A	non-annotated SAGE orf Found forward in NC_001147 between 107
8050_at	7.8	A	non-annotated SAGE orf Found forward in NC_001147 between 107
8051_i_at	9.1	A	non-annotated SAGE orf Found reverse in NC_001147 between 107
8052_r_at	311.2	A	non-annotated SAGE orf Found reverse in NC_001147 between 107
8053_at	524.9	A	snRNA
8054_at	388.1	P	snRNA
8055_i_at	8.3	A	Centromere
8056_at	1982.4	P	snRNA
8057_i_at	763.2	P	snRNA
8058_r_at	534.4	P	snRNA
8059_at	905.2	P	snRNA
8060_at	2072.8	P	snRNA
8061_at	1064.5	P	snRNA
8062_at	7624.4	P	snRNA
8016_at	212.1	A	snRNA
8017_at	4583	P	snRNA
8018_i_at	497.6	P	strong similarity to hypothetical protein YOR389w/putative pseudoge
8019_s_at	1002.1	P	strong similarity to hypothetical protein YOR389w/putative pseudoge
8020_s_at	297.2	A	putative formate dehydrogenase/putative pseudogene
8021_at	4168.9	P	strong similarity to amino-acid transport proteins
8022_at	8768	P	weak similarity to M.leprae metH2 protein, and strong similarity to hy
8023_at	418	P	hypothetical protein
8024_at	11537.4	P	nuclear gene for ATP synthase epsilon subunit
8025_at	3061.3	P	ATP-binding cassette (ABC) transporter family member
8026_at	1162.1	P	Cortical protein required for cytoplasmic microtubule orientation\; loca
8027_at	1033.6	P	phosphoinositide-specific phospholipase C
8028_at	857.2	M	weak similarity to C.elegans transcription factor unc-86
8029_at	5672	P	dimethyladenosine transferase
8030_at	35680.5	P	dicarboxylic amino acid permease
8031_at	2910.1	P	strong similarity to YMR253c

8032_at	2082.4	P	similarity to Kel2p and Kel3p
8033_at	24788.9	P	mitochondrial and cytoplasmic fumarase (fumarate hydralase)
8034_at	32.8	A	questionable ORF
8035_at	2469	P	hypothetical protein
8036_at	966.4	P	medium subunit of the clathrin-associated protein complex
8037_at	724.8	P	similarity to B.subtilis transcriptional activator tenA, and strong simila
8038_at	27.5	A	weak similarity to YIL029c
7993_at	3540.6	P	G(sub)1 cyclin
7994_at	570.4	P	Involved in mitotic cell cycle and meiosis
7995_at	4753.1	P	transcription factor, member of Ada\/Gcn5 protein complex
7996_at	579.5	P	Cik1p homolog
7997_at	14170.8	P	iron-sulfur protein homologous to human adrenodoxin
7998_at	891.7	A	questionable ORF
7999_at	11394.4	P	weak similarity to YMR195w
8000_i_at	12232.7	P	Ribosomal protein L36B (L39) (YL39)
8001_at	272.7	A	similarity to mouse Tbc1 protein
8002_at	1552.1	P	zinc-finger transcription factor of the Zn(2)-Cys(6) binuclear cluster d
8003_at	3074.8	P	similarity to human HAN11 protein and petunia an11 protein
8004_at	8773.1	P	weak similarity to mouse proteinase activated receptor 2
8005_at	4459.9	P	weak similarity to human mutL protein homolog
8006_at	7566.1	P	weak similarity to human UDP-galactose transporter related isozyme
8007_at	1659.1	P	component of signal recognition particle
8008_at	664	P	Homolog of the mammalian IQGAP1 and 2 genes\; probable regulat
8009_at	3872.7	P	involvement in microtubule function
8010_i_at	19959.3	P	heat shock protein
8011_at	18141.1	P	YAR1 encodes a 200-amino-acid protein with two ANK repeat motifs
8012_at	2803	P	questionable ORF
8013_at	22293.7	P	beta subunit of translation initiation factor eIF-2
8014_at	501.7	P	similarity to Prk1p, and serine/threonine protein kinase homolog fro
8015_at	11843.6	P	strong similarity to TATA-binding protein-interacting protein 49 from r
7970_at	24826.8	P	17-kDa subunit C of vacuolar membrane H(+)-ATPase
7971_at	627	P	hypothetical protein
7972_at	5869.3	P	SSO1 and SSO2 encode syntaxin homologs\; act in late stages of se
7973_at	29277.9	P	alpha subunit of fatty acid synthase
7974_at	970.9	A	Up in StarVation
7975_at	2270.9	P	weak similarity to YMR181c
7976_at	725.4	P	mRNA capping enzyme beta subunit (80 kDa), RNA 5 -triphosphata
7977_at	7186.3	P	UDP-glucose:dolichyl-phosphate glucosyltransferase
7978_at	26506.3	P	similarity to translation elongation factor eEF3
7979_at	5847.8	P	hypothetical protein
7980_at	2844.2	P	Protein involved in mitochondrial iron accumulation
7981_at	715	P	Induced by osmotic stress
7982_at	50.2	A	similarity to C.perfringens hypothetical protein
7983_at	8147	P	Bypass of PAM1
7984_s_at	25893.1	P	Ribosomal protein L1A, forms part of the 60S ribosomal subunit
7985_at	2228.6	P	PHO85 cyclin
7986_at	21206.8	P	GTP binding protein
7987_at	7040.8	P	similarity to human hypothetical protein KIAA0187
7988_at	119.5	A	similarity to YGL133w
7989_at	2410.8	P	Protein required for assembly of ubiquinol cytochrome-c reductase c
7990_at	2964.3	P	TMP pyrophosphorylase, hydroxyethylthiazole kinase
7991_at	1502.2	P	similarity to A.thaliana U2 snRNP protein A

7992_at	4438.3	P	intranuclear protein which exhibits a nucleotide-specific intron-depen
7947_at	8562.8	P	Nip7p is required for 60S ribosome subunit biogenesis
7948_at	6382.7	P	component of signal recognition particle
7949_at	641.5	P	Protein kinase
7950_at	1650.2	P	similarity to YHL039w
7951_at	14507.6	P	similarity to hypthetical proteins from A. fulgidus, M. thermoautotrop
7952_at	18618.4	P	weak similarity to glycerophosphoryl diester phosphodiesterases
7953_at	1342.7	P	questionable ORF
7954_at	5888.7	P	casein kinase I isoform
7955_at	3141.9	P	cAMP-dependent protein kinase catalytic subunit
7956_at	495.8	A	similarity to cell size regulation protein Rcs1p
7957_at	276.6	A	hypothetical protein
7958_at	27.5	A	hypothetical protein
7959_at	6041	P	weak similarity to T.cruzi p284 protein
7960_i_at	6323.9	P	Ribosomal protein L7B (L6B) (rp11) (YL8)
7961_f_at	5982.7	P	Ribosomal protein L7B (L6B) (rp11) (YL8)
7962_s_at	27036.9	P	Ribosomal protein L7B (L6B) (rp11) (YL8)
7963_at	1029.2	P	questionable ORF
7964_at	951.2	P	weak similarity to S.pombe hypothetical protein SPAC8C9
7965_at	2318.7	P	delta-like subunit of the yeast AP-3 adaptin component of the membr
7966_at	1080	P	DNA damage checkpoint gene
7967_at	753	P	weak similarity to human centromere protein E
7968_at	111	A	hypothetical protein
7969_at	178.4	P	strong similarity to YGL082w
7924_at	4494.6	P	polyadenylated RNA-binding protein
7925_at	552.1	P	strong similarity to YGL084c
7926_at	3524.2	P	similarity to Utr1p and YEL041w
7927_at	23484	P	mating factor alpha
7928_at	202.7	A	weak similarity to Xenopus protein xlgv7
7929_at	381	A	questionable ORF
7930_at	8599.6	P	weak similarity to Pub1p
7931_at	4960.6	P	ribosomal protein L36, mitochondrial
7932_at	8675.8	P	similarity to Taf90p
7933_at	1248.6	M	questionable ORF
7934_at	978.9	P	weak similarity to YKR029c
7935_at	4090.8	P	weak similarity to human l-caldesmon I
7936_at	10009.3	P	protein phosphatase Q
7937_at	6558.2	P	Small subunit of nuclear cap-binding protein complex
7938_at	9317.6	P	putative DNA binding protein which shows similarity in homeobox do
7939_at	4999.1	P	similarity to chinese hamster transferrin receptor protein
7940_at	1870.3	P	N-acetylglucosaminyl-phosphatidylinositol biosynthetic protein
7941_at	307	P	Nuclear import protein
7942_at	4566.7	P	Mitochondrial ribosomal protein MRPL40 (YmL40)
7943_at	1767.1	P	Putative farnesyl transferase required for heme A synthesis
7944_at	914.6	A	NAD(P)H dehydrogenase
7945_at	5248.4	P	similarity to C.elegans LIM homeobox protein
7946_at	8540.3	P	INvolved in nuclear mRNA export, binds both poly(A)
7902_at	142.9	A	weak similarity to E.coli bfpB protein
7903_at	381.5	P	DNA polymerase
7904_at	74.2	A	weak similarity to paramyosins
7905_at	85.8	A	weak similarity to YHR207c
7906_at	197.8	A	similarity to mismatch repair protein Mlh1p

7907_at	27339.9	P	Serine and threonine rich protein.
7908_at	1431	P	hypothetical protein
7909_at	1065.1	P	Involved in polarity establishment and bud emergence\; interacts wit
7910_at	13954.3	P	cytosolic leucyl tRNA synthetase
7911_at	5271.6	P	weak similarity to YPR151c
7912_at	4226.9	P	weak similarity to human nucleolin
7913_at	1663.6	P	weak similarity to S.pombe hypothetical protein SPAC2G11.15c
7914_at	1568	P	weak similarity to YDL010w
7915_at	1155.8	P	kinesin-related protein
7916_at	21606.4	P	vacuolar proteinase A
7917_at	589.6	P	protein kinase, Mec1p and Tel1p regulate rad53p phosphorylation
7918_at	505.7	P	Resistant to Rapamycin Deletion 2
7919_at	2491.7	P	strong similarity to A.thaliana PRL1 and PRL2 proteins
7920_at	390.8	P	similarity to ser/thr protein kinases
7921_at	1396.3	P	involved in autophagy
7922_at	651.7	A	Phosphopantetheine
7923_at	353.7	P	Pxa1p and Pxa2p appear to be subunits of a peroxisomal ATP-bindi
7879_at	6563.1	P	weak similarity to myosin heavy chain proteins
7880_at	10895.8	P	Homologous to human oxysterol-binding protein\; implicated in ergos
7881_at	4287.5	P	encodes snRNA U3, SNR17A also encodes snRNA U3
7882_f_at	25135.2	P	Ribosomal protein L33A (L37A) (YL37) (rp47)
7883_at	1266.2	P	questionable ORF
7884_at	3732.4	P	strong similarity to protein kinase Kin4p
7885_at	1147.4	P	protein kinase
7886_at	1128.4	P	Transcriptional modulator
7887_at	2479.1	P	weak similarity to fruit fly polycomblike nuclear protein
7888_at	2501.2	P	similarity to microtubule-interacting protein Mhp1p and to hypothetica
7889_at	128	A	questionable ORF
7890_at	7607.9	P	NifU-like protein A
7891_at	1137.8	P	similarity to ADP/ATP carrier proteins
7892_at	1771.1	P	weak similarity to transcription factors
7893_at	2327.5	P	Putative heme A biosynthetic enzyme involved in forming the formyl
7894_at	29100	P	Ribosomal protein L5 (L1a)(YL3)
7895_at	674.1	P	hypothetical protein
7896_at	6811.5	P	TFIIF subunit (transcription initiation factor), 30 kD
7897_at	4014.7	P	TTAGGG repeat binding factor
7898_at	7423.2	P	histone H1
7899_at	7158.1	P	weak similarity to fruit fly TFIID subunit p85
7900_at	3700.5	P	weak similarity to YDR395w and cellular apoptosis susceptibility pro
7901_at	395.1	A	Nuclear import protein
7857_at	263.3	P	similarity to ribonucleases
7858_at	2031.5	P	TFIIH subunit Tfb2\; has homology to CAK and human IIH subunits
7859_at	15.6	A	Meiotic protein required for synapsis and meiotic recombination
7860_at	1884.3	P	Required for sorting and delivery of soluble hydrolases to the vacuol
7861_at	641.6	P	putative ATP-dependent RNA helicase\; Dead box protein
7862_at	1122.1	P	Component of small subunit of the mitochondrial ribosome
7863_at	5253.4	P	Isopentenyl diphosphate:dimethylallyl diphosphate isomerase (IPP is
7864_at	532.8	P	Protein with similarity to Hda1p, Rpd3p, Hos2p, and Hos1p
7865_at	8709.8	P	has GTPase-activating protein activity toward the essential bud-site
7866_at	904.7	P	questionable ORF
7867_at	538.1	P	similarity to glycerate dehydrogenases
7868_at	2304	P	weak similarity to YOR193w

7869_at	7981.5	P	arginase
7870_at	4792.1	P	similarity to C.elegans hypothetical protein, weak similarity to Pho81
7871_at	705.2	P	similarity to aminoglycoside acetyltransferase regulator from P. stuar
7872_at	2549.4	P	hypothetical protein
7873_at	989.2	P	hypothetical protein
7874_at	20085.2	P	HSP70 family member, highly homologous to Ssa1p and Sse2p
7875_at	2931.9	P	similarity to Smy2p
7876_at	1086.9	P	Aspartyl-tRNA synthetase, mitochondrial
7877_at	2877.9	P	similarity to hypothetical M. tuberculosis protein
7878_at	982.3	P	questionable ORF
7834_at	5960.8	P	hypothetical protein
7835_at	3138.2	P	similarity to YFR021w
7836_at	943.6	P	weak similarity to Sulfolobus hypothetical protein
7837_at	6713.9	P	similarity to S.pombe hypothetical protein
7838_at	2571.3	P	Tyrosyl-tRNA synthetase
7839_at	6664.3	P	hypothetical protein
7840_at	1220.1	P	strong similarity to YBR177c
7841_at	14524.3	P	membrane component of ER protein translocation apparatus
7842_at	21467.4	P	similarity to M.jannaschii GTP-binding protein, GTP1/OBG-family, w
7843_at	2391.6	P	sensitive to sulfite
7844_at	13416	P	Glutathione oxidoreductase
7845_s_at	37804.7	P	Ribosomal protein S6A (S10A) (rp9) (YS4)
7846_at	9047.3	P	serum response factor-like protein
7847_at	1273.8	P	similarity to aryl-alcohol dehydrogenases
7848_at	8353.2	P	strong similarity to YBR183w
7849_at	7563.2	P	Histone and other Protein Acetyltransferase\; Has sequence homolo
7850_at	3531.4	P	multidomain vesicle coat protein that interacts with Sec23p
7851_at	1570.5	P	BCK1-like resistance to osmotic shock
7852_at	852.3	P	54kDa subunit of the tetrameric tRNA splicing endonuclease
7853_at	3086.3	P	putative helicase
7854_i_at	3162.5	P	Ribosomal protein S9A (S13) (rp21) (YS11)
7855_f_at	13021.8	P	Ribosomal protein S9A (S13) (rp21) (YS11)
7856_at	559.8	A	hypothetical protein
7811_at	923.7	P	Ribosomal protein L21B
7812_at	5599.6	P	F(1)F(0)-ATPase complex delta subunit, mitochondrial
7813_at	583.4	P	weak similarity to YBR197c
7814_at	2855.1	P	Required for synthesis of N-acetylglucoaminylphosphatidylinositol, th
7815_at	805.4	P	similarity to Vps4p and YER047c
7816_at	63.1	A	questionable ORF
7817_at	609.3	P	encodes putative deubiquitinating enzyme
7818_at	1018	P	hypothetical protein
7819_at	719.8	P	weak similarity to Vps9p
7820_at	643.1	P	geranylgeranyl diphosphate synthase
7821_at	1092.5	P	hypothetical protein
7822_at	3621.5	P	hypothetical protein
7823_at	4558.2	P	hypothetical protein
7824_at	1839.8	P	soluble, hydrophilic protein involved in transport of precursors for sol
7825_at	2549.8	P	weak similarity to S.pombe peptidyl-prolyl cis-trans isomerase
7826_at	10966.9	P	similarity to hypothetical protein YLR019w, YLL010c and S.pombe h
7827_at	795.5	A	hypothetical protein
7828_at	29533.7	P	cytosolic aldehyde dehydrogenase
7829_at	437.1	P	strong similarity to Mrs2p

7830_at	1749.3	P	similarity to glutaredoxins
7831_at	28828	P	multidrug resistance transporter
7832_at	14134.6	P	Multicopy suppressor of cls2-2\; also suppresses rvs161 mutations
7833_at	4944.1	P	hypothetical protein
7788_at	2886.3	P	hypothetical protein
7789_at	2036.6	A	protein of unknown function
7790_at	27334.9	P	mannosylphosphate transferase
7791_at	3527.8	P	hypothetical protein
7792_at	1379.4	M	strong similarity to ADP-ribosylation factors
7793_at	4505.4	P	Protein required for complex glycosylation
7794_at	7380	P	MAP kinase-associated protein
7795_at	14638.3	P	Calcium and phospholipid binding protein homologous to translation
7796_at	3385.8	P	hypothetical protein
7797_at	5029.6	P	Elongin C transcription elongation factor
7798_at	1057.8	P	Vacuolar sorting protein
7799_at	1375.5	P	questionable ORF
7800_at	7088.9	P	RNA recognition motif-containing protein
7801_at	672.4	P	a cyclin(SSN8)-dependent serine\/threonine protein kinase
7802_at	1727.5	P	hypothetical protein
7803_at	1908.4	P	nuclear encoded mitochondrial isoleucyl-tRNA synthetase
7804_at	7947.8	P	hypothetical protein
7805_at	494.8	P	zinc finger DNA binding factor, transcriptional regulator of sulfur ami
7806_at	25701	P	GAL4 enhancer protein, has similarity to human transcription factor
7807_at	6270.4	P	plasma membrane ATPase
7808_at	463.7	M	questionable ORF
7809_at	689.9	P	questionable ORF
7810_at	152.1	A	weak similarity to YLR426w
7766_at	15829.2	P	styryl dye vacuolar localization
7767_at	8626.5	P	negative transcriptional regulator, protein kinase homolog
7768_at	4563.9	P	similarity to C.elegans hypothetical protein
7769_at	1761.5	P	putative ATP-dependent helicase
7770_at	17268	P	acetoacetyl CoA thiolase
7771_at	701.5	A	hypothetical protein
7772_at	4932.2	P	serine\/threonine protein kinase homologous to Ran1p
7773_at	229	A	questionable ORF
7774_at	795.7	M	(N)egative regulator of (C)ts1 (E)xpression
7775_at	5806.6	P	putative methylenetetrahydrofolate reductase (mthfr)
7776_at	1086.2	P	UV endonuclease
7777_at	39.6	A	ExtraCellular Mutant\; similar to SRD1
7778_at	6503	P	weak similarity to Smt4p
7779_at	20117.7	P	strong similarity to YFL004w, similarity to YJL012c
7780_at	166.9	A	Important for chromosome segregation
7781_at	51.4	A	strong similarity to Lpd1p and other dihydrolipoamide dehydrogenase
7782_at	2661.1	P	Zinc-finger transcription factor
7783_at	2401.8	P	Homolog of SIR2
7784_at	5682.8	P	hypothetical protein
7785_at	10544	P	ribosomal protein S16, mitochondrial
7786_at	18894.6	P	hypothetical protein
7787_at	1193.3	P	Component of the TAF(II) complex (TBP-associated protein complex
7743_at	3346.7	P	coatomer complex zeta chain
7744_at	7670.3	P	similarity to M.jannaschii hypothetical protein
7745_at	1129	P	kinetochore protein in the DEAH box family

7746_at	758.2	M	hypothetical protein
7747_at	10425.3	P	predicted transmembrane protein
7748_at	1039.6	P	weak similarity to Nup2p
7749_at	19538.2	P	strong similarity to YGR086c
7750_at	802.3	P	Required for activation of RUB1 (ubiquitin-like protein) together with
7751_at	2900.8	P	appears to be functionally related to SNF7
7752_at	3417.3	P	histone acetyltransferase
7753_at	255.6	A	Mitochondrial isoform of citrate synthase
7754_at	284.2	A	similarity to B.subtilis mmgE protein
7755_at	438	A	similarity to sulphate transporter proteins
7756_at	13500.9	P	strong similarity to electron transfer flavoproteins alpha chain
7757_at	574.4	M	polar 32k Da cytoplasmic protein
7758_at	1210.5	P	Isocitrate lyase, may be nonfunctional
7759_at	61.1	A	hypothetical protein
7760_at	1661.8	P	similarity to transcription factor
7761_at	1417.9	P	similarity to sterol uptake protein Sut1p
7762_at	16029.9	P	RNA polymerase I subunit A135
7763_at	2238.6	P	similarity to ADP/ATP carrier proteins and Graves disease carrier pr
7764_at	1102.8	P	hypothetical protein
7765_at	734.5	A	similarity to transcription factors
7721_at	27.5	A	hypothetical protein
7722_at	229.2	A	similarity to transcription factors
7723_at	34884.7	P	similar to human translation initiation factor 6 (eIF6)
7724_at	1512.1	P	GDP dissociation factor for Sec4p
7725_at	1339.6	P	p90 subunit of yeast omatin Assembly Factor-I (CAF-I)
7726_at	2122.5	P	essential for initiation of DNA replication\; homolog of S. pombe CDC
7727_at	949.4	P	hypothetical protein
7728_at	1555.4	M	similarity to human citrate transporter protein
7729_at	1114.7	P	weak similarity to fruit fly dorsal protein and Snf5p
7730_at	11721.4	P	similarity to human hypothetical protein
7731_at	2557	P	Mitochondrial protein of the CDC48\/PAS1\/SEC18 family of ATPase
7732_at	1791.8	P	novel cyclin gene\; encodes subunits of TFIIK, a subcomplex of tran
7733_at	857.4	P	null mutant is viable\; increased tolerance to dehydration, freezing, a
7734_at	204.9	A	similarity to YNL019c and YNL033w
7735_at	8025.1	P	Ypt Interacting Protein
7736_at	19912.8	P	Ypt Interacting Protein
7737_at	7890.4	P	Gamma-adaptin, large subunit of the clathrin-associated protein (AP
7738_at	979.7	A	similarity to YBL101c
7739_at	1629	P	similarity to human zinc-finger protein BR140
7740_at	2557.6	P	yeast homolog of the Drosphila tumor suppressor, lethal giant larva
7741_at	19746.6	P	cytoplasmic and mitochondrial histidine tRNA synthetases
7742_at	2141	P	Actin-related protein
7698_at	26452.2	P	glutamine synthetase
7699_at	17091.6	P	54-kDa vacuolar H(+) ATPase subunit of V1 sector
7700_at	9491.8	P	similarity to Erv1p and rat ALR protein
7701_at	490.7	A	questionable ORF
7702_g_at	3347.9	A	questionable ORF
7703_at	147.3	A	questionable ORF
7704_at	3398	P	similarity to C.elegans C02C2.6 protein
7705_at	4623.4	P	Translation initiation factor eIF-5
7706_at	5200	P	similarity to Jsn1p
7707_i_at	38562.2	P	Ribosomal protein L43A

7708_f_at	23267.6	P	Ribosomal protein L43A
7709_at	1498	P	questionable ORF
7710_at	919.2	P	similarity to C.elegans hypothetical protein
7711_at	1156.3	P	Required for chromosome segregation
7712_at	693	P	alpha subunit of yeast mitochondrial phenylalanyl-tRNA synthetase
7713_at	6486.6	P	similarity to M.domestica NADPH--ferrihemoprotein reductase and m
7714_at	517.4	A	similarity to Uso1p
7715_at	1438.1	A	questionable ORF
7716_at	6180.4	P	N-acetyltransferase
7717_at	14113.7	P	11-kDa nonhistone chromosomal protein
7718_g_at	17519	P	11-kDa nonhistone chromosomal protein
7719_at	1773.8	P	questionable ORF
7720_at	44.7	A	MAP kinase
7675_at	883	P	121 kDa component of the Exocyst complex, which is required for e
7676_at	987.2	P	Component of RNA polymerase transcription initiation TFIIH (factor
7677_at	3449.4	P	Protein involved in snRNP biogenesis
7678_at	5220.7	P	putative mitochondrial carrier protein
7679_at	166.5	A	questionable ORF
7680_at	6468.4	P	chorismate mutase
7681_at	498.9	P	weak similarity to Synechococcus sp. DnaJ protein
7682_at	19030.9	P	cytosine deaminase
7683_at	10101.6	P	hypothetical protein
7684_at	816.5	A	hypothetical protein
7685_at	4956.5	P	site-specific DNA binding protein, repressor
7686_at	815.6	P	ubiquitin-like protein activating enzyme
7687_at	946.7	P	weak similarity to F.alni nitrogen fixation protein
7688_at	335.1	P	Protein with similarity to Hda1p, Rpd3p, Hos2p, and Hos3p
7689_at	10629.8	P	putrescine aminopropyltransferase (spermidine synthase)
7690_at	1878.2	P	hypothetical protein
7691_at	1093.7	P	strong similarity to YIL029c
7692_at	3075.2	P	member of the NOT complex, a global negative regulator of transcri
7693_at	1323.1	P	18-kDa phosphotyrosine phosphatase of unknown function
7694_at	34487.8	P	Transketolase 1
7695_at	2620.8	P	imparts Far- phenotype
7696_at	113.5	A	questionable ORF
7697_i_at	129.4	A	questionable ORF
7653_s_at	348.5	A	questionable ORF
7654_at	575.4	A	hypothetical protein
7655_at	1022.2	P	weak similarity to human insulin-like growth factor 2 receptor
7656_s_at	26361	P	translational elongation factor EF-1 alpha
7657_at	6579.6	P	strong similarity to glycyl-tRNA synthetases
7658_at	3722.4	P	S. pombe dim1+ in budding yeast
7659_at	1377.1	M	hypothetical protein
7660_at	8797.8	P	hypothetical protein
7661_at	747	M	hypothetical protein
7662_at	27185.6	P	transcription factor TFIIB homolog
7663_at	802.1	P	questionable ORF
7664_at	10236.5	P	Signal recognition particle subunit (homolog of mammalian SRP54)
7665_at	607.1	P	questionable ORF
7666_at	4907.1	P	hypothetical protein
7667_at	966.9	P	weak similarity to C.elegans LIM homeobox protein
7668_at	287.8	A	questionable ORF

7669_at	526.8	M	weak similarity to zinc-finger proteins
7670_at	2456.5	P	weak similarity to chicken lim-3 protein
7671_at	1050.9	P	Suppressor of Ypt3
7672_at	542.4	A	hypothetical protein
7673_at	12835.3	P	hypothetical protein
7674_at	6980.1	P	hypothetical protein
7629_at	551.9	A	questionable ORF
7630_at	5534.8	P	weak similarity to C.elegans hypothetical protein CEC25A1
7631_at	1220.2	P	splicing factor
7632_i_at	36963.8	P	Ribosomal protein L11A (L16A) (rp39A) (YL22)
7633_s_at	32234.7	P	Ribosomal protein L11A (L16A) (rp39A) (YL22)
7634_at	35064.8	P	proteasome subunit
7635_at	625.3	P	Protein with a domain similar to the fork head DNA-binding domain f
7636_at	1657.2	P	hypothetical protein
7637_at	2002.6	P	protein kinase
7638_at	2622.2	P	Yeast 30kDa Homologue
7639_at	23384.8	P	Subunit of the regulatory particle of the proteasome
7640_at	865.4	P	weak similarity to human nicotinic acetylcholine receptor delta chain
7641_at	4773.6	P	RNA polymerase III (C) subunit
7642_at	207.8	A	kinase required for late nuclear division
7643_at	237.8	P	kinase required for late nuclear division
7644_at	2958.3	P	similarity to RNA-binding proteins
7645_at	25466.9	P	phosphatidylinositol synthase
7646_at	19095.1	P	similarity to YJR116w
7647_at	4712.7	P	similarity to probable transcription factor Ask10p, and to YNL047c a
7648_at	70.3	A	hypothetical protein
7649_at	657.9	P	similarity to YLR454w
7650_at	3083.1	P	similarity to M.jannaschii translation initiation factor, eIF-2B
7651_at	1520.6	P	G(sub)2-specific B-type cyclin
7652_at	2385.9	P	B-type cyclin
7607_at	1846.5	P	similarity to B.subtilis transcriptional activator tenA, strong similarity
7608_at	2329.2	P	putative homolog of human insulin-degrading endoprotease
7609_at	1728	A	questionable ORF
7610_at	6769.6	P	High affinity copper transporter into the cell, probable integral memb
7611_at	10211.5	P	suppressor of mrs2-1 mutation
7612_at	2215.4	P	questionable ORF
7613_at	1121.1	P	similarity to C-term. of N.tabacum auxin-induced protein
7614_at	5890.3	P	similarity to carrier protein FLX1
7615_at	5705.3	P	multicopy suppressor of clathrin deficiency
7616_at	1675	M	questionable ORF
7617_at	2976.9	P	similarity to N-acetyltransferases
7618_f_at	34113.4	P	Ribosomal protein S23B (S28B) (rp37) (YS14)
7619_s_at	10321.6	P	Ribosomal protein S23B (S28B) (rp37) (YS14)
7620_at	3459.1	P	similarity to C.elegans hypothetical protein
7621_at	15128.8	P	Translocase of the Outer Mitochondrial membrane
7622_at	1291.9	P	Protein involved in splicing intron a15beta of COX1
7623_at	3163.2	P	DNA polymerase alpha binding protein
7624_at	1118.9	P	questionable ORF
7625_at	12121.9	P	weak similarity to Taf90p
7626_at	7704.6	P	NH4+ transporter, highly similar to Mep1p and Mep2p
7627_at	5176.5	P	hypothetical protein
7628_at	1577.5	P	similarity to human BTHS gene involved in Barth syndrome

7584_at	1819.3	P	kinesin-like nuclear fusion protein
7585_at	1241.9	P	questionable ORF
7586_at	2166.3	P	hypothetical protein
7587_at	4334.5	P	similarity to YDR060w and C.elegans hypothetical protein
7588_at	10421.6	P	asparagine synthetase
7589_at	3125.7	P	questionable ORF
7590_at	4766.8	P	hypothetical protein
7591_at	3939.7	P	hypothetical protein
7592_at	27382.1	P	involved in secretion of proteins that lack classical secretory signal se
7593_at	701.9	A	questionable ORF
7594_at	1621.3	P	weak similarity to YPL159c
7595_at	1043.2	P	hypothetical protein
7596_at	716.7	P	hypothetical protein
7597_at	10091.5	P	similarity to chicken growth factor receptor-binding protein GRB2 hon
7598_at	1163.9	P	Regulates proper expression of subunits 6 (Atp6p) and 8 (Atp8p) of t
7599_i_at	400.7	A	similarity to multidrug resistance proteins
7600_s_at	27315.7	P	similarity to multidrug resistance proteins
7601_at	1055.7	P	strong similarity to YGR141w
7602_at	1165.8	P	similarity to YGR142w
7603_at	15198.2	P	potential beta-glucan synthase
7604_at	836.7	P	Glycogen phosphorylase
7605_at	1721.7	P	CDC28\/cdc2 related protein kinase
7606_at	1649	P	56-kDa subunit of origin recognition complex (ORC)
7561_at	24205.4	P	Translation initiation factor eIF-4B
7562_at	809.9	P	killed in mutagen, sensitive to diepoxybutane and\/or mitomycin C
7563_at	14586.7	P	GTP-binding protein of the rho subfamily of ras-like proteins
7564_at	3497.2	P	14 kDa mitochondrial ribosomal protein\; homologous to E. coli S14
7565_at	1003.6	P	3 phosphoadenylylsulfate reductase
7566_at	181.7	A	negative regulator of URS2 of the HO promoter
7567_at	11421.2	P	hypothetical protein
7568_at	352.7	A	hypothetical protein
7569_at	1570.2	P	hypothetical protein
7570_at	1569.8	P	strong similarity to YLR456w
7571_at	5054.5	P	defective in vacuolar protein sorting
7572_at	930.8	A	weak similarity to Nbp1p
7573_at	903.1	P	DNA polymerase epsilon, subunit B
7574_at	7591.1	P	Geranylgeranyltransferase Type II beta subunit
7575_at	241.8	A	questionable ORF
7576_at	2400.4	P	associated with the U4\/U6 snRNP
7577_at	612.6	P	hypothetical protein
7578_at	1807.7	P	Along with Uba2p forms a heterodimeric activating enzyme for Smt3
7579_at	4516.8	P	cytoplasmic GTPase-activating protein
7580_at	4380	P	Sm or Sm-like snRNP protein
7581_at	18574.9	P	dolichol phosphate mannose synthase
7582_at	2908.2	P	similarity to human 4-alpha-glucanotransferase (EC 2.4.1.25)/amylo-
7583_at	3793.4	P	Autophagy
7538_at	782.5	P	Transcription factor IIIA (TFIIIA) with putative Zn-fingers
7539_at	18606	P	subunit common to RNA polymerases I, II, and III
7540_at	1120.1	P	similarity to calmodulin and calmodulin-related proteins
7541_at	1642.1	P	Contains 8 copies of the TPR domain
7542_at	6558.4	P	82-kDa subunit of RNA polymerase III (C)
7543_at	17382.7	P	40 kDa ubiquinol cytochrome-c reductase core protein 2

7544_at	1019.5	A	similarity to plasma membrane and water channel proteins
7545_at	311.6	A	Histone and other Protein Acetyltransferase\; Has sequence homolog
7546_at	120.1	A	similarity to S.pombe isp4 protein
7547_at	46.7	A	hypothetical protein
7548_at	315.7	A	strong similarity to regulatory protein Mal63p
7549_g_at	13317.3	P	strong similarity to regulatory protein Mal63p
7550_at	208.9	A	questionable ORF
7551_at	5747.4	P	multi-copy suppressor of gal11 null\; member of drug-resistance prot
7552_at	1999.9	P	Similar to transcriptional regulatory elements YAP1 and cad1
7553_at	368.2	A	Required for arsenate but not for arsenite resistance
7554_at	10.6	A	involved in arsenite transport
7555_s_at	4426.3	P	trans-acting positive regulator of the enolase and glyceraldehyde-3-p
7556_at	1194.4	P	non-annotated SAGE orf Found reverse in NC_001148 between 188
7557_at	8767.5	P	non-annotated SAGE orf Found reverse in NC_001148 between 582
7558_at	87.4	A	non-annotated SAGE orf Found forward in NC_001148 between 744
7559_at	355.6	M	non-annotated SAGE orf Found forward in NC_001148 between 744
7560_at	265.9	P	non-annotated SAGE orf Found reverse in NC_001148 between 824
7512_at	1253.8	P	non-annotated SAGE orf Found reverse in NC_001148 between 132
7513_f_at	3427.4	P	non-annotated SAGE orf Found forward in NC_001148 between 809
7514_at	854	P	non-annotated SAGE orf Found forward in NC_001148 between 810
7515_f_at	34.2	A	non-annotated SAGE orf Found forward in NC_001148 between 853
7516_at	5932.2	P	non-annotated SAGE orf Found reverse in NC_001148 between 212
7517_at	3384.3	P	non-annotated SAGE orf Found reverse in NC_001148 between 278
7518_at	633.2	P	non-annotated SAGE orf Found forward in NC_001148 between 411
7519_at	2919.6	P	non-annotated SAGE orf Found forward in NC_001148 between 431
7520_at	19174	P	non-annotated SAGE orf Found reverse in NC_001148 between 592
7521_at	11411.5	P	non-annotated SAGE orf Found reverse in NC_001148 between 624
7522_at	275.3	A	non-annotated SAGE orf Found forward in NC_001148 between 700
7523_at	652.7	P	non-annotated SAGE orf Found forward in NC_001148 between 706
7524_at	1034.2	P	non-annotated SAGE orf Found reverse in NC_001148 between 718
7525_at	4518.8	P	non-annotated SAGE orf Found forward in NC_001148 between 743
7526_i_at	1868.8	M	non-annotated SAGE orf Found reverse in NC_001148 between 773
7527_r_at	225.8	P	non-annotated SAGE orf Found reverse in NC_001148 between 773
7528_f_at	594.3	P	non-annotated SAGE orf Found reverse in NC_001148 between 773
7529_at	107.1	A	non-annotated SAGE orf Found forward in NC_001148 between 819
7530_s_at	1030.9	A	non-annotated SAGE orf Found forward in NC_001148 between 880
7531_at	9597	P	non-annotated SAGE orf Found forward in NC_001148 between 883
7532_at	4094.7	P	non-annotated SAGE orf Found forward in NC_001148 between 897
7533_at	11055.8	P	non-annotated SAGE orf Found forward in NC_001148 between 298
7534_i_at	29.3	A	non-annotated SAGE orf Found reverse in NC_001148 between 700
7535_f_at	23.5	A	non-annotated SAGE orf Found reverse in NC_001148 between 700
7536_at	575.1	P	non-annotated SAGE orf Found forward in NC_001148 between 754
7537_at	1377.9	P	non-annotated SAGE orf Found reverse in NC_001148 between 812
7489_at	405.8	A	non-annotated SAGE orf Found forward in NC_001148 between 860
7490_at	576.8	P	non-annotated SAGE orf Found reverse in NC_001148 between 927
7491_at	1153.9	A	non-annotated SAGE orf Found forward in NC_001148 between 147
7492_at	1430.7	P	non-annotated SAGE orf Found reverse in NC_001148 between 854
7493_at	15629.5	P	non-annotated SAGE orf Found reverse in NC_001148 between 296
7494_at	428.9	A	non-annotated SAGE orf Found forward in NC_001148 between 297
7495_at	38.9	A	non-annotated SAGE orf Found reverse in NC_001148 between 411
7496_at	472.1	A	non-annotated SAGE orf Found reverse in NC_001148 between 445
7497_at	14.7	A	non-annotated SAGE orf Found reverse in NC_001148 between 588

7498_at	74.9	A	non-annotated SAGE orf Found reverse in NC_001148 between 588
7499_at	193.1	A	non-annotated SAGE orf Found reverse in NC_001148 between 678
7500_at	454	A	non-annotated SAGE orf Found reverse in NC_001148 between 769
7501_at	62.5	A	non-annotated SAGE orf Found forward in NC_001148 between 775
7502_at	1490	A	non-annotated SAGE orf Found forward in NC_001148 between 822
7503_i_at	5695.7	M	non-annotated SAGE orf Found reverse in NC_001148 between 880
7504_r_at	911.8	A	non-annotated SAGE orf Found reverse in NC_001148 between 880
7505_at	316	A	non-annotated SAGE orf Found reverse in NC_001148 between 921
7506_at	3251.8	P	non-annotated SAGE orf Found reverse in NC_001148 between 324
7507_at	500.3	A	non-annotated SAGE orf Found reverse in NC_001148 between 408
7508_at	997.8	P	non-annotated SAGE orf Found forward in NC_001148 between 408
7509_at	254.9	A	non-annotated SAGE orf Found reverse in NC_001148 between 409
7510_at	3126.9	P	non-annotated SAGE orf Found forward in NC_001148 between 427
7511_at	1007.6	A	non-annotated SAGE orf Found forward in NC_001148 between 497
7466_at	187.9	A	non-annotated SAGE orf Found forward in NC_001148 between 560
7467_at	38.8	A	non-annotated SAGE orf Found forward in NC_001148 between 596
7468_at	254.9	M	non-annotated SAGE orf Found forward in NC_001148 between 633
7469_at	277.1	P	non-annotated SAGE orf Found forward in NC_001148 between 703
7470_at	16469.6	P	non-annotated SAGE orf Found reverse in NC_001148 between 733
7471_at	184.4	A	non-annotated SAGE orf Found forward in NC_001148 between 780
7472_at	1896.2	A	non-annotated SAGE orf Found forward in NC_001148 between 831
7473_at	2274.7	P	snRNA
7474_at	5908.4	P	snRNA
7475_at	2490	P	snRNA
7476_at	1716	P	snRNA
7477_at	319.9	P	snRNA
7478_s_at	3074.2	P	similarity to subtelomeric encoded proteins
7479_at	1342.3	P	hypothetical protein
7480_at	1249.5	P	yeast homolog of the Drosphila tumor suppressor, lethal giant larvae
7481_at	1458.5	P	putative protein kinase
7482_at	2668.5	P	hypothetical protein
7483_at	2807.6	P	Probable cytochrome c subunit, copper binding
7484_at	8014.2	P	suppressor of sed5 ts mutants
7485_at	1898.5	P	ExtraCellular Mutant
7486_at	651.5	A	questionable ORF
7487_at	14249	P	mitochondrial F1F0-ATPase alpha subunit
7488_at	2266.2	P	similarity to human and D.melanogaster kynurenine 3-monooxygenas
7443_at	410.7	P	BARREN, a gene with sequence similarity to Drosophila barren and
7444_at	4820.4	P	questionable ORF
7445_at	1415.1	P	similarity to C.albicans hypothetical protein
7446_at	632.7	P	questionable ORF
7447_at	1591.6	P	RNA polymerase II holoenzyme\/mediator subunit
7448_at	20143	P	Ribosomal protein L32
7449_at	1097	P	weak similarity to SCS2
7450_at	21392.4	P	methionine aminopeptidase 2
7451_at	807.8	P	Component of the small subunit of mitochondrial ribosomes
7452_at	2441	P	weak similarity to A.thaliana aminoacid permease AAP3
7453_at	584.8	P	putative phosphatidylinositol kinase
7454_s_at	31766.4	P	Ribosomal protein L23A (L17aA) (YL32)
7455_at	531.7	P	involved in sugar metabolism
7456_at	3608.8	P	BEM1-binding protein
7457_at	3392	P	component of the anaphase-promoting complex

7458_i_at	805	P	questionable ORF
7459_s_at	5953.9	P	questionable ORF
7460_at	5578.4	P	putative Dol-P-Man dependent alpha(1-3) mannosyltransferase invol
7461_at	16192.9	P	hypothetical protein
7462_at	419.7	P	62-kDa protein
7463_at	3775.4	P	Nucleoporin highly similar to Nup157p and to mammalian Nup155p (
7464_at	4012.9	P	Form a protein complex with Aut2p, to mediate attachment of autop
7465_at	1353.2	P	questionable ORF
7421_at	17654.6	P	cytoplasmic isoleucyl-tRNA synthetase
7422_at	269.7	A	heat-inducible cytosolic member of the 70 kDa heat shock protein fa
7423_at	653.8	P	splices pre mRNA of the MATa1 cistron
7424_at	273.8	A	questionable ORF
7425_s_at	27564	P	Ribosomal protein S8A (S14A) (rp19) (YS9)
7426_at	1225.8	P	hypothetical protein
7427_at	211.5	A	questionable ORF
7428_at	10576	P	ribose-phosphate pyrophosphokinase 4
7429_at	1525.4	P	ubiquitin carboxyl-terminal hydrolase
7430_at	928.5	A	putative transcription factor
7431_at	523	A	questionable ORF
7432_at	1123.3	P	Homolog to thiol-specific antioxidant
7433_at	769.4	P	kinesin related protein
7434_at	786.3	P	questionable ORF
7435_at	8495.3	P	protoplast regeneration and killer toxin resistance gene, may be a p
7436_at	1265.4	P	hypothetical protein
7437_at	94.8	A	weak similarity to hypothetical protein YER093c-a
7438_at	1261	P	weak similarity to hypothetical protein YER093c-a
7439_at	9989.3	P	isolated as a suppressor of the lethality caused by overexpression of
7440_at	3333.8	P	strong similarity to hypothetical S.pombe protein
7441_at	5950.7	P	protein phosphatase type 2C
7442_at	3101.8	P	similarity to hypothetical S.pombe protein
7398_at	7430.8	P	Homolog to myb transforming proteins
7399_at	1375.5	A	questionable ORF
7400_at	1386.3	P	SAS3 for Something about silencing, gene 3. Influences silencing at
7401_at	12571.6	P	similarity to S.pombe Z66568_C protein
7402_at	4074.5	P	peripheral membrane protein required for vesicular transport betwee
7403_at	810.6	P	hypothetical protein
7404_at	878.6	A	hypothetical protein
7405_at	6467.5	P	USO1 homolog (S. cerevisiae), cytoskeletal-related transport protei
7406_at	6519.3	P	weak similarity to hypothetical protein YOR054c
7407_at	9840.9	P	44 kDa core protein of yeast coenzyme QH2 cytochrome c reductas
7408_at	185.1	A	hypothetical protein
7409_at	1912.4	P	ExtraCellular Mutant
7410_at	24052.6	P	uridine permease
7411_at	13610.2	P	proteasome subunit
7412_at	1802.2	P	encodes the HDEL receptor required for retention of ER proteins
7413_at	29849.3	P	CTP synthase, highly homologus to URA8 CTP synthase
7414_at	3518.8	P	Mitochondrial ribosomal protein MRPL16
7415_at	1302.3	P	clathrin Associated Protein complex Large subunit
7416_at	11301.4	P	Homolog to twitching motility protein (P. aeroginosa)
7417_at	1599.7	P	B subunit of DNA polymerase alpha-primase complex
7418_at	1687.5	P	suppressor of cold-sensitive tub2 mutation\; shown to be a compone
7419_at	10523.3	P	GTP cyclohydrolase II

7420_at	23654.6	P	weak similarity to hnRNP complex protein homolog YBR233w
7374_at	170.9	A	hypothetical protein
7375_at	27358.9	P	mitochondrial ADP\/ATP translocator
7376_at	2871	P	hypothetical protein
7377_at	2166.8	P	involved in mating-type regulation
7378_s_at	37675.6	P	Ribosomal protein L19B (YL14) (L23B) (rpl5L)
7379_i_at	202.6	P	snRNA-associated protein of the Sm class
7380_f_at	53.7	A	snRNA-associated protein of the Sm class
7381_at	2263.9	P	snRNA-associated protein of the Sm class
7382_at	509.6	P	Upstream activation factor subunit
7383_at	13058.6	P	Probable proliferating-cell nucleolar antigen (human p120)
7384_at	6723.3	P	Minichromosome maintenance protein, transcription factor
7385_at	18711.6	P	mitochondrial ATP-dependent protease
7386_at	2786.6	P	transcriptional activator protein of CYC1
7387_at	8700	P	67 kDa integral membrane protein
7388_at	620.7	A	AP endonuclease
7389_at	4910.1	P	integral subunit of RNase P and apparent subunit of RNase MRP
7390_at	7918.9	P	carboxypeptidase Y sorting receptor in late Golgi\; Type I integral me
7391_at	9248.2	P	cdc2+\/CDC28 related kinase with positive role in conjugation
7392_at	2410.9	P	acetyl CoA hydrolase
7393_at	1834.9	P	member of yeast Pol I core factor (CF) also composed of Rrn11p, R
7394_at	101.8	A	Probable met-tRNA formyltransferase, mitochondrial
7395_at	172.1	A	questionable ORF
7396_at	7344.9	P	High copy suppresor of choline-transport mutants
7397_at	143.6	A	hypothetical protein
7352_at	3050.2	P	strong similarity to DNA damage responsive Alk1p
7353_at	827.3	P	putative repressor protein homologous to yeast Tup1p and mammali
7354_at	13669.6	P	contains 3 SH3 domains, interacts with Bee1p
7355_at	4404.5	P	hypothetical protein
7356_at	1178.1	P	Pleiotropic drug resistance protein 3
7357_at	4387	P	weak similarity to Papaya ringspot virus polyprotein
7358_s_at	34854.6	P	Histone H2A (HTA1 and HTA2 code for nearly identical proteins)
7359_at	25102.6	P	Histone H2B (HTB1 and HTB2 code for nearly identical proteins)
7360_at	3725.9	P	ExtraCellular Mutant
7361_at	3286.5	P	Neutral trehalase, highly homologous to Nth1p
7362_at	7928.9	P	strong similarity to hypothetical protein YMR101c
7363_at	6035.8	P	hexaprenyl pyrophosphate synthetase
7364_at	11680	P	similarity to S.pombe hypothetical protein SPAC18B11.05
7365_at	1451.7	P	strong similarity to hypothetical protein YDR003w
7366_at	2625.9	P	hypothetical protein
7367_at	5363.3	P	Major Facilitator Transporter
7368_i_at	20824.6	P	Histone H3 (HHT1 and HHT2 code for identical proteins)
7369_s_at	14568.2	P	Histone H3 (HHT1 and HHT2 code for identical proteins)
7370_at	31006.2	P	Inorganic pyrophosphatase
7371_at	2074.6	P	hypothetical protein
7372_at	574.7	P	hypothetical protein
7373_at	2494.1	P	Glutaredoxin homolog
7328_at	9994.5	P	Type II transmembrane protein
7329_at	15631.8	P	strong similarity to hypothetical proteins YDL012c and YDR210w
7330_at	8086.7	P	karyopherin beta 2, yeast transportin
7331_at	914.8	A	galactose-1-phosphate uridyl transferase
7332_at	298.3	P	UDP-glucose 4-epimerase

7333_at	310.9	A	galactokinase
7334_at	12123.6	P	uracil permease
7335_at	851.2	P	hypothetical protein
7336_at	17851.7	P	chitin synthase 3
7337_at	1680.1	P	SCO1 protein homolog (S. cerevisiae)
7338_at	16301.3	P	probable purine nucleotide-binding protein
7339_at	1725.3	P	Nuclear protein that binds to T-rich strand of core consensus sequen
7340_at	866	A	hypothetical protein
7341_at	1824	P	Probable ser\/thr-specific protein kinase, homolog to YKR2 and YPK
7342_at	16473.7	P	CDP-diacylglycerol synthase, CTP-phosphatidic acid cytidylyltransfe
7343_at	1601.8	P	involved in inositol biosynthesis
7344_i_at	8513.1	A	Ribosomal protein L4A (L2A) (rp2) (YL2)
7345_s_at	32739.4	P	Ribosomal protein L4A (L2A) (rp2) (YL2)
7346_at	2524.9	P	hypothetical protein
7347_at	660.6	A	Probable regulatory Zn-finger protein,\/ homolog to YKL251\/
7348_at	10929.3	P	nuclear protein arginine methyltransferase (mono- and asymmetricall
7349_at	5184	P	pyridoxine (pyridoxiamine) phosphate oxidase
7350_at	17238.7	P	contains 9 or 10 putative membrane spanning regions\; putative Ca2
7351_at	4531.2	P	inner mitochondrial membrane protein
7306_at	9503.6	P	chitin synthase 2
7307_at	25179.4	P	gamma subunit of mitochondrial ATP synthase
7308_at	3749.2	P	integral membrane protein
7309_at	3598.3	P	Fatty acid transporter
7310_at	1272.4	P	Probable membrane-bound small GTPase
7311_at	5031.2	P	similarity to benomyl/methotrexate resistance protein
7312_at	153.7	A	similarity to chaperonin HSP60 proteins
7313_at	14	A	Glc7-interacting protein.
7314_at	3223	P	Homolog to quinone oxidoreductase (E. coli)
7315_at	597.1	A	hypothetical protein
7316_s_at	23766.7	P	Ribosomal protein S11B (S18B) (rp41B) (YS12)
7317_at	3430.2	P	RNA polymerase I enhancer binding protein
7318_at	853.6	P	Possible regulatory subunit for the PP1 family protein phosphatase G
7319_at	337.1	A	questionable ORF
7320_at	2863.4	P	Homolog to YCR004, obr1 (S. pombe), trp repressor binding protein
7321_at	3283.6	P	similarity to rat regucalcin
7322_at	11173.2	P	Homolog to HSP30 heat shock protein YRO1 (S. cerevisiae) 7
7323_at	1520.5	P	RNA splicing factor
7324_at	1302	P	Homolog to glucan-1,3--glucosidase (EC 3.2.1.5\; S. cerevisiae) 2
7325_at	1376.3	P	Muddled Meiosis
7326_at	2721.8	P	Ubiquitin-specific protease
7327_at	1546	P	Probable protein kinase
7283_at	4244	P	origin recognition complex subunit 2
7284_at	5369	P	Homolog to ftsJ protein (E. coli) ,\/ YCR054\/
7285_at	7095.5	P	similarity to rat neurodegeneration associated protein 1
7286_at	1035	P	Probable phosphopanthethein-binding protein
7287_at	201.6	A	questionable ORF
7288_at	533.9	A	ExtraCellular Mutant
7289_at	3417.1	P	Probable Zn-finger protein
7290_at	1104.2	P	cell wall mannoprotein
7291_at	20307.5	P	probable amino acid permease for leucine, valine, and isoleucine
7292_at	7517.8	P	Probable amino acid transport protein
7293_at	2967.2	P	osmotolerance protein

7294_at	6588.8	P	hypothetical protein
7295_at	941.1	P	heat shock protein 26
7296_at	2990.5	P	Putative helicase similar to RAD54
7297_at	3570.1	P	Homolog to aminopeptidase Y (S. cerevisiae)
7298_at	3476.7	P	hypothetical protein
7299_at	130.5	A	ExtraCellular Mutant
7300_at	5756.2	P	hypothetical protein
7301_at	13679.2	P	Homolog to sporulation specific protein SPS2 (S. cerevisiae)
7302_at	923.8	P	Homolog to sporulation specific protein SPS2 (S. cerevisiae)
7303_at	11671.4	P	Exhibits significant sequence similarity with a subunit of the mammal
7304_at	10561.6	P	cytoplasmic protein involved in protein transport between ER and Go
7305_at	1415	P	transcription factor, member of the histone acetyltransferase SAGA
7260_at	22951.4	P	ubiquitin-conjugating enzyme
7261_at	17179.4	P	transcription factor of the TEA\/ATTS DNA-binding domain family, re
7262_at	11929.4	P	mitochondrial C1-tetrahydroflate synthase
7263_at	2689.9	P	mitochondrial ADP\/ATP translocator
7264_at	8478.1	P	Probable transmembrane protein
7265_at	2583.6	P	Subunit 5 of Replication Factor C\; homologous to human RFC 38 kD
7266_at	5173	P	profilerating cell nuclear antigen (PCNA)\; accessory factor for DNA
7267_at	143.6	A	questionable ORF
7268_at	3932.2	P	11-kDa nonhistone chromosomal protein
7269_g_at	1742.5	M	11-kDa nonhistone chromosomal protein
7270_i_at	20191	P	questionable ORF
7271_at	58.3	A	questionable ORF
7272_at	1687.1	P	Nuclear protein involved in mitochondrial intron splicing
7273_at	19961.3	P	Acid phosphatase, constitutive
7274_at	2280	P	Acid phosphatase, repressible
7275_at	2531.2	P	weak similarity to pig tubulin-tyrosine ligase
7276_at	12189.1	P	hypothetical protein
7277_at	4067.6	P	hypothetical protein
7278_at	2218.3	P	Myristoylated Serine\/threonine protein kinase involved in vacuolar pr
7279_at	109.3	A	putative transcriptional (co)activator for DNA damage
7280_at	739.6	P	weak similarity to T.brucei mitochondrion hypothetical protein 6
7281_at	308.1	A	questionable ORF
7282_at	13435.3	P	weak similarity to S.pombe hypothetical protein SPBC3B9.01
7238_at	468.6	P	hypothetical protein
7239_at	3654.9	P	weak similarity to human U3 snoRNP associated 55 kDa protein
7240_at	4874.6	P	mitochondrial carrier protein
7241_at	2894.3	P	involved in fructose-1,6-bisphosphatase degradation
7242_at	32761.5	P	May be a membrane protein involved in inorganic phosphate transpo
7243_at	511.9	A	weak similarity to N.crassa chitin synthase
7244_at	833.2	P	Probable transcription factor
7245_at	10776.2	P	Calmodulin
7246_at	2286.6	P	beta-1,4-mannosyltransferase
7247_at	9675.8	P	Homolog to serendipity protein (D. melanogaster)
7248_at	5277.5	P	Transcription regulatory protein
7249_at	291.2	A	questionable ORF
7250_at	863.7	P	Radiation repair protein, putative DNA helicase
7251_at	15168.6	P	alpha aminoadipate reductase
7252_at	1720	P	questionable ORF
7253_g_at	1409.5	P	questionable ORF
7254_at	204.4	A	transketolase, homologous to tkl1

7255_at	1232.9	P	U1 snRNP A protein
7256_at	799.1	P	Translational activator of COB mRNA
7257_at	35116.1	P	Glycyl-tRNA synthase
7258_at	2015.2	P	Mitochondrial ribosomal protein MRPL36 (YmL36)
7259_at	2166.3	P	transcription factor tau (TFIIIC) subunit 95
7215_at	44.5	A	questionable ORF
7216_at	1732.9	P	Probable phosphoprotein phosphatase (EC 3.1.3.16)
7217_at	8114.1	P	56 kD synthase subunit of trehalose-6-phosphate synthase\/phospha
7218_at	30426	P	H+-transporting ATPase, vacuolar (EC 3.6.1.35)
7219_at	292.2	A	required for autophagy
7220_at	1590.3	P	imparts Far- phenotype
7221_at	5826.4	P	cytoplasmic protein involved in mother-specific HO expression
7222_at	2711.8	P	Calcium Caffeine Zinc sensitivity
7223_at	2152.9	P	Amino acid permease
7224_at	2516.1	P	Negative regulator of swe1 kinase (which regulates cdc28)
7225_at	263.5	A	questionable ORF
7226_at	10587.5	P	subunit of the Cdc28 protein kinase
7227_at	1178.3	P	similar to phosphatidylinositol(PI)3-kinases required for DNA damag
7228_at	2259.5	P	hypothetical protein
7229_at	155.5	P	Unknown
7230_at	2838.5	P	Probable serine-type carboxypeptidase (EC 3.4.16.1)
7231_at	2404.8	P	GTPase activating protein
7232_at	3166.5	P	hypothetical protein
7233_at	6073.7	P	Probable pre-mRNA splicing RNA-helicase
7234_at	23865.5	P	Ominipotent suppressor protein of nonsense codons
7235_at	366	A	hypothetical protein
7236_at	11798.1	P	alcohol dehydrogenase isoenzyme V
7237_at	2306	P	Probable mitochondrial ribosomal protein S9
7193_at	850.7	A	strong similarity to hypothetical protein YOL092w
7194_at	181.4	A	Spore-specific protein
7195_at	4444.3	P	D-arabinose dehydrogenase
7196_at	6286.7	P	Probable Zn-finger protein
7197_at	5260.1	P	weak similarity to potato sucrose cleavage protein
7198_at	243.1	P	U4\/U6.U5-associated snRNP protein\; contains a PEST proteolysis
7199_at	3654.3	P	Riboflavin biosynthesis protein
7200_at	13212.6	P	25-kDa RNA polymerase subunit (common to polymerases I, II and
7201_at	7318.3	P	Stress-inducible riboflavin biosynthetic protein homolog
7202_at	377.9	A	weak similarity to myosins
7203_at	371.9	A	hypothetical protein
7204_at	28262.5	P	hypothetical protein
7205_at	8138.9	P	similarity to human 17-beta-hydroxysteroid dehydrogenase
7206_at	3807.3	P	protein kinase catalytic subunit
7207_at	2254.5	P	Homolog to suppressor of reduced viability of starvation (SUR1, S.
7208_at	20940.6	P	similarity to hypothetical protein YJL171c
7209_at	8483	P	Protein that participates in secretory pathway
7210_at	2552.6	P	hypothetical protein
7211_at	19413.1	P	ADP-ribosylation factor-like protein 1
7212_at	893.9	P	General positive regulator of CDC34\; Suppress some cdc34 mutati
7213_at	5652.9	P	Prephenate dehydrogenase (NADP+)
7214_at	630.7	P	Pop7 protein, an integral subunit of RNase P and apparent subunit
7170_at	654.8	A	weak similarity to hypothetical protein YLR324w
7171_at	2702.7	P	HSP70 family member, highly homologous to Sse1p

7172_at	3469.4	P	Suppressor of SEC63 (S.cerevisiae), novel ER translocation compo
7173_at	14024.2	P	glycoprotein complexed with Sec62p and Sec63p in the Sec63 comp
7174_at	1012.8	P	Kinesin-related protein suppressing myosin defects (MYO2)
7175_at	1363.4	P	20S proteasome maturation factor
7176_at	50.7	A	questionable ORF
7177_at	5192.9	P	Probable GTP-binding protein
7178_at	2511.6	P	Alpha-Ketoisovalerate Hydroxymethyltransferase
7179_at	14915.3	P	Probable membrane receptor
7180_at	73	A	questionable ORF
7181_at	2048	P	homolog of Drosophila melanogaster fuzzy onions gene\; integral pro
7182_at	242.4	A	Probable resistance protein
7183_at	1202.1	P	Probable DNA-binding transcription factor, Homolog to SRF\/SL-2
7184_at	7116.1	P	strong similarity to hypothetical protein YPL087w
7185_at	219.7	P	alpha-galactosidase
7186_at	1959.1	P	respiratory chain assembly protein
7187_at	48.1	A	Putative ATPase
7188_at	22448.2	P	probable membrane protein
7189_at	636.1	P	splicing factor
7190_i_at	26659.3	P	Ribosomal protein S9B (S13) (rp21) (YS11)
7191_f_at	28457.2	P	Ribosomal protein S9B (S13) (rp21) (YS11)
7192_at	658.9	P	questionable ORF
7147_at	4735.5	P	Ribosomal protein L21A
7148_at	3651.7	P	Probable carrier protein, mitochondrial
7149_at	747.6	A	Stoichiometric member of mediator complex
7150_at	1254.6	P	hypothetical protein
7151_at	2957.7	P	p50 subunit of the yeast omatin Assembly Factor-I (CAF-I) negative r
7152_at	27134.2	P	Glucose-6-phosphate isomerase
7153_at	547.1	P	weak similarity to hypothetical protein YPL077c
7154_at	4161.9	P	Probable transcription-associated factor protein, probable -transduci
7155_at	9564.5	P	Putative alpha-1,2-mannosyltransferase
7156_at	2507.4	P	contains two SH3 domains
7157_at	5376.1	P	MCM3 protein homolog (S. cerevisiae)
7158_at	172.3	P	hypothetical protein
7159_at	1830.6	P	Probable serine-active lipase, peroxisomal (EX 3.1.1.-)
7160_at	15729.8	P	Putative alpha-1,2-mannosyltransferase
7161_g_at	24213.9	P	Putative alpha-1,2-mannosyltransferase
7162_at	8022.1	P	questionable ORF
7163_at	9654.9	P	probable membrane protein
7164_at	3095.3	P	Urea amidolyase (contains urea carboxylase and allophanate hydrola
7165_at	287.1	A	hypothetical protein
7166_at	8380.1	P	strong similarity to D.melanogaster cornichon protein
7167_at	601.5	P	regulator of microtubule stability
7168_at	12311.7	P	negative growth regulatory protein
7169_at	3085.2	P	Effector in the expression of PAPS reductase and sulfite reductase
7124_at	2016.6	P	strong similarity to hypothetical protein YGL056c
7125_at	889.9	P	highly charged, basic protein
7126_at	983.5	P	strong similarity to hypothetical protein YGL060w
7127_at	443	M	autophagy
7128_at	28499.7	P	pyruvate carboxylase
7129_at	2276.8	P	similarity to human acetyl-coenzyme A transporter
7130_g_at	2584.1	P	similarity to human acetyl-coenzyme A transporter
7131_at	18939.8	P	beta subunit of pyruvate dehydrogenase (E1 beta)

7132_at	9707.4	P	Probable AMP-binding protein
7133_at	1886.2	P	hypothetical protein
7134_at	1878.7	P	questionable ORF
7135_at	1437.4	P	hypothetical protein
7136_at	543.9	A	questionable ORF
7137_at	2567.2	P	Homolog to ATP-binding protein clpX (E.coli)
7138_at	1959.1	P	similarity to hypothetical A.thaliana protein
7139_at	2835.7	P	Homolog to 1,4-a-glucosidase (S.cerevisiae) (EC 3.2.1.3) 3
7140_at	8440.3	P	hypothetical protein
7141_at	1229.3	P	similarity to human p97 homologous protein
7142_at	638.7	A	questionable ORF
7143_at	915.8	M	Homolog to human hnRNP complex K protein
7144_at	8691	P	similarity to human Arp2/3 protein complex subunit p41-Arc and to hu
7145_at	2222.9	P	similarity to bumetanide-sensitive Na-K-Cl cotransport protein
7146_at	3861.8	P	RNA (guanine-7-)methyltransferase (cap methyltransferase)
7102_at	532.1	P	RNA helicase homolog
7103_at	12893.3	P	strong similarity to general chromatin factor Spt16p
7104_at	2582.8	P	Probable Zn-finger protein
7105_at	1429.3	P	Probable Zn-finger protein
7106_at	5653.5	P	Probable sugar transport protein
7107_at	2854.3	P	Probable ATP\/GTP-binding protein
7108_at	12339.5	P	UDP-N-acetyl-glucosamine-1-P transferase (GPT)
7109_at	1809.7	P	Probable glutathione peroxidase (EC 1.11.1.9)
7110_at	3506.9	P	Homolog to SNF2\/SWI2 DNA-binding regulatory protein
7111_at	7900.6	P	hypothetical protein
7112_at	10732.6	P	Putative 57 kDa protein with an apparent MW of 70 kDa by SDS-PA
7113_at	18903	P	glutamine amidotransferase:cyclase
7114_at	14050	P	3-deoxy-D-arabino-heptulosonate 7-phosphate (DAHP) synthase iso
7115_at	549.4	M	hypothetical protein
7116_at	639.5	P	Probable mitochondrial ribosomal protein S5
7117_at	8028.2	P	dUTP pyrophosphatase (dUTPase)
7118_at	512.3	A	transcription factor, part of Srb\/Mediator complex
7119_at	2153.8	P	probable membrane protein
7120_at	666.9	P	hypothetical protein
7121_at	652.8	P	Riboflavin synthase alpha-chain
7122_at	906.6	A	Required for normal 5.8S rRNA processing and for tRNA processing
7123_at	642.5	P	hypothetical protein
7079_at	1231.8	P	hypothetical protein
7080_at	3847.3	P	similarity to C.elegans GTPase-activating protein
7081_at	6927.3	P	similarity to hypothetical S. pombe protein
7082_at	7087.9	P	questionable ORF
7083_at	17950.1	P	Serine hydroxymethyltransferase, mitochondrial
7084_at	4504.6	P	Probable small GTP-binding protein
7085_at	10153.9	P	probable membrane protein
7086_at	4803.7	P	Probable mitochondrial protein L37
7087_at	1763.5	P	hypothetical protein
7088_at	908.7	A	Probable ATP\/GTP-binding protein
7089_at	3743.9	P	weak similarity to S.pombe uvi22 protein and hypothetical protein YN
7090_at	1477.4	P	Hsm3p may be a member of the yeast MutS homolog family
7091_at	6103.3	P	similarity to hypothetical protein YJL048c
7092_at	2526.5	P	Probable protein kinase (growth factor & cytokine receptor family)
7093_at	3521.6	P	RAP1-interacting factor, involved in establishment of repressed chro

7094_at	3836.2	P	dual specificity protein phosphatase
7095_at	213.7	A	questionable ORF
7096_at	823.5	A	C and C subunits of DNA polymerase II
7097_at	6462.9	P	RNA polymerase II-associated, nuclear protein that may serve as bc
7098_at	2281	P	hypothetical protein
7099_at	2325.4	P	Probable G-protein, -transducin type
7100_at	4606.6	P	Mitochondrial ribosomal protein MRPL27 (YmL27)
7101_at	11886.5	P	Probable SEC61 protein homolog
7057_at	693.7	P	similarity to AMP deaminase
7058_at	58.9	A	hypothetical protein
7059_at	33412	P	Aminopeptidase yscIII
7060_at	8591.4	P	similarity to hypothetical S. pombe protein
7061_at	3738.2	P	clathrin associated protein medium chain
7062_at	4257.9	P	transcriptional activator
7063_at	3365.6	P	metal homeostasis protein\; putative membrane protein
7064_at	5200.2	P	citrate tranporter in mitochondrial inner membrane
7065_at	697.5	P	hypothetical protein
7066_at	7647.6	P	Probable multidrug resistance protein
7067_at	304.3	A	Probable sulfate transport protein
7068_at	2254.7	P	Putative P-type Cu(2+)-transporting ATPase
7069_at	6534.6	P	Homolog to phosphate-repressible phosphate permease
7070_at	1088.8	P	Maltose fermentation regulatory protein
7071_s_at	1088.7	M	maltose permease
7072_s_at	235.7	A	Maltase (EC 3.2.1.20)
7073_at	973.1	A	strong similarity to hypothetical protein YGR293c
7074_f_at	3896.1	P	YKL224 c homolog
7075_at	26.9	A	hypothetical membrane protein
7076_at	2736.8	P	identified by SAGE
7077_at	7199.5	P	identified by SAGE
7078_at	756.7	P	hypothetical protein
7033_at	15.7	A	questionable ORF - upstream ORF of ALG1
7034_i_at	21423.7	P	identified by SAGE
7035_s_at	17945.9	P	identified by SAGE
7036_s_at	3967.3	P	Protein involved in targeting of plasma membrane [H+]ATPase
7037_s_at	1334.8	P	Probable aldehyde dehydrogenase (EC 1.2.1.-)
7038_s_at	2599.2	P	Degradation in the Endoplasmic Reticulum
7039_at	336.6	A	probable membrane protein
7040_g_at	208.6	A	probable membrane protein
7041_s_at	3266.9	P	Probable Zn-finger protein (C2H2 type)
7042_at	1350.1	P	non-annotated SAGE orf Found forward in NC_001134 between 469
7043_at	1813.2	P	non-annotated SAGE orf Found reverse in NC_001134 between 164
7044_at	168.2	A	non-annotated SAGE orf Found reverse in NC_001134 between 164
7045_i_at	334.2	P	non-annotated SAGE orf Found forward in NC_001134 between 490
7046_s_at	7243.8	P	non-annotated SAGE orf Found forward in NC_001134 between 490
7047_at	2830.3	P	non-annotated SAGE orf Found forward in NC_001134 between 680
7048_i_at	841.6	P	non-annotated SAGE orf Found forward in NC_001134 between 680
7049_s_at	2050.6	A	non-annotated SAGE orf Found forward in NC_001134 between 680
7050_at	5253.7	P	non-annotated SAGE orf Found reverse in NC_001134 between 680
7051_at	3.7	A	non-annotated SAGE orf Found forward in NC_001134 between 362
7052_at	1039.8	A	non-annotated SAGE orf Found reverse in NC_001134 between 101
7053_at	32	A	non-annotated SAGE orf Found reverse in NC_001134 between 196
7054_i_at	175.7	A	non-annotated SAGE orf Found forward in NC_001134 between 592

7055_f_at	1629.5	A	non-annotated SAGE orf Found forward in NC_001134 between 592
7056_at	308.8	A	non-annotated SAGE orf Found forward in NC_001134 between 767
7010_at	326.4	P	non-annotated SAGE orf Found reverse in NC_001134 between 882
7011_g_at	4267.6	P	non-annotated SAGE orf Found reverse in NC_001134 between 882
7012_at	12990.4	P	non-annotated SAGE orf Found reverse in NC_001134 between 883
7013_at	63.9	A	non-annotated SAGE orf Found reverse in NC_001134 between 101
7014_at	5865.8	P	non-annotated SAGE orf Found reverse in NC_001134 between 115
7015_at	2204.4	P	non-annotated SAGE orf Found reverse in NC_001134 between 143
7016_at	1817.2	P	non-annotated SAGE orf Found forward in NC_001134 between 172
7017_at	4509.1	P	non-annotated SAGE orf Found reverse in NC_001134 between 241
7018_at	1465.9	P	non-annotated SAGE orf Found reverse in NC_001134 between 256
7019_at	1114.1	P	non-annotated SAGE orf Found forward in NC_001134 between 270
7020_at	16466.4	P	non-annotated SAGE orf Found reverse in NC_001134 between 305
7021_at	16324	P	non-annotated SAGE orf Found reverse in NC_001134 between 373
7022_at	45.5	A	non-annotated SAGE orf Found forward in NC_001134 between 391
7023_at	2238.9	P	non-annotated SAGE orf Found forward in NC_001134 between 407
7024_at	38	A	non-annotated SAGE orf Found reverse in NC_001134 between 480
7025_at	267.1	P	non-annotated SAGE orf Found reverse in NC_001134 between 553
7026_at	1540.2	P	non-annotated SAGE orf Found reverse in NC_001134 between 553
7027_at	17613.2	P	non-annotated SAGE orf Found reverse in NC_001134 between 562
7028_at	77.9	A	non-annotated SAGE orf Found forward in NC_001134 between 592
7029_g_at	176.3	A	non-annotated SAGE orf Found forward in NC_001134 between 592
7030_at	35.9	A	non-annotated SAGE orf Found forward in NC_001134 between 592
7031_at	1857	P	non-annotated SAGE orf Found reverse in NC_001134 between 615
7032_at	16252.1	P	non-annotated SAGE orf Found forward in NC_001134 between 649
6985_at	129.4	A	non-annotated SAGE orf Found reverse in NC_001134 between 741
6986_i_at	77.1	A	non-annotated SAGE orf Found forward in NC_001134 between 356
6987_at	423.8	M	non-annotated SAGE orf Found reverse in NC_001134 between 668
6988_at	273.7	A	non-annotated SAGE orf Found forward in NC_001134 between 181
6989_at	1241.8	P	non-annotated SAGE orf Found reverse in NC_001134 between 593
6990_at	370.5	A	non-annotated SAGE orf Found forward in NC_001134 between 622
6991_i_at	1077.2	P	non-annotated SAGE orf Found reverse in NC_001134 between 694
6992_r_at	97	P	non-annotated SAGE orf Found reverse in NC_001134 between 694
6993_f_at	26723.6	A	non-annotated SAGE orf Found reverse in NC_001134 between 694
6994_at	2012.8	P	non-annotated SAGE orf Found reverse in NC_001134 between 747
6995_at	713.1	P	non-annotated SAGE orf Found forward in NC_001134 between 143
6996_at	364.1	A	non-annotated SAGE orf Found reverse in NC_001134 between 159
6997_at	332.8	A	non-annotated SAGE orf Found forward in NC_001134 between 164
6998_at	126.8	A	non-annotated SAGE orf Found forward in NC_001134 between 165
6999_at	2876.5	P	non-annotated SAGE orf Found forward in NC_001134 between 165
7000_i_at	42.5	A	non-annotated SAGE orf Found reverse in NC_001134 between 197
7001_r_at	150.8	A	non-annotated SAGE orf Found reverse in NC_001134 between 197
7002_at	366.6	P	non-annotated SAGE orf Found reverse in NC_001134 between 235
7003_at	35.2	A	non-annotated SAGE orf Found reverse in NC_001134 between 351
7004_at	202.4	M	non-annotated SAGE orf Found reverse in NC_001134 between 363
7005_at	104.9	A	non-annotated SAGE orf Found forward in NC_001134 between 419
7006_at	43	A	non-annotated SAGE orf Found forward in NC_001134 between 477
7007_at	26.3	A	non-annotated SAGE orf Found forward in NC_001134 between 480
7008_at	5700.5	P	non-annotated SAGE orf Found reverse in NC_001134 between 554
7009_g_at	1043.4	P	non-annotated SAGE orf Found reverse in NC_001134 between 554
6962_at	363.1	A	non-annotated SAGE orf Found reverse in NC_001134 between 554
6963_at	1117.8	P	non-annotated SAGE orf Found forward in NC_001134 between 555

6964_s_at	5503.2	P	non-annotated SAGE orf Found forward in NC_001134 between 555
6965_i_at	6.8	A	non-annotated SAGE orf Found forward in NC_001134 between 555
6966_r_at	308.3	P	non-annotated SAGE orf Found forward in NC_001134 between 555
6967_at	2163.1	P	non-annotated SAGE orf Found reverse in NC_001134 between 624
6968_at	4448.2	P	non-annotated SAGE orf Found reverse in NC_001134 between 681
6969_at	12435.3	P	non-annotated SAGE orf Found reverse in NC_001134 between 681
6970_at	489	A	non-annotated SAGE orf Found reverse in NC_001134 between 681
6971_at	1007.1	P	non-annotated SAGE orf Found forward in NC_001134 between 697
6972_at	46.8	A	non-annotated SAGE orf Found forward in NC_001134 between 744
6973_at	16.9	A	non-annotated SAGE orf Found forward in NC_001134 between 938
6974_at	64.1	A	non-annotated SAGE orf Found forward in NC_001134 between 978
6975_at	9121.4	P	non-annotated SAGE orf Found forward in NC_001134 between 133
6976_at	10871.1	P	non-annotated SAGE orf Found reverse in NC_001134 between 167
6977_at	6512.9	P	non-annotated SAGE orf Found forward in NC_001134 between 283
6978_at	516.7	P	non-annotated SAGE orf Found reverse in NC_001134 between 308
6979_at	6961.7	P	non-annotated SAGE orf Found forward in NC_001134 between 333
6980_at	50	A	non-annotated SAGE orf Found reverse in NC_001134 between 376
6981_at	10247.2	P	non-annotated SAGE orf Found reverse in NC_001134 between 398
6982_at	134	A	non-annotated SAGE orf Found forward in NC_001134 between 479
6983_at	248.3	P	non-annotated SAGE orf Found forward in NC_001134 between 741
6984_at	301.9	P	non-annotated SAGE orf Found forward in NC_001134 between 741
6938_at	3490.8	P	Saccharomyces cerevisiae chromosome II, complete chromosome s
6939_g_at	2251.1	P	Saccharomyces cerevisiae chromosome II, complete chromosome s
6940_s_at	336.9	P	Saccharomyces cerevisiae chromosome II, complete chromosome s
6941_s_at	964.3	P	Saccharomyces cerevisiae chromosome II, complete chromosome s
6942_at	1575.8	A	Saccharomyces cerevisiae chromosome II, complete chromosome s
6943_g_at	636.5	P	Saccharomyces cerevisiae chromosome II, complete chromosome s
6944_at	141.5	A	Saccharomyces cerevisiae chromosome II, complete chromosome s
6945_g_at	6710.3	P	Saccharomyces cerevisiae chromosome II, complete chromosome s
6946_at	6006.4	P	Saccharomyces cerevisiae chromosome II, complete chromosome s
6947_g_at	16522.2	P	Saccharomyces cerevisiae chromosome II, complete chromosome s
6948_i_at	320.8	A	Saccharomyces cerevisiae chromosome II, complete chromosome s
6949_f_at	3954	P	Saccharomyces cerevisiae chromosome II, complete chromosome s
6950_at	1815.7	P	snRNA
6951_at	6277.9	P	telomerase RNA component
6952_at	7337.1	P	telomerase RNA component
6953_at	142.6	A	snRNA
6954_at	227.3	A	snRNA
6955_s_at	53.1	A	putative pseudo-TY5
6956_s_at	765.8	A	Reverse transcriptase
6957_s_at	1133.7	P	Bud site selection
6958_s_at	5133.1	P	Mating type protein alpha-2
6959_s_at	4691.5	P	transcripton factor involved in the regulation of the alpha-specific gen
6960_at	5.5	A	questionable ORF
6961_g_at	13173.1	P	questionable ORF
6915_at	2263.5	P	catabolic serine (threonine) dehydratase
6916_at	3048	P	weak similarity to yeast translation regulator Gcd6p
6917_at	1065.8	P	similarity to myosin heavy chain form b from Chicken and Xenopus
6918_at	10357.7	P	strong similarity to human Rev interacting protein Rip-1
6919_at	1876.5	M	hypothetical protein
6920_at	9933.9	P	Saccharolysin (oligopeptidase yscD)
6921_at	16864.3	P	hypothetical protein

6922_at	2907.7	P	May assist Ste12p in pheromone-dependent expression of KAR3 an
6923_at	3675.1	P	Methyltransferase
6924_at	4882.8	P	Protease B Non-derepressible
6925_at	1176.4	P	involved in laminarinase resistance
6926_at	9198.4	P	diadenosine 5 ,5 -P1,P4-tetraphosphate phosphorylase I
6927_at	4892.9	P	hypothetical protein
6928_at	17.1	A	strong similarity to sporulation-specific protein Sps2p
6929_at	519.9	P	hypothetical protein
6930_at	2371.3	P	weak similarity to human ORF
6931_at	21.3	A	questionable ORF
6932_at	3984.6	P	hypothetical protein
6933_at	21377.4	P	protein disulfide isomerase
6934_at	913.3	P	questionable ORF
6935_at	1866.3	M	questionable ORF
6936_g_at	8155.7	P	questionable ORF
6937_at	24848.3	P	Glucokinase
6893_at	1356.9	P	regulatory protein
6894_at	7567.6	P	Membrane transporter
6895_at	27037.7	P	SRO9 may overlap in function with tropomyosin and may be involved
6896_at	8751.6	P	similarity to hypothetical protein YDR514c
6897_at	12656.4	P	Glutaredoxin (thiol-transferase)
6898_at	3129.2	P	similarity to hypothetical S.pombe protein
6899_at	2343.4	P	Transcription regulator
6900_at	894.4	P	possesses a SAM (sterile alpha motif)\; interacts with G protein and
6901_at	3393.5	P	involved in pre-rRNA processing and ribosome assembly
6902_at	25893.9	P	histidinol dehydrogenase
6903_at	3134	P	Microtubule-binding protein
6904_at	12270.6	P	weak similarity to glutenins, high molecular weight chain
6905_at	4345.6	P	serine\/threonine-rich membrane protein
6906_at	987.8	P	Protein involved in the integration of lipid signaling pathways with cell
6907_at	5063.1	P	Amino acid permease
6908_at	382	A	questionable ORF
6909_at	8836.4	P	beta-IPM (isopropylmalate) dehydrogenase
6910_at	13655.4	P	NifS-like protein
6911_at	1973.9	P	hypothetical protein
6912_at	1033.5	P	Cell cycle regulated protein required for axial bud formation\; co-ass
6913_at	3100.1	P	part of budding protein Bud3p due to frameshift in DNA sequence
6914_at	22260.1	P	Protein with RNA recognition motifs
6870_at	785	P	strong similarity to Saccharomyces pastorianus hypothetical protein
6871_at	18491.9	P	Small regulatory subunit of Acetolactate synthase
6872_at	307.8	P	Calcofluor White Hypersensitivity
6873_at	693.8	P	questionable ORF
6874_at	3931.2	P	strong similarity to Saccharomyces pastorianus hypothetical protein
6875_at	739.1	P	17-kDa phosphatidylserine synthase
6876_at	3882.7	P	strong similarity to Saccharomyces pastorianus hypothetical protein
6877_at	10823.8	P	Protein involved in retention of membrane proteins, including Sec12
6878_at	60.7	A	similarity to Dom34p
6879_at	225.6	A	hypothetical protein
6880_at	7788.9	P	conserved potential GTP-ginding protein
6881_at	1080	P	Mitochondrial ribosomal protein MRPL32 (YmL32)
6882_at	5939.5	P	FMN-binding protein
6883_at	16162.4	P	non-mitochondrial citrate synthase

6884_at	188	A	hypothetical protein
6885_at	5614.6	P	Ser\/Thr protein kinase
6886_at	6330.5	P	Reduced viability on starvation protein RVS161
6887_at	708	P	strong similarity to Y.lipolytica GPR1 protein and Fun34p
6888_at	6088.4	P	Active transport ATPase
6889_at	684.5	P	weak similarity to M.leprae B1496_F1_41 protein
6890_at	1272.7	P	3-phosphoglycerate kinase
6891_at	936.8	P	DNA polymerase IV
6892_at	999.4	P	hypothetical protein
6848_at	1433.9	P	hypothetical protein
6849_at	22108.7	P	similarity to hypothetical S.pombe protein
6850_at	1155.8	P	Transcription regulator
6851_at	1350.1	P	MAK32 sugar kinase
6852_at	781.1	A	Transcription regulator
6853_at	2671.1	P	MAK31 snRNP
6854_at	1292.1	P	Protein induced by heat shock, ethanol treatment, and entry into stat
6855_at	422.7	A	hypothetical protein
6856_at	6864.4	P	Membrane transporter
6857_at	1318	P	Asn-tRNA synthetase
6858_f_at	31861.3	P	Proteolipid associated with plasma membrane H(+)-ATPase (Pma1p
6859_at	524.5	A	hypothetical protein
6860_at	1645.5	P	Membrane phospho-diesterase
6861_at	456.4	P	GTPase (RAS-related)
6862_at	1441.3	P	Amino acid permease
6863_at	14018.1	P	required for mitochondrial DNA replication
6864_at	16796.7	P	required for mitochondrial DNA replication
6865_at	3500.7	P	weak similarity to S.pombe hypothetical protein SPBC4C3.06
6866_at	25137.3	P	Ribosomal protein S14A (rp59A)
6867_at	871.9	P	Beige Protein Homologue 1
6868_at	4863.3	P	similarity to mouse nuclear receptor co-repressor N-Cor
6869_at	23624.2	P	Probable subunit of 1,3-beta-glucan synthase\; homolog of ELO1
6825_at	3226	P	Component of the exosome 3->5 exoribonuclease complex with Rrp
6826_at	7171.2	P	ribokinase
6827_at	12648.4	P	May collaborate with Pho86p and Pho84p in inorganic phosphate upt
6828_at	1084.2	P	GTP\/GDP exchange factor for Rsr1 protein
6829_at	39.1	A	questionable ORF
6830_at	2275.4	P	TATA binding protein-associated factor (TAF)
6831_at	2934.5	P	hypothetical protein
6832_at	2063	P	involved in manganese homeostasis
6833_at	395.1	A	Protease
6834_at	5009	P	required for respiration and maintenance of mitochondrial genome
6835_at	6616.4	P	Protein carboxyl methylase
6836_at	155.4	A	questionable ORF
6837_at	10002.9	P	Acyl-CoA cholesterol acyltransferase (sterol-ester synthetase)
6838_at	167.2	A	questionable ORF
6839_at	2424.9	P	weak similarity to ankyrins
6840_at	4522.1	P	a subunit of RSC, a fifteen-protein chromatin remodeling complex ar
6841_at	12054.1	P	threonine synthase
6842_at	2044.6	P	CTR86 shares a terminator region with THR4. CTR86 contains aGC
6843_at	3227.1	P	regulatory protein
6844_at	2703.3	P	weak similarity to hypothetical protein YDL177c
6845_at	5354.2	P	regulatory protein

6846_at	9758.7	P	hypothetical protein
6847_g_at	7901.6	P	hypothetical protein
6803_at	7862.1	P	similarity to Ytp1p protein
6804_at	518.1	A	questionable ORF
6805_at	2283.3	A	G10-like protein
6806_at	8918.3	P	Transcription factor (fork head domain)
6807_at	645.8	P	Zn finger protein, putative ATPase
6808_at	9056.6	P	Intracellular transport protein
6809_at	206.6	A	similarity to hypothetical S.pombe protein
6810_g_at	882.8	A	similarity to hypothetical S.pombe protein
6811_at	5523.9	P	cyclophilin homolog
6812_at	881.6	P	(required for) Integrity of Mitochondrial Genome 2
6813_at	6946.6	P	regulatory protein
6814_at	2148	P	protein kinase
6815_at	16041.6	P	shows similarity to glucose-6-phosphate dehydrogenase non-catalyti
6816_at	2959.3	P	ERS1 protein, ER defect supressor
6817_at	4160.4	P	hypothetical protein
6818_at	21131.5	P	Necessary for accurate chromosome transmission during cell divisio
6819_at	1927.7	P	weak similarity to A.thaliana protein phosphatase 2C
6820_at	1162.7	P	activation mediator subcomplex of RNA polymerase I holoenzyme
6821_at	2829.3	P	weak similarity to Rbk1p
6822_at	1926.9	P	Thioredoxin type II
6823_at	18213.9	P	glucose repression regulatory protein, exhibits similarity to beta subu
6824_at	496.1	M	hypothetical protein
6780_at	1817.2	P	hypothetical protein
6781_at	1190.1	P	questionable ORF
6782_at	3189.5	P	nucleic acid-binding protein
6783_at	9391.7	P	Actin binding protein
6784_at	4986.1	P	predicted GPI-anchored cell wall protein
6785_at	2257.1	P	hypothetical protein
6786_at	29.7	A	Putative serine\/threonine protein kinase most similar to cyclic nucle
6787_at	677	P	mutS homolog, forms a complex with Msh2p to repair insertion-dele
6788_at	1831.7	P	nuclear protein that negatively regulates basal transcription
6789_at	5168	P	Cell Division Cycle mutant
6790_at	964.2	P	hypothetical protein
6791_s_at	1.5	A	Homeobox-domain containing protein which, together with alpha2, r
6792_s_at	97.9	A	Homeobox-domain containing protein which, together with alpha2, r
6793_at	1033.9	P	permease involved in the uptake of glycerophosphoinositol (GroPIns
6794_at	129.2	A	strong similarity to Pep1p
6795_at	1620	P	strong similarity to Pep1p
6796_at	81.3	A	strong similarity to Pep1p
6797_at	3052.7	P	Alcohol dehydrogenase
6798_f_at	2615	P	member of the seripauperin protein\/gene family (see Gene_class P
6799_at	1967.6	P	Alcohol dehydrogenase
6800_at	559.9	P	Transcription regulator
6801_at	144.2	A	hypothetical protein
6802_at	510.6	P	hypothetical protein
6755_i_at	36.4	A	hypothetical protein
6756_at	227.9	P	high-temperature lethal
6757_i_at	39.4	A	Homeobox-domain containing protein which, together with alpha2, r
6758_at	301.7	P	hypothetical protein identified by SAGE
6759_at	3939.6	P	identified by SAGE

6760_g_at	12147.3	P	identified by SAGE
6761_at	207.1	A	similarity to starvation induced pSI-7 protein of C. fluvum
6762_s_at	1003.4	P	Ser\/Thr protein kinase
6763_at	3994.5	P	homologous to mouse and human Tsg101 tumor susceptibility genes
6764_g_at	1223.3	P	homologous to mouse and human Tsg101 tumor susceptibility genes
6765_at	258	A	non-annotated SAGE orf Found forward in NC_001135 between 414
6766_at	657.7	A	non-annotated SAGE orf Found forward in NC_001135 between 157
6767_at	431.2	A	non-annotated SAGE orf Found forward in NC_001135 between 171
6768_at	4335.4	P	non-annotated SAGE orf Found reverse in NC_001135 between 175
6769_at	123.2	P	non-annotated SAGE orf Found forward in NC_001135 between 289
6770_i_at	1102.2	A	non-annotated SAGE orf Found forward in NC_001135 between 127
6771_s_at	450.5	A	non-annotated SAGE orf Found forward in NC_001135 between 127
6772_at	418.3	A	non-annotated SAGE orf Found forward in NC_001135 between 127
6773_at	1230.4	P	non-annotated SAGE orf Found forward in NC_001135 between 185
6774_at	526.5	P	non-annotated SAGE orf Found forward in NC_001135 between 109
6775_at	16578.1	P	non-annotated SAGE orf Found reverse in NC_001135 between 130
6776_at	795.3	P	non-annotated SAGE orf Found reverse in NC_001135 between 171
6777_at	2249.8	P	non-annotated SAGE orf Found reverse in NC_001135 between 172
6778_i_at	1257.6	P	non-annotated SAGE orf Found reverse in NC_001135 between 204
6779_r_at	282.9	P	non-annotated SAGE orf Found reverse in NC_001135 between 204
6731_at	471.5	P	non-annotated SAGE orf Found reverse in NC_001135 between 286
6732_at	18407.3	P	non-annotated SAGE orf Found reverse in NC_001135 between 162
6733_at	32527.9	P	non-annotated SAGE orf Found reverse in NC_001135 between 162
6734_at	17.6	A	non-annotated SAGE orf Found reverse in NC_001135 between 205
6735_i_at	1419.2	P	non-annotated SAGE orf Found forward in NC_001135 between 258
6736_r_at	1.1	A	non-annotated SAGE orf Found forward in NC_001135 between 258
6737_at	242.9	A	non-annotated SAGE orf Found reverse in NC_001135 between 895
6738_at	702.2	P	non-annotated SAGE orf Found reverse in NC_001135 between 926
6739_at	504.4	A	non-annotated SAGE orf Found forward in NC_001135 between 154
6740_at	264.3	A	non-annotated SAGE orf Found forward in NC_001135 between 240
6741_at	28.9	A	non-annotated SAGE orf Found reverse in NC_001135 between 414
6742_at	3012.6	A	non-annotated SAGE orf Found reverse in NC_001135 between 416
6743_at	353.5	P	non-annotated SAGE orf Found reverse in NC_001135 between 123
6744_at	682.3	A	non-annotated SAGE orf Found forward in NC_001135 between 125
6745_at	3246.4	P	non-annotated SAGE orf Found reverse in NC_001135 between 168
6746_at	354.7	A	non-annotated SAGE orf Found forward in NC_001135 between 288
6747_at	8136.6	P	non-annotated SAGE orf Found reverse in NC_001135 between 209
6748_at	485.6	A	non-annotated SAGE orf Found reverse in NC_001135 between 213
6749_at	179.7	A	non-annotated SAGE orf Found forward in NC_001135 between 265
6750_i_at	961.7	A	TY5-1
6751_at	904.9	P	snRNA
6752_i_at	36	A	Centromere
6753_at	12059.3	P	snRNA
6754_at	59.2	A	snRNA
6708_at	458.5	P	snRNA
6709_i_at	76.3	A	strong similarity to sugar transport proteins
6710_at	859.3	P	Hypothetical aryl-alcohol dehydrogenase
6711_at	25.1	A	strong similarity to hypothetical protein YPR079w
6712_at	1011.7	P	hypothetical protein
6713_at	1937.8	P	Protein similar to LIM-domain proteins and to rho\/rac GTPase-activa
6714_at	467.5	P	hypothetical protein
6715_at	619.4	A	similarity to E.coli hypothetical protein and to chlorohydrolases

6716_at	7415.9	P	hypothetical protein
6717_at	28756.5	P	p-nitrophenyl phosphatase
6718_at	3332.7	P	Two-component phosphorelay intermediate
6719_at	973	P	protein of unknown function
6720_at	883.6	P	hypothetical protein
6721_at	16964.7	P	3.6-kDa protein, probably membrane-located
6722_at	1799	P	hypothetical protein
6723_at	2230.9	P	phosphotyrosine-specific protein phosphatase
6724_at	1618.2	P	similarity to A.klebsiana glutamate dehydrogenase
6725_at	11295.9	P	Homothallic switching endonuclease
6726_at	5063.1	P	ADP-ribosylation factor GTPase-activating protein (ARF GAP)
6727_at	4211.8	P	similarity to Cdc11p, Cdc3p and human CDC10 protein
6728_at	3700.2	P	Possible RNA binding protein. Homolog of Whi3.
6729_at	2436.7	P	weak similarity to mucin
6730_at	1725.8	A	strong similarity to hypothetical protein YNL194c and similarity to YM
6686_at	119.9	A	questionable ORF
6687_at	4069.2	P	binds to single-stranded TG1-3 telomere G-tails
6688_at	2652.3	P	strong similarity to S.equisimilis hypothetical protein
6689_at	2932.2	P	strong similarity to S.equisimilis hypothetical protein
6690_at	487.8	P	weak similarity to hypothetical protein YNR061c
6691_at	4302.9	P	Mitochondrial inner membrane protein involved in import of proteins
6692_at	444.5	P	similarity to Jun activation domain binding protein homologue of A. th
6693_at	3752.5	P	NAD-dependent glutamate dehydrogenase
6694_at	35.6	A	strong similarity to putative protein kinase NPR1
6695_at	6745.1	P	has an RNA recognition domain in the N-terminal region
6696_at	23658.7	P	Integral membrane component of the endoplasmic reticulum
6697_at	436.7	A	similarity to hypothetical protein YNL176c
6698_at	548	A	GABA-specific transport protein
6699_at	3577.7	P	similarity to hypothetical S. pombe protein
6700_at	19791.1	P	HMG-like nuclear protein
6701_at	3121.5	P	Nuclear-export-signal (NES)-containing protein
6702_at	925.4	P	weak similarity to transporter proteins
6703_at	1895.1	P	phorphobilinogen deaminase (uroporphyrinogen synthase), the third
6704_at	178.5	A	similarity to hypothetical protein YDR233c
6705_at	4248.5	P	similarity to Skt5p
6706_at	1138.9	P	Mitochondrial ribosomal protein MRPL11 (YmL11)
6707_at	3713.7	P	strong similarity to human D1075-like protein
6663_at	2400.9	P	6-O-methylguanine-DNA methylase
6664_at	342.9	A	similarity to sugar transporter proteins
6665_at	6229	P	high copy suppressor of abf2 lacking the HMG1-like mitochondrial H
6666_at	1589.6	P	Anti-silencing protein that causes depression of silent loci when over
6667_at	1562.6	A	hypothetical protein
6668_at	21980.1	P	involved in protein transport from endoplasmic reticulum to Golgi
6669_at	505.5	P	glucose transporter
6670_at	1379.9	P	similarity to N.crassa hypothetical 32 kDa protein
6671_at	846.2	P	ADP-ribosylation factor
6672_s_at	12992.8	P	Ribosomal protein L35A
6673_at	4457.8	P	ubiquitin fusion degradation protein
6674_at	623.5	P	hypothetical protein
6675_at	1300.2	P	hypothetical protein
6676_at	6047.4	P	serine-threonine protein phosphatase 2A
6677_at	1207.5	P	questionable ORF

6678_at	35.4	A	hypothetical protein
6679_at	14117.3	P	encodes a protein with three regions (ABC) that is spliced to yield th
6680_s_at	1898.2	P	Ribosomal protein L41A (YL41) (L47A)
6681_at	917.1	P	weak similarity to S.pombe hypothetical protein SPAC23H3
6682_at	20688.3	P	homocitrate synthase, highly homologous to YDL131W
6683_g_at	24715.5	P	homocitrate synthase, highly homologous to YDL131W
6684_at	1709.5	P	ATPase inhibitor
6685_at	2736.5	P	hypothetical protein
6641_at	2745.4	P	PHO85 cyclin
6642_at	8933.2	P	D-Lactate Dehydrogenase (Cytochrome)
6643_at	822.9	P	similarity to hypothetical protein YCR059c
6644_at	541.3	P	hypothetical protein
6645_at	663.5	P	strong similarity to hypothetical protein YIL079c and weak similarity t
6646_at	14023.1	P	mitochondrial enzyme D-lactate ferricytochrome c oxidoreductase
6647_at	4798.8	P	hypothetical protein
6648_at	1166.8	A	questionable ORF
6649_at	22212.7	P	Glutamate synthase (NADPH)
6650_at	1178.9	P	zinc-finger transcription factor of the Zn(2)-Cys(6) binuclear cluster d
6651_at	174.2	A	protein of unknown function
6652_at	7055.4	P	Long-chain alcohol dehydrogenase (glutathione-dependent formalde
6653_at	3647	P	Asparagine-rich protein
6654_at	3607.4	P	weak similarity to Pyrococcus horikoshii hypothetical protein PHBJ01
6655_at	3448.4	P	nuclear protein that negatively regulates basal transcription
6656_at	5142.6	P	DNA ligase
6657_at	38.7	A	questionable ORF
6658_at	98.9	A	hypothetical protein
6659_at	3659.1	P	strong similarity to hypothetical protein YLR206w and to human KIAA
6660_at	19441.7	P	Putative RNA helicase of DEAD box family, required for Rap1p local
6661_at	2554.5	P	MEK homolog
6662_at	8617.3	P	questionable ORF
6618_at	19241.9	P	hypothetical protein
6619_at	527.6	A	weak similarity to Pas7p
6620_at	3984.8	P	G(sub)2-specific B-type cyclin
6621_at	600.1	P	MutS homolog involved in chromosome exchange
6622_at	20685.1	P	Something About Silencing 10
6623_at	751.5	M	questionable ORF
6624_at	614.1	A	questionable ORF
6625_at	6257.9	P	RNA polymerase III (C) subunit, homologus to human BN51 protein
6626_at	388.5	M	hypothetical protein
6627_at	6365.1	P	similarity to human mRNA clone RES4-25
6628_at	10184.7	P	Subunit of the regulatory particle of the proteasome
6629_at	964.5	P	weak similarity to Orc3p
6630_at	24061.4	P	alpha subunit of the coatamer complex\; gamma-alpha-COP
6631_at	4608.3	P	hypothetical protein
6632_at	10671.5	P	Cytoplasmic chaperonin subunit required for actin cytoskeleton asse
6633_at	1129	P	Cardiolipin synthase
6634_at	4152.3	P	Biotin:apoprotein ligase
6635_at	5582	P	RNA polymerase II large subunit
6636_at	634.2	P	hypothetical protein
6637_at	1351.2	P	suppressor of snf3 mutant
6638_at	29093.7	P	ADP-ribosylation factor 2
6639_at	8157.9	P	Rho GDP dissociation inhibitor with activity toward Rho1p

6640_at	1859.2	P	serine-threonine protein phosphatase 2A
6595_at	2624.8	P	hypothetical protein
6596_at	3161.9	P	Acts together with Cdc4p and Cdc34p to control the G1-S phase tra
6597_at	24080.1	P	homocitrate synthase, highly homologous to YDL182W
6598_at	14351.8	P	ATPase stabilizing factor
6599_at	32287.1	P	Ribosomal protein P1B (L44) (YP1beta) (Ax)
6600_at	1262.6	P	Ribosomal protein P1B (L44) (YP1beta) (Ax)
6601_at	3725.3	P	hypothetical protein
6602_at	14493.6	P	vacuolar H+\/Ca2+ exchanger
6603_at	3558.3	P	G1 cyclin
6604_at	27638.3	P	Microsomal protein of CDC48\/PAS1\/SEC18 family of ATPases\; fu
6605_at	13932.3	P	Yeast member of the Histidine Triad protein family (HIT)
6606_at	1100.1	A	Yeast member of the Histidine Triad protein family (HIT)
6607_at	3254.3	P	similarity to aldose reductases
6608_at	5858.4	P	similarity to hypothetical protein YJL151c
6609_at	11181.9	P	Ubiquitin-specific protease
6610_at	2627	P	hypothetical protein
6611_at	2012.5	P	Mitochondrial protein that regulates mitochondrial iron accumulation
6612_at	1022.3	P	similarity to bovine Graves disease carrier protein
6613_at	469	A	questionable ORF
6614_at	3026.1	P	similarity to hypothetical S. pombe protein
6615_at	9879.3	P	Protein with homology to mammalian Nup107p
6616_at	1414.8	P	hypothetical protein
6617_at	23.9	A	weak similarity to Rhizobium nodulation protein nodG
6573_at	320	P	similarity to hypothetical protein YDR425w
6574_at	6678	P	similarity to C-terminus of human TRP-185 protein
6575_at	5052.5	P	Component of the exosome 3->5 exoribonuclease complex with Rrp
6576_at	1361.9	P	hypothetical protein
6577_at	1385.2	P	strong similarity to thiamine-repressed protein Thi4p
6578_at	1012.3	P	serine-threonine kinase, subunit of transcription factor TFIIK, a subc
6579_at	376	A	cox1 pre-mRNA splicing factor
6580_at	553.1	P	Homeobox-domain containing protein which is a positive regulator of
6581_at	833.9	A	protein of unknown function
6582_at	501.6	A	similarity to H.influenzae sialoglycoprotease (gcp)
6583_at	2847.2	P	UDP-N-acetylglucosamine pyrophosphorylase
6584_at	1170.3	P	largest and catalytic subunit of DNA polymerase III (delta)
6585_at	1592.8	P	protein kinase
6586_at	10434.7	P	similarity to E.coli arsenical pump-driving ATPase
6587_at	6912.1	P	weak similarity to myosin heavy chain proteins
6588_at	706.5	P	hypothetical protein
6589_at	11553.5	P	Subunit of the regulatory particle of the proteasome
6590_at	1233.7	P	questionable ORF
6591_at	14985.9	P	dolichyl phosphate-D-mannose:protein O-D-mannosyltransferase
6592_at	198.5	A	questionable ORF
6593_at	4016	P	dolichyl phosphate-D-mannose:protein O-D-mannosyltransferase
6594_at	3389.1	P	Signal recognition particle subunit
6550_at	854.6	P	weak similarity to mouse FAF1 protein
6551_at	3275	P	beta subunit of farnesyltransferase
6552_at	3282.5	P	hypothetical protein
6553_at	2274	P	Suppressor of thermosensitive mutations in the DNA polymerase del
6554_at	880.7	P	Living Under Cap-binding complex expression
6555_at	11984.7	P	similarity to hypothetical Synechocystis protein

6556_at	97.7	A	strong similarity to NADH dehydrogenase (ubiquinone)
6557_at	22169.9	P	suppressor of the cold-sensitive snRNP biogenesis mutant brr1-1
6558_i_at	27246.2	P	Ribosomal protein S16B (rp61R)
6559_f_at	19027	P	Ribosomal protein S16B (rp61R)
6560_at	25869.9	P	Ribosomal protein L13A
6561_at	26554.5	P	Acidic ribosomal protein P1A (YP1alpha) (A1)
6562_at	2108.7	P	positive regulatory factor with thiamin pyrophosphate-binding motif fo
6563_at	1008.3	A	MDS1 related protein kinase
6564_at	38.9	A	MDS1 related protein kinase
6565_at	4770.3	P	malate dehydrogenase
6566_at	1511.4	P	Required for the vacuolar morphogenesis in yeast
6567_at	1546.1	P	hypothetical protein
6568_f_at	29743.7	P	Ribosomal protein L31A (L34A) (YL28)
6569_at	10041.8	P	Ribosomal protein L31A (L34A) (YL28)
6570_at	2161.1	P	weak similarity to spindle pole body protein NUF1
6571_at	2783.1	P	weak similarity to Cyprinus carpio calcium channel protein
6572_at	3364.3	P	weak similarity to hypothetical protein YMR040w
6527_at	2663.1	P	questionable ORF
6528_at	4161.6	P	Bromodomain protein, homolog of Bdf1
6529_at	965.8	P	translational activator of cytochrome b
6530_at	746.9	A	questionable ORF
6531_at	9312.6	P	Subunit VIIa of cytochrome c oxidase
6532_at	19627	P	Mitochondrial form of NADP-specific isocitrate dehydrogenase
6533_at	5383.1	P	40 kDa farnesylated protein associated with peroxisomes
6534_at	6112.2	P	ubiquitin-conjugating enzyme
6535_at	3684.6	P	weak similarity to human estrogen-responsive finger protein
6536_at	94.8	A	questionable ORF
6537_f_at	35936	P	Ribosomal protein S29B (S36B) (YS29)
6538_at	19158.2	P	similarity to C.elegans hypothetical protein
6539_at	652	A	A mutation in this gene results in RADiation sensitivity and recombin
6540_at	1135.6	P	Integrin analogue gene
6541_at	731.4	A	hypothetical protein
6542_at	1042.8	P	transcription factor
6543_at	24407.6	P	mannose-1-phosphate guanyltransferase, GDP-mannose pyrophosp
6544_at	3282.5	P	hypothetical protein
6545_at	7003.2	P	hypothetical protein
6546_at	7151.4	P	putative 1-acyl-sn-gylcerol-3-phosphate acyl transferase
6547_at	8358.3	P	Protein homologous to human La (SS-B) autoantigen
6548_at	2321.9	P	questionable ORF
6549_at	603	A	KRE9 homolog
6504_at	5338.2	P	SIT4 suppress mutations in DBF2
6505_at	24098.7	P	hypothetical protein
6506_at	12870.2	P	homologous to Yml37p, component of the 37 S subunit of mitochonc
6507_at	1087.3	P	FAD synthetase
6508_at	3161.8	P	Necessary for the stability and\/or processing of some large mitochor
6509_at	693.6	P	snRNA-associated protein
6510_at	3360.4	P	regulator of silent mating loci
6511_at	1110.9	M	questionable ORF
6512_at	8721.1	P	N-terminal acetyltransferase
6513_at	20072.2	P	questionable ORF
6514_at	16921.9	P	similarity to mucin proteins
6515_at	3241.4	P	strong similarity to glucan 1,4-alpha-glucosidase

6516_at	2362.1	P	strong similarity to RIB2 protein
6517_at	3778	P	G-protein coupled receptor
6518_at	281.7	A	questionable ORF
6519_at	1886	P	similarity to H.influenzae hypothetical protein HI0174
6520_at	606.4	A	questionable ORF
6521_at	8158.5	P	DEAD box protein 10
6522_at	1458.8	P	RNA splicing factor
6523_at	16624.5	P	actin-related protein
6524_at	983.5	P	serine\/threonine\/tyrosine protein kinase (dual specificity), able to au
6525_at	878.8	P	hypothetical protein
6526_at	608.9	A	questionable ORF
6482_at	1088.8	A	ser/thr protein kinase of the DEAD/DEAH box family
6483_at	1346.8	P	strong similarity to acid phosphatase
6484_at	76.8	A	questionable ORF
6485_at	8205.5	P	glycerol-3-phosphate dehydrogenase
6486_at	547.6	P	Similar to GPM1 (phosphoglycerate mutase)
6487_at	3192.3	P	involved in ubiquitin degradation pathway
6488_at	5938	P	similarity to Osh1p
6489_at	241.4	P	p24 protein involved in membrane trafficking
6490_at	1616.6	P	serine\/threonine protein kinase
6491_at	192.8	A	questionable ORF
6492_at	21647.3	P	similarity to rat synaptic glycoprotein SC2
6493_at	31537.4	P	nucleolar protein, homologous to mammalian fibrillarin
6494_at	2840.8	P	Protein involved in hexose metabolism
6495_at	8110.3	P	strong similarity to hypothetical protein YBR016w and YDR210w
6496_at	484.1	A	questionable ORF
6497_at	2520.4	P	similarity to hypothetical protein YBR014c and glutaredoxins
6498_at	1326.1	P	questionable ORF
6499_at	1806.4	P	subunit of the anaphase promoting complex (APC)
6500_at	5732.5	P	Probable 26S protease subunit and member of CDC48\/PAS1\/SEC1
6501_at	818	P	serine-threonine protein phosphatase
6502_at	1650.8	P	Stoichiometric member of mediator complex
6503_at	11841.7	P	ATP synthase delta subunit
6459_at	1292.2	P	Mitotic omosome Determinant\; similar to S. pombe RAD21\; may fur
6460_at	1235.8	P	HMG1-box containing protein
6461_at	1107.2	P	similarity to hypothetical protein YFR048w, YDR282c and S.pombe
6462_at	2993.8	P	neutral trehalase (alpha,alpha-trehalase)
6463_at	26713.8	P	Yeast Ran Binder #1\; suppressor of FUS1\; homolog of mouse HTF
6464_at	776.1	P	strong similarity to hypothetical protein YBR005w
6465_at	2037.5	P	RecA homolog (similar to DMC1, RAD51, and RAD55), interacts wit
6466_at	1254.6	P	required for sorting of Mod5p
6467_at	3144.5	P	gene dosage suppressors of the conditional growth defect of several
6468_at	3299.6	P	n-(5 -phosphoribosyl)-anthranilate isomerase
6469_at	456.7	A	questionable ORF
6470_at	458.1	A	galactokinase
6471_at	305	A	hypothetical protein
6472_at	13521.4	P	ABC transporter
6473_i_at	35021.6	P	Ribosomal protein L4B (L2B) (rp2) (YL2)
6474_at	675.1	P	similarity to human hypothetical KIAA0186 protein
6475_at	240	A	weak similarity to chicken neurofilament triplet M protein
6476_at	480.7	A	hypothetical protein
6477_at	1825.6	P	hypothetical protein

6478_at	5510.2	P	Shows homology to basic leucine zipper family of transcription factor
6479_at	236.9	A	strong similarity to hypothetical protein YBR042c
6480_at	1260.9	P	glycine cleavage T protein (T subunit of glycine decarboxylase comp
6481_at	37.7	A	weak similarity to uridine kinases and phosphoribulokinases
6436_at	1502.1	P	DEAD-box protein, putative RNA helicase
6437_at	96.5	A	cik1 suppressor
6438_at	21418.6	P	seryl-tRNA synthetase
6439_at	640.6	A	hypothetical protein
6440_at	2540.2	P	strong similarity to DNA-binding protein Reb1p
6441_at	2188.8	P	Loss Upsets Vacuole
6442_at	910.9	P	regulatory subunit for protein phosphatase Glc7p
6443_at	842.1	P	hypothetical protein
6444_at	829.1	P	Protein involved in the same pathway as Rad26p, has beta-transduc
6445_at	863.2	P	hypothetical protein
6446_at	13491.4	P	strong similarity to S.pombe obr1
6447_at	28015.4	P	strong similarity to putative heat shock protein YRO2
6448_at	1077.5	P	Transcriptional activator of lysine pathway genes with 2-aminoadipat
6449_at	377.3	A	identified by SAGE expression analysis
6450_at	18314.4	P	DAHP synthase\; a.k.a. phospho-2-dehydro-3-deoxyheptonate aldol
6451_at	8326.6	P	similarity to enoyl CoA hydratase
6452_at	29815	P	lysyl-tRNA synthetase
6453_at	1404	P	P-type ATPase involved in Na+ efflux
6454_g_at	11903.2	P	P-type ATPase involved in Na+ efflux
6455_s_at	14848.8	P	plasma membrane protein\; putative Na+ pump\; P-type ATPase
6456_at	3045.6	P	weak similarity to bacterial ribosomal S10 proteins
6457_at	280.2	A	hypothetical protein
6458_at	1063	P	Suppressor of SNf
6413_at	4409.1	P	Coproporphyrinogen III oxidase
6414_at	6410	P	strong similarity to S.acidocaldarius transcription elongation factor tfs
6415_at	9986.7	P	Valine transporter
6416_at	11694.5	P	uroporphyrinogen decarboxylase
6417_at	33.4	A	questionable ORF
6418_at	1631.3	P	similarity to C.elegans K06H7.3 protein
6419_at	16232.4	P	triosephosphate isomerase
6420_at	10712.1	P	similarity to hypothetical A. thaliana protein BAC F7G19
6421_at	859.5	P	cyclin-like kinase required for late nuclear division
6422_at	587.7	A	questionable ORF
6423_at	975.6	P	ubiquitin-conjugating enzyme, E2
6424_at	12024.4	P	strong similarity to SPS2 protein
6425_at	6020.7	P	hypothetical protein
6426_at	825.6	P	weak similarity to L.lactis mleR protein
6427_at	909	P	TriGlyceride Lipase
6428_at	2793.1	P	ubiquitin-conjugating enzyme
6429_at	2307.9	P	similarity to mouse putative CCAAT binding factor CBF1 and CBF2
6430_at	2182.8	P	similarity to E.coli modF and photorepair protein phrA
6431_at	26461.3	P	Probable component of serine palmitoyltransferase, which catalyzes
6432_at	2015.1	P	weak similarity to glia maturation factor beta
6433_at	26235.6	P	Ribosomal protein S13 (S27a) (YS15)
6434_at	658.6	P	hypothetical protein
6435_at	648.1	P	similarity to hypothetical protein YER139c
6391_at	374.8	A	similarity to YNL099c
6392_at	4661.6	P	involved in genome stability

6393_at	1300.4	P	ubiquitin isopeptidase
6394_at	390.4	A	hypothetical protein
6395_at	5224	P	similarity to O.aries arylalkylamine N-acetyltransferase
6396_at	2602.5	P	inositolphosphotransferase 1
6397_at	1043	P	component of SWI\/SNF global transcription activator complex
6398_at	9541.6	P	Trehalose-6-phosphate phosphatase
6399_at	2070.8	P	protein phosphatase type 2A
6400_at	412.1	A	RecA homolog (related to DMC1, RAD51, RAD57), interacts with Ra
6401_at	4022.3	P	putative cell surface glycoprotein
6402_at	2284.1	P	Preferential Use of Neither donor locus during mating type switching.
6403_at	1962	P	cytochrome c oxidase-specific assembly factor
6404_at	1457	P	vacuolar protein sorting
6405_at	4838.7	P	Asparagine and serine-rich protein
6406_at	807.8	P	Involved in telemere length regulation, may be functional in telemere
6407_at	18726.2	P	similarity to hypothetical S.pombe protein
6408_at	7071.8	P	similarity to hypothetical C.elegans protein
6409_at	1925.8	P	coordinates regulation of alpha-factor receptor signalling and inductic
6410_at	9377.7	P	endoplasmic reticulum protein that is part of the Sec61 trimeric comp
6411_at	5866.9	P	involved in processing rRNA precursor species to mature rRNAs
6412_at	1562	P	involved in 3 splice site choices and 2nd step of splicing
6368_at	1983.5	P	weak similarity to Streptococcus transposase
6369_at	3699.9	P	weak similarity to YRO2 protein
6370_at	28799.2	P	strong similarity to human RNase L inhibitor and M.jannaschii ABC tr
6371_at	8203.1	P	ubiquitin-conjugating enzyme
6372_at	3682.9	P	similarity to P.falciparum ATPase 2
6373_g_at	9608	P	similarity to P.falciparum ATPase 2
6374_at	2840.9	P	questionable ORF
6375_at	4597.6	P	hypothetical protein
6376_at	1379.5	P	putative zinc finger protein
6377_at	5963.5	P	Homolog of the human GTBP protein, forms a complex with Msh2p
6378_at	4292.9	P	similarity to Legionella glutaredoxin-like protein
6379_at	23710.4	P	Homolog of mammalian 14-3-3 proteins
6380_at	4133.1	P	similarity to Dictyostelium development-specific membrane protein
6381_at	9532	P	weak similarity to proliferation-associated protein
6382_at	40.7	A	hypothetical protein
6383_at	2175.7	P	Protein of the pheromone pathway
6384_at	737.8	P	hypothetical protein
6385_at	5121.9	P	similarity to mouse hypothetical protein
6386_at	744.4	P	Actin-related protein
6387_at	1811.4	P	strong similarity to Emp70 protein
6388_at	778.9	P	Probably has role late in meiosis following DNA replication
6389_at	773	P	similarity to Mpa43p
6390_at	1103.4	P	DNA replication fork blocking protein
6346_at	801.2	P	strong similarity to alanine transaminase
6347_at	236.5	A	questionable ORF
6348_at	153.1	A	42-kDa nuclear protein
6349_at	163.1	A	questionable ORF
6350_at	1646.7	M	similarity to bacterial ribosomal L34 proteins
6351_at	1229.4	P	similarity to bacterial ribosomal L1 proteins
6352_at	3149.7	P	similarity to mouse ligatin, a trafficking receptor for phosphoglycopro
6353_at	674.4	P	subunit of the anaphase promoting complex (APC)
6354_at	8102.9	P	similarity to B.subtilis tetracyclin resistance

6355_at	12502	P	N2,N2-dimethylguanosine-specific tRNA methyltransferase
6356_at	2868.8	P	weak similarity to YNC2beta protein
6357_at	1215.7	P	Serine\/threonine protein kinase
6358_at	504.3	A	helix-loop-helix protein
6359_at	616.1	A	hypothetical protein
6360_at	43.6	A	ExtraCellular Mutant
6361_at	3571.2	P	similarity to hypothetical protein YLR246w and YOL003c
6362_at	18107.4	P	pentafunctional arom polypeptide (contains: 3-dehydroquinate synth
6363_at	3440.4	P	weak similarity to Sec27p, YMR131c and human retinoblastoma-bin
6364_at	9121.4	P	fibrim homolog (actin-filament bundling protein)
6365_at	566.5	P	weak similarity to sea urchin myosin heavy chain
6366_at	774.7	P	similarity to hypothetical protein YJL149w
6367_at	637.7	P	strong similarity to hypothetical protein YLR108c
6323_at	25366.7	P	questionable ORF
6324_g_at	28804.9	P	questionable ORF
6325_at	6574.3	P	Metal resistance protein with similarity to human cystic fibrosis protei
6326_at	201.4	A	questionable ORF
6327_at	2180.7	P	Reduced growth phenotype
6328_at	838.4	P	Hyperrecombination protein that suppresses intrachromosomal excis
6329_at	9142	P	ubiquitin-like protein
6330_at	3664.9	P	ubiquitin-like protein
6331_at	2522.2	P	weak similarity H.influenzae protoporphyrinogen oxidase (hemK) ho
6332_at	1647.4	P	hypothetical protein
6333_at	838.4	P	Member of beta-transducin-related (WD-40) protein family
6334_at	6774.6	P	mating-type regulation protein
6335_at	20280.4	P	aspartyl protease related to Yap3p
6336_at	921.1	P	TFIID subunit
6337_at	3257.3	P	transcriptional activator
6338_at	1344	P	Ethanolamine Kinase
6339_at	11462.4	P	dihydrolipoyl transsuccinylase component of alpha-ketoglutarate deh
6340_at	681.3	A	questionable ORF
6341_at	2113.8	P	Protein with variable number of tandem repeats of a 64 amino-acid
6342_at	1285.8	P	member of the CCCH zinc finger protein family that has two or more
6343_at	4690.4	P	weak similarity to C.elegans hypothetical protein CET26E3
6344_at	4544.9	P	hypothetical protein
6345_at	22456.4	P	questionable ORF
6300_g_at	25015.4	P	questionable ORF
6301_at	17529.7	P	cyclophilin peptidyl-prolyl cis-trans isomerase
6302_at	14620.7	P	RNA polymerase I subunit A14
6303_at	1849.2	P	questionable ORF
6304_at	9673	P	aspartic beta semi-aldehyde dehydrogenase
6305_at	1708.6	P	Leucine permease transcriptional regulator
6306_at	2102.8	P	Ssy1p controls expression of several transporter genes, including B
6307_at	3536.5	P	protein phosphatase Two C-Interacting protein
6308_at	2121.8	P	Nap1p-binding protein
6309_at	1448.1	P	weak similarity to S.pombe hypothetical protein
6310_at	929	P	Hydrophilic protein involved at the late stage of secretion
6311_at	4852.9	P	weak similarity to hypothetical C.elegans protein
6312_at	2649.3	P	107 kDa component of the Exocyst complex\; required for exocytosis
6313_at	6872.5	P	TFIID subunit
6314_at	14955.6	P	Cell cycle protein necessary for passage through START
6315_at	1029.9	P	Binds Sin3p in two-hybrid assay

6316_at	9398	P	Guanine nucleotide exchange protein for ARF
6317_at	2599.6	P	Similar to HSP26\; expression is regulated by stress conditions
6318_at	11388.1	P	putative translation factor
6319_at	1936.1	P	Regulator of arginine-responsive genes with ARG80 and ARG81
6320_at	11562	P	Non-histone protein
6321_at	2301.8	P	similarity to S.pombe hypothetical protein SPAC2F7.15
6322_at	1479.3	P	transcription factor\; genetic and mutant analyses suggest that Ngg1
6278_at	23575.6	P	ubiquitin-conjugating enzyme
6279_at	23888.5	P	succinate dehydrogenase membrane anchor subunit
6280_at	244.5	P	hypothetical protein
6281_at	355.7	A	hypothetical protein
6282_at	1085.5	P	Sister chromatid cohesion protein
6283_at	1097.3	P	Involved in silencing at telomeres, HML and HMR
6284_at	5614.6	P	Protein that affects bud emergence, intrachromosomal recombinatio
6285_at	1375.4	P	weak similarity to thioredoxin
6286_at	3605.6	P	Aip Three Complex\; interacts with AIP3, localized to the nucleus
6287_at	644.8	P	strong similarity to Msf1p
6288_at	608	P	hypothetical protein
6289_at	475.4	A	questionable ORF
6290_at	14413.7	P	Cytoplasmic chaperonin of the Cct ring complex (previously called T
6291_at	2577	P	Hydrophilic suppressor of ypt1 involved in vesicle trafficking between
6292_at	12273.6	P	strong similarity to TATA-binding protein-interacting protein 49 - rat
6293_at	1124.8	P	Homolog of SIR2
6294_at	806.9	P	nucleoporin
6295_at	128.1	A	questionable ORF
6296_at	9429.6	P	Mitochondrial RNA helicase of the DEAD box family
6297_at	1312.7	P	RNA-binding protein involved in cleavage step of mRNA 3 -end form
6298_at	2246.1	P	similarity to C.elegans hypothetical protein T05G5.5
6299_at	613.3	P	cytochrome b translational activator
6255_at	836.4	P	hypothetical protein
6256_at	663.3	A	questionable ORF
6257_at	1093.1	P	similarity to hypothetical protein YLR238w
6258_at	9570.7	P	component of spindle pole
6259_at	1065.8	P	hypothetical protein
6260_at	151.3	A	questionable ORF
6261_at	2321.8	P	Involved in ubiquinone biosynthesis
6262_at	4081.5	P	similarity to A.eutrophus cation efflux system membrane protein czcl
6263_at	2243.2	P	EST1-like bcy1 Suppressor
6264_at	3437	P	Ume6p is a C6 zinc finger URS1-binding protein that is a key regulat
6265_at	4672.7	P	Phosphatidylinositol 4-phosphate kinase
6266_at	1320.8	P	questionable ORF
6267_at	9014.3	P	strong similarity to hypothetical protein YBR016w
6268_at	6505.7	P	Translation initiation factor eIF-2B epsilon subunit
6269_at	12671.6	P	chaperonin subunit alpha
6270_at	714.8	P	regulatory protein involved in control of sterol uptake
6271_at	5886.1	P	similarity to hypothetical protein YNL281w
6272_at	854.6	A	hypothetical protein
6273_at	1170.4	P	positive transcriptional regulator of ADH2 and peroxisomal protein ge
6274_at	1804.7	P	cell cycle arrest protein
6275_at	131	A	Septin-related protein expressed during sporulation
6276_at	575.8	P	hypothetical protein
6277_at	1487.1	A	questionable ORF

6232_at	940	P	weak similarity to the beta subunit of an ER luminal alpha-glucosidas
6233_at	12884.8	P	strong similarity to hypothetical protein YLR225c
6234_at	241.4	P	similarity to Ifh1p
6235_at	21186.1	P	Histone H2B (HTB1 and HTB2 code for nearly identical proteins)
6236_i_at	35397.9	A	Histone H2A (HTA1 and HTA2 code for nearly identical proteins)
6237_at	13839	P	cytosolic adenylate kinase
6238_at	618.9	P	regulator of silent mating loci
6239_at	1526.2	P	Component of pre-mRNA cleavage and polyadenylation factor I, inte
6240_at	1141.9	P	hypothetical protein
6241_at	667.3	A	questionable ORF
6242_at	1709	P	hypothetical protein
6243_at	15569.6	P	5-aminolevulinate synthase
6244_at	20876.2	P	similarity to hypothetical protein YDL204w
6245_at	26470.8	P	homoaconitase
6246_at	1679.5	P	U1 snRNP protein that shares 50\% sequence similarity with Prp39p
6247_at	1003.4	P	similarity to hypothetical A. thaliana protein
6248_at	1561.2	A	Mitochondrial ribosomal protein MRPL7 (YmL7)
6249_at	18289.4	P	encodes a subunit of yeast coatomer
6250_at	4031.9	P	hypothetical protein
6251_at	321.1	A	Snurp = Small nuclear ribonucleoprotein particle of MW 56 kDa. Ass
6252_at	102.7	A	questionable ORF
6253_at	904.2	P	putative amidase
6254_at	591.7	P	Required for the first step of splicing in vitro
6209_at	700.2	P	69-kDa protein containing tetratricopeptide repeat (TPR)
6210_at	7638.6	P	galactosyltransferase
6211_at	6571	P	involved in targeting and fusion of ER to golgi transport vesicles
6212_at	5310	P	strong similarity to Sks1p
6213_at	4574.9	P	strong similarity to E.coli thermoresistant gluconokinase
6214_at	1029.7	P	weak similarity to cytochrome b
6215_at	597.9	P	hypothetical protein
6216_at	2292.4	P	coiled-coil protein multicopy suppressor of loss of PP2A
6217_at	1055.6	M	Negative effect on expression of several genes transcribed by RNA
6218_at	305.5	A	zinc finger DNA binding factor, transcriptional regulator of sulfur ami
6219_at	496.6	P	Protein necessary for stability of ARS-CEN plasmids\; suggested to
6220_at	1894.1	P	weak similarity to hypothetical S.pombe hypothetical protein SPBC29
6221_at	277.4	A	catalase A
6222_at	869.4	P	Transcription regulator
6223_at	2683.1	P	Mitochondrial heat shock protein 78 kDa
6224_at	128.8	A	bZIP protein
6225_at	4387.7	P	hypothetical protein
6226_at	2485.3	P	Exo-1,3-b-glucanase
6227_at	8420.4	P	hypothetical protein
6228_at	1020.3	P	DNA-damage inducible gene
6229_at	4343.1	P	Ankyrin repeat-containing protein
6230_at	844.5	A	C3HC4 zinc-binding integral peroxisomal membrane protein
6231_at	3749.6	P	similarity to hypothetical C.elegans protein
6187_at	4285.1	P	weak similarity to human TAFII100 and other WD-40 repeat containi
6188_at	1822.3	P	mitochondrial tryptophanyl-tRNA synthetase
6189_at	266.8	A	questionable ORF
6190_at	4660.7	P	Copper-transporting P-type ATPase with similarity to human Menkes
6191_at	299.3	A	questionable ORF
6192_at	1967	P	Cytoplasmic glyoxylase-II

6193_at	1091.5	P	weak similarity to YOR042w
6194_at	747.3	A	hypothetical protein
6195_at	2470.1	P	weak similarity to YOR042w
6196_at	24762.4	P	strong similarity to Hordeum vulgare blt101 protein
6197_at	534.6	P	Protein is 61\% identical to Msn3p
6198_at	184.1	A	hypothetical protein
6199_at	434.2	P	hypothetical protein
6200_at	10606.8	P	Putative 3 ->5 exoribonuclease\; component of exosome complex o
6201_at	2987.8	P	hypothetical protein
6202_at	1636.3	P	similarity to hypothetical protein YDL001w, YFR048w and S.pombe
6203_at	1227.5	P	eukaryotic initiation factor 2 alpha (eIF2-alpha) kinase
6204_at	4136.2	P	Diacylglycerol Pyrophosphate Phosphatase
6205_at	70.4	A	Synaptonemal complex protein, component of the central element
6206_at	749.1	P	hypothetical protein
6207_at	1387.6	P	similarity to inositolmonophosphatases
6208_at	516.7	P	hypothetical protein
6163_at	754	P	hypothetical protein
6164_at	28.5	A	questionable ORF
6165_at	3158.7	P	similarity to B.subtilis helicases
6166_at	2943.1	P	signal recognition particle receptor - alpha subunit
6167_at	6429.6	P	putative protein phosphatase
6168_at	15720.1	P	dihydrosphingosine phosphate lyase (also known as sphingosine ph
6169_at	601.4	P	weak similarity to Uso1p, YPR179c and fruit fly tropomyosin
6170_at	5208.9	P	hypothetical protein
6171_at	6912.2	P	Syringomycin response protein 2
6172_at	4347.1	P	ATP synthase subunit 5\; oligomycin sensitivity-conferring protein
6173_at	2704.4	P	involved in protein transport step at the Brefeldin A blocks
6174_at	4439.6	P	gamma-glutamyl kinase
6175_at	2919.3	P	Component of pre-mRNA cleavage factor II (CFII)\; 150-kDa protein
6176_at	12176.2	P	weak similarity to human GPI-anchor biosynthesis protein
6177_at	1187.1	P	similarity to transcriptional regulator proteins
6178_at	6083	P	Cyclophilin D, Peptidyl-prolyl cis-trans isomerase D
6179_at	3103.4	P	Yeast member of the Histidine Triad protein family (HIT)
6180_i_at	280	M	Yeast member of the Histidine Triad protein family (HIT)
6181_r_at	76.8	A	Yeast member of the Histidine Triad protein family (HIT)
6182_f_at	473.1	A	Yeast member of the Histidine Triad protein family (HIT)
6183_at	3269.4	P	weak similarity to S.pombe hypothetical protein SPAC6F6
6184_at	6386.1	P	similarity to Pmt1p, Pmt2p, Pmt3p and Pmt5p
6185_at	1848.5	P	RNA polymerase II holoenzyme component
6186_at	22671.8	P	GTPase-interacting component 2
6140_at	4788.4	P	Suppresor of mar1-1 (sir2) mutation
6141_at	1113	P	Component of transcription initiation factor IIb, 75 kDa subunit
6142_i_at	2003.6	P	high copy suppressor of G beta subunit temperature sensitive mutati
6143_f_at	3246.4	P	high copy suppressor of G beta subunit temperature sensitive mutati
6144_at	946.6	M	Phosphatidylinositol(3)-phosphate binding
6145_at	244.5	A	weak similarity to hypothetical S.pombe protein
6146_at	894.2	P	hypothetical protein
6147_at	4621.6	P	hypothetical protein
6148_at	256.9	A	hypothetical protein
6149_at	1578.1	P	Involved in minichromosome maintenance
6150_at	1626.1	P	hypothetical protein
6151_at	590.1	P	similarity to hypothetical S. pombe protein and weak similarity to bovi

6152_at	18526.6	P	Asparaginase I, intracellular isozyme
6153_at	2131.1	P	Mitochondrial ribosomal protein MRPL35 (YmL35)
6154_at	17617.1	P	subunit e of mitochondrial F1F0-ATPase
6155_at	27.2	A	cytosolic and peripheral membrane protein with three zinc fingers\; cy
6156_at	3339.5	P	weak similarity to beta transducin from S. pombe and other WD-40 re
6157_at	963.5	P	weak similarity to S.pombe hypothetical protein SPAC1B9
6158_at	533.8	P	strong similarity to YHR080c, similarity to YFL042c and YLR072w
6159_at	517.4	A	questionable ORF
6160_at	4607.3	P	Skp1p encodes Cbf3d, a 29 Kd kinetochore protein subunit of CBF3
6161_at	816.9	P	48-kDa peroxisomal integral membrane protein
6162_at	2127.9	P	similarity to hypothetical S. pombe protein
6117_at	6311.7	P	Protein involved in the attachment of glycosylphosphatidylinositol (GF
6118_at	1064.2	P	similarity to E.coli hypothetical protein and weak similarity to RNA hel
6119_at	2366.8	P	similarity to hypothetical S. pombe protein
6120_at	711	P	similarity to nuclear Sth1p, Snf2p and related proteins
6121_at	11257.5	P	Multicopy suppressor of snf1 mutation
6122_at	2486.9	P	weak similarity to B.subtilis hypothetical protein X
6123_at	5291.1	P	Mitochondrial ribosomal protein MRPS28 (E. coli S15)
6124_at	5802	P	similarity to Erc1p
6125_at	4960.5	P	weak similarity to hypothetical protein YOR004w
6126_at	222	A	questionable ORF
6127_at	31363.3	P	strong similarity to arginine-tRNA ligase
6128_f_at	22489.2	P	Hexose transporter
6129_f_at	23646.4	P	Hexose transporter
6130_at	412.3	A	hypothetical protein
6131_at	20755	P	High-affinity glucose transporter
6132_at	4586.8	P	similarity to hypothetical S.pombe protein
6133_at	4326.5	P	37 kDa mitochondrial ribosomal protein
6134_at	1554.5	P	similarity to hypothetical protein YHR097c
6135_at	4928.5	P	GPI-anchored aspartic protease
6136_at	2028.6	P	protein of unknown function
6137_at	4443.6	P	required for bud growth
6138_at	1302.9	P	weak similarity to hypothetical proteins YOL092w, YBR147w and YM
6139_at	14121.4	P	Thioredoxin reductase
6095_at	2685.9	P	anthranilate phosphoribosyl transferase
6096_at	74.2	A	questionable ORF
6097_at	863.3	P	component of the spindle pole body that interacts with Spc42p, calm
6098_at	679.4	P	hypothetical protein
6099_at	511.7	P	strong similarity to hypothetical protein YHR108w and weak similarity
6100_at	1631.8	P	hypothetical protein
6101_at	35.9	A	questionable ORF
6102_at	1628	P	hypothetical protein
6103_at	3073.9	P	91 kDa tau91 subunit of transcription factor IIIC (TFIIIC)
6104_at	1092.3	P	Establishes Silent omatin
6105_at	4912.8	P	Homolog of DSS1\; similar to hypothetical protein from S. pombe
6106_at	2511.9	P	Member of the beta transducin family
6107_at	6424.5	P	weak similarity to Streptococcus M protein
6108_at	73.1	A	similarity to YOL106w and YER181c
6109_at	3697.4	P	hypothetical protein
6110_at	14807.5	P	homologous to the aldo-keto reductase protein family
6111_at	274.1	A	DNA repair protein
6112_at	1526.9	P	hypothetical protein

6113_at	103.2	A	similarity to chitinases
6114_at	1395.8	P	similarity to hypothetical S. pombe protein
6115_at	15929.3	P	strong similarity to human BDR-1 protein and other calcium binding p
6116_at	406.3	A	similarity to hypothetical A. thaliana protein BAC F21M12
6072_at	1354.3	P	Mitochondrial protein of the CDC48\/PAS1\/SEC18 ATPase family, r
6073_at	3298.7	P	adrenodoxin oxidoreductase homolog
6074_at	2990.2	P	ATP synthase subunit f
6075_at	1676.2	P	Sm-like protein
6076_at	922.4	P	Contains a Rho-GAP domain and two LIM domains. Has strong simil
6077_at	12613.7	P	similarity to Pdc6p, Thi3p and to pyruvate decarboxylases
6078_at	14334.6	P	Nuclear RNA-binding RNA annealing protein
6079_at	9864.3	P	Nuclear RNA-binding RNA annealing protein
6080_at	17001.4	P	Ribosomal protein P2B (YP2beta) (L45)
6081_at	377.4	A	weak similarity to S.pombe paramyosin
6082_at	14970.5	P	strong similarity to Y.lipolytica GPR1 gene
6083_at	183.7	A	MMS and UV Sensitive\; Mus81p and Rad54p are found together in a
6084_at	1144.3	P	similarity to Itr1p and Itr2p and E.coli araE
6085_at	16552.3	P	involved in endocytosis
6086_at	2131.7	P	GTPase activating protein (GAP) for RHO1
6087_at	1608.2	P	Protein with homology to mammalian ubiquitin activating (E1) enzyme
6088_at	1139.9	P	strong similarity to hypothetical protein YOR013w
6089_at	1359.4	P	transcription factor, member of the histone acetyltransferase SAGA
6090_at	291	P	mRNA (identified by a library screen) that causes growth arrest when
6091_at	4042.8	P	probable 26S protease subunit and member of the CDC48\/PAS1\/SE
6092_at	6925.5	P	Sxm1p
6093_at	660.9	P	hypothetical protein
6094_at	2536.5	P	repressor of class II transcription
6049_at	5411.6	P	similarity to human KIAA0007 gene
6050_at	5243.6	P	Hypoxanthine Phosphoribosyltransferase
6051_at	7761.9	P	similarity to C. fasciculata inosine-uridine preferring nucleoside hydro
6052_at	60.7	A	Cytochrome P450 56, Dit2p catalyzes oxidation of N-formyl tyrosine
6053_at	430.7	A	questionable ORF
6054_at	379.4	A	first enzyme in dityrosine synthesis in the outer layer of the spore wa
6055_at	10697.8	P	dissociable subunit of RNA polymerase II
6056_at	1711.3	P	263-amino acid mitochondrial ribosomal large subunit protein\; simila
6057_at	2008.7	P	probable multidrug resistance transporter
6058_at	2118.1	P	weak similarity to Myo1p
6059_at	2305.9	P	glycinamide ribotide transformylase
6060_at	771.3	P	similarity to Nfi1p
6061_at	5756.2	P	farnesyl cysteine-carboxyl methyltransferase
6062_at	3652.2	P	weak similarity to Der1p
6063_at	2767.9	A	weak similarity to NADH dehydrogenase
6064_at	3446.8	P	questionable ORF
6065_at	1085.9	P	Protein required for retention of luminal ER proteins
6066_at	2617.8	P	strong similarity to bacterial leucyl aminopeptidase
6067_at	1459.9	P	SYnthetic lethal with cdcForty
6068_at	429.3	P	questionable ORF
6069_i_at	32354.9	P	Ribosomal protein L12B (L15B) (YL23)
6070_s_at	31033.3	P	Ribosomal protein L12B (L15B) (YL23)
6071_at	524.3	P	similar to E. coli DinB and S. cerevisiae REV1
6026_at	5266.3	P	Type 1 membrane protein with EF hand motif
6027_at	591.4	P	hypothetical protein

6028_at	2083.3	P	SNF1 protein kinase substrate
6029_at	1881.9	P	Transcriptional activator involved in resistance to 1,10-phenanthrolin
6030_at	5983.5	P	putative light chain of dynein
6031_at	1679.6	P	similarity to hypothetical protein YDL113c
6032_at	355	A	questionable ORF
6033_at	12039.8	P	Subunit of the regulatory particle of the proteasome
6034_at	4657.8	P	hypothetical protein
6035_at	12777.6	P	Translation initiation factor 3 p33 subunit
6036_at	2199.1	P	similarity to C.perfringens hypothetical hypA protein
6037_at	82.1	A	questionable ORF
6038_at	25803.5	P	nuclear shuttling protein with an RNA recognition motif
6039_g_at	28482.8	P	nuclear shuttling protein with an RNA recognition motif
6040_i_at	36802.3	P	questionable ORF
6041_at	6213.4	P	similarity to S.pombe hypothetical protein
6042_at	2661.2	P	similarity to YOL141w and hypothetical C.elegans protein
6043_at	890.5	A	serine-threonine phosphatase Z
6044_at	196.3	A	hypothetical protein
6045_at	1353	P	strong similarity to hypothetical protein YML018c
6046_at	681.1	A	Loss of rDNA silencing
6047_at	1840.9	P	Pachytene CHeckpoint
6048_at	10261.1	P	Adenine phosphoribosyltransferase
6003_at	60.6	A	questionable ORF
6004_at	2414.7	P	RNA polymerase II holoenzyme component
6005_at	1007.9	P	similarity to hypothetical protein YGL144c and YDL109c
6006_at	623.4	A	questionable ORF
6007_at	303.5	A	ExtraCellular Mutant
6008_at	2348.5	P	transcription factor, member of ADA and SAGA, two transcriptional
6009_at	1677.5	P	hypothetical protein
6010_at	2721.6	P	strong similarity to Yox1p
6011_at	4621.1	P	similarity to human sphingomyelin phosphodiesterase
6012_at	593.9	P	strong similarity to thiol-specific antioxidant proteins
6013_at	17249	P	guanylate kinase
6014_at	167.8	A	questionable ORF
6015_at	5670.8	P	Na+\/H+ exchanger
6016_at	9762.2	P	hect-domain-containing protein, required for G2\/M transition\; simila
6017_at	1049.6	P	similarity to hypothetical protein YML034w and YML033w
6018_at	893.1	P	weak similarity to YNL326c
6019_at	1496.9	P	TFIIH subunit Tfb3 , contains ring finger motif\; similar to mammalia
6020_r_at	1064	A	a-factor mating pheromone precursor
6021_f_at	241.8	A	a-factor mating pheromone precursor
6022_at	1575.2	P	Mitochondrial ribosomal protein MRPL28 (YmL28)
6023_at	2325.2	P	Nuclear-localized protein containing zinc finger motifs
6024_at	892.2	P	negative regulator of prp genes
6025_at	15063.2	P	Protein arginine methyltransferase
5980_at	3935.4	P	similarity to ser/thr protein kinase
5981_at	1314	A	questionable ORF
5982_at	1997.1	P	tSNARE that affects a Late Golgi compartment
5983_at	1171.8	P	hypothetical protein
5984_at	458.1	P	similarity to chromosome segregation protein Cse1p
5985_at	35396.2	P	Ribosomal protein L27B
5986_at	2001.8	P	similarity to P.falciparum 41-2 protein antigen
5987_at	2020.6	P	essential splicing factor

5988_at	1571.7	P	similarity to C-terminal region of YOR019w
5989_at	50.7	A	hypothetical protein
5990_at	6296.2	P	hypothetical protein
5991_at	2904.4	P	protein serine\/threonine kinase
5992_at	2399.8	P	RNAse MRP protein component
5993_at	1064	P	weak similarity to YHR150w
5994_at	1373.5	A	MAP kinase-associated protein
5995_at	10292.2	P	repressible alkaline phosphatase
5996_at	330.8	A	hypothetical protein
5997_at	12379.8	P	alpha-1,2-mannosyltransferase
5998_at	655.3	P	May interact with actin as a component or controller of the assembly
5999_at	1143.1	P	similarity to trichohyalin
6000_at	1425.1	P	weak similarity to Snf7p
6001_at	12095.9	P	3,4-dihydroxy-2-butanone 4-phosphate synthase
6002_at	3370.5	P	Protein required in the absence of Cin8p
5958_at	562.2	P	hypothetical protein
5959_at	1255.3	P	Ser\/Thr protein kinase
5960_at	1211.7	A	questionable ORF
5961_at	24570.6	P	strong similarity to hypothetical protein YOL002c
5962_at	762.4	P	hypothetical protein
5963_at	3979.5	P	hypothetical protein
5964_at	439.3	P	Vacuolar sorting protein
5965_at	3415.4	P	similarity to hypothetical human and C.elegans proteins
5966_at	28506.1	P	myo-inositol transporter
5967_at	3039.8	P	membrane glycoprotein, sorted by HDEL retrieval system
5968_at	919.8	P	weak similarity to hypothetical C.elegans protein, M.genitalium pepti
5969_at	28018.1	P	60S ribosomal protein L37B (L43) (YL35)
5970_at	306.1	M	similarity to hypothetical protein YLR183c
5971_at	31661.8	P	S-adenosylmethionine synthetase
5972_at	928.2	P	Lipid phosphate phosphatase
5973_at	13688.3	P	similarity to hypothetical T.brucei protein
5974_at	3199.5	P	high copy suppressor of ts mutations in DNA polymerase alpha
5975_at	1944.9	P	similarity to FET3, YFL041w and F.floriforme diphenol oxidase
5976_at	8671	P	putative serine\/threonine kinase
5977_at	19252.9	P	high-affinity glutamine permease
5978_at	357	A	questionable ORF
5979_at	6145.7	P	may be involved in function and\/or structure of the eukaryotic kineto
5935_at	1711.4	P	weak similarity to C. elegans protein F25H9.7 and to the human com
5936_at	4266.7	P	questionable ORF
5937_at	5156.2	P	Glutaredoxin (thioltransferase) (glutathione reductase)
5938_at	4063.1	P	strong similarity to hypothetical protein YCL036w
5939_at	1154.1	P	regulates the copper-dependent mineralization of copper sulfide com
5940_at	7646.9	P	strong similarity to glucokinase
5941_at	2621.3	P	weak similarity to hypothetical S.pombe protein
5942_at	2178.1	P	Protein disulfide isomerase homolog
5943_at	5833.4	P	FKBP (FK506 binding protein) 13\; peptidylprolyl cis-trans isomerase
5944_at	887.9	P	weak similarity to transcription factors of the zinc finger class
5945_at	454.3	A	questionable ORF
5946_at	34.7	A	Middle\/late gene of meiosis
5947_at	557.1	P	serine\/threonine kinase homologous to Ste20p\; expressed in middl
5948_at	2035.1	P	similarity to hypothetical human protein and YIL044c
5949_at	231.5	A	hypothetical protein

5950_at	655.5	A	questionable ORF
5951_at	4238.4	P	weak similarity to Plasmodium yoelii rhoptry protein
5952_at	1812.6	P	similarity to Lre1p
5953_at	9826.3	P	ubiquinol-cytochrome c oxidoreductase subunit 7 (14 kDa)
5954_at	1287.4	P	5 ,5 -P-1,P-4-tetraphosphate phosphorylase II
5955_at	6250.6	P	similarity to hypothetical A. thaliana and C. elegans proteins
5956_at	388.6	P	weak similarity Plasmodium repeat organellar protein
5957_at	16966.6	P	strong similarity to hypothetical proteins YPL280w, YOR391c and Y
5913_at	1086.2	P	similarity to YOR383c,Sta1p and pig mucin
5914_at	1080.8	M	hypothetical protein
5915_at	54.4	A	sugar transporter-like protein
5916_at	262.8	A	questionable ORF
5917_at	5894.1	P	Phenylacrylic acid decarboxylase
5918_at	6598.3	P	similarity to E.coli hypothetical 55.3 kDa protein in rfah-rfe intergenic
5919_at	181	A	hypothetical protein
5920_at	1156.1	P	similarity to dihydroflavonol-4-reductases
5921_at	10637.5	P	hypothetical protein identified by SAGE
5922_s_at	6177.7	P	homing endonuclease with protein splicing activity
5923_at	3975.4	P	identified by SAGE
5924_at	1272.1	P	identified by SAGE
5925_at	923.7	P	identified by SAGE
5926_g_at	923.7	A	identified by SAGE
5927_at	8402.5	P	Involved in pre-tRNA splicing and in uptake of branched-chain amino
5928_at	728.6	P	non-annotated SAGE orf Found forward in NC_001136 between 169
5929_at	1126	P	non-annotated SAGE orf Found reverse in NC_001136 between 340
5930_at	1222.9	P	non-annotated SAGE orf Found reverse in NC_001136 between 372
5931_at	5865.5	P	non-annotated SAGE orf Found forward in NC_001136 between 578
5932_at	2058.9	P	non-annotated SAGE orf Found reverse in NC_001136 between 603
5933_at	697.9	A	non-annotated SAGE orf Found forward in NC_001136 between 691
5934_at	1203.2	P	non-annotated SAGE orf Found reverse in NC_001136 between 110
5887_i_at	34.3	A	non-annotated SAGE orf Found reverse in NC_001136 between 148
5888_at	52.4	A	non-annotated SAGE orf Found reverse in NC_001136 between 169
5889_at	70.9	A	non-annotated SAGE orf Found reverse in NC_001136 between 436
5890_i_at	53.9	A	non-annotated SAGE orf Found forward in NC_001136 between 43
5891_f_at	2.1	A	non-annotated SAGE orf Found forward in NC_001136 between 43
5892_at	249.1	A	non-annotated SAGE orf Found reverse in NC_001136 between 512
5893_at	19.9	A	non-annotated SAGE orf Found forward in NC_001136 between 629
5894_at	33.2	A	non-annotated SAGE orf Found reverse in NC_001136 between 130
5895_at	2389.3	P	non-annotated SAGE orf Found forward in NC_001136 between 319
5896_at	950.9	A	non-annotated SAGE orf Found forward in NC_001136 between 541
5897_at	1309.1	A	non-annotated SAGE orf Found reverse in NC_001136 between 769
5898_at	968.8	A	non-annotated SAGE orf Found reverse in NC_001136 between 104
5899_i_at	98.5	A	non-annotated SAGE orf Found forward in NC_001136 between 130
5900_at	58.8	A	non-annotated SAGE orf Found forward in NC_001136 between 130
5901_at	4022.1	P	non-annotated SAGE orf Found forward in NC_001136 between 192
5902_at	58.4	A	non-annotated SAGE orf Found forward in NC_001136 between 217
5903_at	378.7	A	non-annotated SAGE orf Found forward in NC_001136 between 241
5904_at	14972.7	P	non-annotated SAGE orf Found forward in NC_001136 between 370
5905_i_at	1317.3	P	non-annotated SAGE orf Found forward in NC_001136 between 370
5906_r_at	2461.5	P	non-annotated SAGE orf Found forward in NC_001136 between 370
5907_at	112.8	A	non-annotated SAGE orf Found forward in NC_001136 between 473
5908_at	26854.3	P	non-annotated SAGE orf Found forward in NC_001136 between 509

5909_at	291.8	P	non-annotated SAGE orf Found reverse in NC_001136 between 542
5910_at	4195.7	P	non-annotated SAGE orf Found forward in NC_001136 between 654
5911_at	469	P	non-annotated SAGE orf Found reverse in NC_001136 between 683
5912_at	775.4	A	non-annotated SAGE orf Found forward in NC_001136 between 886
5864_at	831.6	P	non-annotated SAGE orf Found forward in NC_001136 between 930
5865_at	301	A	non-annotated SAGE orf Found reverse in NC_001136 between 971
5866_at	1806.6	P	non-annotated SAGE orf Found reverse in NC_001136 between 971
5867_at	1259.2	P	non-annotated SAGE orf Found reverse in NC_001136 between 101
5868_at	1357.6	P	non-annotated SAGE orf Found forward in NC_001136 between 102
5869_at	749.2	P	non-annotated SAGE orf Found reverse in NC_001136 between 107
5870_at	151.7	P	non-annotated SAGE orf Found reverse in NC_001136 between 114
5871_at	305.6	A	non-annotated SAGE orf Found reverse in NC_001136 between 116
5872_at	654.9	P	non-annotated SAGE orf Found forward in NC_001136 between 122
5873_at	473.7	P	non-annotated SAGE orf Found reverse in NC_001136 between 127
5874_at	878.5	A	non-annotated SAGE orf Found forward in NC_001136 between 138
5875_s_at	942.1	A	non-annotated SAGE orf Found forward in NC_001136 between 138
5876_at	10646	P	non-annotated SAGE orf Found reverse in NC_001136 between 141
5877_i_at	1489.4	P	non-annotated SAGE orf Found reverse in NC_001136 between 340
5878_r_at	1270.5	A	non-annotated SAGE orf Found reverse in NC_001136 between 340
5879_at	2886.1	P	non-annotated SAGE orf Found forward in NC_001136 between 160
5880_at	921.5	M	non-annotated SAGE orf Found reverse in NC_001136 between 217
5881_at	712.1	A	non-annotated SAGE orf Found forward in NC_001136 between 309
5882_at	1221.7	P	non-annotated SAGE orf Found forward in NC_001136 between 681
5883_i_at	256.4	P	non-annotated SAGE orf Found forward in NC_001136 between 871
5884_r_at	3.8	A	non-annotated SAGE orf Found forward in NC_001136 between 871
5885_at	1630.2	P	non-annotated SAGE orf Found forward in NC_001136 between 937
5886_at	751	P	non-annotated SAGE orf Found forward in NC_001136 between 102
5841_at	367.9	P	non-annotated SAGE orf Found forward in NC_001136 between 102
5842_at	122.2	A	non-annotated SAGE orf Found reverse in NC_001136 between 104
5843_at	23.1	A	non-annotated SAGE orf Found forward in NC_001136 between 109
5844_at	56	A	non-annotated SAGE orf Found reverse in NC_001136 between 116
5845_at	2197.9	P	non-annotated SAGE orf Found reverse in NC_001136 between 120
5846_at	1136.2	P	non-annotated SAGE orf Found forward in NC_001136 between 148
5847_at	7.9	A	non-annotated SAGE orf Found reverse in NC_001136 between 484
5848_at	19.8	A	non-annotated SAGE orf Found reverse in NC_001136 between 485
5849_at	1526	P	non-annotated SAGE orf Found reverse in NC_001136 between 169
5850_at	533.2	P	non-annotated SAGE orf Found forward in NC_001136 between 362
5851_at	473.4	A	non-annotated SAGE orf Found reverse in NC_001136 between 366
5852_at	376.7	A	non-annotated SAGE orf Found reverse in NC_001136 between 369
5853_at	99.3	A	non-annotated SAGE orf Found reverse in NC_001136 between 386
5854_at	1295.3	A	non-annotated SAGE orf Found reverse in NC_001136 between 471
5855_at	97	A	non-annotated SAGE orf Found forward in NC_001136 between 542
5856_at	264	P	non-annotated SAGE orf Found reverse in NC_001136 between 545
5857_g_at	259.6	A	non-annotated SAGE orf Found reverse in NC_001136 between 545
5858_at	50.1	A	non-annotated SAGE orf Found reverse in NC_001136 between 545
5859_at	137.2	A	non-annotated SAGE orf Found reverse in NC_001136 between 721
5860_g_at	625.3	A	non-annotated SAGE orf Found reverse in NC_001136 between 721
5861_at	1665.5	A	non-annotated SAGE orf Found reverse in NC_001136 between 721
5862_at	733.9	A	non-annotated SAGE orf Found reverse in NC_001136 between 909
5863_at	274.6	M	non-annotated SAGE orf Found reverse in NC_001136 between 118
5817_at	877.7	A	non-annotated SAGE orf Found reverse in NC_001136 between 125
5818_at	17.6	A	non-annotated SAGE orf Found reverse in NC_001136 between 125

5819_at	3478	P	non-annotated SAGE orf Found reverse in NC_001136 between 135
5820_at	100.3	A	non-annotated SAGE orf Found reverse in NC_001136 between 138
5821_at	28.1	A	non-annotated SAGE orf Found reverse in NC_001136 between 139
5822_at	502.6	M	non-annotated SAGE orf Found reverse in NC_001136 between 151
5823_at	771.2	A	non-annotated SAGE orf Found reverse in NC_001136 between 151
5824_i_at	20.6	A	non-annotated SAGE orf Found forward in NC_001136 between 174
5825_r_at	4.1	A	non-annotated SAGE orf Found forward in NC_001136 between 174
5826_at	2067.9	P	non-annotated SAGE orf Found reverse in NC_001136 between 235
5827_at	50.7	A	non-annotated SAGE orf Found reverse in NC_001136 between 286
5828_at	5915.5	P	non-annotated SAGE orf Found forward in NC_001136 between 371
5829_at	485.2	A	non-annotated SAGE orf Found reverse in NC_001136 between 423
5830_at	511.7	A	non-annotated SAGE orf Found reverse in NC_001136 between 428
5831_at	344.7	A	non-annotated SAGE orf Found reverse in NC_001136 between 463
5832_i_at	195.5	A	non-annotated SAGE orf Found reverse in NC_001136 between 541
5833_r_at	234.3	A	non-annotated SAGE orf Found reverse in NC_001136 between 541
5834_s_at	1429.8	P	non-annotated SAGE orf Found reverse in NC_001136 between 541
5835_i_at	236.6	A	non-annotated SAGE orf Found reverse in NC_001136 between 541
5836_at	39.7	A	non-annotated SAGE orf Found reverse in NC_001136 between 558
5837_at	137	A	non-annotated SAGE orf Found reverse in NC_001136 between 664
5838_at	3982.2	P	non-annotated SAGE orf Found reverse in NC_001136 between 678
5839_at	3015.4	P	non-annotated SAGE orf Found forward in NC_001136 between 733
5840_at	10838.8	P	non-annotated SAGE orf Found reverse in NC_001136 between 792
5792_at	2638.8	P	non-annotated SAGE orf Found reverse in NC_001136 between 812
5793_at	979.7	P	non-annotated SAGE orf Found forward in NC_001136 between 909
5794_i_at	6644.5	M	non-annotated SAGE orf Found forward in NC_001136 between 945
5795_at	91.5	A	non-annotated SAGE orf Found reverse in NC_001136 between 976
5796_at	286.2	A	non-annotated SAGE orf Found forward in NC_001136 between 979
5797_at	155.5	A	non-annotated SAGE orf Found forward in NC_001136 between 101
5798_at	1564.5	A	non-annotated SAGE orf Found forward in NC_001136 between 101
5799_at	2443.4	P	non-annotated SAGE orf Found forward in NC_001136 between 110
5800_at	6146.1	P	non-annotated SAGE orf Found reverse in NC_001136 between 123
5801_at	61	A	non-annotated SAGE orf Found forward in NC_001136 between 135
5802_at	58.5	A	non-annotated SAGE orf Found forward in NC_001136 between 136
5803_at	713	A	non-annotated SAGE orf Found reverse in NC_001136 between 150
5804_at	2194.1	P	snRNA
5805_i_at	2.4	A	Centromere
5806_i_at	884.9	P	snRNA
5807_at	9191.5	P	snRNA
5808_i_at	24.4	A	questionable ORF
5809_i_at	1161.3	A	similarity to subtelomeric encoded proteins
5810_s_at	5558.1	P	similarity to subtelomeric encoded proteins
5811_at	90.4	A	similarity to YJR108w
5812_at	140.4	A	hypothetical protein
5813_at	8967.2	P	strong similarity to Aip2p
5814_at	482.2	P	hypothetical protein
5815_at	67.3	A	weak similarity to YKL083w
5816_at	2075.9	P	Histone and other Protein Acetyltransferase\; Has sequence homolo
5769_at	2093.7	P	probably multidrug resistance protein
5770_at	1582.2	P	similarity to YBL089w
5771_at	7680.9	P	arginine permease
5772_at	628.9	P	Non-membrane-embedded, PEST sequence-containing protein
5773_at	1022.4	P	Kinesin-related protein involved in establishment and maintenance o

5774_at	23101.6	P	vacuolar protease B
5775_at	4286.1	P	high copy suppressor of imp1 mutation, may be required for the func
5776_at	826.1	A	hypothetical protein
5777_at	15834.1	P	Phosphoacetylglucosamine Mutase
5778_at	231.8	A	hypothetical protein
5779_at	5859.2	P	subunit of a cytoplasmic histone acetyltransferase
5780_at	7374.8	P	DNA polymerase V that has motifs typical of DNA polymerase family
5781_i_at	24606	P	Ribosomal protein L12A (L15A) (YL23)
5782_at	1800.9	P	glucose-repressible protein
5783_at	4670.7	P	ATPase family gene
5784_at	7910	P	Vacuolar H-ATPase D subunit of the V1 catalytic sector
5785_at	3318.2	P	Mitochondrial ribosomal protein L2 of the large subunit
5786_f_at	1936.3	A	member of the seripauperin protein\/gene family (see Gene_class P
5787_at	263	A	hypothetical protein
5788_at	26582.5	P	strong similarity to Osm1p
5789_at	21556.9	P	Threonine Aldolase
5790_at	1655.1	P	weak similarity to cytochrome c oxidase III of T.brucei kinetoplast
5791_at	4295.7	P	hypothetical protein
5747_at	12597.2	P	weak similarity to Mad1p
5748_at	18452.1	P	Guanosine diphosphatase of Golgi membrane
5749_at	268.3	A	strong similarity to Utr1p
5750_at	29457.5	P	weak similarity to Bacillus 1,3-1,4-beta-glucanase
5751_at	1137	P	iso-2-cytochrome c
5752_at	6137.2	P	similarity to K.oxytoca enolase-phosphatase E-1
5753_at	10490	P	ubiquitin-like protein
5754_at	10602.7	P	Mannan 8\; Protein of the endoplasmic reticulum with a role in retent
5755_at	87.7	A	protein of unknown function
5756_at	14728.6	P	Translation initiation factor eIF-5A
5757_at	569.9	A	weak similarity to Sauroleishmania mitochondrial hypothetical ORF-5
5758_at	4389.5	P	Member of complex that acts at ARS s to initiate replication
5759_at	27902	P	P-type ATPase
5760_at	343.4	A	ExtraCellular Mutant
5761_at	2504.8	P	similarity to hypothetical protein YNR027w
5762_at	209.4	A	hypothetical protein
5763_at	11588.3	P	Vacuolar ATP synthase 17-kDa proteolipid C subunit of VO sector\;
5764_at	26665.5	P	strong similarity to high mobility group-like protein Nhp2p
5765_at	836.8	P	hypothetical protein
5766_at	20437.1	P	Rieske iron-sulfur protein of the mitochondrial cytochrome bc1 compl
5767_at	194.6	A	hypothetical protein
5768_at	562.8	M	ARF GTP\/GDP exchange factor
5724_at	997.1	A	orotidine-5 -phosphate decarboxylase
5725_at	1785.6	P	similarity to O.formigenes oxalyl-CoA decarboxylase
5726_at	44	A	Protein involved in DNA repair
5727_at	6974.8	P	weak similarity to Rad50p
5728_i_at	2164.9	M	Proteolipid associated with plasma membrane H(+)-ATPase (Pma1p
5729_f_at	13847.5	P	Proteolipid associated with plasma membrane H(+)-ATPase (Pma1p
5730_at	15247.9	P	hypothetical protein
5731_at	1638.7	P	similarity to human nucleotide pyrophosphatase
5732_at	3704.1	P	weak similarity to Spa2p
5733_at	1287.7	M	hypothetical protein
5734_at	6346.2	P	An armadillo repeat-containing protein localized on the vacuolar mem
5735_at	1007.2	P	1,4-glucan-6-(1,4-glucano)-transferase

5736_at	92.5	A	hypothetical protein
5737_at	26878.2	P	transcriptional activator of amino acid biosynthetic genes
5738_at	64.3	A	hypothetical protein
5739_at	20140.2	P	similarity to S.pombe pac2 protein
5740_at	2091.4	P	similarity to peroxisomal membrane and mitochondrial carrier protein
5741_at	1166.9	P	hypothetical protein
5742_at	1873.2	P	Shows sequence similarity to GOG5, a gene involved in vanadate re
5743_at	3709.2	P	Putative homolog of subunit 2 of bovine prefoldin, a chaperone com
5744_at	23326	P	oligosaccharyl transferase glycoprotein complex, beta subunit
5745_at	15271.4	P	hypothetical protein
5746_at	7456.9	P	Alpha-1,3-mannosyltransferase
5701_at	12277.9	P	weak similarity to chicken microfibril-associated protein
5702_at	18109.2	P	mannose-6-phosphate isomerase
5703_at	17799.9	P	similarity to hypothetical E.coli and C.elegans proteins
5704_at	2288.7	P	similarity to Gda1p
5705_at	12795.4	P	similarity to P.polycephalum myosin-related protein mlpA
5706_at	1188	P	Required for viability in the absence of the kinesin-related mitotic mo
5707_at	9677.2	P	putattive ORF identified by SAGE
5708_at	1952.3	P	SEC3 encodes the 144 kD and 91 kD components of the Exocyst co
5709_at	22725.8	P	May coordinate the Ran-dependent (GSP1\/GSP2) association and
5710_at	2983.2	P	similarity to L.pneumophila dlpA protein
5711_at	8499.3	P	Cold-shock induced protein of the Srp1p\/Tip1p family of serine-alani
5712_at	12365.6	P	22.6 kDa proteasome subunit
5713_at	1543.4	P	helicase-like protein
5714_at	1891.7	P	protoporphyrinogen oxidase
5715_at	185.4	A	Acyl-CoA synthetase (fatty acid activator 2)
5716_at	2032.7	P	BInding to Microtubules
5717_at	10732.2	P	ATP-dependent metalloprotease
5718_at	1967.6	A	component of spindle pole
5719_at	8804.6	P	putative neutral sphingomyelinase
5720_at	11642.6	P	homologous to Sbh1p
5721_at	6420.1	P	nucleotide binding regulatory protein
5722_at	5544.7	P	component of the regulatory module of the 26S proteasome, homol
5723_at	1568.8	P	subunit of RNA polymerase II holoenzyme\/mediator complex
5678_at	13316.2	P	delta 1-pyrroline-5-carboxylate reductase
5679_at	717.8	P	similarity to carnitine O-acetyltransferase Yat1p
5680_at	25308.5	P	gamma subunit of translational initiation factor eIF-2
5681_at	8264	P	phosphatidylserine synthase
5682_at	4951.3	P	glucose repression protein
5683_at	430.5	P	similarity to Mig1p
5684_at	2519.2	P	Associated with U1 snRNP as part of the Sm-core that is common to
5685_at	5316.2	P	similarity to mouse nucleolin
5686_at	6044.1	P	ras-like GTPase, highly homologous to YPT32
5687_at	2201.5	P	Putative participant in 3 mRNA processing
5688_at	2644.2	P	weak similarity to Nmd2p, Kex1p and hamster nucleolin
5689_at	1283.6	P	hypothetical protein
5690_at	2857.9	A	hypothetical protein
5691_at	31010.7	P	strong similarity to members of the ABC transporter family
5692_at	318.3	A	strong similarity to hypothetical protein YGL224c
5693_at	332.8	A	hypothetical protein
5694_at	1410.7	A	Homologous to VRG4
5695_at	1015.9	P	positive nitrogen regulatory protein

5696_at	1080.7	P	weak similarity to DNA repair protein Rad2p and Dsh1p
5697_at	1500.7	P	responsible for the reduction of methionine sulfoxide
5698_at	24248.3	P	putative S-adenosyl-L-homocysteine hydrolase
5699_at	8435.6	P	hypothetical protein
5700_at	234.6	A	Required for full sporulation. Dispensable for axial cores but requirec
5655_n_at	42.6	A	Required for full sporulation. Dispensable for axial cores but requirec
5656_at	1601.8	P	weak similarity to transcription factor Sko1p
5657_at	627.2	P	hypothetical protein
5658_at	1971.1	P	member of the AAA ATPase family of proteins
5659_at	13368	P	Homologous to E. coli DnaJ\; contains leucine zipper-like motif
5660_at	1508.7	P	putative ORF identified by SAGE
5661_at	11389.1	P	strong similarity to hypothetical S.pombe protein YER049W
5662_at	5660.2	P	hypothetical protein
5663_at	355.4	P	similarity to C.elegans hypothetical protein
5664_at	9587.5	P	Aspartate kinase (L-aspartate 4-P-transferase) (EC 2.7.2.4)
5665_at	4058.2	P	strong similarity to mitochondrial phosphate carrier protein
5666_at	278	P	Glc7-interacting protein\; shares homology with PIG2\; contains cons
5667_at	30807.8	P	ATP phosphoribosyltransferase
5668_at	20923.4	P	purine-cytosine permease
5669_g_at	23081.2	P	purine-cytosine permease
5670_i_at	29827.7	P	Ribosomal protein L34A
5671_s_at	24796.5	P	Ribosomal protein L34A
5672_at	12678.1	P	Inhibitor of cell Growth\; heat shock inducible
5673_at	2806	P	cytochrome c oxidase assembly factor
5674_at	706.4	P	PHO85 cyclin
5675_at	5537.8	P	purine-cytosine permease
5676_at	630.6	A	purine-cytosine permease
5677_at	623.1	A	Protein homologous to beta-keto-acyl synthase
5633_at	7605.9	P	DL-glycerol-3-phosphatase
5634_at	9264.7	P	Suppressor of the Transcriptional (T) defect of Hpr1 (H) by Overexpr
5635_at	14261.8	P	similarity to hypothetical protein YIL056w
5636_at	1269.4	P	isocitrate lyase
5637_at	1528.4	P	strong similarity to cell division control protein Cdc4p
5638_g_at	4303	P	strong similarity to cell division control protein Cdc4p
5639_at	510.5	A	hypothetical protein
5640_at	831	P	strong similarity to hypothetical protein YIL057c
5641_at	1818.3	P	putative zinc finger protein
5642_at	16156.3	P	N-acetyl-gamma-glutamyl-phosphate reductase and acetylglutamate
5643_at	23083.4	P	ribonucleotide reductase
5644_at	499.9	A	hypothetical protein
5645_at	30473.9	P	Homolog of S. pombe Nrf1 (97\% identical in predicted amino acid s
5646_at	14921.7	P	aldehyde dehydrogenase (NAD+)
5647_s_at	24405	P	40S ribosomal protein S24A
5648_at	1275.6	P	Protein tyrosine phosphatase
5649_at	1140	M	similarity to killer toxin Khr1p
5650_at	597.2	P	hypothetical protein
5651_at	1369.3	P	similarity to E.coli X-Pro aminopeptidase II
5652_at	1504	P	hypothetical protein
5653_at	5518.1	P	hypothetical protein
5654_at	2045.1	P	strong similarity to phosphoglycerate dehydrogenases
5610_at	3670.8	P	similarity to M.sexta steroid regulated MNG10 protein
5611_at	16271	P	hypothetical protein

5612_at	2761.9	P	questionable ORF
5613_at	186.3	A	weak similarity to myosins
5614_at	24344.3	P	threonine deaminase
5615_at	1904.5	P	similarity to E.coli prolyl-tRNA synthetase
5616_at	9842.8	P	homologous to Sbh2p
5617_at	6955.8	P	Derepression Of Telomeric silencing
5618_at	7115.8	P	Protein phosphatase type 2C
5619_at	19451.2	P	anthranilate synthase Component I
5620_at	27379.6	P	vitamin B12-(cobalamin)-independent isozyme of methionine synthas
5621_at	1912.1	P	hypothetical protein
5622_at	2155.3	P	weak similarity to S.epidermidis PepB protein
5623_at	1033.3	P	similarity to hypothetical protein YBL059w
5624_at	2024.3	P	similarity to hypothetical protein YBL059w
5625_at	8297.6	P	20S proteasome subunit (beta3)
5626_at	13933	P	RecA homolog\; Rad51p colocalizes to ~65 spots with Dmc1p prior t
5627_at	768	P	sporulation-specific homolog of csd4
5628_at	47.1	A	weak similarity to ribosomal S3 proteins
5629_at	629.3	A	ubiquitin carboxyl-terminal hydrolase
5630_at	5259.4	P	ribose-phosphate pyrophosphokinase 2
5631_at	2402.5	P	ubiquitin-conjugating enzyme
5632_at	2418.5	P	Protein involved in targeting of plasma membrane [H+]ATPase
5588_at	2033.4	P	member of 70 kDa heat shock protein family
5589_at	492.6	A	hypothetical protein
5590_at	9956.6	P	Nucleoporin similar to Nup157p and to mammalian Nup155p
5591_at	411	A	hypothetical protein
5592_at	6934.8	P	homologous to S. pombe RAE1 gene\; 2-hybrid analysis demonstrate
5593_at	1846.2	P	putative transcriptional activator of FLO1
5594_at	93.3	A	putative transcriptional activator of FLO1
5595_at	14129.9	P	Karyopherin beta 4
5596_at	487.5	P	transcription factor
5597_at	3749.7	P	U6 snRNA associated protein
5598_at	6636.7	P	similarity to Emp70p
5599_at	4199.7	P	Protein which binds Bem1p and contains a proline-rich sequence, ar
5600_at	3317.3	P	sporulation-specific protein
5601_at	719.7	A	zinc-finger protein
5602_at	2650.1	P	Transmembrane osmosensor
5603_at	2586.3	P	weak similarity to E.herbicola tyrosine permease
5604_at	11.8	A	questionable ORF
5605_at	22388.8	P	Likely to be involved in regulating INO1 expression, suppressor of a
5606_at	896.9	A	hypothetical protein
5607_at	10093.5	P	Zinc-finger-containing protein with similarity to Gcs1p and Sps18p
5608_at	785	P	plasma membrane-bound casein kinase I homolog
5609_at	3389	P	weak similarity to Dictyostelium WD40 repeat protein 2
5565_at	10239.2	P	Rsp5p encodes a hect (homologous to E6-AP C terminus) and enco
5566_at	8355.7	P	weak similarity to E.coli colicin N
5567_at	4192.4	P	Lethal with conditional pap1 allele
5568_at	1659.1	P	hypothetical protein
5569_at	720.9	A	DNA polymerase alpha suppressing protein kinase
5570_at	1863.4	P	similarity to Msn2p and weak similarity to Msn4p
5571_at	10334.4	P	Ribosomal protein S26B
5572_at	2699.1	P	Paralog of MDS3
5573_at	2089.3	P	protein phosphatase type I

5574_at	17204.6	P	protein phosphatase type I
5575_at	1409.4	P	weak similarity to S.pombe SPBC13G1 and C.elegans F26F2.d hypo
5576_at	232.4	A	hypothetical protein
5577_at	17842.3	P	GDP dissociation inhibitor
5578_at	926.3	P	weak similarity to Mycoplasma hominis P120 protein
5579_at	177.6	P	similarity to hypothetical protein YDR066c
5580_at	1372.7	P	hypothetical protein
5581_at	27295.3	P	cytochrome oxidase assembly factor
5582_at	1722.6	P	3-methyladenine DNA glycosylase
5583_at	2301.5	P	DNA Damage Inducible
5584_at	3717	P	Putative Ubiquitin-specific protease
5585_at	15397.1	P	Iron permease
5586_at	3412.3	P	Sm-like protein
5587_at	2118.1	P	weak similarity to mouse NAD(P)H dehydrogenase (quinone)
5542_at	11687.7	P	TATA-binding protein (tfIId)
5543_at	1455.2	P	Protein with coiled-coil domain
5544_at	2135.3	A	strong similarity to putative cell surface glycoprotein Sed1p
5545_at	1722.3	P	Ubiquitin-specific protease
5546_at	7156.3	P	weak similarity to E.coli hypothetical protein f470
5547_at	152.4	A	translational activator of cytochrome c oxidase subunit III
5548_at	19811.2	P	Required for correct assembly of the cytochrome c oxidase and the
5549_at	4360.8	P	Rho-type GTPase activating protein (GAP)
5550_at	11403.1	P	similarity to hypothetical C. elegans protein C27H6.5
5551_at	757.4	P	hypothetical protein
5552_at	3761.1	P	weak similarity to Afr1p
5553_at	4365	P	Transcriptional regulator which functions in modulating the activity of
5554_at	2569.6	P	non-specific DNA binding protein (sin1)
5555_at	1235.6	P	Nucleotide excision repair protein
5556_at	2904.9	P	weak similarity to E.coli cation transport protein
5557_at	1660.7	P	transcriptional regulator
5558_at	25288.9	P	Poly(A) binding protein, cytoplasmic and nuclear
5559_at	3900.1	P	similarity to ATPase P.falciparum ATPase 2
5560_at	1258.5	P	Serine\/threonine protein kinase
5561_at	1768.6	P	tRNA nucleotidyltransferase (tRNA CCA-pyrophosphorylase)
5562_at	2887.6	P	Repressor of PHR1 transcription\; binds to PHR1 URS
5563_at	884.1	P	Adenylate kinase (mitochondrial GTP:AMP phosphotransferase)
5564_at	2014.4	P	DNA repair helicase component of transcription factor b
5520_at	1058.3	P	putative ATP-dependent RNA helicase
5521_at	1235.9	P	checkpoint protein
5522_at	2519	P	similarity to Legionella glutaredoxin-like protein
5523_at	475.4	P	similarity to hypothetical protein YHR209w
5524_at	5032.4	P	DNA Helicase I
5525_at	21695.5	P	Ribosomal protein L23B (L17aB) (YL32)
5526_at	16911.9	P	alpha subunit of pyruvate dehydrogenase (E1 alpha)
5527_at	1126	A	meiosis-specific protein related to RecA and Rad51p. Dmc1p coloca
5528_at	303.3	A	meiosis-specific protein related to RecA and Rad51p. Dmc1p coloca
5529_at	1158.6	P	Meiosis-specific protein required for spore formation
5530_at	155.4	A	questionable ORF
5531_at	1271	P	hypothetical protein
5532_at	1587.6	P	similarity to human 5,10-methenyltetrahydrofolate synthetase
5533_at	520.5	A	similarity to multidrug resistance proteins Pdr3p and Pdr1p
5534_at	543.1	P	strong similarity to Rtm1p

5535_at	5651.4	P	weak similarity to hypothetical protein YMR316w
5536_at	656	M	similarity to killer toxin KHS precursor
5537_at	268.4	A	hypothetical protein
5538_at	2461.7	P	Translocase in inner membrane of mitochondria involved in mitochor
5539_at	382.8	A	hypothetical protein
5540_at	46.4	A	hypothetical protein identified by SAGE
5541_at	434.4	P	questionable ORF
5497_at	751.4	A	questionable ORF
5498_at	165.9	A	questionable ORF
5499_at	551.3	A	questionable ORF
5500_at	459.3	A	questionable ORF
5501_at	173	A	questionable ORF
5502_at	1488.3	A	questionable ORF
5503_at	514.6	A	questionable ORF
5504_at	807.5	A	questionable ORF
5505_at	65	A	hypothetical protein
5506_s_at	1757.8	P	ubiquitin-conjugating enzyme\; ubiquitin-protein ligase
5507_at	3047.7	P	non-annotated SAGE orf Found forward in NC_001137 between 671
5508_at	38.2	A	non-annotated SAGE orf Found reverse in NC_001137 between 159
5509_at	466.6	P	non-annotated SAGE orf Found reverse in NC_001137 between 187
5510_at	225.7	A	non-annotated SAGE orf Found reverse in NC_001137 between 251
5511_at	567.9	P	non-annotated SAGE orf Found reverse in NC_001137 between 288
5512_at	1040.2	A	non-annotated SAGE orf Found reverse in NC_001137 between 550
5513_at	93.6	A	non-annotated SAGE orf Found reverse in NC_001137 between 900
5514_at	26156.1	P	non-annotated SAGE orf Found reverse in NC_001137 between 314
5515_at	1963.7	P	non-annotated SAGE orf Found reverse in NC_001137 between 642
5516_at	28485.3	P	non-annotated SAGE orf Found reverse in NC_001137 between 673
5517_at	35635.5	P	non-annotated SAGE orf Found reverse in NC_001137 between 122
5518_at	649.8	P	non-annotated SAGE orf Found forward in NC_001137 between 251
5519_at	358.9	P	non-annotated SAGE orf Found reverse in NC_001137 between 258
5473_at	2438.9	P	non-annotated SAGE orf Found reverse in NC_001137 between 308
5474_at	175	A	non-annotated SAGE orf Found reverse in NC_001137 between 314
5475_at	5080.3	P	non-annotated SAGE orf Found forward in NC_001137 between 401
5476_at	18123.4	P	non-annotated SAGE orf Found reverse in NC_001137 between 407
5477_at	14777.1	P	non-annotated SAGE orf Found reverse in NC_001137 between 499
5478_i_at	4818.1	P	non-annotated SAGE orf Found reverse in NC_001137 between 561
5479_r_at	2568.1	P	non-annotated SAGE orf Found reverse in NC_001137 between 561
5480_f_at	416.7	A	non-annotated SAGE orf Found reverse in NC_001137 between 561
5481_at	1619.2	A	non-annotated SAGE orf Found reverse in NC_001137 between 848
5482_at	877.7	P	non-annotated SAGE orf Found reverse in NC_001137 between 118
5483_at	8921.2	P	non-annotated SAGE orf Found forward in NC_001137 between 251
5484_at	351.4	A	non-annotated SAGE orf Found forward in NC_001137 between 303
5485_at	668.3	A	non-annotated SAGE orf Found reverse in NC_001137 between 545
5486_at	282	P	non-annotated SAGE orf Found reverse in NC_001137 between 156
5487_at	498.6	A	non-annotated SAGE orf Found reverse in NC_001137 between 460
5488_at	188.6	A	non-annotated SAGE orf Found reverse in NC_001137 between 117
5489_at	236.7	A	non-annotated SAGE orf Found reverse in NC_001137 between 117
5490_at	21	A	non-annotated SAGE orf Found reverse in NC_001137 between 135
5491_at	16.7	A	non-annotated SAGE orf Found reverse in NC_001137 between 137
5492_at	51.2	A	non-annotated SAGE orf Found reverse in NC_001137 between 144
5493_at	99.7	A	non-annotated SAGE orf Found forward in NC_001137 between 167
5494_at	326.9	A	non-annotated SAGE orf Found reverse in NC_001137 between 177

5495_at	338.5	A	non-annotated SAGE orf Found forward in NC_001137 between 194
5496_g_at	1196	A	non-annotated SAGE orf Found forward in NC_001137 between 194
5449_at	102.1	A	non-annotated SAGE orf Found reverse in NC_001137 between 225
5450_g_at	145.6	A	non-annotated SAGE orf Found reverse in NC_001137 between 225
5451_at	3.5	A	non-annotated SAGE orf Found forward in NC_001137 between 249
5452_at	16.2	A	non-annotated SAGE orf Found forward in NC_001137 between 284
5453_at	356.2	A	non-annotated SAGE orf Found forward in NC_001137 between 284
5454_at	1107.9	P	non-annotated SAGE orf Found forward in NC_001137 between 289
5455_at	855.3	P	non-annotated SAGE orf Found reverse in NC_001137 between 311
5456_at	102.6	A	non-annotated SAGE orf Found reverse in NC_001137 between 312
5457_at	1263.3	P	non-annotated SAGE orf Found forward in NC_001137 between 382
5458_at	9	A	non-annotated SAGE orf Found forward in NC_001137 between 434
5459_at	4.5	A	non-annotated SAGE orf Found forward in NC_001137 between 434
5460_at	263.1	A	non-annotated SAGE orf Found reverse in NC_001137 between 467
5461_at	448.9	A	non-annotated SAGE orf Found reverse in NC_001137 between 504
5462_at	552.3	A	non-annotated SAGE orf Found forward in NC_001137 between 564
5463_r_at	6120.7	P	non-annotated SAGE orf Found reverse in NC_001137 between 523
5464_i_at	24798.5	A	non-annotated SAGE orf Found reverse in NC_001137 between 523
5465_f_at	850.4	P	non-annotated SAGE orf Found reverse in NC_001137 between 523
5466_i_at	181.5	A	non-annotated SAGE orf Found reverse in NC_001137 between 523
5467_f_at	4781.6	P	non-annotated SAGE orf Found reverse in NC_001137 between 523
5468_at	245.8	A	non-annotated SAGE orf Found forward in NC_001137 between 774
5469_at	426.3	A	non-annotated SAGE orf Found forward in NC_001137 between 849
5470_at	3225.5	P	non-annotated SAGE orf Found forward in NC_001137 between 898
5471_at	2486.8	P	non-annotated SAGE orf Found forward in NC_001137 between 122
5472_at	279.4	A	non-annotated SAGE orf Found reverse in NC_001137 between 212
5436_i_at	13.2	A	non-annotated SAGE orf Found reverse in NC_001137 between 212
5437_s_at	25.2	A	non-annotated SAGE orf Found reverse in NC_001137 between 212
5438_at	463.8	A	non-annotated SAGE orf Found reverse in NC_001137 between 250
5439_at	204.3	A	non-annotated SAGE orf Found forward in NC_001137 between 272
5440_at	884.1	P	non-annotated SAGE orf Found forward in NC_001137 between 367
5441_at	5206	P	non-annotated SAGE orf Found forward in NC_001137 between 412
5442_at	1031.8	A	non-annotated SAGE orf Found forward in NC_001137 between 422
5443_g_at	253.7	A	non-annotated SAGE orf Found forward in NC_001137 between 422
5444_at	1453.4	A	non-annotated SAGE orf Found forward in NC_001137 between 422
5445_i_at	7382	P	non-annotated SAGE orf Found reverse in NC_001137 between 441
5446_r_at	314.7	P	non-annotated SAGE orf Found reverse in NC_001137 between 441
5447_at	7466.8	P	non-annotated SAGE orf Found forward in NC_001137 between 546
5448_at	8283.5	P	snRNA
5412_at	260	A	snRNA
5413_at	1899.8	P	RNase P RNA
5414_i_at	1.2	A	Centromere
5415_r_at	0.4	A	Centromere
5416_at	868	A	snRNA R14
5417_at	18870	P	snRNA U4
5418_at	540	P	snRNA
5419_at	432.8	P	small cytoplasmic RNA
5420_s_at	2342.7	P	weak similarity to hypothetical E.coli protein
5421_i_at	13	A	similarity to mouse period clock protein
5422_s_at	1350.1	A	similarity to mouse period clock protein
5423_s_at	2182.7	P	strong similarity to aryl-alcohol dehydrogenases
5424_at	140.4	A	Hypothetical aryl-alcohol dehydrogenase (AAD)

5425_at	492.7	M	Amino acid permease
5426_at	976.9	P	similarity to channel proteins
5427_at	647.9	A	dihydroxyacetone kinase
5428_at	119.6	A	strong similarity to Mal63p, YPR196w and Mal13p
5429_at	229.6	A	putative pseudogene
5430_at	1032.6	A	ALuminium Resistance 2
5431_at	1201.2	P	weak similarity to Npl6p
5432_at	6810	P	47 kDa type I transmembrane protein localized to the Golgi
5433_at	4088.3	P	similarity to S.pombe hypothetical protein SPAC2F7.18c
5434_at	6866.4	P	weak similarity to middle part of C.elegans myosin heavy chain A
5435_at	26318.3	P	phosphomannomutase
5389_at	2769.6	P	weak similarity to human dystrophin
5390_at	7665.5	P	multicopper oxidase, type 1 integral membrane protein
5391_at	128.8	A	similarity to yeast glucose transport proteins
5392_at	2454.6	P	Actin
5393_at	20395.6	P	Ras-like GTP-binding protein\; most similar to mammalian Rab1A pr
5394_at	32282.9	P	beta-tubulin
5395_at	7125.1	P	mitochondrial RNA polymerase II
5396_at	13550.7	P	Ribosomal protein L22B (L1c) (rp4) (YL31)
5397_at	679.7	P	similarity to hypothetical S. pombe protein and to C.elegans F35D11
5398_at	1024.4	P	Trehalose-associated protein kinase related to S. pombe cek1+
5399_at	9.6	A	questionable ORF
5400_at	781.8	A	similarity to several transaminases
5401_at	1262.8	P	Cyclin-dependent kinase-activating kinase
5402_at	2213	P	ABC ATPase
5403_at	1230.3	P	weak similarity to P.falciparum Pfmdr2 protein
5404_at	243.7	P	alpha-factor pheromone receptor\; seven-transmembrane domain pr
5405_at	3060.2	P	Negatively regulates COPII vesicle formation
5406_at	787.7	P	Probable chromatin protein because of homology to Drosophila Ena
5407_at	1493.6	P	similarity to repeat structures in a Plasmodium falciparum protein (M
5408_at	11887	P	Phenylalanyl-tRNA synthetase, beta subunit, cytoplasmic
5409_at	1985.3	M	transcriptional activator with GATA-1-type Zn finger DNA-binding mo
5410_f_at	1461.1	P	member of the seripauperin protein\/gene family (see Gene_class P
5411_at	150.2	A	hypothetical protein
5367_at	22349.3	P	dihydrolipoamide dehydrogenase precursor (mature protein is the E3
5368_at	1752.5	P	snRNP G protein (the homologue of the human Sm-G)
5369_at	8280.6	P	similarity to hypothetical S. pombe protein and to hypothetical C.eleg
5370_at	6943.8	P	DnaJ homolog involved in mitochondrial biogenesis and protein foldi
5371_at	1016.4	A	weak similarity to YDR504c
5372_at	1366.4	P	12 kDa heat shock protein
5373_at	3397.9	P	weak similarity to Dictyostelium protein kinase
5374_at	46.5	A	questionable ORF
5375_at	31.3	A	hypothetical protein
5376_at	429.5	A	High-affinity hexose transporter
5377_at	777.2	P	Involved in ammonia regulation of GAP1 activity
5378_at	8908.1	P	questionable ORF
5379_at	2264	P	beta subunit of large (heterotrimeric) G-proteins (beta-transducin)
5380_at	2915.8	P	omosome segregation protein
5381_at	6326.8	P	weak similarity to Mms19p
5382_at	4028.2	P	hypothetical protein
5383_at	4674.3	P	Ras-like small GTP-binding protein
5384_at	19522.7	P	strong similarity to hypothetical protein YPL019c

5385_at	445.5	M	meiosis specific protein, E.coli MutS protein, localizes to discrete sit
5386_at	5679.9	P	ATP-dependent RNA helicase
5387_at	1873.9	P	Depressed growth-rate protein
5388_at	20449.2	P	weak similarity to rabbit triadin Spp41p
5344_at	4118.7	P	96 kDa nucleoporin-interacting component
5345_at	2500.3	P	hypothetical protein
5346_at	11849.5	P	Similar to S. pombe PAD1 gene product
5347_at	1155.8	P	similarity to hypothetical A. thaliana proteins
5348_at	16159.1	P	similarity to X-Pro dipeptidases
5349_at	1074.9	M	weak similarity to YER176w
5350_at	488.2	P	weak similarity to human centromere protein E
5351_at	18684.3	P	Member of ATP-binding cassette (ABC) family of proteins
5352_at	25237	P	encodes putative deubiquitinating enzyme
5353_at	2116.2	P	ochre suppressor tyr-tRNA
5354_at	707.9	M	similarity to hypothetical protein YOL019w
5355_at	1863.8	P	similarity to YOL017w
5356_at	386.2	P	Calmodulin-dependent protein kinase
5357_at	847.9	P	Glycogen synthase (UDP-gluocse--starch glucosyltransferase)
5358_at	3059.3	P	similarity to mammalian neurofilament proteins and to Dictyostelium
5359_at	618.7	P	hypothetical protein
5360_at	7575.1	P	similarity to human glutaminyl-peptide cyclotransferase
5361_at	2642.5	P	type II PI(4)P5-kinase (PIP4,5 kinase) similar to human PIP5K-II
5362_at	3198.7	P	hypothetical protein
5363_at	2612.5	P	similarity to hypothetical protein YPL100w
5364_at	263.5	A	similarity to Rod1p
5365_at	17.6	A	poly(A) binding protein\; related to PES4 protein homolog YHR015w
5366_s_at	3279.4	P	similarity to Acanthamoeba myosin heavy chain IC and weak similari
5322_at	1134.6	P	Histidinolphosphatase
5323_at	480	A	hypothetical protein
5324_at	783.7	P	hypothetical protein
5325_at	2130	P	soluble tyrosine-specific protein phosphatase
5326_at	741.1	P	Regulator of expression of the PTR2, GAP1, and BAP2 genes\; invo
5327_at	810.6	P	subunit of assimilatory sulfite reductase
5328_at	6311.2	P	nuclear protein related to ScII (chicken), XCAPE (xenopus), and cut
5329_s_at	6500.8	P	Ribosomal protein L2A (L5A) (rp8) (YL6)
5330_at	883.8	M	weak similarity to S.pombe polyadenylate-binding protein, YPR112c
5331_at	12711.1	P	Ribosomal protein L29 (YL43)
5332_at	13841.8	P	ubiquinol-cytochrome c oxidoreductase subunit 6 (17 kDa)
5333_at	2492.7	P	myc-type helix-loop-helix transcription factor
5334_at	603.7	A	hypothetical protein
5335_at	1390.4	P	cell division control protein
5336_at	4343	P	Rsc8 is the eighth largest subunit of RSC, a fifteen-protein chromati
5337_at	984	P	strong similarity to mouse lymphocyte specific helicase
5338_at	2506.6	P	similarity to hypothetical protein YGL228w
5339_at	4285.8	P	155 kDa SIT4 protein phosphatase-associated protein
5340_at	870.3	P	weak similarity to dnaJ-like heat shock proteins
5341_at	1308.2	P	hypothetical protein
5342_at	745.5	P	hypothetical protein
5343_at	30817.2	P	similarity to hypothetical protein YBR281c
5299_at	420.8	P	similarity to mitochondrial citrate transport proteins
5300_at	833	A	hypothetical protein
5301_at	9700.4	P	strong similarity to human quinolinate phosphoribosyltransferase

5302_at	860.5	P	similarity to hypothetical S.pombe protein SPAC12G12.14 and to YD
5303_at	2548.4	P	mitochondrial ribosomal protein (precursor)
5304_at	18649.9	P	proteasome subunit necessary for peptidyl glutamyl peptide hydrolyzi
5305_at	17928.2	P	Coatomer (COPI) complex delta subunit
5306_at	9552.7	P	cytoplasmic 32 - 34 kDa protein
5307_at	11361.6	P	Hexokinase I (PI) (also called Hexokinase A)
5308_at	590.1	A	hypothetical protein
5309_at	189.3	A	questionable ORF
5310_at	10760.5	P	strong similarity to beta-cystathionases
5311_at	29.7	A	weak similarity to Cha4p
5312_s_at	2249.3	P	hypothetical protein
5313_s_at	2489.9	P	Mob1p-like protein
5314_at	610.2	A	hypothetical protein
5315_at	293.3	A	questionable ORF
5316_at	1005.3	P	questionable ORF
5317_s_at	866.2	P	similarity to hypothetical protein YLR072w
5318_s_at	10176.2	P	bZIP (basic-leucine zipper) protein
5319_at	5381.9	P	non-annotated SAGE orf Found reverse in NC_001138 between 763
5320_at	150.9	A	non-annotated SAGE orf Found forward in NC_001138 between 101
5321_at	507.6	P	non-annotated SAGE orf Found forward in NC_001138 between 234
5274_at	8876.9	P	non-annotated SAGE orf Found reverse in NC_001138 between 444
5275_i_at	120.1	A	non-annotated SAGE orf Found reverse in NC_001138 between 101
5276_r_at	16.5	A	non-annotated SAGE orf Found reverse in NC_001138 between 101
5277_at	12384.5	P	non-annotated SAGE orf Found reverse in NC_001138 between 224
5278_at	1389	P	non-annotated SAGE orf Found forward in NC_001138 between 226
5279_at	311.9	A	non-annotated SAGE orf Found reverse in NC_001138 between 184
5280_i_at	11.1	A	non-annotated SAGE orf Found reverse in NC_001138 between 580
5281_f_at	84.2	A	non-annotated SAGE orf Found reverse in NC_001138 between 580
5282_at	1347.7	A	non-annotated SAGE orf Found reverse in NC_001138 between 480
5283_at	196.6	A	non-annotated SAGE orf Found forward in NC_001138 between 485
5284_at	1017.4	P	non-annotated SAGE orf Found forward in NC_001138 between 487
5285_at	2559.5	P	non-annotated SAGE orf Found reverse in NC_001138 between 111
5286_at	304	P	non-annotated SAGE orf Found forward in NC_001138 between 119
5287_at	642.2	A	non-annotated SAGE orf Found forward in NC_001138 between 184
5288_at	77.1	A	non-annotated SAGE orf Found forward in NC_001138 between 265
5289_at	631.3	A	non-annotated SAGE orf Found forward in NC_001138 between 279
5290_at	156.5	A	non-annotated SAGE orf Found forward in NC_001138 between 975
5291_at	654.2	P	non-annotated SAGE orf Found forward in NC_001138 between 161
5292_at	1293.9	P	non-annotated SAGE orf Found reverse in NC_001138 between 181
5293_g_at	420.5	A	non-annotated SAGE orf Found reverse in NC_001138 between 181
5294_at	401.4	A	ARS605 Found forward in NC_001138 between 135973 and 136029
5295_f_at	117.6	A	ARS607 Found forward in NC_001138 between 199390 and 199446
5296_i_at	354.2	A	ARS608 Found forward in NC_001138 between 216458 and 216508
5297_at	23.1	A	Protein with strong similarity to subtelomerically-encoded proteins in
5298_at	26.6	A	similarity to hypothetical protein YER187w
5251_f_at	3136	P	strong similarity to members of the Srp1/Tip1 family
5252_at	399	A	GPI-anchored aspartic protease
5253_g_at	426.3	A	GPI-anchored aspartic protease
5254_i_at	128.9	A	strong similarity to hypothetical protein YOR387c
5255_s_at	973.4	A	strong similarity to hypothetical protein YOR387c
5256_at	3695.7	P	similarity to Mnn1p
5257_at	9553	P	alcohol dehydrogenase isoenzyme IV

5258_at	6723.1	P	high-affinity zinc transport protein
5259_at	1856.4	P	putative transcription factor, has five zinc fingers
5260_at	22395.8	P	Hexokinase II (PII) (also called Hexokinase B)
5261_at	4770	P	Protein involved in interorganelle communication between mitochon
5262_at	319.9	P	C4 zinc finger DNA-binding protein of low sequence specificity in vitr
5263_at	227.2	A	hypothetical protein
5264_at	98.3	A	Required for ZIPpering up meiotic chromosomes during chromoson
5265_at	2569.5	P	3 ,5 -Cyclic-nucleotide phosphodiesterase, low affinity
5266_at	2194.1	P	similarity to hypothetical protein YHR036w
5267_at	1053.1	P	weak similarity to C.elegans dom-3 protein
5268_at	32519.3	P	strong similarity to glutamine--tRNA ligase
5269_at	1959	P	Nuclear protein
5270_at	826.3	P	tRNA-specific adenosine deaminase 1 (TAD1)\; Tad1p\/scADAT1
5271_at	17466.1	P	weak similarity to Drosophila ANK protein
5272_at	2107.1	P	similarity to Cse1p
5273_at	579.9	A	Doc1p and Cdc26p are associated with the anaphase-promoting con
5229_at	242.1	P	questionable ORF
5230_at	5702.4	P	Protein required for accurate mitotic chromosome segregation
5231_at	1283.5	P	transcriptional activator protein of CYC1
5232_at	1920.2	P	strong similarity to gidA E.coli protein
5233_at	52.6	A	questionable ORF
5234_at	28608.4	P	glycinamide ribotide synthetase and aminoimidazole ribotide synthet
5235_at	1685.8	P	113kD component of the Exocyst complex, which contains the gene
5236_n_at	985.7	P	weak similarity to P.falciparum dihydropteroate synthase
5237_at	1783.2	P	weak similarity to P.falciparum dihydropteroate synthase
5238_at	5054.6	P	hypothetical protein
5239_at	36.5	A	hypothetical protein
5240_at	1171.2	P	SAP4 is related to SAP155, SAP185, and SAP190, all of which asso
5241_at	9293.3	P	mRNA (identified by a library screen) that causes growth arrest when
5242_at	811.1	P	TOR inhibitor
5243_at	14958.4	P	9.5-kDa zeta subunit of oligosaccharyltransferase complex
5244_at	2512.5	P	similarity to N.crassa cytochrome-c oxidase chain V
5245_at	30371.4	P	May regulate Golgi function and glycosylation in Golgi
5246_at	3147.2	P	strong similarity to hypothetical protein YER037w
5247_at	1759.6	P	weak similarity to Clostridium regulatory protein
5248_at	113.8	A	hypothetical protein
5249_at	1061	P	Ngg1p-interacting factor 3
5250_at	16168.7	P	weak similarity to V.alginolyticus bolA protein
5206_at	1450.7	P	hypothetical protein
5207_at	65.6	A	questionable ORF
5208_at	359.7	A	questionable ORF
5209_at	726.5	P	Kinesin-related protein
5210_at	3199.6	P	Cyclin-like protein that interacts with Pho85p in affinity chromatograp
5211_at	59.8	A	questionable ORF
5212_at	5509.9	P	antiviral protein, mRNA is induced early in meiosis
5213_at	627.3	A	hydrophilic protein, heptad repeat motif
5214_at	2334.8	P	similarity to M.jannaschii hypothetical proteins MJ1157 and MJ1478
5215_at	1777.3	P	ras-like GTPase, highly homologous to YPT31
5216_at	6626	P	Protein containing zinc fingers very similar to zinc fingers in Mig1p
5217_at	965.1	P	Member of a family of proteins, including Sip1p and Gal83p, that inte
5218_at	8482.8	P	transcription factor
5219_at	12606.6	P	presumed vesicle coat protein

5220_at	195.7	A	fatty-acyl coenzyme A oxidase
5221_at	721.9	P	questionable ORF
5222_at	1615.9	P	carboxypeptidase B-like processing protease
5223_at	25831.8	P	aromatic amino acid aminotransferase
5224_at	2064.5	P	Member of the MCM\/P1 family of proteins involved in DNA replicatio
5225_at	26160.4	P	type I transmemebrane protein, component of COPII-coated, ER-de
5226_at	910.5	A	questionable ORF
5227_at	8259.3	P	weak similarity to Yip1p
5228_at	1420.4	P	Mck1 Dosage Suppressor 3\; negative regulator of early meiotic gene
5183_at	5160.7	P	hypothetical protein
5184_at	9583.7	P	translational activator of GCN4 through activation of GCN2 in respon
5185_at	492.2	P	Protein with similarity to Hda1p, Rpd3p, Hos1p, and Hos3p
5186_at	5070.3	P	questionable ORF
5187_at	187.5	A	IME4 appears to activate IME1 in response to cell-type and nutritiona
5188_at	8625.6	P	subunit VIa of cytochrome c oxidase, may specifically interact with A
5189_at	1028.8	P	Protein phosphatase 2A regulatory subunit B
5190_i_at	924.1	A	Ribosomal protein S26A
5191_f_at	30821.2	P	Ribosomal protein S26A
5192_at	337.1	M	hypothetical protein
5193_at	4662.1	P	subunit IV of cytochrome c oxidase
5194_at	12106.4	P	similarity to hypothetical protein Fcy21p and weak similarity to FCY2
5195_at	4132.6	P	weak similarity to dehydrogenases
5196_at	1277.7	P	strong similarity to Emericella nidulans cystathionine beta-lyase
5197_at	7.1	A	hypothetical protein
5198_at	148.7	A	questionable ORF
5199_at	1430.4	P	Glycine-threonine-serine repeat protein
5200_at	1512.3	P	Protein kinase
5201_at	956.4	P	ser/thr protein kinase
5202_at	1137.6	A	questionable ORF
5203_at	22260.1	P	multicopy suppressor of POP2
5204_at	2395	P	weak similarity to Oryctolagus calcium channel BIII
5205_at	29.8	A	involved in meiotic recombination and chromosome metabolism
5161_at	1335.8	P	weak similarity to C.elegans hypothetical protein R08D7.1
5162_at	10801.9	P	DNA strand-transfer protein exoribonuclease I\; catalyzes the formati
5163_at	8345	P	nuclear pore complex protein with GLFG repetitive sequence motif
5164_at	6518.4	P	Contains domains found in the DEAD protein family of ATP-depende
5165_at	134.2	A	hypothetical protein
5166_at	880.8	P	Protein involved in translation initiation
5167_at	666.1	P	questionable ORF
5168_at	13926	P	Ca++-Pump, ATPase
5169_at	1714.2	P	Activator of transcription
5170_at	1051.8	A	questionable ORF
5171_at	5209.1	P	similarity to S.pombe hypothetical protein SPAC31A2.10
5172_at	1619.2	P	Required for X-ray damage repair, mitotic recombination, and full me
5173_at	1592.1	P	Involved in sterol uptake
5174_at	9531.5	P	hypothetical protein
5175_at	487.3	P	similarity to hypothetical protein YLR047c and Fre2p
5176_at	2424.8	P	hypothetical protein
5177_at	37.4	A	Serine\/threonine protein kinase
5178_at	2468.6	P	similarity to V.vinifera dihydroflavonol 4-reductase
5179_at	1081.3	A	vacuolar alpha mannosidase
5180_at	571.7	P	polypeptide subunit of a yeast type 1 protein geranylgeranyltransfera

5181_at	2621.9	P	aminoadipate-semialdehyde dehydrogenase small subunit (alpha-am
5182_at	475.7	A	questionable ORF
5137_at	5650.9	P	Peroxisomal peripheral membrane protein (peroxin) involved in impo
5138_at	953.2	P	negative regulator of URS2 of the HO promoter
5139_at	4183.7	P	Shows similarity to the Snf2p family of DNA-dependent ATPases
5140_at	904.6	P	questionable ORF
5141_at	18047.8	P	Chorismate synthase
5142_i_at	9913.1	P	Ribosomal protein L9A (L8A) (rp24) (YL11)
5143_at	312	A	hypothetical protein
5144_at	1412.5	P	transport protein that interacts with Sec20p\; required for protein tran
5145_at	986.8	P	strong similarity to hypothetical protein YDL109c
5146_at	690.3	M	Mitochondrial polypeptide chain release factor
5147_at	3009	P	Most likely an alpha 1,2 mannosyltransferase utilized for the additio
5148_at	3100.9	P	similarity to human human E6-associated protein
5149_at	2357.7	P	weak similarity to Lactobacillus putative histidine protein kinase Sppk
5150_at	5101.9	P	strong similarity to hypothetical protein YPL221w
5151_at	23	A	hypothetical protein
5152_at	12217.1	P	encodes beta -subunit of yeast coatomer
5153_at	859.7	P	weak similarity to E.coli ftsJ protein
5154_at	786.2	P	PHO85 cyclin
5155_at	756.8	P	similarity to hypothetical protein YPL216w
5156_at	113.5	A	questionable ORF
5157_at	1058.7	P	weak similarity to S.pombe hypothetical protein C3H1.12C
5158_at	6455.4	P	mRNA guanylyltransferase (mRNA capping enzyme), alpha subunit
5159_at	1331.9	P	hypothetical protein
5160_at	3618.3	P	weak similarity to rat cysteine string protein
5115_at	4911.3	P	SOH1 encodes a novel 14-kD protein with limited sequence similarit
5116_at	5678.4	P	required for inositol prototrophy
5117_at	20736.4	P	putative methylenetetrahydrofolate reductase (mthfr)
5118_at	1115.2	P	similarity to S.pombe hypothetical protein
5119_at	22242.7	P	Ribosomal protein S2 (S4) (rp12) (YS5)
5120_at	12960.6	P	nuclear polyadenylated RNA binding protein
5121_at	393.6	M	hypothetical protein
5122_at	21216	P	pre-mRNA processing factor involved in disassembly of spliceosome
5123_at	1838.2	P	multicopy suppressor of a cytochrome b mRNA translation defect, e
5124_at	290.4	P	questionable ORF
5125_at	567.7	P	hypothetical protein
5126_at	2514	P	beta-transducin homolog
5127_at	4781.2	P	associates with Snf1p
5128_at	3271.6	P	weak similarity to H.influenzae permease
5129_at	1340.3	P	weak similarity to YOR165w
5130_at	5633.7	P	TATA-binding protein-associated-factor
5131_at	9660.9	P	hypothetical protein
5132_at	2591.2	P	hypothetical protein
5133_at	758.5	A	questionable ORF
5134_at	1467.6	P	weak similarity to hypotetical S.pombe protein
5135_at	2783.3	P	strong similarity to hypothetical protein YBR238c
5136_at	10150.1	P	light chain for myosin Myo2p
5092_at	21668.9	P	Associated with tRNA and amino acyl-tRNA synthetases\; has affinity
5093_at	718.5	P	similarity to glucose transport proteins
5094_at	30824.2	P	Ribosomal protein L28 (L29) (rp44) (YL24)
5095_at	2208.4	P	questionable ORF

5096_at	1859.6	P	strong similarity to hypothetical protein YBR242w
5097_at	3384.3	P	nuclear pore protein, homologous to sec13
5098_at	5044.9	P	similarity to putative human GTP-binding protein MMR1
5099_at	764.1	P	hypothetical protein
5100_at	16741.1	P	pheromone response pathway suppressor
5101_at	1015.2	P	similarity to copper homeostasis protein Cup9p
5102_at	1079.8	P	cytosolic and peripheral membrane protein
5103_at	824.2	A	135-kDa protein that is subunit of poly(A) ribonuclease
5104_at	4403	P	component of spindle pole
5105_at	4688.2	P	Nuclear pore complex protein with GLFG motif
5106_at	1635.8	P	35 kDa nucleotide binding protein
5107_at	753.2	P	Ligase Interacting Factor 1\; physically interacts with DNA ligase 4 pr
5108_at	26151.6	P	alpha mating factor
5109_at	1850	P	questionable ORF
5110_at	2068	P	Similar to ubiquitin conjugating protein family
5111_at	2786.5	P	Coiled-coil protein involved in spindle-assembly checkpoint
5112_at	1564.4	P	weak similarity to Staphylococcus aureus nuclease (SNase)
5113_at	6501.7	P	strong similarity to hypothetical protein YPL189w
5114_at	1226.9	P	suppressor of GTPase mutant
5069_at	11612.6	P	strong similarity to hypothetical protein YPL191c
5070_at	255.9	A	hypothetical protein
5071_at	2539.5	P	strong similarity to C.elegans R07E5.13 protein
5072_at	3550.6	P	hypothetical protein
5073_at	15081.6	P	ATP-dependent RNA helicase CA3 of the DEAD\/DEAH box family
5074_at	12076.6	P	Transporter (permease) for choline and nitrogen mustard\; share hor
5075_i_at	28521.3	P	Ribosomal protein L7A (L6A) (rp11) (YL8)
5076_f_at	23920.1	P	Ribosomal protein L7A (L6A) (rp11) (YL8)
5077_at	482.1	A	Mitotic Membrane Component
5078_at	22.6	A	questionable ORF
5079_at	2509.8	P	heat shock transcription factor
5080_at	1379.8	P	questionable ORF
5081_at	4012	P	Putative transcription factor that binds the consensus site PyPuCAC
5082_at	6466	P	RNA polymerase II subunit
5083_at	92	A	questionable ORF
5084_at	2528.7	P	probable ribosomal protein L12
5085_at	4183.6	P	weak similarity to H.influenzae hypothetical protein
5086_at	2620.8	P	hypothetical protein
5087_at	4861.4	P	glycosyltransferase
5088_at	1500.5	P	similarity to YLR276c and YKR024c
5089_at	656.5	A	pseudouridine synthase 2
5090_at	17209.4	P	pyruvate carboxylase
5091_at	922.1	P	Death Upon Overexpression
5047_at	1842.5	P	strong similarity to hypothetical protein YBR216c
5048_at	110.3	A	similarity to rat branched-chain alpha-ketoacid dehydrogenase kinas
5049_at	5043.9	P	ubiquitin conjugating (E2) enzyme, separate domains of Rad6p inter
5050_at	1274.8	P	hypothetical protein
5051_at	14015.5	P	homologue of pombe SDS23\; localizes to spindle pole body
5052_at	27784.2	P	delta-9-fatty acid desaturase
5053_at	6117.8	P	strong similarity to D.melagonaster cni protein
5054_at	1436.3	P	strong similarity to hypothetical proteins YAR031w, YGL051w, YAR
5055_at	194	M	questionable ORF
5056_at	882.1	P	strong similarity to YAR033w protein

5057_at	2828.4	P	hypothetical protein
5058_at	811	P	mRNA cap-binding protein (eIF-4F), 130K subunit
5059_at	19835.8	P	ATPase
5060_at	1169.3	P	similarity to hypothetical S. pombe protein
5061_at	259.2	A	hypothetical protein
5062_at	595.9	A	hypothetical protein
5063_at	2120.3	P	component of the cleavage and polyadenylation factor CF I involved
5064_at	1837.2	P	RNA polymerase II elongation factor
5065_at	518	P	questionable ORF
5066_at	126	A	weak similarity to YJL109c
5067_at	16302.2	P	delta-aminolevulinate dehydratase (porphobilinogen synthase)
5068_at	5967.7	P	similarity to V. vinifera dihydroflavonol reductase
5024_at	3592.9	P	membrane-bound mannosyltransferase
5025_at	6307	P	similarity to E.coli hypothetical 23K protein
5026_at	1253.4	P	Mtf1 Two Hybrid Clone 2
5027_at	930	P	C2H2 zinc finger protein which resembles the mammalian Egr and W
5028_at	277.9	A	questionable ORF
5029_at	257.1	M	Meiosis-specific gene required for the pairing of homologous chromo
5030_at	283.4	A	adhesion subunit of a-agglutinin
5031_at	23523.1	P	Ribosomal protein L24A (rp29) (YL21) (L30A)
5032_at	25619.9	P	Large ribosomal subunit protein L30 (L32) (rp73) (YL38)
5033_at	3650.9	P	weak similarity to human chromatin assembly factor I p150 chain
5034_at	18565.3	P	glucanase gene family member
5035_at	6616.1	P	glucosidase I
5036_at	31269.8	P	tryptophan synthetase
5037_at	920	P	Probable transcription factor, polyglutamine domain protein
5038_at	2144.4	A	questionable ORF
5039_at	11551.9	P	weak similarity to Vsp27p
5040_at	15291.4	P	required for protein glycosylation
5041_at	2220.8	P	DNA damage-responsive protein
5042_at	7995.5	P	hypothetical protein
5043_at	11360.1	P	beta (38kDa) subunit of casein kinase II (CKII)
5044_at	1930.3	P	Homolog of E. coli Hsc20 co-chaperone protein
5045_at	1313.6	P	arginyl-tRNA-protein transferase
5046_at	4410.1	P	pleiotropic drug resistance regulatory protein
5002_at	350.3	P	hypothetical protein
5003_at	9244.3	P	similarity to Drosophila pumilio protein and Mpt5p protein
5004_at	3276.3	P	zinc-finger transcription factor of the Zn(2)-Cys(6) binuclear cluster d
5005_at	29533.5	P	Sterol C-24 reductase
5006_at	8975.9	P	Proteasome subunit YC7alpha\/Y8 (protease yscE subunit 7)
5007_at	1270.3	P	similarity to hypothetical S. pombe protein
5008_at	9513.3	P	isopropylmalate isomerase
5009_at	28181.5	P	plasma membrane H+-ATPase
5010_at	811.4	A	questionable ORF
5011_at	4037.8	P	putative vacuolar Ca2+ ATPase
5012_at	779.3	P	weak similarity to Xenopus kinesin-related protein Eg5
5013_at	1246.5	P	weak similarity to Tup1p
5014_at	1151.2	P	protein required for Clb2 and Ase1 degradation
5015_at	1728.6	P	p24 protein involved in membrane trafficking
5016_at	11086.4	P	putative 3-beta-hydroxysteroid dehydrogenase
5017_at	4676.9	P	similarity to C.elegans hypothetical M142.5 protein
5018_at	2908.2	P	similarity to C.elegans hypothetical M142.5 protein

5019_at	904.3	P	similarity to hypothetical S. pombe protein
5020_at	1142.3	P	similarity to D.melanogaster lin19 protein
5021_at	1435.7	P	strong similarity to hypothetical protein YLR324w
5022_at	2310.2	P	transcription initiation factor TFIIF middle subunit
5023_at	384.9	A	RNA splicing factor associated with U5 snRNP
4979_at	5595.1	P	choline phosphate cytidylyltransferase (also called phosphoethanola
4980_at	5112.1	P	ATPase stabilizing factor
4981_at	3573	P	Putative t-SNARE of the plasma membrane
4982_at	1684.1	P	strong similarity to hypothetical protein YLR328w
4983_g_at	4167.2	P	strong similarity to hypothetical protein YLR328w
4984_at	1801.5	P	questionable ORF
4985_at	3368.2	P	similarity to E.nidulans cysteine synthase
4986_at	890.7	P	Associated with U1 snRNP (no counterpart in mammalian U1 snRN
4987_at	15428.6	P	putative integral membrane protein
4988_at	641.8	P	similarity to hypothetical protein YGR031w
4989_at	151	A	weak similarity to M.jannaschii hypothetical protein MJ1317
4990_at	2525.7	P	hypothetical protein
4991_at	615.4	A	questionable ORF
4992_at	1121	P	gamma-aminobutyrate (GABA) transaminase (4-aminobutyrate amin
4993_at	9177.1	P	Vacuolar H-ATPase 14 kDa subunit (subunit F) of the catalytic (V1) s
4994_at	1325.4	P	similarity to M.leprae yfcA protein
4995_at	833	A	questionable ORF
4996_at	1156.6	P	acts in concert with Mid2p to transduce cell wall stress signals
4997_at	6833.3	P	weak similarity to Methanobacterium thermoautotrophicum hypotheti
4998_at	752.1	A	questionable ORF
4999_at	12373.1	P	hypothetical protein
5000_i_at	8508	P	Ribosomal protein S25A (S31A) (rp45) (YS23)
5001_f_at	20875.8	P	Ribosomal protein S25A (S31A) (rp45) (YS23)
4956_at	2043	P	40 kDa putative membrane-spanning ATPase
4957_at	972.3	P	integral subunit of RNase P and apparent subunit of RNase MRP
4958_at	1630.9	P	similarity to hypothetical protein YGR015c and weak similarity H.influ
4959_at	7111.4	P	catalytic component of 1,3-beta-D-glucan synthase
4960_at	4380.7	P	hypothetical protein
4961_at	834.2	A	hypothetical protein
4962_at	844.5	P	Cwh8p contains 3 short stretches of amino acids that are characteri
4963_at	29246.4	P	Acyl-CoA-binding protein (ACBP)\/Diazepam binding inhibitor (DBI)\/
4964_at	13242.5	P	strong similarity to hypothetical protein YLR350w
4965_at	664.5	P	questionable ORF
4966_at	545.3	P	MAP protein kinase homolog involved in pheromone signal transduct
4967_at	3580.1	P	Among a group of genes whose products are necessary for bud-site
4968_at	793.3	P	hypothetical protein
4969_at	897.9	P	strong similarity to transaldolase
4970_at	2980	P	zinc finger protein\; negative regulator of meiosis\; directly repressed
4971_at	395.9	M	questionable ORF
4972_at	565.6	P	hypothetical protein
4973_at	3965.6	P	transcription factor tau (TFIIIC) subunit 131
4974_at	1091.6	P	ubiquitin fusion degradation protein
4975_at	12862.3	P	Protein that suppresses ts allele of CDC4 when overexpressed
4976_at	1319.9	P	questionable ORF
4977_at	152.9	A	questionable ORF
4978_at	481.7	A	similarity to ser/thr protein kinases
4934_at	348	A	hypothetical protein

4935_at	4736.4	P	similarity to C.elegans E04D5.1 protein
4936_at	14523.5	P	high affinity methionine permease
4937_at	2461.4	P	Member of RSC complex
4938_at	981.8	P	Required for amino acid permease transport from the Golgi to the ce
4939_at	1124.8	P	similarity to mouse calcium-binding protein
4940_at	250.9	P	a sporulation-specific homologue of the yeast CDC3\/10\/11\/12 famil
4941_at	18990.5	P	C-4 sterol methyl oxidase
4942_at	26201.4	P	5 -phosphoribosylformyl glycinamidine synthetase
4943_at	4991.4	P	Cytochrome OXidase gene 18
4944_at	7885.6	P	Zn-finger protein, transcriptional regulator
4945_at	864.4	P	questionable ORF
4946_at	9932.4	P	similarity to P.putida phthalate transporter
4947_at	178.3	A	similarity to hypothetical protein YBR105c
4948_at	1225.1	P	weak similarity to transcription factors
4949_at	1224.8	A	weak similarity to Rod1p
4950_at	251.9	A	questionable ORF
4951_at	904.9	M	GDP-GTP Exchange Protein (GEP) for the Rho1p Small GTP-bindin
4952_at	1777.1	P	similarity to hypothetical protein YLR373c
4953_at	1489.7	P	factor stimulating decay of mRNAs containing premature stop codon
4954_at	733.3	P	questionable ORF
4955_at	1106.3	P	Homolog of human core snRNP protein D1, involved in snRNA matu
4911_at	519.2	P	RNA splicing factor
4912_at	2435.2	P	Mitochondrial ribosomal protein MRPL25 (YmL25)
4913_at	11116.6	P	peroxisome associated protein containing a PTS1 signal
4914_at	2853.3	P	Polypeptide 3 of a Yeast Non-native Actin Binding Complex, homolo
4915_at	5278.3	P	hypothetical protein
4916_at	7226.8	P	Twinfilin A, an actin monomer sequestering protein
4917_at	1323.7	P	weak similarity to mammalian myosin heavy chain
4918_at	8819.4	P	20 kDa mitochondrial outer membrane protein import receptor
4919_at	3780	P	translation initiation factor eIF2B, 71 kDa (delta) subunit\; translation
4920_at	3650.7	P	35 kDa mitochondrial ribosomal small subunit protein
4921_i_at	34352.6	P	60S ribosomal protein L11B (L16B) (rp39B) (YL22)
4922_at	10851.7	P	strong similarity to hypothetical protein YPL004c
4923_at	129.5	A	Third, minor isozyme of pyruvate decarboxylase
4924_at	360.2	A	cytoplasmic catalase T
4925_at	445.2	P	weak similarity to rat tropomyosin
4926_at	4459.2	P	hypothetical protein
4927_at	915.8	P	pre-mRNA splicing protein
4928_at	2165.9	P	Serine\/threonine protein kinase
4929_at	5059.1	P	similarity to hypothetical S.pombe protein
4930_at	29145.5	P	mitochondrial and cytoplasmic valyl-tRNA synthetase
4931_at	4357.6	P	Putative 3 ->5 exoribonuclease\; component of exosome complex o
4932_at	1202.9	P	similarity to bovine Graves disease carrier protein
4933_at	9207.9	P	transcriptional activator of the SKN7 mediated two-component regu
4888_at	2022.9	P	Esp1 promotes sister chromatid separation by mediating dissociation
4889_at	1528.1	P	involved in controlling telomere length
4890_at	1258.1	P	Mac1-dependent regulator
4891_at	6077.3	P	weak similarity to B.subtilis YqgP
4892_at	1818.4	P	hypothetical protein
4893_at	2135.1	P	similarity to zebrafish essential for embryonic development gene pes
4894_at	773	A	subunit of RNA polymerase II holoenzyme\/mediator complex
4895_at	6993	P	Protein involved in vacuolar H-ATPase assembly or function

4896_at	22186.2	P	hypothetical protein
4897_at	95.5	A	questionable ORF
4898_at	4430.3	P	G(sub)2-specific B-type cyclin
4899_at	653.4	P	B-type cyclin
4900_at	265.1	P	weak similarity to YLR099c and YDR125c
4901_at	1585.3	P	weak similarity to mosquito carboxylesterase
4902_at	1114.8	P	mitochondrial protein with homology to the mammalian SURF-1 gen
4903_at	1515.6	P	Duo1 And Mps1 interacting
4904_at	328.3	A	questionable ORF
4905_g_at	1965.3	P	questionable ORF
4906_at	26.6	A	questionable ORF
4907_at	1626.5	P	transcriptional regulator, interacts with histones, primarily histone H3
4908_at	1812.6	P	hypothetical protein
4909_f_at	32483.3	P	Ribosomal protein S23A (S28A) (rp37) (YS14)
4910_at	3087.8	P	Contains GLFG repeats in N-terminal half and heptad repeats in C-te
4865_at	1863.2	P	required for ER to golgi vesicle docking
4866_at	2785.1	P	ammonia permease
4867_at	874.5	P	hypothetical protein
4868_at	4435.1	P	serine\/threonine phosphatase
4869_at	24203	P	asparagine synthetase
4870_at	5635.8	P	similarity to S.pombe hypothetical protein SPAC24H6.11c
4871_at	166.8	A	weak similarity to hypothetical protein YPR156c
4872_at	2082.1	A	weak similarity to mouse T10 protein
4873_at	8017.1	P	hypothetical protein
4874_at	1477.8	P	SYnthetic lethal with cdcForty
4875_at	763	P	weak similarity to myosin heavy chain proteins
4876_at	363.3	P	strong similarity to Nce2p
4877_at	5873.5	P	mitochondrial protein, prohibitin homolog\; similar to S. cerevisiae P
4878_at	115.4	A	Member of ubiquitin-conjugating protein family
4879_at	1805.3	P	hypothetical protein
4880_at	11397.1	P	proteasome component Y13
4881_at	7502.2	P	weak similarity to chicken growth factor receptor-binding protein GR
4882_g_at	2963.7	P	weak similarity to chicken growth factor receptor-binding protein GR
4883_at	1376.5	P	questionable ORF
4884_i_at	29187.2	P	similarity to multidrug resistance proteins
4885_at	89	A	questionable ORF
4886_at	805.5	P	110 kDa subunit of the centromere binding factor CBF3
4887_at	3051.3	P	strong similarity to hypothetical protein YPR157w
4842_at	4022	P	similarity to hypothetical protein YPR158w
4843_at	15307.7	P	encodes a predicted type II membrane protein highly homologous to
4844_at	494.3	A	component of the biosynthetic pathway producing the thiazole precur
4845_at	9268.7	P	similarity to C.elegans hypothetical protein
4846_at	9687.9	P	hypothetical protein
4847_at	2145.3	P	N alpha-acetyltransferase that acts on methionine termini
4848_at	6867.2	P	Ribosomal protein L24B (rp29) (YL21) (L30B)
4849_at	2365	P	hypothetical protein
4850_at	690.1	P	hypothetical protein
4851_i_at	16645.4	P	questionable ORF
4852_s_at	5424.2	P	questionable ORF
4853_at	932.3	P	GTP-binding protein of the ras superfamily involved in bud site select
4854_at	311.8	A	hypothetical protein
4855_at	855.3	P	strong similarity to hypothetical proteins YKR076w and YMR251w

4856_at	35230.3	P	Cystathionine beta-synthase
4857_at	1547.1	P	hypothetical protein
4858_at	7704.6	P	Phosphatidyl-ethanolamine N-methyltransferase
4859_at	1844.4	P	involved in mRNA transport
4860_at	21536.8	P	nuclear localization sequence binding protein
4861_at	1071.5	A	questionable ORF
4862_at	2003.7	P	hypothetical protein
4863_at	6057.6	P	mRNA cap-binding protein (eIF-4F), 150K subunit , highly homologo
4864_at	2079.5	P	GTP-binding protein
4819_at	11.2	A	questionable ORF
4820_at	2418.4	P	hypothetical protein
4821_at	5678.5	P	Involved in biosynthetic pathway for cell wall beta-glucans
4822_at	10916.5	P	Clathrin light chain
4823_at	741.8	A	hypothetical protein
4824_at	2255.3	P	similarity to Rib2p
4825_at	1321	P	phosphatidylserine decarboxylase located in vacuole or Golgi
4826_at	4260.8	P	mitochondrial methionyl-tRNA synthetase
4827_at	5293.7	P	Golgi membrane protein
4828_at	7350.1	P	strong similarity to human GTP-binding protein
4829_at	1206.7	P	Essential for the expression and activity of ubiquinol-cytochrome c re
4830_at	24493.5	P	Squalene monooxygenase
4831_at	80	A	questionable ORF
4832_at	5665.4	P	Alcohol acetyltransferase
4833_at	9891	P	Poly(A)-binding protein binding protein
4834_at	1186.3	P	hypothetical protein
4835_at	29578.8	P	Ribonucleotide Reductase
4836_at	6920.3	P	similarity to YHR004c-a
4837_at	2582.4	P	questionable ORF
4838_at	4607.6	P	7.3 kDa subunit 9 of the ubiquinol cytochrome c oxidoreductase com
4839_at	4063.7	P	Ubiquitin-protein ligase
4840_at	18459.9	P	tyrosyl-tRNA synthetase, cytoplasmic
4841_at	3526.5	P	Transcription factor TFIIF large subunit
4797_at	9382.9	P	HMG1\/2 homolog
4798_at	253.3	A	Serine\/threonine protein kinase required for cell cycle arrest in respo
4799_at	25236.5	P	similarity to Aspergillus fumigatus rAsp
4800_at	424.9	A	questionable ORF
4801_at	10074.9	P	histidine permease
4802_i_at	923.8	A	Glyceraldehyde-3-phosphate dehydrogenase 3
4803_at	2462.3	P	Protein X component of mitochondrial pyruvate dehydrogenase comp
4804_at	1177	P	xylulokinase
4805_at	4903.6	P	homolog of RNAse PH
4806_at	1092.7	P	weak similarity to Tetrahymena acidic repetitive protein arp1
4807_at	6394.7	P	involved in nitrosoguanidine resistance
4808_at	4718.8	P	hypothetical protein
4809_at	11158.5	P	dolichyl phosphate-D-mannose:protein O-D-mannosyltransferase
4810_at	3699.5	P	weak similarity to rape guanine nucleotide regulatory protein
4811_at	606.4	P	strong similarity to translation elongation factor eEF1 alpha chain Ca
4812_at	1083.3	P	phosphorylcholine transferase\; or cholinephosphate cytidylyltransfer
4813_at	4864.5	P	weak similarity to X.laevis protein-tyrosin-phosphatase cdc homolog
4814_at	25092.3	P	encodes the cytoplasmic trifunctional enzyme C1-tetrahydrofolate sy
4815_at	1170.7	P	similarity to S.pombe hypothetical protein D89234
4816_at	963.8	P	similarity to Xenopus transcription factor Oct-1.17

4817_at	1101.9	P	electron-transferring flavoprotein, beta chain
4818_at	6200.9	P	phosphoserine phosphatase
4774_at	10821.3	P	thioredoxin
4775_at	10146.4	P	similarity to M.jannaschii GTP-binding protein and to M.capricolum hy
4776_at	5148.6	P	zinc finger protein
4777_at	229.1	P	weak similarity to S.pombe hypothetical protein SPAC18B11.03c
4778_at	309	A	involved in 7-aminocholesterol resistance
4779_f_at	19588.9	P	Ribosomal protein S0A
4780_at	29221.2	P	Ribosomal protein S0A
4781_at	1636.8	P	strong similarity to hypothetical S. pombe protein
4782_at	2182.8	P	Participates in synthesis of N-acetylglucoaminylphosphatidylinositol,
4783_at	1934.3	P	putative calcium channel
4784_at	782.6	P	omosome region maintenance protein
4785_at	680.6	P	questionable ORF
4786_at	4385.8	P	Mitochondrial ribosomal protein MRPL9 (YmL9) (E. coli L3) (human
4787_at	719.7	A	similarity to hypothetical protein YHR149c
4788_at	3000.5	P	translational activator of cytochrome c oxidase subunit III
4789_at	1248.1	P	weak similarity to hypothetical protein YFR021w
4790_at	1807.1	P	strong similarity to drug resistance protein SGE1
4791_at	239.3	A	weak similarity to human p55CDC and Cdc20p
4792_at	57.5	A	hypothetical protein
4793_at	9825.6	P	De-repression of ITR1 Expression
4794_at	979.4	P	questionable ORF
4795_at	3023.2	P	57 kDa nuclear protein
4796_at	346.9	M	questionable ORF
4751_at	12317.3	P	mitochondrial protein, prohibitin homolog\; homolog of mammalian
4752_at	3208.3	P	possible homolog of human 26S proteasome regulatory subunit p28
4753_at	13320.4	P	Positive regulatory protein of phosphate pathway
4754_at	31179.6	P	Flavohemoglobin
4755_at	6385.2	P	hypothetical protein
4756_at	366.3	A	questionable ORF
4757_at	934.8	P	weak similarity to YOR019w
4758_at	1081.6	P	protein containing kelch repeats, similar to YHR158c and YPL263c
4759_at	614	P	weak similarity to hypothetical protein YHR160c
4760_at	27530.3	P	phosphofructokinase alpha subunit
4761_at	2101.3	P	Yeast Assembly Polypeptide, member of AP180 protein family, bind
4762_at	470.4	A	questionable ORF
4763_at	234.2	A	strong similarity to hypothetical protein YHR162w
4764_at	6407.9	P	Succinate-CoA Ligase (ADP-Forming)
4765_at	8312.2	P	similarity to hypothetical S.pombe protein
4766_at	5825.2	P	RNA polymerase III transcription factor with homology to TFIIB
4767_at	1399.7	P	hypothetical protein
4768_at	1196.6	P	similar to SOL3
4769_at	706.6	P	Mga1p shows similarity to heat shock transcription factor
4770_at	1654.1	P	weak similarity to human cleavage stimulation factor 64K chain
4771_at	2706.7	P	hypothetical protein
4772_at	1472.5	P	histone acetyltransferase
4773_at	10116.6	P	Proteasome subunit
4729_i_at	28315.6	P	enolase I
4730_s_at	11972.3	P	enolase I
4731_at	4407.3	P	COQ6 monooxygenase
4732_at	1126.5	A	6-phosphogluconate dehydrogenase

4733_at	3375.2	P	similarity to C.elegans C16C10.1
4734_at	2391.3	P	homolog of xeroderma pigmentosum group G (XPG) protein, copufu
4735_at	909.5	A	questionable ORF
4736_at	27478.1	P	similarity to allantoate transport protein
4737_at	6689.7	P	putative beta adaptin component of the membrane-associate clathrin
4738_at	884.8	P	ser/thr protein kinase
4739_at	1620.7	P	weak similarity to E.coli lipase like enzyme
4740_at	24237.6	P	methionyl tRNA synthetase
4741_at	77.6	A	questionable ORF
4742_at	4539.6	P	hypothetical protein
4743_at	5322.6	P	GTP-cyclohydrolase I
4744_at	2002.8	P	weak similarity to S.pombe hypothetical protein SPAC17A5
4745_at	335.7	A	questionable ORF
4746_at	1562.4	P	Member of CDC48\/PAS1\/SEC18 family of ATPases
4747_at	1496.1	P	strong similarity to S.pombe RNA helicase
4748_at	2910.1	P	similarity to hypothetical S.pombe protein SPAC12G12.02
4749_at	68.2	A	similarity to hypothetical protein YMR295c
4750_at	3917.8	P	Component of the TAFII complex required for activated transcription
4705_at	8988	P	hypothetical protein
4706_at	3857.2	P	ribonuclease H
4707_at	8304.9	P	similarity to hypothetical S.pombe protein
4708_at	536.4	A	similarity to C.elegans LET-858
4709_at	18221.3	P	glucanase gene family member
4710_at	20144.8	P	weak similarity to Cbf5p
4711_at	4247.2	P	ABC transporter
4712_at	24992.2	P	Cell wall endo-beta-1,3-glucanase
4713_at	2576.7	P	similarity to hypothetical protein YMR310c
4714_at	9045.8	P	similarity to mouse Surf-4 protein
4715_at	27352.4	P	Zuotin, putative Z-DNA binding protein
4716_at	9714.7	P	Biotin synthase
4717_at	262	P	strong similarity to maltase
4718_at	886.1	P	maltose pathway regulatory protein
4719_at	1176.3	P	alpha-glucoside transporter
4720_at	983.9	A	hypothetical protein
4721_at	68.2	A	hypothetical protein
4722_s_at	856.8	P	strong similarity to hypothetical protein YBR300c
4723_f_at	3478.6	P	strong similarity to members of the Srp1p/Tip1p family
4724_i_at	6907.5	P	hypothetical protein
4725_f_at	170	A	hypothetical protein
4726_at	175.3	A	identified by SAGE
4727_s_at	3120.5	P	Protein essential for mitochondrial biogenesis and cell viability
4728_at	297.9	A	non-annotated SAGE orf Found reverse in NC_001139 between 110
4681_at	1660.4	P	non-annotated SAGE orf Found reverse in NC_001139 between 323
4682_at	15816.2	P	non-annotated SAGE orf Found reverse in NC_001139 between 836
4683_at	4015.2	P	non-annotated SAGE orf Found reverse in NC_001139 between 836
4684_at	1790.8	P	non-annotated SAGE orf Found reverse in NC_001139 between 904
4685_at	6124	P	non-annotated SAGE orf Found reverse in NC_001139 between 905
4686_s_at	269	A	non-annotated SAGE orf Found reverse in NC_001139 between 939
4687_at	1395.5	P	non-annotated SAGE orf Found reverse in NC_001139 between 225
4688_at	47.8	A	non-annotated SAGE orf Found forward in NC_001139 between 323
4689_at	1354.1	P	non-annotated SAGE orf Found reverse in NC_001139 between 324
4690_at	390.1	P	non-annotated SAGE orf Found forward in NC_001139 between 363

4691_at	28	A	non-annotated SAGE orf Found forward in NC_001139 between 437
4692_f_at	3119	P	non-annotated SAGE orf Found reverse in NC_001139 between 536
4693_i_at	3.3	A	non-annotated SAGE orf Found reverse in NC_001139 between 931
4694_at	184.9	A	non-annotated SAGE orf Found reverse in NC_001139 between 974
4695_at	1474.6	A	non-annotated SAGE orf Found forward in NC_001139 between 299
4696_at	7612.6	P	non-annotated SAGE orf Found forward in NC_001139 between 312
4697_at	1658.3	P	non-annotated SAGE orf Found forward in NC_001139 between 326
4698_at	1152.8	P	non-annotated SAGE orf Found reverse in NC_001139 between 366
4699_at	1221.5	P	non-annotated SAGE orf Found forward in NC_001139 between 393
4700_at	1850.8	P	non-annotated SAGE orf Found forward in NC_001139 between 400
4701_at	8301.5	P	non-annotated SAGE orf Found reverse in NC_001139 between 554
4702_at	5500.2	P	non-annotated SAGE orf Found forward in NC_001139 between 669
4703_at	118.5	A	non-annotated SAGE orf Found forward in NC_001139 between 670
4704_at	707	P	non-annotated SAGE orf Found reverse in NC_001139 between 736
4658_at	2412	P	non-annotated SAGE orf Found forward in NC_001139 between 772
4659_at	3165.5	P	non-annotated SAGE orf Found forward in NC_001139 between 777
4660_i_at	2354.4	P	non-annotated SAGE orf Found forward in NC_001139 between 783
4661_r_at	130.8	A	non-annotated SAGE orf Found forward in NC_001139 between 783
4662_at	24596.7	P	non-annotated SAGE orf Found forward in NC_001139 between 827
4663_at	3043.6	P	non-annotated SAGE orf Found forward in NC_001139 between 836
4664_at	621.9	A	non-annotated SAGE orf Found reverse in NC_001139 between 853
4665_at	62.9	A	non-annotated SAGE orf Found reverse in NC_001139 between 949
4666_r_at	10111.6	P	non-annotated SAGE orf Found reverse in NC_001139 between 970
4667_at	339.6	P	non-annotated SAGE orf Found forward in NC_001139 between 973
4668_at	311.5	A	non-annotated SAGE orf Found forward in NC_001139 between 974
4669_i_at	5	A	non-annotated SAGE orf Found reverse in NC_001139 between 103
4670_f_at	14904.2	P	non-annotated SAGE orf Found reverse in NC_001139 between 103
4671_at	1165.2	P	non-annotated SAGE orf Found reverse in NC_001139 between 103
4672_at	81.2	A	non-annotated SAGE orf Found forward in NC_001139 between 110
4673_at	420	P	non-annotated SAGE orf Found reverse in NC_001139 between 255
4674_at	248.6	A	non-annotated SAGE orf Found forward in NC_001139 between 255
4675_at	416	A	non-annotated SAGE orf Found forward in NC_001139 between 384
4676_at	80.7	A	non-annotated SAGE orf Found reverse in NC_001139 between 394
4677_at	58.8	A	non-annotated SAGE orf Found forward in NC_001139 between 773
4678_at	43.5	A	non-annotated SAGE orf Found forward in NC_001139 between 106
4679_at	303.4	P	non-annotated SAGE orf Found forward in NC_001139 between 108
4680_at	56.1	A	non-annotated SAGE orf Found reverse in NC_001139 between 101
4631_at	150.4	A	non-annotated SAGE orf Found reverse in NC_001139 between 745
4632_g_at	53.5	A	non-annotated SAGE orf Found reverse in NC_001139 between 745
4633_at	661.6	A	non-annotated SAGE orf Found reverse in NC_001139 between 746
4634_at	960.4	A	non-annotated SAGE orf Found reverse in NC_001139 between 933
4635_g_at	1687.1	A	non-annotated SAGE orf Found reverse in NC_001139 between 933
4636_i_at	286.2	A	non-annotated SAGE orf Found reverse in NC_001139 between 934
4637_r_at	186.3	A	non-annotated SAGE orf Found reverse in NC_001139 between 934
4638_i_at	10.8	A	non-annotated SAGE orf Found reverse in NC_001139 between 148
4639_f_at	99.1	A	non-annotated SAGE orf Found reverse in NC_001139 between 148
4640_at	493.8	A	non-annotated SAGE orf Found forward in NC_001139 between 319
4641_s_at	381.5	A	non-annotated SAGE orf Found forward in NC_001139 between 319
4642_i_at	20.6	A	non-annotated SAGE orf Found reverse in NC_001139 between 401
4643_f_at	90.6	A	non-annotated SAGE orf Found reverse in NC_001139 between 401
4644_i_at	145.8	A	non-annotated SAGE orf Found forward in NC_001139 between 405
4645_at	110.4	A	non-annotated SAGE orf Found reverse in NC_001139 between 544

4646_at	68.9	A	non-annotated SAGE orf Found forward in NC_001139 between 619
4647_at	183.7	A	non-annotated SAGE orf Found forward in NC_001139 between 700
4648_i_at	4	A	non-annotated SAGE orf Found reverse in NC_001139 between 701
4649_r_at	198.6	M	non-annotated SAGE orf Found reverse in NC_001139 between 701
4650_f_at	46.4	A	non-annotated SAGE orf Found reverse in NC_001139 between 701
4651_at	4906.6	P	non-annotated SAGE orf Found reverse in NC_001139 between 707
4652_at	8966.9	P	non-annotated SAGE orf Found reverse in NC_001139 between 707
4653_at	2129.9	P	non-annotated SAGE orf Found reverse in NC_001139 between 708
4654_at	540.5	A	non-annotated SAGE orf Found reverse in NC_001139 between 711
4655_at	208.9	A	non-annotated SAGE orf Found reverse in NC_001139 between 801
4656_f_at	2893	A	non-annotated SAGE orf Found forward in NC_001139 between 818
4657_at	296.6	P	non-annotated SAGE orf Found reverse in NC_001139 between 823
4608_g_at	402.9	A	non-annotated SAGE orf Found reverse in NC_001139 between 823
4609_at	494.8	A	non-annotated SAGE orf Found reverse in NC_001139 between 919
4610_at	133.7	A	non-annotated SAGE orf Found reverse in NC_001139 between 994
4611_at	22.3	A	non-annotated SAGE orf Found reverse in NC_001139 between 994
4612_at	34.4	A	non-annotated SAGE orf Found reverse in NC_001139 between 994
4613_at	1253	M	non-annotated SAGE orf Found forward in NC_001139 between 233
4614_at	1676.8	P	non-annotated SAGE orf Found reverse in NC_001139 between 525
4615_at	1853.8	P	non-annotated SAGE orf Found forward in NC_001139 between 944
4616_at	571.2	P	non-annotated SAGE orf Found forward in NC_001139 between 129
4617_at	771.1	M	non-annotated SAGE orf Found reverse in NC_001139 between 139
4618_at	1829.9	P	non-annotated SAGE orf Found reverse in NC_001139 between 163
4619_at	1312.8	P	non-annotated SAGE orf Found reverse in NC_001139 between 199
4620_at	1267.3	A	non-annotated SAGE orf Found reverse in NC_001139 between 249
4621_at	7256.1	P	non-annotated SAGE orf Found forward in NC_001139 between 274
4622_at	3792.1	P	non-annotated SAGE orf Found forward in NC_001139 between 318
4623_at	4355.8	P	non-annotated SAGE orf Found reverse in NC_001139 between 474
4624_at	585.8	P	non-annotated SAGE orf Found forward in NC_001139 between 512
4625_at	18479.2	P	non-annotated SAGE orf Found reverse in NC_001139 between 533
4626_at	2615.5	P	non-annotated SAGE orf Found forward in NC_001139 between 576
4627_at	1860.5	P	non-annotated SAGE orf Found reverse in NC_001139 between 604
4628_at	579.9	P	non-annotated SAGE orf Found forward in NC_001139 between 682
4629_at	399.7	P	non-annotated SAGE orf Found reverse in NC_001139 between 727
4630_at	2637	P	non-annotated SAGE orf Found forward in NC_001139 between 733
4585_at	1640.8	P	non-annotated SAGE orf Found forward in NC_001139 between 757
4586_at	458.7	M	non-annotated SAGE orf Found forward in NC_001139 between 787
4587_at	269.1	A	non-annotated SAGE orf Found forward in NC_001139 between 788
4588_at	264.3	A	non-annotated SAGE orf Found forward in NC_001139 between 810
4589_g_at	497.8	P	non-annotated SAGE orf Found forward in NC_001139 between 810
4590_at	1006.6	P	non-annotated SAGE orf Found forward in NC_001139 between 810
4591_at	2350.8	P	non-annotated SAGE orf Found forward in NC_001139 between 810
4592_at	31.3	A	non-annotated SAGE orf Found forward in NC_001139 between 867
4593_at	80.2	A	non-annotated SAGE orf Found reverse in NC_001139 between 878
4594_at	410.3	A	non-annotated SAGE orf Found forward in NC_001139 between 965
4595_at	824.9	A	non-annotated SAGE orf Found reverse in NC_001139 between 974
4596_at	76	A	non-annotated SAGE orf Found forward in NC_001139 between 100
4597_at	832.6	P	non-annotated SAGE orf Found forward in NC_001139 between 101
4598_g_at	321.5	A	non-annotated SAGE orf Found forward in NC_001139 between 101
4599_i_at	673.5	A	non-annotated SAGE orf Found forward in NC_001139 between 101
4600_at	3500.3	P	non-annotated SAGE orf Found forward in NC_001139 between 101
4601_at	2126	P	non-annotated SAGE orf Found forward in NC_001139 between 105

4602_at	3980.2	P	non-annotated SAGE orf Found reverse in NC_001139 between 105
4603_at	1472	P	snRNA
4604_i_at	1003.8	P	snRNA
4605_s_at	1306.3	P	snRNA
4606_at	883.6	P	snRNA
4607_at	1871.8	P	snRNA
4561_s_at	410.4	M	snRNA
4562_at	207.8	A	similarity to C.carbonum toxin pump
4563_f_at	6113.2	P	strong similarity to members of the Srp1p/Tip1p family
4564_at	163.4	A	similarity to subtelomeric encoded proteins
4565_at	415.7	A	ExtraCellular Mutant
4566_at	335.3	A	similarity to subtelomeric encoded proteins
4567_at	619.7	A	weak similarity to Drosophila hypothetical protein 6
4568_at	2361.9	P	similarity to C.carbonum toxin pump
4569_at	2910.3	P	weak similarity to YPL208w
4570_at	59.7	A	Cytochrome B pre-mRNA processing protein
4571_at	421.8	A	hypothetical protein
4572_at	2518.6	P	very low affinity methionine permease
4573_at	903.8	P	ABC transporter
4574_at	10688	P	Single-strand nucleic acid binding protein
4575_i_at	28572.1	P	Ribosomal protein L8A (rp6) (YL5) (L4A)
4576_at	751.3	A	glyerol kinase (converts glycerol to glycerol-3-phosphate
4577_at	3134.8	P	SNARE protein with a C-terminal membrane anchor
4578_at	1724.8	P	ExtraCellular Mutant
4579_at	10694.3	P	hypothetical protein
4580_at	5115	P	Putative integral membrane protein containing novel cysteine motif.
4581_at	20233.5	P	Meiotic regulatory protein\; Cys-His zinc fingers
4582_at	1952.3	P	hypothetical protein
4583_at	3412.2	P	transcriptional regulator
4584_at	1335.3	P	RNA binding domain (N-term) with asparagine rich region?
4539_at	949.4	P	hypothetical protein
4540_at	79.2	A	Encodes one of the earliest meiosis-specific recombination functions
4541_at	2109.2	P	weak similarity to Pseudomonas gamma-butyrobetaine hydroxylase
4542_at	7257.3	P	negative regulator of phospholipid biosynthesis
4543_at	645	A	Similiar to clathrin coat proteins
4544_at	90.2	A	Dimerization cofactor of homeodomian protein NF1-alpha
4545_at	5497.6	P	Probable transmembrane protein PTM1
4546_at	1591.3	M	Urea transporter
4547_at	14395.8	P	Ribosomal protein S20
4548_at	598.8	A	GTP-binding protein and glycogen phosphorylase (weak)
4549_at	4983.5	P	similarity to C.elegans hypothetical protein F21D5.2
4550_at	20.9	A	UDP Glucose pyrophosphorylase
4551_at	14759.9	P	ribose-phosphate pyrophosphokinase 3
4552_at	514.3	P	similarity to C.elegans hypothetical protein
4553_at	330.5	P	bZip DNA binding proteins
4554_at	4980.6	P	Potential formate transporter nirC
4555_at	2944.4	P	serine\/threonine protein kinase
4556_at	1186.2	A	hypothetical protein
4557_at	30.1	A	hypothetical protein
4558_at	3147.8	P	mitochondrial ribosomal protein, homologous to E. coli ribosomal pr
4559_at	1744.9	P	YKL008c
4560_at	2864.6	P	SH3 domain

4515_i_at	20232	A	Ribosomal protein L14B
4516_f_at	15925.1	P	Ribosomal protein L14B
4517_at	5283.4	P	60kD chaperonin (weak)
4518_at	19175.3	P	8.5 kDa subunit of the ubiqunol-cytochrome c oxidoreductase comple
4519_at	1367.4	P	Mitochondrial carrier protein\/Grave s disease carrier protein
4520_at	4358.6	P	thiF, moeB, ubiquitin activating enzyme (all weak)
4521_at	1185.3	P	similarity to YLL010c, YLR019w
4522_at	3933.9	P	alpha subunit of G protein coupled to mating factor receptors
4523_at	21188.1	P	May act cooperatively with Mrs5p in mitochondrial protein import or o
4524_at	1871.7	P	Zinc finger (Cys(2)-His(2))
4525_at	33553.6	P	cytochrome P450 lanosterol 14a-demethylase
4526_at	15106.6	P	Manganese-containing superoxide dismutase
4527_at	8674.7	P	similarity to S.pombe hypothetical protein
4528_i_at	18034.2	P	Ribosomal protein L27A
4529_f_at	13269.7	P	Ribosomal protein L27A
4530_at	488.9	P	Seryl-tRNA synthetase
4531_at	4485	P	Vacuolar protein sorting
4532_at	1918.5	P	subunit of the major N alpha-acetyltransferase, complexes with the
4533_at	166.2	P	Encodes a 33.4 kDa basic protein that localizes to the nucleus. Thou
4534_at	954.4	A	PolyA-binding protein
4535_at	1323.2	P	SH3 domain in C-terminus
4536_at	3987	P	strong similarity to S.douglasii YSD83
4537_at	8240.4	P	argininosuccinate lyase
4538_at	24630.8	P	Asparaginyl-tRNA synthetase
4493_at	23112.9	P	Aminoacyl tRNA-synthetase
4494_at	29914.4	P	40S Ribosomal protein S27B (rp61) (YS20)
4495_at	36.7	A	ExtraCellular Mutant
4496_at	184.1	M	RAS-related protein
4497_at	899.6	P	Class II Myosin
4498_at	2941.8	P	53 kDa subunit of the mitochondrial processing protease
4499_at	27630.5	P	homoserine kinase
4500_at	21928.4	P	proteolipid protein of the proton ATPase
4501_at	11791.4	P	Subunit of 26S Proteasome (PA700 subunit)
4502_at	5464.5	P	Dipeptidyl aminopeptidase B (DPAP B)
4503_at	1329.6	P	Thymidylate synthase (putative\; weak)
4504_at	17431	P	putative protein kinase
4505_at	2404.9	P	Pif1p, mitochondrial DNA repair and recombination protein
4506_at	8237.1	P	ethionine resistance protein
4507_at	1859.7	P	Pro1p (Gamma-glutamyl kinase)
4508_at	1124.2	P	hypothetical protein
4509_at	243.2	A	Sec23p (weak)
4510_at	1079.1	P	similarity to hypothetical protein YGL247w
4511_at	3926.3	P	delta-1-pyrroline-5-carboxylate dehydrogenase
4512_at	343.6	A	Killed in Mutagen, sensitive to Diepoxybutane and\/or Mitomycin C
4513_at	8740.1	P	Aldehyde dehydrogenases
4514_at	26940.1	P	13-kDa vacuolar H-ATPase subunit
4469_at	1642.7	P	weak similarity to Hit1p
4470_at	2468.6	P	RNA polymerase II holoenzyme\/mediator subunit
4471_at	24325.7	P	NADP-cytochrome P450 reductase
4472_s_at	2898.6	P	2-deoxyglucose-6-phosphate phosphatase
4473_i_at	98.7	A	2-deoxyglucose-6-phosphate phosphatase
4474_at	7539.4	P	hypothetical protein

4475_at	9078	P	Inositol monophosphatase
4476_at	7949.5	P	arginine\/alanine aminopeptidase
4477_at	689.3	M	similarity to multidrug resistance proteins
4478_at	3858.6	P	similarity to S.pombe dihydrofolate reductase and YOR280c
4479_at	1019.5	P	questionable ORF
4480_at	5221.2	P	localized to mitochondrial membrane
4481_at	11606.8	P	subunit VI of cytochrome c oxidase
4482_at	3055.2	P	weak similarity to P.yoelii rhoptry protein
4483_s_at	31134	P	copper-binding metallothionein
4484_s_at	9966.8	P	weak similarity to YOR262w
4485_at	10230.4	P	Peptidylprolyl isomerase (cyclophilin) ER or secreted
4486_at	1138.3	P	RNA polymerase II transcriptional regulation mediator
4487_at	639.6	P	weak similarity to Ustilago hordei B east mating protein 2
4488_at	1931.3	P	required for V-ATPase activity
4489_at	7676.8	P	GTPase-interacting component 1
4490_at	2383.8	P	Protein subunit of nuclear ribonuclease P (RNase P)
4491_at	6519.8	P	weak similarity to translational activator CBS2
4492_at	24827	P	Hsp70 Protein
4446_at	6760.2	P	RRP3 is a DEAD box gene homologous to eIF-4a which encodes an
4447_at	2103	P	homologous to Ssf2p
4448_at	866.6	P	hypothetical protein
4449_at	30917	P	Deoxyhypusine synthase
4450_at	2636	P	3->5 exoribonuclease\; Component of the exosome 3->5 exonucleas
4451_at	4136.4	P	strong similarity to N.crassa met-10+ protein
4452_at	13989.7	P	G1\/S cyclin (weak)
4453_at	12615.8	P	2,3-oxidosqualene-lanosterol cyclase
4454_at	511.5	P	Oxysterol-binding protein
4455_at	3926.8	P	weak similarity to B.subtilis spore outgrowth factor B
4456_at	1523.5	P	ribosomal protein of the small subunit, mitochondrial
4457_at	1929.1	P	weak similarity to C.elegans hypothetical protein CEW09D10
4458_at	6710.8	P	hypothetical protein
4459_at	646.2	P	Ire1p is a transmembrane protein that has both serine-threonine kina
4460_i_at	9	A	Ire1p is a transmembrane protein that has both serine-threonine kina
4461_r_at	141.6	A	Ire1p is a transmembrane protein that has both serine-threonine kina
4462_at	1382.4	P	similarity to hypothetical protein YDR326c, YFL042c and YLR072w
4463_at	3131.7	P	weak similarity to human C1D protein
4464_at	4925.3	P	Ser\/Thr protein kinase
4465_at	1810.3	P	hypothetical protein
4466_at	5705.4	P	Transcription factor
4467_at	2032.1	P	weak similarity to fruit fly brahma transcriptional activator
4468_at	23233	P	putative RNA binding protein, involved in meiosis-specific splicing of
4423_at	903.7	P	hypothetical protein
4424_at	3757.9	P	similarity to hypothetical protein YNL075w
4425_at	18480.7	P	small nucleolar RNP proteins
4426_at	2456.7	P	NuBbiN
4427_at	3785.2	P	Arginyl-tRNA synthetase
4428_at	14788.6	P	High-affinity glucose transporter
4429_at	687	P	the AHT1 DNA sequence is upstream of HXT4 and contains an HXT
4430_at	31632.7	P	High-affinity hexose (glucose) transporter
4431_at	184.1	A	hypothetical protein
4432_at	583.6	A	hexose transporter
4433_at	1131.7	A	strong similarity to hypothetical protein YDR348c

4434_at	1390.8	P	strong similarity to hypothetical protein YDR348c
4435_at	8431.6	P	binds to Sed5p and Sec23p by distinct domains
4436_at	4727	P	ATM\/Mec1\/TOR1+2-related
4437_at	1531.4	P	hypothetical protein
4438_at	1530.6	P	Bad in glucose or big cells
4439_at	565.1	A	Bad in glucose or big cells
4440_at	2070.6	P	Ser\/Thr protein kinase
4441_at	3569.6	P	functionally redundant and similar in structure to SBE2
4442_at	4960.2	P	Aldo-keto reductase
4443_at	268.4	A	weak similarity to Mvp1p
4444_at	2912.5	P	Thioredoxin reductase
4445_at	2084.3	P	Component of 10 nm filaments of mother-bud neck (septin)
4401_at	15009.7	P	strong similarity to hypothetical protein YDR358w
4402_at	230.1	A	hypothetical protein
4403_at	995.1	P	p24 protein involved in membrane trafficking
4404_at	1469.5	P	moeB, thiF, UBA1
4405_at	6952.6	P	Cystathionine gamma-synthase
4406_at	5663.1	P	Vacuolar aminopeptidase
4407_at	1932.8	P	SH3 domain
4408_at	1940.3	P	strong similarity to hypothetical protein YNL116w
4409_at	594.5	P	hypothetical protein
4410_at	734.9	P	71-kDa component of the protein translocase of the outer membrane
4411_at	416.1	P	50-kDa subunit of ORC
4412_at	2567.5	P	trithorax
4413_at	3382.6	P	mutS homolog involved in mitochondrial DNA repair
4414_at	3790.9	P	weak similarity to C.elegans hypothetical protein
4415_at	1254.7	P	similarity to hypothetical C. elegans protein F45G2.a
4416_at	1842.4	P	sn-1,2-diacylglycerol ethanolamine- and cholinephosphotranferase
4417_at	5046	P	sn-1,2-diacylglycerol ethanolamine- and cholinephosphotranferase
4418_at	52	A	meiosis-specific gene, mRNA is sporulation-specific
4419_at	182.2	A	questionable ORF
4420_at	392.5	A	hypothetical protein
4421_at	1476	P	(H)igh copy (S)uppressor of (N)34 dominant negative allele of SEC4.
4422_at	22610.2	P	UPRTase
4378_at	853.8	P	Centractin
4379_at	3077.9	P	weak similarity to T.brucei H+-transporting ATP synthase
4380_at	3454.3	P	Highly acidic C-terminus
4381_at	13169.1	P	Carboxypeptidase
4382_at	23307.2	P	similarity to hypothetical protein YNL156c
4383_at	735.1	P	hypothetical protein
4384_at	5081.7	P	membrane-bound casein kinase I homolog
4385_at	9103.5	P	17 kDa protein
4386_at	18312.5	P	aromatic amino acid aminotransferase II
4387_at	2306.9	P	hypothetical protein
4388_at	334.8	A	sporulation-specific wall maturation protein
4389_at	24.6	A	hypothetical protein
4390_at	110.8	A	hypothetical protein
4391_at	21257.8	P	weak similarity to cytochrome-c oxidases
4392_at	24655.7	P	Ser-Thr rich protein
4393_at	5341.7	P	subunit of RNA polymerase II
4394_at	4401.9	P	dCMP deaminase
4395_at	570.6	A	questionable ORF

4396_at	8903.1	P	similarity to pheromone-response G-protein Mdg1p
4397_at	6930.9	P	Mitochondrial ribosomal protein MRPL6 (YmL6)
4398_at	2678.6	P	ribosomal protein (weak similarity)
4399_at	2981.9	P	similarity to hypothetical protein YGR221c
4400_at	601.7	A	weak similarity to YDR479c
4356_at	2538.3	P	hypothetical protein
4357_at	5215.9	P	20 kDa protein with negatively charged C-terminus required for functi
4358_at	347.8	P	sporulation protein
4359_at	2915.2	P	Establishes Silent omatin
4360_at	1400.8	P	Snf1-interacting protein Sip3p
4361_at	1048.4	P	weak similarity to mouse kinesin KIF3B
4362_at	196.7	A	mRNA is induced early in meiosis
4363_at	2004.5	P	protein containing kelch repeats, similar to YGR238c
4364_at	360.7	A	hypothetical protein
4365_at	145.5	A	weak similarity to hypothetical protein YGR239c
4366_at	2636.5	P	Yeast Assembly Polypeptide, member of AP180 protein family, binds
4367_at	7711.7	P	strong similarity to hypothetical protein YGR243w
4368_at	10118.3	P	shows similarity to glucose-6-phosphate dehydrogenase non-catalyti
4369_at	1456	P	DNA replication helicase
4370_at	4699.3	P	RNA splicing factor
4371_at	407.8	A	Cell division cycle protein
4372_at	1477	P	hypothetical protein
4373_at	1793.6	P	GTP-binding protein
4374_at	4151	P	DEAD-box protein
4375_at	9297.1	P	putative Upf1p-interacting protein
4376_at	780	P	autophagy
4377_at	1488.1	P	spindle pole body component, associates in a complex with Spc98p
4333_at	99.3	A	hypothetical protein
4334_i_at	8280.6	P	enolase
4335_at	10832	P	Putative low-affinity copper transport protein
4336_at	697.8	A	Dimethylaniline monoxygenase
4337_at	580.4	P	weak similarity to Spombe pac2 protein
4338_at	1605	P	Zinc finger (6-Cys)
4339_at	24310.5	P	NAPDH dehydrogenase (old yellow enzyme), isoform 2
4340_at	960.3	P	hypothetical protein
4341_at	12653.2	P	similarity to mouse TEG-261 protein
4342_at	1066.3	P	hypothetical protein
4343_at	27666.3	P	Phosphogluconate Dehydrogenase (Decarboxylating)
4344_at	110.9	A	Involved in the control of meiotic nuclear divisions and spore formatio
4345_at	123.5	A	hypothetical protein
4346_at	1845.9	P	similarity to C.elegans hypothetical protein C10C5.6
4347_at	475	P	confers sensitivity to killer toxin
4348_at	7391.9	P	similarity to hypothetical C. elegans proteins F17c11.7
4349_at	311.2	A	similarity to peptidyl-tRNA hydrolases
4350_at	15683.9	P	squalene synthetase
4351_at	3283.5	P	protein of unknown function
4352_at	1985.1	P	hypothetical protein
4353_at	26231.5	P	GAL4 enhancer protein, homolog of human alpha NAC subunit of th
4354_at	2064.1	P	similarity to hypothetical protein YOR147w
4355_at	3888.7	P	hypothetical protein
4310_at	4581.1	P	hypothetical protein
4311_at	13768.9	P	hypothetical protein

4312_at	2168.7	P	strong similarity to hypothetical protein YHR199c
4313_at	5783.8	P	strong similarity to hypothetical protein YHR198c
4314_at	11682.6	P	homolog of the mammalian S5a protein, component of 26S proteas
4315_at	4147.6	P	Cytosolic exopolyphosphatase
4316_at	3941.3	P	similarity to S.pombe hypothetical protein SPAC17G6
4317_at	4363.5	P	similarity to alpha-mannosidases
4318_at	3320.2	P	cAMP-dependent protein kinase homolog, suppressor of cdc25ts
4319_at	7426	P	Protein with similarity to DNA-binding region of heat shock transcripti
4320_at	6558.1	P	weak similarity to YPL165c
4321_at	34595.8	P	branched-chain amino acid transaminase, highly similar to mammali
4322_at	796.1	P	UDP-glucose-4-epimerase (GAL10, galE)
4323_f_at	19063.4	P	IMP dehydrogenase\; probable PUR5 gene
4324_s_at	3693.8	P	gene in Y repeat region
4325_at	179.7	A	questionable ORF
4326_at	1408.3	P	questionable ORF
4327_at	69.2	A	questionable ORF
4328_at	727.8	A	questionable ORF
4329_at	114.6	A	questionable ORF
4330_at	1198.9	P	questionable ORF
4331_at	225.7	A	questionable ORF
4332_at	56.8	A	questionable ORF
4286_s_at	2691.1	P	Highly acidic C-terminus
4287_s_at	820.6	P	similarity to hypothetical protein YER175c
4288_at	3225.6	P	non-annotated SAGE orf Found reverse in NC_001140 between 345
4289_at	34.1	A	non-annotated SAGE orf Found reverse in NC_001140 between 518
4290_at	541	P	non-annotated SAGE orf Found reverse in NC_001140 between 519
4291_i_at	25.2	A	non-annotated SAGE orf Found reverse in NC_001140 between 917
4292_at	1339.9	P	non-annotated SAGE orf Found reverse in NC_001140 between 146
4293_at	2495.4	P	non-annotated SAGE orf Found forward in NC_001140 between 370
4294_at	1032.7	A	non-annotated SAGE orf Found forward in NC_001140 between 560
4295_at	944	P	non-annotated SAGE orf Found forward in NC_001140 between 804
4296_at	939	A	non-annotated SAGE orf Found reverse in NC_001140 between 122
4297_at	84.6	A	non-annotated SAGE orf Found forward in NC_001140 between 146
4298_at	118.3	A	non-annotated SAGE orf Found reverse in NC_001140 between 167
4299_at	915.8	P	non-annotated SAGE orf Found reverse in NC_001140 between 225
4300_at	793.6	P	non-annotated SAGE orf Found reverse in NC_001140 between 374
4301_at	66	A	non-annotated SAGE orf Found forward in NC_001140 between 508
4302_at	1847.7	P	non-annotated SAGE orf Found forward in NC_001140 between 209
4303_at	4297.4	P	non-annotated SAGE orf Found forward in NC_001140 between 467
4304_f_at	339.4	A	non-annotated SAGE orf Found forward in NC_001140 between 528
4305_at	1402.6	P	non-annotated SAGE orf Found reverse in NC_001140 between 566
4306_i_at	41.1	A	non-annotated SAGE orf Found reverse in NC_001140 between 577
4307_f_at	18.9	A	non-annotated SAGE orf Found reverse in NC_001140 between 577
4308_at	281.3	P	non-annotated SAGE orf Found reverse in NC_001140 between 202
4309_i_at	70.8	A	non-annotated SAGE orf Found forward in NC_001140 between 203
4261_s_at	10.2	A	non-annotated SAGE orf Found forward in NC_001140 between 203
4262_i_at	15.3	A	non-annotated SAGE orf Found forward in NC_001140 between 203
4263_at	347.2	A	non-annotated SAGE orf Found reverse in NC_001140 between 204
4264_at	770.6	P	non-annotated SAGE orf Found reverse in NC_001140 between 422
4265_s_at	368.6	A	non-annotated SAGE orf Found reverse in NC_001140 between 422
4266_at	1432.5	P	non-annotated SAGE orf Found reverse in NC_001140 between 422
4267_at	220.1	A	non-annotated SAGE orf Found reverse in NC_001140 between 458

4268_at	15.4	A	non-annotated SAGE orf Found reverse in NC_001140 between 522
4269_f_at	563.7	A	non-annotated SAGE orf Found forward in NC_001140 between 530
4270_f_at	167.9	A	non-annotated SAGE orf Found reverse in NC_001140 between 530
4271_at	31.2	A	non-annotated SAGE orf Found reverse in NC_001140 between 531
4272_at	7596.6	P	non-annotated SAGE orf Found reverse in NC_001140 between 111
4273_at	385.6	A	non-annotated SAGE orf Found forward in NC_001140 between 157
4274_at	4741.2	P	non-annotated SAGE orf Found forward in NC_001140 between 175
4275_at	356.7	A	non-annotated SAGE orf Found forward in NC_001140 between 198
4276_at	75.2	A	non-annotated SAGE orf Found reverse in NC_001140 between 410
4277_i_at	0.4	A	Centromere
4278_at	479.7	M	snRNA
4279_at	3974.7	P	snRNA
4280_f_at	4948.4	P	strong similarity to members of the Srp1p/Tip1p family
4281_i_at	4517.5	A	High-affinity hexose transporter
4282_f_at	346.7	A	High-affinity hexose transporter
4283_at	161.8	A	L-serine dehydratase
4284_at	26.7	A	serine dehydratase
4285_at	698.1	P	similarity to allantoate permease Dal5p
4237_at	1348.3	P	putative pseudogene
4238_at	1238.2	A	Nit1 nitrilase
4239_at	125.1	A	questionable ORF
4240_at	8739.9	P	hypothetical protein
4241_at	728	A	peroxisomal 3-oxoacyl CoA thiolase
4242_at	158.7	A	Bni1p-related protein, helps regulate reorganization of the actin cytos
4243_at	4765	P	similarity to hypothetical protein YKR100c
4244_at	1236.5	P	hypothetical protein
4245_at	513.9	P	Ubiquitin-specific protease
4246_at	5589.9	P	glycerol-3-phosphate dehydrogenase, mitochondrial
4247_at	2770.4	P	transcription factor
4248_at	4459.8	P	Resistant to Rapamycin Deletion
4249_at	1543.4	P	hypothetical protein
4250_at	1094.6	P	similarity to mitochondrial aldehyde dehydrogenase Ald1p
4251_at	365.4	P	Protein required for S-phase (DNA synthesis) initiation or completion
4252_at	2084.6	P	similarity to Mlp1p and myosin heavy chains
4253_i_at	26289.7	A	Ribosomal protein L40A
4254_at	3702.7	P	histidine kinase osmosensor that regulates an osmosensing MAP ki
4255_at	2012.6	P	ExtraCellular Mutant
4256_at	1436	P	similarity to E.coli pantothenate synthetase
4257_at	410.9	A	Dmc1p interacting protein
4258_at	1919.3	P	DNA helicase homolog\; homolog of human XPBC, ERCC3
4259_at	14420.5	P	molecular chaperone
4260_at	3424.3	P	questionable ORF
4215_g_at	2056.2	P	questionable ORF
4216_at	3667.2	P	localizes to the plasma membrane
4217_at	452.1	P	subunit of DNA polymerase-zeta (Pol-zeta), an enzyme whose sole
4218_at	1438.2	P	Tropomyosin isoform 2
4219_at	3811.1	P	similarity to M.musculus aminopeptidase
4220_at	460	A	45-kDa mitochondrial outer membrane protein
4221_at	6166.5	P	similarity to Ymk1p
4222_at	882.5	P	mitochondrial inner membrane carrier protein for FAD
4223_at	21474.3	P	Ribosomal protein L16A (L21A) (rp22) (YL15)
4224_at	539.4	A	hypothetical protein

4225_at	3252.7	P	similarity to Drosophila fork head protein
4226_at	7811.4	P	similarity to Put3p and to hypothetical protein YJL206c
4227_at	5424.7	P	similarity to hypothetical human protein
4228_at	2085.5	P	Involved in nucleotide excision repair and regulation of TFIIH
4229_at	2387.6	P	weak similarity to Smy2p
4230_at	2905	P	helicase related protein, snf2 homolog
4231_at	17539.9	P	alpha-ketoglutarate dehydrogenase
4232_at	7619.8	P	similarity to C.perfringens nanH protein
4233_at	28599	P	involved in cell cycle regulation and aging
4234_at	1009.9	P	hypothetical protein
4235_at	818.8	M	similarity to antibiotic resistance proteins
4236_at	921	A	similarity to antibiotic resistance proteins
4192_at	2850.7	P	inhibitor of ras
4193_at	2559.4	P	ras homolog--GTP binding protein
4194_at	3600.8	P	hydrophobic transmembrane domain
4195_at	1409.5	P	histidinol-phosphate aminotransferase
4196_at	1212.3	P	159-kDa nucleoporin with coiled-coil domain and repeated motifs typ
4197_at	3824.9	P	voltage dependent anion channel (YVDAC2)
4198_at	58	A	strong similarity to dual-specificity phosphatase Msg5p
4199_at	1062	M	similarity to ankyrin and coiled-coil proteins
4200_at	115.6	A	Cytochrome-c oxidase chain Vb
4201_at	2881.8	P	weak similarity to hypothetical C.elegans protein
4202_at	7888.5	P	The Sec23p-Sec24p complex is one of three cytoplamic COPII facto
4203_at	6633.1	P	similarity to hypothetical S. pombe protein
4204_at	362.3	A	6-Phosphofructose-2-kinase
4205_at	526.2	P	weak similarity to probable transcription factor Ask10p
4206_at	803	P	similarity to hypothetical S. pombe protein
4207_at	3400	P	weak similarity to Dph2 protein
4208_at	34.7	A	strong similarity to YIL014c-a
4209_at	118.2	A	DNA-binding transcriptional repressor
4210_at	248.5	A	similarity to mouse Gcap1 protein and fruit fly Bkm-like sex-determin
4211_at	1858.8	P	intracellular glucoamylase
4212_g_at	139.4	A	intracellular glucoamylase
4213_at	900.7	P	Formation of Mitochondrial Cytochromes 1
4214_at	742.9	P	hypothetical protein
4170_at	10375	P	hypothetical protein
4171_at	201.5	A	probable serine\/threonine-protein kinase
4172_at	10702.5	P	Homo-isocitrate dehydrogenase
4173_at	634.8	P	weak similarity to S.pombe hypothetical protein SPBC16A3
4174_at	483.7	P	hypothetical protein
4175_at	3359.9	P	weak similarity to spt5p
4176_at	4044.7	P	similarity to hypothetical S. pombe protein
4177_at	791.9	P	similarity to hypothetical protein YLR036c
4178_at	16058.7	P	weak similarity to A.thaliana aminoacid permease AAP4
4179_at	3394.2	P	hypothetical protein
4180_at	129.6	A	hypothetical protein
4181_at	3026.7	P	Putative mannosyltransferase of the KRE2 family
4182_at	434.7	M	Functions are similar to those of SIN3 and RPD3
4183_at	5374.7	P	hypothetical protein
4184_s_at	2755.1	P	Ty3-2 orf C fragment
4185_at	2376.4	P	strong similarity to hypothetical protein YDL175c
4186_at	27264.9	P	Threonyl-tRNA synthetase, cytoplasmic

4187_at	681.4	P	hypothetical protein
4188_at	8720.3	P	epsilon-COP coatomer subunit Sec28p
4189_at	18930	P	RPN2p is a component of the 26S proteosome
4190_at	7495.7	P	strong similarity to E.coli phosphoglycerate dehydrogenase
4191_at	74.4	A	weak similarity to mouse polycystic kidney disease-related protein
4147_at	228.9	A	Meiosis-specific protein involved in homologous chromosome synaps
4148_at	372.4	P	hypothetical protein
4149_at	11726.1	P	mitochondrial acidic matrix protein
4150_at	4778.5	P	88 kD component of the Exocyst complex, which contains the gene
4151_at	2889.3	P	hypothetical protein
4152_at	2153.6	P	similarity to C.elegans hypothetical protein
4153_at	3880.7	P	weak similarity to fowlpox virus major core protein
4154_at	1365.7	P	nuclear protein, interacts with Gsp1p and Crm1p
4155_at	6428.5	P	Arp Complex Subunit
4156_at	143.4	A	U1snRNP 70K protein homolog
4157_at	529.1	P	questionable ORF
4158_at	1882.7	P	hypothetical protein
4159_at	314.1	A	hypothetical protein
4160_at	153.2	A	strong similarity to YER067w
4161_at	6703.4	P	similarity to YER064c
4162_at	479.3	P	hypothetical protein
4163_at	561.8	P	weak similarity to fruit fly NADH dehydrogenase
4164_at	28460	P	DL-glycerol-3-phosphatase
4165_i_at	32567.3	P	Ribosomal protein L34B
4166_at	22353.3	P	Maintenance of Mitochondrial DNA 1
4167_at	4417.8	P	PHO85 cyclin
4168_at	5487.6	P	Protein required for filamentous growth, cell polarity, and cellular elo
4169_at	10657	P	ATPase that leads to neomycin-resistant protein when overexpresse
4124_at	21890.1	P	plasma membrane protein
4125_at	1922.9	P	Met30p contains five copies of WD40 motif and interacts with and re
4126_at	233.9	A	Protein with 30\%% identity to protein corresponding to YER054
4127_at	2331	P	weak similarity to zinc finger protein Gcs1p
4128_at	13692.5	P	cytochrome b reductase
4129_at	1402.2	P	similarity to rat branched-chain alpha-ketoacid dehydrogenase kinas
4130_at	13159.6	P	similarity to S.pombe hypothetical protein
4131_at	7373.5	P	weak similarity to T.brucei NADH dehydrogenase
4132_at	12718.7	P	hypothetical protein
4133_at	2477.6	P	General negative regulator of transcription\; may inhibit RNA polymer
4134_at	89.3	A	hypothetical protein
4135_at	1687.4	P	weak similarity to human cAMP responce element-binding protein
4136_at	3520.5	P	alpha subunit of casein kinase II
4137_at	2096.1	P	beta subunit of capping protein
4138_at	9083.8	P	regulatory subunit of cAMP-dependent protein kinase
4139_at	1149.6	M	hypothetical protein
4140_at	724.4	P	Suppressor of Mif Two
4141_at	9240.7	P	integral nuclear membrane protein
4142_at	199	M	strong similarity to hypothetical protein YPR071w
4143_at	351.2	A	putative pseudogene
4144_at	7364.6	P	hypothetical protein
4145_at	738.9	P	Irregular
4146_at	21.2	A	weak similarity to E.gracilis RNA polymerase subunit
4101_at	1122.4	P	hypothetical protein

4102_at	3793.3	P	similarity to mouse MHC H-2K/t-w5-linked ORF precursor
4103_at	6762.2	P	48.8 kDa protein involved in mitochondrial protein import
4104_at	5780.3	P	45 kDa subunit of RNA polymerase II
4105_at	3186.4	P	phosphoribosyl-5-amino-1-phosphoribosyl-4-imidazolecarboxiamide
4106_at	714.3	P	weak similarity to S.pombe hypothetical protein SPAC3F10
4107_at	439.6	P	hypothetical protein
4108_at	1917.1	P	18.3 kD integral membrane protein
4109_at	92.8	A	encodes a-cell barrier activity on alpha factor
4110_at	24.7	A	strong similarity to hypothetical protein YIL102c
4111_at	4211.2	P	similarity to Mnn1p
4112_at	992.5	P	Putative member of the ABC family of membrane transporters
4113_at	213.9	A	hypothetical protein
4114_at	12559.3	P	strong similarity to members of the Srp1p/Tip1p family
4115_at	3902.8	P	Derepression Of Telomeric silencing
4116_at	933.9	P	181aa protein - 20.5 kD
4117_at	287.7	A	181aa protein - 20.5 kD
4118_at	7746.4	P	Acyl CoA synthase
4119_at	6786.3	P	hypothetical protein
4120_at	435.8	A	similarity to C.elegans hypothetical protein
4121_at	1409.6	P	similarity to Flx1p
4122_at	5253.7	P	similarity to protein disulfide isomerases
4123_at	2591.3	P	Synaptobrevin (t-SNARE) homolog present on ER vesicles recycling
4079_at	1737.5	P	strong similarity to Nbp35p and human nucleotide-binding protein
4080_at	1906.3	P	phosphatidylinositol 4,5-bisphosphate 5-phosphatase
4081_at	1218	P	similarity to S.pombe hypothetical protein, weak similarity to human
4082_at	888.4	P	similarity to D.melanogaster RNA binding protein
4083_at	2037.3	P	weak similarity to ATP-dependent RNA helicases
4084_at	2968.1	P	weak similarity to mammalian neurofilament triplet H proteins
4085_at	1006.2	P	DnaJ-like protein required for Peroxisome biogenesis\; Djp1p is locat
4086_at	570.7	A	similarity to RNA-binding proteins
4087_at	14640.7	P	polyA-specific ribonuclease
4088_at	994.1	P	hypothetical protein
4089_at	3963	P	p48 polypeptide of DNA primase
4090_at	1002.4	P	encodes YU2B, a component of yeast U2 snRNP
4091_at	2752.4	P	hypothetical protein
4092_at	5582.9	P	restores protein transport when overexpressed and rRNA stability to
4093_at	10552.7	P	contains multiple WD repeats and interacts with Qsr1p in two hybrid
4094_at	504.4	A	strong similarity to YLR013w, similarity to YMR136w
4095_at	446.6	P	hypothetical protein
4096_at	436.1	A	an integral subunit of RNase P but not RNase MRP
4097_at	3027.9	P	weak similarity to YOL036w
4098_at	684.8	A	Transcriptional activator of sulfur amino acid metabolism
4099_at	1131.9	A	bZIP protein\; transcription factor
4100_at	18753.2	P	cell surface flocculin with structure similar to serine\/threonine-rich G
4056_at	628.5	P	hypothetical protein
4057_at	1083	P	mitochondrial RNA splicing
4058_at	5265	P	signal peptidase subunit
4059_at	1788.7	P	Transcriptional activator for allantoin and GABA catabolic genes, co
4060_at	1301.6	P	G1 Factor needed for normal G1 phase
4061_at	820.2	P	hypothetical protein
4062_at	6922.3	P	nitrogen starvation-induced protein phosphatase
4063_at	211.4	A	allantoinase

4064_at	345.9	A	allantoin permease
4065_at	407.7	A	allantoicase
4066_at	701.7	P	involved in nitrogen-catabolite metabolism
4067_at	248.4	A	Malate synthase 2
4068_at	127.9	A	ureidoglycolate hydrolase
4069_at	808.3	P	may be involved in the remodeling chromatin structure
4070_at	5883.8	P	saccharopine dehydrogenase
4071_at	4969.3	P	similarity to human corticosteroid 11-beta-dehydrogenase
4072_at	2880.7	P	similarity to E.coli fabD
4073_at	10535.8	P	putative glutathione-peroxidase
4074_at	1586.4	P	Glutathione transferase
4075_at	365	A	GPI-anchored aspartic protease
4076_f_at	1100.1	P	similarity to members of the Srp1p/Tip1p family
4077_at	882.6	P	weak similarity to B.licheniformi hypothetical protein P20
4078_i_at	497.7	M	putative pseudogene
4032_f_at	169	A	putative pseudogene
4033_f_at	9200.3	P	putative pseudogene
4034_at	58	A	hypothetical protein
4035_at	98.6	A	questionable ORF
4036_at	127.3	A	questionable ORF
4037_at	44	A	questionable ORF
4038_at	629	M	questionable ORF
4039_at	117.2	A	questionable ORF
4040_at	577.8	A	questionable ORF
4041_at	196.6	A	hypothetical protein
4042_at	1573.1	P	questionable ORF
4043_s_at	1038.6	M	invertase (sucrose hydrolyzing enzyme)
4044_s_at	1135.3	P	Mps One Binder
4045_s_at	163.8	A	Ribonucleotide reductase (ribonucleoside-diphosphate reductase) la
4046_at	67.5	A	non-annotated SAGE orf Found forward in NC_001141 between 197
4047_at	553.9	A	non-annotated SAGE orf Found forward in NC_001141 between 268
4048_at	28.3	A	non-annotated SAGE orf Found forward in NC_001141 between 414
4049_at	754.4	A	non-annotated SAGE orf Found forward in NC_001141 between 438
4050_at	1139.9	P	non-annotated SAGE orf Found forward in NC_001141 between 144
4051_at	298.2	A	non-annotated SAGE orf Found forward in NC_001141 between 173
4052_i_at	14.8	A	non-annotated SAGE orf Found forward in NC_001141 between 324
4053_s_at	2899.6	P	non-annotated SAGE orf Found forward in NC_001141 between 324
4054_at	3394.4	P	non-annotated SAGE orf Found forward in NC_001141 between 350
4055_at	150.8	A	non-annotated SAGE orf Found forward in NC_001141 between 398
4009_at	10645.9	P	non-annotated SAGE orf Found forward in NC_001141 between 269
4010_at	28.7	A	non-annotated SAGE orf Found reverse in NC_001141 between 139
4011_at	1183.6	P	non-annotated SAGE orf Found reverse in NC_001141 between 139
4012_at	292.3	A	non-annotated SAGE orf Found forward in NC_001141 between 169
4013_i_at	54	A	non-annotated SAGE orf Found reverse in NC_001141 between 210
4014_at	2259.2	A	non-annotated SAGE orf Found forward in NC_001141 between 230
4015_at	450.8	M	non-annotated SAGE orf Found forward in NC_001141 between 258
4016_at	1446	P	non-annotated SAGE orf Found forward in NC_001141 between 258
4017_at	736.9	P	non-annotated SAGE orf Found reverse in NC_001141 between 324
4018_at	1038.1	A	non-annotated SAGE orf Found reverse in NC_001141 between 385
4019_at	905.7	A	non-annotated SAGE orf Found reverse in NC_001141 between 385
4020_at	989	M	non-annotated SAGE orf Found reverse in NC_001141 between 386
4021_at	339.2	A	non-annotated SAGE orf Found forward in NC_001141 between 387

4022_at	401.1	A	non-annotated SAGE orf Found forward in NC_001141 between 425
4023_s_at	91.3	A	non-annotated SAGE orf Found forward in NC_001141 between 213
4024_at	386.9	P	non-annotated SAGE orf Found reverse in NC_001141 between 306
4025_i_at	3362.9	P	non-annotated SAGE orf Found reverse in NC_001141 between 516
4026_at	294.3	A	non-annotated SAGE orf Found forward in NC_001141 between 122
4027_at	311.6	P	non-annotated SAGE orf Found forward in NC_001141 between 154
4028_at	673.4	A	non-annotated SAGE orf Found reverse in NC_001141 between 231
4029_at	4224.8	P	non-annotated SAGE orf Found reverse in NC_001141 between 355
4030_at	1102.2	P	non-annotated SAGE orf Found forward in NC_001141 between 385
4031_at	2316.1	P	snRNA
3983_at	104	A	cytochrome-c oxidase subunit II
3984_r_at	45.1	A	questionable ORF Found forward in NC_001224 between 74495 and
3985_i_at	283.9	A	questionable ORF Found forward in NC_001224 between 74495 and
3986_f_at	358.8	A	questionable ORF Found forward in NC_001224 between 74495 and
3987_at	13.2	A	similarity to Podospora cytb intron 1a and coII intron protein 2 Found
3988_at	377.8	A	cytochrome-c oxidase chain III
3989_at	71.2	A	strong similarity to maturase-related hypothetical protein RF2
3990_i_at	9.1	A	similarity to hypothetical protein Sgc2p Found forward in NC_001224
3991_r_at	5.8	A	similarity to hypothetical protein Sgc2p Found forward in NC_001224
3992_f_at	6	A	similarity to hypothetical protein Sgc2p Found forward in NC_001224
3993_at	3.9	A	strong similarity to Yeast (S.uvarum) mitochondria RF2 gene and ma
3994_at	661.9	P	similarity to Sauroleishmania NADH dehydrogenase (ubiquinone) ch
3995_i_at	48.2	A	RF2 protein Found forward in NC_001224 between 8526 and 8736 w
3996_s_at	884.3	P	cytochrome-c oxidase subunit I Found forward in NC_001224 betwee
3997_at	435.1	A	questionable ORF Found reverse in NC_001224 between 13748 and
3998_at	255.9	P	COX1 intron 1 protein Found forward in NC_001224 between 13818
3999_at	3.5	A	COX1 intron 2 protein Found forward in NC_001224 between 16473
4000_at	15.8	A	COX1 intron 3 protein Found forward in NC_001224 between 18992
4001_at	6882.2	P	cytochrome-c oxidase subunit I Found forward in NC_001224 betwee
4002_at	138.6	P	DNA endonuclease I-SceII Found forward in NC_001224 between 2
4003_s_at	2492.6	P	cytochrome-c oxidase subunit I Found forward in NC_001224 betwee
4004_at	625	P	probable mRNA maturase aI5-alpha Found forward in NC_001224 b
4005_at	14885	P	cytochrome-c oxidase subunit I Found forward in NC_001224 betwee
4006_at	65.8	A	COX1 intron protein aI5-beta Found forward in NC_001224 between
4007_at	968.5	P	cytochrome-c oxidase subunit I Found forward in NC_001224 betwee
4008_at	1140.5	P	cytochrome-c oxidase subunit I Found forward in NC_001224 betwee
3956_i_at	228.4	A	F1F0-ATPase complex, F0 subunit 8 Found forward in NC_001224
3957_r_at	434.5	P	F1F0-ATPase complex, F0 subunit 8 Found forward in NC_001224
3958_r_at	68.2	A	similarity to mouse Gcap1 Found forward in NC_001224 between 28
3959_at	917	P	F1F0-ATPase complex, FO A subunit Found forward in NC_00122
3960_at	7.2	A	endonuclease SCEI, small subunit Found forward in NC_001224 be
3961_i_at	0	A	endonuclease SCEI, small subunit Found forward in NC_001224 be
3962_f_at	2213	A	endonuclease SCEI, small subunit Found forward in NC_001224 be
3963_at	0.5	A	endonuclease SCEI, small subunit Found forward in NC_001224 be
3964_at	3.6	A	endonuclease SCEI, small subunit Found forward in NC_001224 be
3965_i_at	12.8	A	ORF5 Found forward in NC_001224 between 30874 and 31014 with
3966_i_at	34.2	A	similarity to T.brucei mitochondrion protein SGC6 Found reverse in
3967_r_at	22.4	A	similarity to T.brucei mitochondrion protein SGC6 Found reverse in
3968_s_at	2750.3	P	ubiquinol--cytochrome-c reductase subunit (cytochrome B) Found fo
3969_at	11.5	A	mRNA maturase bI2 Found forward in NC_001224 between 37723 a
3970_s_at	2869.2	P	ubiquinol--cytochrome-c reductase subunit (cytochrome B) Found fo
3971_at	2.2	A	mRNA maturase bI3 Found forward in NC_001224 between 39141 a

3972_s_at	2451.6	P	ubiquinol--cytochrome-c reductase subunit (cytochrome B) Found for
3973_at	275.4	P	mRNA maturase bI4 Found forward in NC_001224 between 40815 a
3974_at	2432.9	P	ubiquinol--cytochrome-c reductase subunit (cytochrome B) Found for
3975_at	1014.1	P	ubiquinol--cytochrome-c reductase subunit (cytochrome B) Found for
3976_at	16701.4	P	F1F0-ATPase complex, F0 subunit 9 Found forward in NC_001224
3977_i_at	481.3	A	similarity to honeybee mitochondrion NADH dehydrogenase chain 6
3978_r_at	12.8	A	similarity to honeybee mitochondrion NADH dehydrogenase chain 6
3979_i_at	7.2	A	mitochondrial ribosomal protein Found forward in NC_001224 betwe
3980_r_at	13.5	A	mitochondrial ribosomal protein Found forward in NC_001224 betwe
3981_at	195.6	P	probable mRNA maturase in 21S rRNA intron Found forward in NC_
3982_at	59.1	A	kanamycin resistance casette
3932_at	17.8	A	MAL-activator 23 (MAL23) gene
3933_s_at	2706.3	P	Required for the catabolism of melibiose and regulated by several G
3934_at	2521.5	P	Protein that confers resistance to molasses
3935_at	27.6	A	Tropomyosin-related protein with transmembrane domain and basic
3936_at	1319.9	P	invertase (sucrose hydrolyzing enzyme)
3937_g_at	7734.8	P	invertase (sucrose hydrolyzing enzyme)
3938_at	2257.3	P	Protein involved in targeting of plasma membrane [H+]ATPase
3939_at	932.6	P	Probable aldehyde dehydrogenase (EC 1.2.1.-)
3940_at	537.9	P	Degradation in the Endoplasmic Reticulum
3941_at	1939.5	P	Ser\/Thr protein kinase
3942_at	10008.3	P	bZIP (basic-leucine zipper) protein
3943_i_at	30087.7	P	bZIP (basic-leucine zipper) protein
3944_f_at	13755.9	A	bZIP (basic-leucine zipper) protein
3945_at	1076.7	P	Protein essential for mitochondrial biogenesis and cell viability
3946_at	873.1	P	Protein essential for mitochondrial biogenesis and cell viability
3947_at	10708.1	P	strong similarity to holacid-halidohydrolase
3948_s_at	1114.8	P	probable serine\/threonine-specific protein kinase (EC 2.7.1.-)
3949_i_at	11346.4	P	protein of unknown function
3950_at	1468.8	P	Rho family GTPase
3951_at	2192.2	P	2 micron plasmid recombinase
3952_at	12535.2	P	2 micron plasmid rep1 protein
3953_at	17202.5	P	2 micron plasmid D protein
3954_at	6674.1	P	2 micron plasmid rep2 protein
3955_at	611.9	P	2 micron plasmid recombinase
3907_f_at	4183.3	P	strong similarity to subtelomeric encoded proteins
3908_i_at	145.2	P	Ty1 LTR
3909_f_at	198.7	A	Ty1 LTR
3910_at	29.1	A	Ty1 LTR
3911_at	5	A	Ty1 LTR
3912_f_at	23568.3	P	Ty1 LTR
3913_s_at	21435	P	Full length Ty1
3914_s_at	35270.3	P	Full length Ty1
3915_s_at	31870.3	P	Full length Ty1
3916_s_at	22618.7	P	Full length Ty1
3917_f_at	11896.7	P	Full length Ty1
3918_f_at	29020.7	P	Full length Ty1
3919_f_at	15970.9	P	Saccharomyces cerevisiae chromosome I, complete chromosome se
3920_f_at	37249.5	P	Saccharomyces cerevisiae chromosome I, complete chromosome se
3921_s_at	28173.3	P	Saccharomyces cerevisiae chromosome I, complete chromosome se
3922_f_at	27395.4	P	Ty1 LTR
3923_f_at	5608.2	P	tRNA-Ala

3924_f_at	3986.1	P	tRNA-Ser
3925_f_at	8787.5	P	Ty3 LTR Found forward in NC_001133 between 182610 and 182949
3926_f_at	4863.9	P	Ty1 LTR
3927_f_at	5824.2	P	Ty2 LTR
3928_f_at	187.5	M	Ty1 LTR
3929_s_at	1256.9	P	tRNA-Thr
3930_i_at	45.3	A	Ty1 LTR
3931_f_at	874.8	P	Ty1 LTR
3884_f_at	12926.7	P	tRNA-Glu
3885_f_at	9038.4	P	tRNA-Ala
3886_f_at	328.4	A	Ty3 LTR
3887_f_at	1373	P	Ty4 LTR
3888_s_at	108.7	A	Saccharomyces cerevisiae chromosome X, complete chromosome s
3889_s_at	309.7	A	Saccharomyces cerevisiae chromosome X, complete chromosome s
3890_s_at	8.5	A	Saccharomyces cerevisiae chromosome X, complete chromosome s
3891_s_at	33.4	A	Saccharomyces cerevisiae chromosome X, complete chromosome s
3892_s_at	250.7	A	Saccharomyces cerevisiae chromosome X, complete chromosome s
3893_s_at	15.1	A	Saccharomyces cerevisiae chromosome X, complete chromosome s
3894_s_at	17.8	A	Saccharomyces cerevisiae chromosome X, complete chromosome s
3895_s_at	506.4	P	Saccharomyces cerevisiae chromosome X, complete chromosome s
3896_s_at	9	A	Full length Ty4
3897_s_at	10.9	A	Full length Ty4
3898_s_at	2.1	A	Full length Ty4
3899_s_at	192.2	M	Full length Ty4
3900_f_at	3691.7	P	Full length Ty4
3901_f_at	1541.8	P	Ty4 LTR
3902_f_at	8986.7	P	Ty1 LTR
3903_i_at	3.6	A	Ty1 LTR
3904_f_at	665.9	P	Ty1 LTR
3905_s_at	7313.4	P	tRNA-Asp
3906_f_at	1014.2	P	tRNA-Arg
3859_i_at	237.6	A	Ty1 LTR
3860_f_at	18345.6	P	Ty1 LTR
3861_f_at	17487	P	Ty1 LTR
3862_f_at	784.8	P	tRNA-Arg
3863_f_at	672.9	P	tRNA-Arg
3864_i_at	492.5	A	Ty1 LTR
3865_f_at	8.7	A	Ty1 LTR
3866_at	84.7	A	Ty1 LTR
3867_s_at	12876.4	P	tRNA-Val
3868_s_at	362.2	P	tRNA-Met
3869_f_at	5286.1	P	tRNA-Gly
3870_s_at	1556.3	P	tRNA-Lys
3871_at	3.8	A	Ty4 LTR
3872_i_at	128.2	A	Ty1 LTR
3873_f_at	15.7	A	Ty1 LTR
3874_i_at	1.2	A	Ty1 LTR
3875_f_at	118.5	A	Ty1 LTR
3876_at	172.6	P	Ty4 LTR
3877_at	616.6	M	Ty1 LTR
3878_s_at	10646.5	P	tRNA-Leu
3879_f_at	20919.2	P	Ty1 LTR

3880_f_at	19433.9	P	Saccharomyces cerevisiae chromosome X, complete chromosome s
3881_f_at	16508.6	P	Full length Ty1
3882_f_at	24536.2	P	Full length Ty1
3883_f_at	15074	P	Ty1 LTR
3835_s_at	36293.3	P	Saccharomyces cerevisiae chromosome X, complete chromosome s
3836_f_at	16343.9	P	Full length Ty1
3837_f_at	24454.8	P	Ty1 LTR
3838_s_at	954.3	A	tRNA-Met
3839_at	8.4	A	Ty1 LTR
3840_f_at	3892.7	P	tRNA-Ser
3841_at	531.7	M	Ty1 LTR
3842_f_at	5872.5	P	tRNA-Gly
3843_at	902	P	Ty1 LTR
3844_f_at	22324.6	P	Ty1 LTR
3845_i_at	50.3	A	tRNA-Arg
3846_f_at	37.5	A	tRNA-Arg
3847_i_at	14.2	A	Ty1 LTR
3848_f_at	2674	P	Ty1 LTR
3849_f_at	944.5	P	Ty1 LTR
3850_at	1663.4	P	Ty1 LTR
3851_s_at	9666.8	P	Protein with similarity to members of the Ybr302p\/Ycr007p\/Cos8p\/
3852_f_at	3705.5	P	Protein with similarity to members of the Ybr302p\/Ycr007p\/Cos8p\/
3853_f_at	2584.3	P	strong similarity to subtelomeric encoded proteins
3854_f_at	535.1	P	strong similarity to Gin11p, YKL225w and other subtelomeric encode
3855_s_at	10.8	A	strong similarity to subtelomeric encoded proteins
3856_at	192.4	A	tRNA-Thr
3857_at	9.9	A	Ty1 LTR
3858_s_at	564.8	A	tRNA-Asn
3812_at	780.9	A	Ty1 LTR
3813_f_at	12607.8	P	tRNA-Glu
3814_f_at	733.7	P	tRNA-Arg
3815_i_at	5.8	A	Ty1 LTR
3816_f_at	237.5	A	Ty1 LTR
3817_f_at	9788.2	P	Ty3 LTR
3818_at	143.6	A	Ty1 LTR
3819_f_at	7490.1	P	tRNA-Ala
3820_f_at	1278.1	P	Ty1 LTR
3821_f_at	3316.7	P	tRNA-His
3822_f_at	1189.1	P	Ty1 LTR
3823_f_at	7772.8	P	Ty1 LTR
3824_f_at	20530.4	P	Ty1 LTR
3825_at	25.7	A	Ty1 LTR
3826_at	40.8	A	Ty1 LTR
3827_f_at	1137.2	P	tRNA-Arg
3828_f_at	913.5	P	Ty1 LTR
3829_f_at	23658.9	P	Ty1 LTR
3830_f_at	8928.7	P	tRNA-Ala
3831_s_at	56.8	A	strong similarity to subtelomeric encoded proteins
3832_s_at	21.7	A	strong similarity to subtelomeric encoded proteins
3833_f_at	5.9	A	Ty5 LTR
3834_s_at	5612.1	P	strong similarity to subtelomeric encoded proteins
3789_s_at	8413.1	P	strong similarity to subtelomeric encoded proteins

3790_s_at	17181.3	P	strong similarity to subtelomeric encoded proteins
3791_s_at	148.7	A	strong similarity to subtelomeric encoded proteins
3792_s_at	14215.8	P	strong similarity to subtelomeric encoded proteins
3793_f_at	1540.7	P	Ty1 LTR
3794_f_at	3790.3	P	tRNA-Ser
3795_at	14.6	A	Ty3 LTR
3796_f_at	6086.9	P	tRNA-Ala
3797_f_at	21510.8	P	Ty1 LTR
3798_s_at	32466.9	P	Saccharomyces cerevisiae chromosome XII, complete chromosome
3799_f_at	16950.7	P	Ty1 LTR
3800_at	13.9	A	Ty1 LTR
3801_f_at	163.9	A	Ty1 LTR
3802_f_at	5056.6	P	Ty3 LTR
3803_f_at	1016	P	tRNA-Arg
3804_f_at	12721.7	P	tRNA-Gln
3805_f_at	807	P	Ty1 LTR
3806_s_at	21946.3	P	35S ribosomal RNA
3807_s_at	3316.5	P	35S ribosomal RNA
3808_s_at	25082.9	P	35S ribosomal RNA
3809_s_at	23118.3	P	35S ribosomal RNA
3810_s_at	4307.8	P	35S ribosomal RNA
3811_s_at	4280.4	P	35S ribosomal RNA
3764_s_at	6882.3	P	35S ribosomal RNA
3765_s_at	4802.9	P	25S ribosomal RNA
3766_s_at	24936.9	P	25S ribosomal RNA
3767_s_at	1022.7	P	18S ribosomal RNA
3768_i_at	37884.8	A	5S ribosomal RNA
3769_s_at	30117.9	P	5S ribosomal RNA
3770_i_at	33408.5	A	5S ribosomal RNA
3771_f_at	25180.3	P	Ty1 LTR
3772_f_at	23006.5	P	Full length Ty1
3773_f_at	31394.6	P	Full length Ty1
3774_f_at	27717.5	P	Saccharomyces cerevisiae chromosome XII, complete chromosome
3775_f_at	22071.6	P	Ty1 LTR
3776_i_at	9.1	A	Ty1 LTR
3777_f_at	56.2	A	Ty1 LTR
3778_f_at	16380.3	P	Ty1 LTR
3779_f_at	16814.7	P	Saccharomyces cerevisiae chromosome XII, complete chromosome
3780_f_at	7948.9	P	Full length Ty1
3781_f_at	25566	P	Full length Ty1
3782_f_at	20481.7	P	Ty1 LTR
3783_at	800.7	A	Ty1 LTR
3784_at	14.8	A	Ty4 LTR
3785_f_at	21511.6	P	Ty1 LTR
3786_s_at	29262	P	TY1B protein Found forward in NC_001144 between 652918 and 65
3787_f_at	15618	P	Saccharomyces cerevisiae chromosome XII, complete chromosome
3788_f_at	39437.1	P	Saccharomyces cerevisiae chromosome XII, complete chromosome
3740_f_at	10304.8	P	Full length Ty1
3741_f_at	21075.7	P	Full length Ty1
3742_f_at	16107.2	P	Ty1 LTR
3743_f_at	9509.7	P	tRNA-Ala
3744_i_at	5669.6	P	Ty3 LTR

3745_f_at	1436.2	P	Ty3 LTR
3746_at	293.9	A	Ty1 LTR
3747_at	6.1	A	Ty1 LTR
3748_i_at	3.5	A	Ty1 LTR
3749_r_at	39.8	A	Ty1 LTR
3750_f_at	64.5	A	Ty1 LTR
3751_f_at	17572.7	P	Ty2 LTR
3752_f_at	174.9	P	Ty1 LTR
3753_s_at	874.9	A	tRNA-Ile
3754_s_at	5175.7	P	tRNA-Ser
3755_f_at	381	P	Ty3 LTR
3756_i_at	63.6	A	Ty1 LTR
3757_f_at	304	M	Ty1 LTR
3758_f_at	13848.8	P	tRNA-Glu
3759_f_at	4668.4	P	Ty1 LTR
3760_at	2183.9	A	tRNA-Arg
3761_f_at	23365.4	P	Ty2 LTR
3762_s_at	6043.9	P	Saccharomyces cerevisiae chromosome XII, complete chromosome
3763_s_at	4324.3	P	Saccharomyces cerevisiae chromosome XII, complete chromosome
3717_s_at	20251.9	P	Saccharomyces cerevisiae chromosome XII, complete chromosome
3718_s_at	12284.9	P	Saccharomyces cerevisiae chromosome XII, complete chromosome
3719_s_at	21324.7	P	Saccharomyces cerevisiae chromosome XII, complete chromosome
3720_f_at	34151.2	P	Saccharomyces cerevisiae chromosome XII, complete chromosome
3721_s_at	12685.1	P	Full length Ty2
3722_s_at	19705	P	Full length Ty2
3723_f_at	19317	P	Full length Ty2
3724_f_at	21120.9	P	Ty2 LTR
3725_at	279.9	P	Ty1 LTR
3726_f_at	10348	P	Ty2 LTR
3727_f_at	12687.4	P	Full length Ty2
3728_f_at	20428.8	P	Saccharomyces cerevisiae chromosome XII, complete chromosome
3729_f_at	10949.6	P	Ty2 LTR
3730_at	1275.7	P	Ty1 LTR
3731_s_at	583.8	A	strong similarity to subtelomeric encoded proteins
3732_s_at	665.5	P	strong similarity to subtelomeric encoded proteins
3733_s_at	1442.8	A	strong similarity to subtelomeric encoded proteins
3734_s_at	1108	P	strong similarity to subtelomeric encoded proteins
3735_f_at	23257.9	P	strong similarity to subtelomeric encoded proteins
3736_s_at	994.2	P	strong similarity to subtelomeric encoded proteins
3737_s_at	841.2	P	strong similarity to subtelomeric encoded proteins
3738_s_at	18339.7	P	Protein with strong similarity to subtelomerically-encoded proteins su
3739_f_at	20039.8	P	Protein with strong similarity to subtelomerically-encoded proteins su
3695_f_at	763.2	P	tRNA-Arg
3696_at	252.3	A	Ty1 LTR
3697_f_at	13909.2	P	Ty2 LTR
3698_f_at	5739.1	P	tRNA-Gly
3699_f_at	27526.1	P	Ty1 LTR
3700_f_at	11900.2	P	Full length Ty1
3701_f_at	23258.5	P	Ty1 LTR
3702_f_at	25783.8	P	Ty1 LTR
3703_f_at	26746.3	P	Saccharomyces cerevisiae chromosome XIII, complete chromosome
3704_f_at	12750.2	P	Full length Ty1

3705_f_at	25225.1	P	Full length Ty1
3706_f_at	20548.1	P	Ty1 LTR
3707_f_at	3671.8	P	tRNA-Ser
3708_at	49.1	A	Ty4 LTR
3709_f_at	12393.4	P	tRNA-Glu
3710_f_at	7850.2	P	tRNA-Ala
3711_f_at	21316.7	P	Ty1 LTR
3712_s_at	4180.5	P	Full length Ty1
3713_s_at	11711.8	P	Full length Ty1
3714_f_at	9928.2	P	Full length Ty1
3715_f_at	21839.6	P	Ty1 LTR
3716_f_at	3493.6	P	tRNA-His
3671_f_at	19691.9	P	Ty1 LTR
3672_f_at	11205.2	P	Full length Ty1
3673_f_at	21137	P	Ty1 LTR
3674_i_at	517.2	A	Ty1 LTR
3675_r_at	360.3	A	Ty1 LTR
3676_f_at	466.4	P	Ty1 LTR
3677_f_at	485.5	A	Ty1 LTR
3678_at	9.2	A	Ty1 LTR
3679_at	9.7	A	Ty1 LTR
3680_i_at	110.1	A	Ty1 LTR
3681_s_at	34.5	A	Ty1 LTR
3682_i_at	3.4	A	Ty1 LTR
3683_f_at	107.9	A	Ty1 LTR
3684_f_at	1310.2	P	Ty4 LTR
3685_f_at	4267.6	P	Ty1 LTR
3686_f_at	264.2	P	Ty1 LTR
3687_f_at	826.2	P	tRNA-Arg
3688_f_at	7962.4	P	tRNA-Ala
3689_f_at	13145.7	P	Ty2 LTR
3690_f_at	4722.9	P	tRNA-Gln
3691_f_at	1664	P	Ty4 LTR
3692_at	13.6	A	Ty1 LTR
3693_f_at	368.3	P	Ty1 LTR
3694_at	603.3	A	strong similarity to subtelomeric encoded proteins
3646_s_at	38.9	A	strong similarity to subtelomeric encoded proteins
3647_f_at	5278.1	P	strong similarity to subtelomeric encoded proteins
3648_f_at	14241.4	P	Protein with similarity to subtelomerically-encoded proteins such as
3649_f_at	437	A	tRNA-Gly
3650_f_at	1322.4	P	Ty4 LTR
3651_f_at	21650	P	Ty1 LTR
3652_f_at	13034.2	P	Full length Ty1
3653_f_at	20609.5	P	Ty1 LTR
3654_i_at	49	A	Ty3 LTR
3655_f_at	139.7	A	Ty3 LTR
3656_f_at	18598.1	P	Ty1 LTR
3657_f_at	15639.6	P	Saccharomyces cerevisiae chromosome XIV, complete chromosome
3658_f_at	9175.6	P	Full length Ty1
3659_f_at	13272.8	P	Full length Ty1
3660_f_at	18852.6	P	Ty1 LTR
3661_at	2092.8	P	Ty3 LTR

3662_f_at	9147.7	P	Ty3 LTR
3663_f_at	1774.6	P	Ty4 LTR
3664_f_at	18828.4	P	Ty2 LTR
3665_f_at	19163.7	P	Full length Ty2
3666_f_at	18932.6	P	Saccharomyces cerevisiae chromosome XIV, complete chromosome
3667_f_at	19882.5	P	Ty2 LTR
3668_f_at	21007.8	M	tRNA-Pro
3669_f_at	8267.4	P	Ty1 LTR
3670_f_at	534.7	P	Ty4 LTR
3621_i_at	7.1	A	Ty3 LTR
3622_f_at	7942.7	P	Ty3 LTR
3623_f_at	16343.2	P	Ty1 LTR
3624_at	955.3	P	Ty1 LTR
3625_at	497.3	P	Protein with strong similarity to subtelomerically-encoded proteins su
3626_i_at	1149.2	M	Protein with strong similarity to subtelomerically-encoded proteins su
3627_r_at	781.9	A	Protein with strong similarity to subtelomerically-encoded proteins su
3628_f_at	5.5	A	Protein with strong similarity to subtelomerically-encoded proteins su
3629_f_at	2277.4	M	strong similarity to subtelomeric encoded proteins
3630_at	2.5	A	Ty1 LTR
3631_s_at	1513.9	P	Ty4 LTR
3632_at	9.4	A	Ty1 LTR
3633_f_at	151	A	tRNA-Gly
3634_f_at	1291.4	P	Ty1 LTR
3635_f_at	27756.8	P	Ty1 LTR
3636_f_at	27875.2	P	Saccharomyces cerevisiae chromosome XV, complete chromosome
3637_f_at	11635	P	Full length Ty1
3638_f_at	27914	P	Full length Ty1
3639_f_at	27400.4	P	Ty1 LTR
3640_f_at	6859.9	P	tRNA-Gly
3641_f_at	38.4	A	Ty3 LTR
3642_at	128.2	A	Ty1 LTR
3643_i_at	9.2	A	Ty1 LTR
3644_f_at	883.8	P	Ty1 LTR
3645_f_at	6036.3	P	tRNA-Gly
3597_at	175.8	A	Ty1 LTR
3598_f_at	967.1	P	tRNA-Arg
3599_at	6.9	A	Ty1 LTR
3600_i_at	19.2	A	Ty3 LTR
3601_f_at	31.1	A	Ty3 LTR
3602_at	111.9	A	Ty1 LTR
3603_at	182.6	A	Ty1 LTR
3604_f_at	131.3	A	tRNA-Gly
3605_f_at	517.3	M	Ty1 LTR
3606_f_at	18064.8	P	Ty1 LTR
3607_f_at	11754.6	P	Full length Ty1
3608_f_at	19788	P	Ty1 LTR
3609_i_at	165	A	Ty1 LTR
3610_f_at	198.9	A	Ty1 LTR
3611_f_at	603.1	A	Ty1 LTR
3612_f_at	15022.4	P	Ty2 LTR
3613_i_at	636.2	A	Ty1 LTR
3614_f_at	470.2	A	Ty1 LTR

3615_i_at	11	A	Ty1 LTR
3616_f_at	84.9	A	Ty1 LTR
3617_f_at	1296.3	P	Ty4 LTR
3618_f_at	16554.5	P	Ty2 LTR
3619_f_at	8868.9	P	Full length Ty2
3620_f_at	30177.6	P	Saccharomyces cerevisiae chromosome XV, complete chromosome
3572_f_at	16226.9	P	Ty2 LTR
3573_f_at	2346.7	P	Ty4 LTR
3574_f_at	4886.2	P	tRNA-Ala
3575_f_at	8659.7	P	Ty3 LTR
3576_f_at	660.6	A	Ty3 LTR
3577_at	313.1	P	Ty1 LTR
3578_f_at	9584.7	P	Ty2 LTR
3579_f_at	27138.4	P	Saccharomyces cerevisiae chromosome XV, complete chromosome
3580_f_at	24581.2	P	Full length Ty2
3581_f_at	9477.2	P	Ty2 LTR
3582_f_at	15149.3	P	Ty1 LTR
3583_i_at	328.4	A	Ty1 LTR
3584_f_at	402.7	P	Ty1 LTR
3585_f_at	5.3	A	Ty3 LTR
3586_f_at	23253.5	P	Ty1 LTR
3587_f_at	22372	P	Saccharomyces cerevisiae chromosome XVI, complete chromosome
3588_f_at	13685.1	P	Full length Ty1
3589_f_at	27309	P	Full length Ty1
3590_f_at	21840.6	P	Ty1 LTR
3591_f_at	10921.6	P	Ty2 LTR
3592_i_at	144.7	A	Ty1 LTR
3593_f_at	4287.3	P	Ty1 LTR
3594_f_at	13404	P	tRNA-Glu
3595_at	56.4	A	Ty1 LTR
3596_f_at	15035.1	P	Ty2 LTR
3548_s_at	2726.8	P	tRNA-Cys
3549_f_at	8.2	A	Ty1 LTR
3550_i_at	1.4	A	Ty1 LTR
3551_f_at	504	M	Ty1 LTR
3552_f_at	23.8	A	Ty1 LTR
3553_f_at	1474.6	P	Ty4 LTR
3554_f_at	2501.4	P	Full length Ty4
3555_s_at	262.7	P	Saccharomyces cerevisiae chromosome XVI, complete chromosome
3556_s_at	23.9	A	Saccharomyces cerevisiae chromosome XVI, complete chromosome
3557_s_at	8.9	A	Saccharomyces cerevisiae chromosome XVI, complete chromosome
3558_f_at	1302.5	P	Ty4 LTR
3559_f_at	25996.5	P	Ty1 LTR
3560_at	192.4	A	Ty1 LTR
3561_f_at	5336.7	P	tRNA-Gly
3562_f_at	8958.7	P	tRNA-Ser
3563_s_at	875.8	P	tRNA-Thr
3564_f_at	13773.3	P	Ty3 LTR
3565_at	607.1	P	Ty1 LTR
3566_i_at	17.7	A	Ty1 LTR
3567_r_at	31.2	A	Ty1 LTR
3568_f_at	1149.8	P	Ty1 LTR

3569_at	73	A	Ty1 LTR
3570_f_at	1832.9	P	Ty1 LTR
3571_f_at	16775.3	P	Ty1 LTR
3524_f_at	6741.2	P	Full length Ty1
3525_f_at	22829.5	P	Full length Ty1
3526_f_at	15377	P	Saccharomyces cerevisiae chromosome XVI, complete chromosom
3527_f_at	16608.8	P	Ty1 LTR
3528_f_at	22343.9	P	Ty1 LTR
3529_f_at	26665.5	P	Full length Ty3
3530_f_at	22289.4	P	Ty1 LTR
3531_at	462.2	P	Ty1 LTR
3532_f_at	25768.4	P	Ty1 LTR
3533_f_at	29644.3	P	Full length Ty1
3534_f_at	27496.8	P	Ty1 LTR
3535_i_at	321.3	A	Ty3 LTR
3536_f_at	7477.9	P	Ty3 LTR
3537_f_at	8735.7	P	tRNA-Ala
3538_f_at	6303.8	P	tRNA-Gly
3539_f_at	628.8	P	Ty3 LTR
3540_at	204.2	A	Ty4 LTR
3541_at	413.5	A	Ty4 LTR
3542_f_at	23629.9	P	strong similarity to subtelomeric encoded proteins
3543_s_at	20756.7	P	strong similarity to subtelomeric encoded proteins
3544_at	300.5	A	strong similarity to subtelomeric encoded proteins
3545_i_at	153.1	A	Ty1 LTR
3546_f_at	7	A	Ty1 LTR
3547_f_at	7114.9	P	Ty2 LTR
3500_f_at	22.1	A	Ty1 LTR
3501_f_at	10946	P	Ty2 LTR
3502_f_at	25445.9	P	Saccharomyces cerevisiae chromosome II, complete chromosome s
3503_f_at	7820.6	P	Full length Ty2
3504_f_at	10283.4	P	Ty2 LTR
3505_s_at	1773.8	P	Ty1 LTR
3506_s_at	1702.7	P	Ty4 LTR
3507_at	38.9	A	Ty1 LTR
3508_f_at	5114.5	P	tRNA-Gly
3509_f_at	6045.2	P	Ty3 LTR
3510_s_at	1312.2	P	Ty1 LTR
3511_f_at	21769.3	P	Ty1 LTR
3512_f_at	12224.6	P	Full length Ty1
3513_f_at	20864.9	P	Ty1 LTR
3514_f_at	3578.2	P	tRNA-Ser
3515_at	626.8	P	Ty1 LTR
3516_f_at	18021.1	P	Ty1 LTR
3517_f_at	10078.8	P	Full length Ty1
3518_f_at	12761.5	P	Ty1 LTR
3519_f_at	135.1	A	Ty1 LTR
3520_s_at	3341.5	P	tRNA-Val
3521_i_at	6.4	A	Ty1 LTR
3522_f_at	293.2	P	Ty1 LTR
3523_at	505.5	A	Ty1 LTR
3477_at	151.3	A	Ty1 LTR

3478_f_at	13787.3	P	tRNA-Gln
3479_f_at	650.2	P	tRNA-Arg
3480_at	45.6	A	Ty1 LTR
3481_at	196.3	A	Ty1 LTR
3482_f_at	13768.4	P	tRNA-Glu
3483_f_at	21301.8	P	Protein with similarity to members of the Cos3\/Cos5\/Cos1\/Cos4\/C
3484_f_at	3	A	Ty5 LTR
3485_at	19.9	A	Full length Ty5
3486_at	153.6	A	Full length Ty5
3487_g_at	65.6	A	Full length Ty5
3488_at	258.7	P	Full length Ty5
3489_f_at	24.8	A	Full length Ty5
3490_f_at	17.4	A	Ty5 LTR
3491_f_at	12709.3	P	tRNA-Glu
3492_f_at	2222.4	P	Ty1 LTR
3493_f_at	9926.1	P	Ty1 LTR
3494_f_at	15473.7	P	Ty1 LTR
3495_f_at	550.5	P	Ty1 LTR
3496_f_at	20594.2	P	Ty2 LTR
3497_f_at	21750.2	P	Saccharomyces cerevisiae chromosome III, complete chromosome s
3498_f_at	24840.5	P	Full length Ty2
3499_f_at	18488.7	P	Ty2 LTR
3451_f_at	19284.2	M	tRNA-Pro
3452_f_at	17515	P	Ty1 LTR
3453_at	111	A	strong similarity to subtelomeric encoded proteins
3454_s_at	769.5	P	tRNA-Asn
3455_f_at	5211.1	P	tRNA-Gly
3456_i_at	12.6	A	Ty1 LTR
3457_f_at	3195.6	P	Ty1 LTR
3458_f_at	596.3	P	Ty1 LTR
3459_at	653.4	A	Ty1 LTR
3460_at	50.3	A	Ty4 LTR
3461_f_at	21780.9	P	Ty1 LTR
3462_f_at	13442.7	P	tRNA-Gln
3463_at	636	P	Ty1 LTR
3464_at	264.7	P	Ty1 LTR
3465_at	13.7	A	Ty5 LTR
3466_i_at	4.1	A	Ty1 LTR
3467_f_at	388.1	A	Ty1 LTR
3468_i_at	35.2	A	Ty1 LTR
3469_f_at	25	A	Ty1 LTR
3470_i_at	1863.1	P	Protein with strong similarity to other subtelomerically-encoded prote
3471_f_at	3716.6	P	Protein with strong similarity to other subtelomerically-encoded prote
3472_f_at	5529.8	P	tRNA-Gly
3473_f_at	7963	P	tRNA-Ala
3474_f_at	3520.5	P	Ty1 LTR
3475_f_at	1428.4	P	Ty4 LTR
3476_f_at	3437.6	P	tRNA-Ser
3427_at	124.2	A	Ty1 LTR
3428_f_at	6598.5	P	Ty1 LTR
3429_f_at	19800	P	Ty2 LTR
3430_f_at	23154.5	P	Full length Ty2

3431_f_at	28149.3	P	Saccharomyces cerevisiae chromosome IV, complete chromosome
3432_f_at	8391.2	P	Ty2 LTR
3433_i_at	2.7	A	Ty1 LTR
3434_f_at	362.1	P	Ty1 LTR
3435_f_at	2277.1	P	Ty1 LTR
3436_f_at	12111.8	P	tRNA-Gln
3437_f_at	660.8	P	tRNA-Arg
3438_f_at	735.3	P	tRNA-Arg
3439_f_at	11854.5	P	tRNA-Gln
3440_f_at	13400.6	P	Ty1 LTR
3441_f_at	14314.7	P	Full length Ty1
3442_f_at	23457.5	P	Full length Ty1
3443_f_at	28656.1	P	Saccharomyces cerevisiae chromosome IV, complete chromosome
3444_f_at	16958.6	P	Ty1 LTR
3445_f_at	2490.2	P	Ty3 LTR
3446_i_at	9.9	A	Ty1 LTR
3447_f_at	707.3	A	Ty1 LTR
3448_s_at	9241	P	Ty3 LTR
3449_i_at	283.2	P	Ty1 LTR
3450_r_at	0.8	A	Ty1 LTR
3404_f_at	1352.9	P	Ty1 LTR
3405_f_at	14331.5	P	tRNA-Gln
3406_f_at	24598.4	P	Ty1 LTR
3407_at	2052.5	P	Saccharomyces cerevisiae chromosome IV, complete chromosome
3408_f_at	14656.5	P	Ty1 LTR
3409_f_at	38192.2	P	Saccharomyces cerevisiae chromosome IV, complete chromosome
3410_f_at	8639.7	P	Full length Ty2
3411_f_at	13279.5	P	Ty1 LTR
3412_f_at	9502.5	P	Full length Ty1
3413_f_at	21641.8	P	Full length Ty1
3414_f_at	18602.1	P	Saccharomyces cerevisiae chromosome IV, complete chromosome
3415_i_at	36.5	A	Ty1 LTR
3416_s_at	4016.1	P	Ty1 LTR
3417_f_at	7759.8	P	Ty3 LTR
3418_f_at	4000.4	P	tRNA-Ser
3419_f_at	9758.3	P	Ty1 LTR
3420_f_at	24075.1	P	Saccharomyces cerevisiae chromosome IV, complete chromosome
3421_f_at	15994.3	P	Full length Ty2
3422_f_at	14175.3	P	Ty1 LTR
3423_f_at	14366.2	P	Ty1 LTR
3424_f_at	11515.1	P	Full length Ty1
3425_f_at	16111.3	P	Full length Ty1
3426_f_at	10258.6	P	Saccharomyces cerevisiae chromosome IV, complete chromosome
3379_f_at	15642.7	P	Ty1 LTR
3380_i_at	133.3	P	Ty3 LTR
3381_f_at	3.2	A	Ty3 LTR
3382_f_at	5379.3	P	tRNA-Gly
3383_f_at	6162.8	P	tRNA-Glu
3384_f_at	7275.9	P	Ty3 LTR
3385_s_at	5005.6	P	tRNA-Val
3386_f_at	24317.7	P	Ty1 LTR
3387_f_at	11303.5	P	Full length Ty1

3388_f_at	28286.5	P	Ty1 LTR
3389_f_at	4150	P	Ty1 LTR
3390_at	81.6	A	Ty3 LTR
3391_f_at	3215	P	Ty1 LTR
3392_f_at	22239.7	P	Ty1 LTR
3393_f_at	36178.4	P	Saccharomyces cerevisiae chromosome IV, complete chromosome
3394_f_at	6450.2	P	Full length Ty1
3395_f_at	24274.6	P	Full length Ty1
3396_f_at	18892.6	P	Ty1 LTR
3397_f_at	156.6	A	tRNA-Gly
3398_f_at	2575.8	A	tRNA-Ser
3399_f_at	11329.7	P	Ty1 LTR
3400_i_at	103.9	A	Ty1 LTR
3401_f_at	130.2	A	Ty1 LTR
3402_at	46.9	A	Ty1 LTR
3403_f_at	2920.1	P	strong similarity to subtelomeric encoded proteins
3356_f_at	4112.6	P	strong similarity to subtelomeric encoded proteins
3357_at	511.7	A	strong similarity to subtelomeric encoded proteins
3358_f_at	5041.3	P	tRNA-Gly
3359_f_at	17753.5	P	Ty1 LTR
3360_at	31.5	A	Ty1 LTR
3361_f_at	3115.2	P	tRNA-Ser
3362_at	5.6	A	Ty1 LTR
3363_at	14.1	A	Ty4 LTR
3364_f_at	10168	P	tRNA-Gln
3365_f_at	12925.3	P	Ty1 LTR
3366_at	26.4	A	Ty1 LTR
3367_f_at	894.2	M	Ty1 LTR
3368_f_at	743.5	P	tRNA-Arg
3369_i_at	11.3	A	Ty1 LTR
3370_f_at	559.5	P	Ty1 LTR
3371_f_at	12145.2	P	tRNA-Glu
3372_f_at	3758.2	P	tRNA-His
3373_at	900.4	P	Ty1 LTR
3374_at	834.7	P	Ty1 LTR
3375_f_at	5688.2	P	Ty3 LTR
3376_f_at	13211.8	P	tRNA-Gln
3377_at	178.5	A	Ty1 LTR
3378_f_at	8312.3	P	tRNA-Ser
3332_i_at	85.9	A	Ty1 LTR
3333_f_at	3739.1	P	Ty1 LTR
3334_at	70.9	A	Ty1 LTR
3335_at	71.8	A	Ty1 LTR
3336_f_at	1447.6	P	Ty4 LTR
3337_i_at	1502.8	A	Ty3 LTR
3338_f_at	14.3	A	Ty3 LTR
3340_f_at	19179.5	P	Ty1 LTR
3342_f_at	7039.2	P	Ty3 LTR
3343_i_at	2064.3	P	Ty1 LTR
3344_f_at	1169.8	P	Ty1 LTR
3345_f_at	6520.3	P	Ty1 LTR
3346_at	320.6	A	Ty4 LTR

3347_s_at	3882.6	P	Ty1 LTR
3348_f_at	15894.3	P	Ty1 LTR
3350_f_at	25902.8	P	Full length Ty1
3352_s_at	19469	P	Ty1 LTR
3354_s_at	2297.8	P	Ty1 LTR
3355_s_at	2971.9	P	Ty1 LTR
3307_s_at	2285.6	P	Ty1 LTR
3308_s_at	3420.3	P	Ty1 LTR
3309_s_at	1500.4	P	Ty1 LTR
3310_s_at	11353.9	P	Ty1 LTR
3311_f_at	12302.1	P	Ty1 LTR
3313_f_at	9178	P	Ty1 LTR
3315_f_at	27242.4	P	Ty3 LTR
3316_f_at	30303.7	P	Ty3 LTR
3317_f_at	29724.7	P	Ty1 LTR
3319_f_at	31740	P	Ty1 LTR
3320_i_at	27.3	A	Ty1 LTR
3321_f_at	397.9	A	Ty1 LTR
3322_at	40.3	A	Ty1 LTR
3323_i_at	5.6	A	Ty5 LTR
3324_at	134.6	A	Ty5 LTR
3325_f_at	8702.5	P	strong similarity to subtelomeric encoded proteins
3326_at	456.1	P	strong similarity to subtelomeric encoded proteins
3327_f_at	23998.4	P	Protein with strong similarity to subtelomerically-encoded proteins su
3328_at	195.6	A	Ty1 LTR
3329_f_at	2033.2	P	Ty1 LTR
3330_f_at	20957.6	P	Ty2 LTR
3283_f_at	30730.2	P	Saccharomyces cerevisiae chromosome VI, complete chromosome
3284_f_at	26277.2	P	Full length Ty2
3285_f_at	17334	P	Ty2 LTR
3286_f_at	1900.7	P	Ty1 LTR
3287_s_at	169.5	P	Ty4 LTR
3288_at	139.4	A	Ty1 LTR
3289_i_at	126	A	Ty1 LTR
3290_f_at	368.4	M	Ty1 LTR
3291_f_at	2651.2	P	Ty1 LTR
3294_at	15.4	A	Ty1 LTR
3296_at	55.5	A	Ty1 LTR
3297_i_at	6.7	A	Ty5 LTR
3298_f_at	6.8	A	Ty5 LTR
3299_f_at	63.7	A	strong similarity to subtelomeric encoded proteins
3301_f_at	851.5	P	Ty4 LTR
3302_f_at	7544.1	P	Ty1 LTR
3303_f_at	243.1	P	Ty1 LTR
3304_f_at	958.8	A	Ty1 LTR
3305_at	167.2	A	Ty4 LTR
3306_i_at	1489	P	Ty1 LTR
3258_f_at	227.2	P	Ty1 LTR
3259_at	2255.4	P	Ty1 LTR
3260_f_at	4345.1	P	Ty3 LTR
3262_at	44.5	A	Ty4 LTR
3263_i_at	160.6	A	Ty1 LTR

3264_f_at	732.4	P	Ty1 LTR
3267_f_at	2800.1	P	Ty3 LTR
3268_f_at	26518.6	P	Ty1 LTR
3269_f_at	660.7	P	Ty1 LTR
3270_f_at	19427.7	P	Ty1 LTR
3271_i_at	40.4	A	Ty3 LTR
3272_f_at	2095.2	P	Ty3 LTR
3274_at	834.8	M	Ty1 LTR
3276_i_at	1.6	A	Ty1 LTR
3277_f_at	66.6	A	Ty1 LTR
3279_f_at	9565.1	P	Full length Ty1
3235_f_at	12813.9	P	Ty1 LTR
3236_f_at	12647.7	P	Full length Ty1
3237_f_at	27199.3	P	Full length Ty1
3239_f_at	20749.9	P	Ty1 LTR
3240_f_at	14294.3	P	Ty2 LTR
3241_f_at	11169.7	P	Full length Ty2
3243_at	3460.1	P	tRNA-Leu
3244_i_at	5	A	Ty1 LTR
3245_f_at	391.6	P	Ty1 LTR
3247_s_at	669.5	A	TY3B protein Found forward in NC_001139 between 707604 and 70
3248_s_at	561.3	A	Saccharomyces cerevisiae chromosome VII, complete chromosome
3249_s_at	1133.2	P	Saccharomyces cerevisiae chromosome VII, complete chromosome
3250_s_at	1006.2	A	Saccharomyces cerevisiae chromosome VII, complete chromosome
3251_s_at	356.1	A	Full length Ty3
3252_s_at	1542.6	P	Full length Ty3
3253_f_at	10238.6	P	Full length Ty3
3255_at	596.8	P	Ty1 LTR
3256_at	35.3	A	Ty1 LTR
3257_f_at	8198	P	Ty3 LTR
3212_f_at	1589.2	P	Ty1 LTR
3214_at	197.4	P	Ty1 LTR
3215_f_at	264.2	A	Ty1 LTR
3216_at	40.1	A	Ty1 LTR
3218_at	12.4	A	Ty1 LTR
3222_f_at	17328.8	P	Full length Ty2
3223_f_at	18105.1	P	Ty2 LTR
3225_f_at	13139	P	Full length Ty1
3226_f_at	22282.7	P	Ty1 LTR
3228_at	745.3	A	Ty3 LTR
3230_f_at	10781.6	P	Ty1 LTR
3232_f_at	2027.1	P	Ty4 LTR
3233_f_at	26252.9	P	Ty1 LTR
3234_at	14768.4	P	Protein with strong similarity to other subtelomerically-encoded prote
3187_s_at	2623	P	strong similarity to subtelomeric encoded proteins
3188_at	2550	M	Protein with similarity to subtelomerically-encoded proteins such as
3189_i_at	222.4	A	Protein with similarity to subtelomerically-encoded proteins such as
3190_f_at	381.9	P	Protein with similarity to subtelomerically-encoded proteins such as
3191_i_at	1.9	A	Ty5 LTR
3192_f_at	5.1	A	Ty5 LTR
3193_at	251.5	A	strong similarity to subtelomeric encoded proteins
3195_f_at	10579.7	P	Ty3 LTR

3196_f_at	1309.8	P	Ty4 LTR
3199_f_at	17591.8	P	Ty1 LTR
3200_i_at	387.8	A	Ty1 LTR
3201_r_at	69.9	A	Ty1 LTR
3202_f_at	6.9	A	Ty1 LTR
3203_f_at	23633.8	P	Ty1 LTR
3204_at	803.9	A	Ty1 LTR
3206_at	31.4	A	Ty1 LTR
3207_i_at	510.7	A	Ty1 LTR
3208_f_at	129.8	A	Ty1 LTR
3209_f_at	17121.4	P	Ty1 LTR
3161_f_at	4378.5	P	Ty3 LTR
3162_at	923.4	P	Ty4 LTR
3163_i_at	66.8	A	Ty1 LTR
3164_f_at	15.2	A	Ty1 LTR
3165_at	16.7	A	Ty4 LTR
3166_i_at	317.4	A	Ty1 LTR
3167_r_at	119	A	Ty1 LTR
3168_f_at	158.3	A	Ty1 LTR
3169_f_at	18564.7	P	Ty2 LTR
3170_i_at	59.3	A	Ty1 LTR
3171_r_at	17.5	A	Ty1 LTR
3172_f_at	318.6	A	Ty1 LTR
3173_i_at	2.6	A	Ty1 LTR
3174_f_at	5.9	A	Ty1 LTR
3175_i_at	906.5	A	Ty1 LTR
3176_f_at	625.2	P	Ty1 LTR
3177_f_at	1013.3	A	Ty3 LTR
3178_f_at	53	A	Ty1 LTR
3180_f_at	11458	P	Full length Ty1
3181_f_at	24338.1	P	Ty1 LTR
3182_i_at	172.9	A	strong similarity to subtelomeric encoded YDR544c
3183_f_at	24795	P	strong similarity to subtelomeric encoded proteins
3184_s_at	185.5	A	strong similarity to subtelomeric encoded proteins
3185_s_at	151.7	A	strong similarity to subtelomeric encoded proteins
3133_f_at	1280.9	P	Ty1 LTR
3136_s_at	3369.3	P	Saccharomyces cerevisiae chromosome IX, complete chromosome
3137_s_at	1828.6	P	Full length Ty3
3139_f_at	563.1	P	Ty2 LTR
3141_i_at	17.1	A	Ty1 LTR
3142_f_at	3513	P	Ty1 LTR
3143_f_at	477.8	P	Ty3 LTR
3144_f_at	1454.6	P	Ty1 LTR
3145_at	647.2	P	Ty1 LTR
3147_at	165.9	A	Ty1 LTR
3148_s_at	8264	P	mating hormone a2
3149_at	1120.3	A	Saccharomyces cerevisiae chromosome I, complete chromosome se
3150_at	1059.6	P	Saccharomyces cerevisiae chromosome I, complete chromosome se
3151_g_at	558.9	P	Saccharomyces cerevisiae chromosome I, complete chromosome se
3152_at	1983.3	P	Saccharomyces cerevisiae chromosome I, complete chromosome se
3153_at	186.1	A	Saccharomyces cerevisiae chromosome I, complete chromosome se
3154_at	396.1	A	Saccharomyces cerevisiae chromosome I, complete chromosome se

3155_at	69.7	A	Saccharomyces cerevisiae chromosome I, complete chromosome se
3156_at	24.6	A	Saccharomyces cerevisiae chromosome I, complete chromosome se
3157_at	538.8	P	Saccharomyces cerevisiae chromosome I, complete chromosome se
3158_at	286.3	A	Saccharomyces cerevisiae chromosome I, complete chromosome se
3159_at	174.3	A	Saccharomyces cerevisiae chromosome I, complete chromosome se
3088_at	173.5	A	Saccharomyces cerevisiae chromosome I, complete chromosome se
3089_g_at	49.9	A	Saccharomyces cerevisiae chromosome I, complete chromosome se
3090_s_at	977.7	A	Saccharomyces cerevisiae chromosome I, complete chromosome se
3091_at	22.1	A	Saccharomyces cerevisiae chromosome I, complete chromosome se
3092_f_at	119.2	A	Saccharomyces cerevisiae chromosome I, complete chromosome se
3093_f_at	854.9	A	Saccharomyces cerevisiae chromosome I, complete chromosome se
3096_f_at	2532.6	P	Saccharomyces cerevisiae chromosome I, complete chromosome se
3097_at	203.3	A	Saccharomyces cerevisiae chromosome I, complete chromosome se
3098_at	138.3	A	Saccharomyces cerevisiae chromosome I, complete chromosome se
3099_at	864.5	A	Saccharomyces cerevisiae chromosome I, complete chromosome se
3100_s_at	1120.5	P	Saccharomyces cerevisiae chromosome I, complete chromosome se
3101_at	681.7	M	Saccharomyces cerevisiae chromosome I, complete chromosome se
3102_s_at	562	P	Saccharomyces cerevisiae chromosome I, complete chromosome se
3103_at	303.7	P	Saccharomyces cerevisiae chromosome I, complete chromosome se
3104_at	249.4	P	Saccharomyces cerevisiae chromosome I, complete chromosome se
3105_g_at	14.5	A	Saccharomyces cerevisiae chromosome I, complete chromosome se
3106_s_at	362	A	Saccharomyces cerevisiae chromosome I, complete chromosome se
3107_s_at	474.6	A	Saccharomyces cerevisiae chromosome I, complete chromosome se
3108_at	524.4	A	Saccharomyces cerevisiae chromosome X, complete chromosome s
3109_at	572.3	A	Saccharomyces cerevisiae chromosome X, complete chromosome s
3110_s_at	18.4	A	Saccharomyces cerevisiae chromosome X, complete chromosome s
3111_s_at	215.6	A	Saccharomyces cerevisiae chromosome X, complete chromosome s
3112_s_at	49.9	A	Saccharomyces cerevisiae chromosome X, complete chromosome s
3113_s_at	647.5	P	Saccharomyces cerevisiae chromosome X, complete chromosome s
3114_s_at	1336.2	P	Saccharomyces cerevisiae chromosome X, complete chromosome s
3115_at	280.6	A	Saccharomyces cerevisiae chromosome X, complete chromosome s
3116_at	1147	A	Saccharomyces cerevisiae chromosome X, complete chromosome s
3117_at	993.7	A	Saccharomyces cerevisiae chromosome X, complete chromosome s
3118_at	252.4	P	Saccharomyces cerevisiae chromosome X, complete chromosome s
3119_at	9.2	A	Saccharomyces cerevisiae chromosome X, complete chromosome s
3120_at	347.6	A	Saccharomyces cerevisiae chromosome X, complete chromosome s
3121_at	847.2	A	Saccharomyces cerevisiae chromosome X, complete chromosome s
3122_at	925.1	P	Saccharomyces cerevisiae chromosome X, complete chromosome s
3123_at	102.6	A	Saccharomyces cerevisiae chromosome X, complete chromosome s
3124_at	934.2	A	Saccharomyces cerevisiae chromosome X, complete chromosome s
3125_at	468.1	A	Saccharomyces cerevisiae chromosome X, complete chromosome s
3126_at	471.9	A	Saccharomyces cerevisiae chromosome X, complete chromosome s
3127_at	33.3	A	Saccharomyces cerevisiae chromosome X, complete chromosome s
3128_at	1993.4	P	Saccharomyces cerevisiae chromosome X, complete chromosome s
3129_at	823.5	A	Saccharomyces cerevisiae chromosome X, complete chromosome s
3130_at	467.7	A	Saccharomyces cerevisiae chromosome X, complete chromosome s
3131_g_at	218.8	A	Saccharomyces cerevisiae chromosome X, complete chromosome s
3045_s_at	660.9	A	Saccharomyces cerevisiae chromosome X, complete chromosome s
3046_at	125.7	A	Saccharomyces cerevisiae chromosome X, complete chromosome s
3047_at	259.8	A	Saccharomyces cerevisiae chromosome X, complete chromosome s
3048_at	32	A	Saccharomyces cerevisiae chromosome X, complete chromosome s
3049_at	5	A	Saccharomyces cerevisiae chromosome X, complete chromosome s

3050_at	196.5	P	Saccharomyces cerevisiae chromosome X, complete chromosome s
3051_at	572.6	P	Saccharomyces cerevisiae chromosome X, complete chromosome s
3052_at	20.5	A	Saccharomyces cerevisiae chromosome X, complete chromosome s
3053_at	105.2	A	Saccharomyces cerevisiae chromosome X, complete chromosome s
3054_at	48.5	A	Saccharomyces cerevisiae chromosome X, complete chromosome s
3055_g_at	329.8	A	Saccharomyces cerevisiae chromosome X, complete chromosome s
3056_s_at	15.7	A	Saccharomyces cerevisiae chromosome X, complete chromosome s
3057_s_at	692.2	P	Saccharomyces cerevisiae chromosome X, complete chromosome s
3058_s_at	825.5	P	Saccharomyces cerevisiae chromosome X, complete chromosome s
3059_at	5.9	A	Saccharomyces cerevisiae chromosome X, complete chromosome s
3060_at	306.1	A	Saccharomyces cerevisiae chromosome X, complete chromosome s
3061_at	26.4	A	Saccharomyces cerevisiae chromosome X, complete chromosome s
3062_at	12.1	A	Saccharomyces cerevisiae chromosome X, complete chromosome s
3063_at	138.6	A	Saccharomyces cerevisiae chromosome X, complete chromosome s
3064_at	94	A	Saccharomyces cerevisiae chromosome X, complete chromosome s
3065_g_at	643.6	A	Saccharomyces cerevisiae chromosome X, complete chromosome s
3066_at	108.6	A	Saccharomyces cerevisiae chromosome X, complete chromosome s
3067_g_at	61.3	A	Saccharomyces cerevisiae chromosome X, complete chromosome s
3068_s_at	1122.3	A	Saccharomyces cerevisiae chromosome X, complete chromosome s
3069_s_at	194.3	A	Saccharomyces cerevisiae chromosome X, complete chromosome s
3070_s_at	179.5	A	Saccharomyces cerevisiae chromosome X, complete chromosome s
3071_s_at	274.5	A	Saccharomyces cerevisiae chromosome X, complete chromosome s
3072_s_at	2520	M	Saccharomyces cerevisiae chromosome X, complete chromosome s
3073_s_at	197.2	M	Saccharomyces cerevisiae chromosome X, complete chromosome s
3074_at	25.5	A	Saccharomyces cerevisiae chromosome X, complete chromosome s
3075_at	384.6	A	Saccharomyces cerevisiae chromosome X, complete chromosome s
3076_at	4.8	A	Saccharomyces cerevisiae chromosome X, complete chromosome s
3077_at	173.2	A	Saccharomyces cerevisiae chromosome X, complete chromosome s
3078_g_at	910.7	P	Saccharomyces cerevisiae chromosome X, complete chromosome s
3079_s_at	4050.9	P	Saccharomyces cerevisiae chromosome X, complete chromosome s
3080_f_at	8320.5	P	Saccharomyces cerevisiae chromosome X, complete chromosome s
3081_at	958.2	P	Saccharomyces cerevisiae chromosome X, complete chromosome s
3082_at	11.8	A	Saccharomyces cerevisiae chromosome X, complete chromosome s
3083_g_at	15.9	A	Saccharomyces cerevisiae chromosome X, complete chromosome s
3084_s_at	40	A	Saccharomyces cerevisiae chromosome X, complete chromosome s
3085_s_at	787.9	A	Saccharomyces cerevisiae chromosome X, complete chromosome s
3086_s_at	40.8	A	Saccharomyces cerevisiae chromosome X, complete chromosome s
3087_s_at	63	A	Saccharomyces cerevisiae chromosome X, complete chromosome s
3003_s_at	650.7	P	Saccharomyces cerevisiae chromosome X, complete chromosome s
3004_s_at	1203.2	A	Saccharomyces cerevisiae chromosome X, complete chromosome s
3005_at	79	A	Saccharomyces cerevisiae chromosome X, complete chromosome s
3006_at	413.7	A	Saccharomyces cerevisiae chromosome X, complete chromosome s
3007_at	1490.4	A	Saccharomyces cerevisiae chromosome X, complete chromosome s
3008_at	280.8	A	Saccharomyces cerevisiae chromosome X, complete chromosome s
3009_g_at	764.2	P	Saccharomyces cerevisiae chromosome X, complete chromosome s
3010_s_at	22.1	A	Saccharomyces cerevisiae chromosome X, complete chromosome s
3011_s_at	109.4	A	Saccharomyces cerevisiae chromosome X, complete chromosome s
3012_s_at	758.1	P	Saccharomyces cerevisiae chromosome X, complete chromosome s
3013_at	270.8	A	Saccharomyces cerevisiae chromosome X, complete chromosome s
3014_at	155.4	A	Saccharomyces cerevisiae chromosome X, complete chromosome s
3015_at	282.5	A	Saccharomyces cerevisiae chromosome X, complete chromosome s
3016_at	848.4	A	Saccharomyces cerevisiae chromosome X, complete chromosome s

3017_g_at	438.5	P	Saccharomyces cerevisiae chromosome X, complete chromosome s
3018_s_at	628	P	Saccharomyces cerevisiae chromosome X, complete chromosome s
3019_at	23.3	A	Saccharomyces cerevisiae chromosome X, complete chromosome s
3020_at	17.3	A	Saccharomyces cerevisiae chromosome X, complete chromosome s
3021_at	60.5	A	Saccharomyces cerevisiae chromosome X, complete chromosome s
3022_at	58.6	A	Saccharomyces cerevisiae chromosome X, complete chromosome s
3023_at	137.4	A	Saccharomyces cerevisiae chromosome X, complete chromosome s
3024_g_at	198.8	A	Saccharomyces cerevisiae chromosome X, complete chromosome s
3025_s_at	964.3	P	Saccharomyces cerevisiae chromosome X, complete chromosome s
3026_at	545.3	A	Saccharomyces cerevisiae chromosome X, complete chromosome s
3027_at	383.5	M	Saccharomyces cerevisiae chromosome X, complete chromosome s
3028_at	96.1	A	Saccharomyces cerevisiae chromosome X, complete chromosome s
3029_at	178.3	A	Saccharomyces cerevisiae chromosome X, complete chromosome s
3030_at	204.4	A	Saccharomyces cerevisiae chromosome X, complete chromosome s
3031_at	326.9	A	Saccharomyces cerevisiae chromosome X, complete chromosome s
3032_at	350.2	A	Saccharomyces cerevisiae chromosome X, complete chromosome s
3033_s_at	456	A	Saccharomyces cerevisiae chromosome X, complete chromosome s
3034_at	632.8	A	Saccharomyces cerevisiae chromosome XI, complete chromosome
3035_at	361.6	P	Saccharomyces cerevisiae chromosome XI, complete chromosome
3036_at	421	A	Saccharomyces cerevisiae chromosome XI, complete chromosome
3037_at	390.5	A	Saccharomyces cerevisiae chromosome XI, complete chromosome
3038_at	102.7	A	Saccharomyces cerevisiae chromosome XI, complete chromosome
3039_s_at	1610.2	P	Saccharomyces cerevisiae chromosome XI, complete chromosome
3040_at	1182.5	A	Saccharomyces cerevisiae chromosome XI, complete chromosome
3041_at	287.9	A	Saccharomyces cerevisiae chromosome XI, complete chromosome
3042_at	347.3	A	Saccharomyces cerevisiae chromosome XI, complete chromosome
3043_at	174	A	Saccharomyces cerevisiae chromosome XI, complete chromosome
3044_at	20.1	A	Saccharomyces cerevisiae chromosome XI, complete chromosome
2960_at	176.3	A	Saccharomyces cerevisiae chromosome XI, complete chromosome
2961_at	1326	A	Saccharomyces cerevisiae chromosome XI, complete chromosome
2962_at	2075.7	P	Saccharomyces cerevisiae chromosome XI, complete chromosome
2963_at	59.2	A	Saccharomyces cerevisiae chromosome XI, complete chromosome
2964_at	19465.2	P	Saccharomyces cerevisiae chromosome XI, complete chromosome
2965_g_at	8230.8	P	Saccharomyces cerevisiae chromosome XI, complete chromosome
2966_s_at	12620.5	P	Saccharomyces cerevisiae chromosome XI, complete chromosome
2967_s_at	7591.2	P	Saccharomyces cerevisiae chromosome XI, complete chromosome
2968_s_at	3611.7	P	Saccharomyces cerevisiae chromosome XI, complete chromosome
2969_s_at	11278.9	P	Saccharomyces cerevisiae chromosome XI, complete chromosome
2970_s_at	26230.6	P	Saccharomyces cerevisiae chromosome XI, complete chromosome
2971_at	471.3	A	Saccharomyces cerevisiae chromosome XI, complete chromosome
2972_at	422.1	A	Saccharomyces cerevisiae chromosome XI, complete chromosome
2973_at	27.7	A	Saccharomyces cerevisiae chromosome XI, complete chromosome
2974_at	81	A	Saccharomyces cerevisiae chromosome XI, complete chromosome
2975_at	331.1	A	Saccharomyces cerevisiae chromosome XI, complete chromosome
2976_at	519.6	A	Saccharomyces cerevisiae chromosome XI, complete chromosome
2977_at	84.8	A	Saccharomyces cerevisiae chromosome XI, complete chromosome
2978_at	580.3	A	Saccharomyces cerevisiae chromosome XI, complete chromosome
2979_at	29.3	A	Saccharomyces cerevisiae chromosome XI, complete chromosome
2980_at	279.6	A	Saccharomyces cerevisiae chromosome XI, complete chromosome
2981_at	147.4	A	Saccharomyces cerevisiae chromosome XI, complete chromosome
2982_at	113.6	A	Saccharomyces cerevisiae chromosome XI, complete chromosome
2983_at	29.1	A	Saccharomyces cerevisiae chromosome XI, complete chromosome

2984_at	213.2	A	Saccharomyces cerevisiae chromosome XI, complete chromosome
2985_at	17.3	A	Saccharomyces cerevisiae chromosome XI, complete chromosome
2986_at	208.3	A	Saccharomyces cerevisiae chromosome XI, complete chromosome
2987_at	786.9	P	Saccharomyces cerevisiae chromosome XI, complete chromosome
2988_at	67.2	A	Saccharomyces cerevisiae chromosome XI, complete chromosome
2989_at	620.8	P	Saccharomyces cerevisiae chromosome XI, complete chromosome
2990_g_at	1092.3	A	Saccharomyces cerevisiae chromosome XI, complete chromosome
2991_at	252.1	A	Saccharomyces cerevisiae chromosome XI, complete chromosome
2992_g_at	62.6	A	Saccharomyces cerevisiae chromosome XI, complete chromosome
2993_s_at	237.4	A	Saccharomyces cerevisiae chromosome XI, complete chromosome
2994_s_at	131.9	P	Saccharomyces cerevisiae chromosome XI, complete chromosome
2995_s_at	413.9	P	Saccharomyces cerevisiae chromosome XI, complete chromosome
2996_s_at	1578	P	Saccharomyces cerevisiae chromosome XI, complete chromosome
2997_s_at	171.3	P	Saccharomyces cerevisiae chromosome XI, complete chromosome
2998_at	492.4	A	Saccharomyces cerevisiae chromosome XI, complete chromosome
2999_at	380.6	A	Saccharomyces cerevisiae chromosome XI, complete chromosome
3000_at	683.8	A	Saccharomyces cerevisiae chromosome XI, complete chromosome
3001_at	5.5	A	Saccharomyces cerevisiae chromosome XI, complete chromosome
3002_g_at	123.3	A	Saccharomyces cerevisiae chromosome XI, complete chromosome
2917_s_at	60	A	Saccharomyces cerevisiae chromosome XI, complete chromosome
2918_s_at	1335.1	A	Saccharomyces cerevisiae chromosome XI, complete chromosome
2919_s_at	1097.3	P	Saccharomyces cerevisiae chromosome XI, complete chromosome
2920_at	919.8	A	Saccharomyces cerevisiae chromosome XI, complete chromosome
2921_at	444.8	A	Saccharomyces cerevisiae chromosome XI, complete chromosome
2922_at	446.3	A	Saccharomyces cerevisiae chromosome XI, complete chromosome
2923_at	358.7	A	Saccharomyces cerevisiae chromosome XI, complete chromosome
2924_g_at	236.6	A	Saccharomyces cerevisiae chromosome XI, complete chromosome
2925_s_at	517	A	Saccharomyces cerevisiae chromosome XI, complete chromosome
2926_s_at	435.6	A	Saccharomyces cerevisiae chromosome XI, complete chromosome
2927_s_at	754.7	A	Saccharomyces cerevisiae chromosome XI, complete chromosome
2928_at	217.1	A	Saccharomyces cerevisiae chromosome XI, complete chromosome
2929_at	498.9	A	Saccharomyces cerevisiae chromosome XI, complete chromosome
2930_at	640.4	A	Saccharomyces cerevisiae chromosome XI, complete chromosome
2931_at	79.6	A	Saccharomyces cerevisiae chromosome XI, complete chromosome
2932_at	24.9	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2933_at	1023.7	M	Saccharomyces cerevisiae chromosome XII, complete chromosome
2934_at	39	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2935_at	195.7	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2936_at	603.1	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2937_at	227.8	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2938_at	36.7	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2939_at	51.2	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2940_at	41.7	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2941_at	31.2	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2942_at	208.4	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2943_at	503.6	M	Saccharomyces cerevisiae chromosome XII, complete chromosome
2944_g_at	1131.1	P	Saccharomyces cerevisiae chromosome XII, complete chromosome
2945_s_at	2612.9	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2946_s_at	537.8	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2947_s_at	3057.4	P	Saccharomyces cerevisiae chromosome XII, complete chromosome
2948_s_at	1718.5	P	Saccharomyces cerevisiae chromosome XII, complete chromosome
2949_at	61.3	A	Saccharomyces cerevisiae chromosome XII, complete chromosome

2950_at	332.3	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2951_at	15.1	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2952_at	12.8	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2953_at	18.2	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2954_at	21.5	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2955_at	5.2	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2956_g_at	2748.8	P	Saccharomyces cerevisiae chromosome XII, complete chromosome
2957_at	13.6	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2958_at	221.6	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2959_at	379.4	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2875_at	159.6	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2876_at	53.3	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2877_at	6.9	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2878_at	13	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2879_at	232.2	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2880_at	264.6	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2881_at	265.4	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2882_at	509.4	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2883_at	57.2	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2884_g_at	381.5	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2885_s_at	1589.8	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2886_s_at	1285.4	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2887_s_at	2494	P	Saccharomyces cerevisiae chromosome XII, complete chromosome
2888_at	871.4	P	Saccharomyces cerevisiae chromosome XII, complete chromosome
2889_at	1156.4	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2890_at	9.2	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2891_at	608.1	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2892_at	43.5	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2893_at	73.9	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2894_at	75.8	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2895_at	18.6	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2896_at	29.6	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2897_at	203.4	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2898_at	20.5	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2899_at	532.9	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2900_at	49.5	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2901_at	53.5	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2902_at	9.8	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2903_g_at	642.2	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2904_s_at	2679.4	P	Saccharomyces cerevisiae chromosome XII, complete chromosome
2905_at	44	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2906_at	557.2	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2907_at	19.7	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2908_at	358.2	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2909_at	58.5	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2910_at	22.3	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2911_s_at	2886.1	P	Saccharomyces cerevisiae chromosome XII, complete chromosome
2912_at	144.7	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2913_at	1123.3	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2914_at	6.5	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2915_g_at	176.7	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2916_s_at	201.1	A	Saccharomyces cerevisiae chromosome XII, complete chromosome

2832_s_at	577.3	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2833_s_at	429.8	P	Saccharomyces cerevisiae chromosome XII, complete chromosome
2834_at	405.4	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2835_at	583.8	P	Saccharomyces cerevisiae chromosome XII, complete chromosome
2836_g_at	7548.5	P	Saccharomyces cerevisiae chromosome XII, complete chromosome
2837_s_at	2545.2	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2838_s_at	4515.6	P	Saccharomyces cerevisiae chromosome XII, complete chromosome
2839_s_at	9123.3	P	Saccharomyces cerevisiae chromosome XII, complete chromosome
2840_s_at	21497.6	P	Saccharomyces cerevisiae chromosome XII, complete chromosome
2841_s_at	33329	P	Saccharomyces cerevisiae chromosome XII, complete chromosome
2842_at	77.3	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2843_at	219.8	P	Saccharomyces cerevisiae chromosome XII, complete chromosome
2844_at	22.4	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2845_g_at	451.4	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2846_s_at	558.4	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2847_s_at	2068.8	P	Saccharomyces cerevisiae chromosome XII, complete chromosome
2848_s_at	3953.8	P	Saccharomyces cerevisiae chromosome XII, complete chromosome
2849_at	425	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2850_g_at	451.1	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2851_s_at	259.4	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2852_s_at	316.9	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2853_s_at	180.7	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2854_s_at	68.6	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2855_s_at	1752.1	P	Saccharomyces cerevisiae chromosome XII, complete chromosome
2856_at	2997	P	Saccharomyces cerevisiae chromosome XII, complete chromosome
2857_at	2796.5	P	Saccharomyces cerevisiae chromosome XII, complete chromosome
2858_at	531.4	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2859_at	33.7	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2860_g_at	524.2	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2861_s_at	77.4	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2862_s_at	693.6	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2863_s_at	456.5	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2864_at	804.3	P	Saccharomyces cerevisiae chromosome XII, complete chromosome
2865_g_at	388.1	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2866_s_at	676.7	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2867_s_at	632.2	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2868_s_at	348.6	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2869_s_at	42.3	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2870_s_at	768.9	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2871_s_at	3332.7	P	Saccharomyces cerevisiae chromosome XII, complete chromosome
2872_at	942.4	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2873_at	300.5	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2874_g_at	293.3	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2789_s_at	42.9	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2790_s_at	181.1	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2791_s_at	185	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2792_s_at	144	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2793_s_at	166.4	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2794_s_at	273.9	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2795_s_at	2390.3	P	Saccharomyces cerevisiae chromosome XII, complete chromosome
2796_f_at	6380.3	P	Saccharomyces cerevisiae chromosome XII, complete chromosome
2797_at	315	A	Saccharomyces cerevisiae chromosome XII, complete chromosome

2798_g_at	102	A	Saccharomyces cerevisiae chromosome XII, complete chromosome
2799_at	16.6	A	Saccharomyces cerevisiae chromosome XIII, complete chromosome
2800_at	669	A	Saccharomyces cerevisiae chromosome XIII, complete chromosome
2801_at	3.9	A	Saccharomyces cerevisiae chromosome XIII, complete chromosome
2802_at	10.2	A	Saccharomyces cerevisiae chromosome XIII, complete chromosome
2803_at	291.6	A	Saccharomyces cerevisiae chromosome XIII, complete chromosome
2804_at	1030.2	A	Saccharomyces cerevisiae chromosome XIII, complete chromosome
2805_g_at	2309	P	Saccharomyces cerevisiae chromosome XIII, complete chromosome
2806_s_at	3241.2	P	Saccharomyces cerevisiae chromosome XIII, complete chromosome
2807_at	440.7	A	Saccharomyces cerevisiae chromosome XIII, complete chromosome
2808_at	645.3	A	Saccharomyces cerevisiae chromosome XIII, complete chromosome
2809_at	63	A	Saccharomyces cerevisiae chromosome XIII, complete chromosome
2810_at	186	A	Saccharomyces cerevisiae chromosome XIII, complete chromosome
2811_at	593.9	A	Saccharomyces cerevisiae chromosome XIII, complete chromosome
2812_at	13	A	Saccharomyces cerevisiae chromosome XIII, complete chromosome
2813_at	2312.6	P	Saccharomyces cerevisiae chromosome XIII, complete chromosome
2814_at	67.1	A	Saccharomyces cerevisiae chromosome XIII, complete chromosome
2815_at	2063.4	P	Saccharomyces cerevisiae chromosome XIII, complete chromosome
2816_at	6107.9	P	Saccharomyces cerevisiae chromosome XIII, complete chromosome
2817_at	10634.2	P	Saccharomyces cerevisiae chromosome XIII, complete chromosome
2818_at	867.6	M	Saccharomyces cerevisiae chromosome XIII, complete chromosome
2819_s_at	2826.9	P	Saccharomyces cerevisiae chromosome XIII, complete chromosome
2821_at	648	A	Saccharomyces cerevisiae chromosome XIII, complete chromosome
2822_at	1402.2	P	Saccharomyces cerevisiae chromosome XIII, complete chromosome
2823_at	949.2	A	Saccharomyces cerevisiae chromosome XIII, complete chromosome
2824_at	790.1	P	Saccharomyces cerevisiae chromosome XIII, complete chromosome
2825_at	251.7	P	Saccharomyces cerevisiae chromosome XIII, complete chromosome
2826_at	82.3	A	Saccharomyces cerevisiae chromosome XIII, complete chromosome
2827_g_at	101.7	A	Saccharomyces cerevisiae chromosome XIII, complete chromosome
2828_at	2.9	A	Saccharomyces cerevisiae chromosome XIII, complete chromosome
2829_f_at	3215.8	P	Saccharomyces cerevisiae chromosome XIII, complete chromosome
2748_at	18.5	A	Saccharomyces cerevisiae chromosome XIII, complete chromosome
2749_s_at	828.3	P	Saccharomyces cerevisiae chromosome XIII, complete chromosome
2750_at	450.8	A	Saccharomyces cerevisiae chromosome XIII, complete chromosome
2751_at	135.5	A	Saccharomyces cerevisiae chromosome XIII, complete chromosome
2752_at	68.2	A	Saccharomyces cerevisiae chromosome XIII, complete chromosome
2753_at	427	A	Saccharomyces cerevisiae chromosome XIII, complete chromosome
2754_at	29.5	A	Saccharomyces cerevisiae chromosome XIII, complete chromosome
2755_at	19.4	A	Saccharomyces cerevisiae chromosome XIII, complete chromosome
2756_at	3002.2	A	Saccharomyces cerevisiae chromosome XIII, complete chromosome
2757_g_at	10280.2	P	Saccharomyces cerevisiae chromosome XIII, complete chromosome
2758_s_at	10931.4	P	Saccharomyces cerevisiae chromosome XIII, complete chromosome
2759_at	81.3	A	Saccharomyces cerevisiae chromosome XIII, complete chromosome
2760_at	496	P	Saccharomyces cerevisiae chromosome XIII, complete chromosome
2761_at	86.6	A	Saccharomyces cerevisiae chromosome XIII, complete chromosome
2762_at	10.6	A	Saccharomyces cerevisiae chromosome XIII, complete chromosome
2763_s_at	34.2	A	Saccharomyces cerevisiae chromosome XIII, complete chromosome
2764_s_at	769.4	P	Saccharomyces cerevisiae chromosome XIII, complete chromosome
2765_s_at	37.4	A	Saccharomyces cerevisiae chromosome XIII, complete chromosome
2766_s_at	570.4	A	Saccharomyces cerevisiae chromosome XIII, complete chromosome
2767_at	903.2	A	Saccharomyces cerevisiae chromosome XIII, complete chromosome
2768_at	513.6	A	Saccharomyces cerevisiae chromosome XIII, complete chromosome

2769_at	15.8	A	Saccharomyces cerevisiae chromosome XIII, complete chromosome
2770_at	311.4	A	Saccharomyces cerevisiae chromosome XIII, complete chromosome
2771_at	578.2	A	Saccharomyces cerevisiae chromosome XIII, complete chromosome
2772_at	1198.6	A	Saccharomyces cerevisiae chromosome XIII, complete chromosome
2773_at	780.5	A	Saccharomyces cerevisiae chromosome XIII, complete chromosome
2774_at	210.5	A	Saccharomyces cerevisiae chromosome XIII, complete chromosome
2775_at	155.4	A	Saccharomyces cerevisiae chromosome XIII, complete chromosome
2776_at	488.5	A	Saccharomyces cerevisiae chromosome XIII, complete chromosome
2777_at	99.8	A	Saccharomyces cerevisiae chromosome XIII, complete chromosome
2778_g_at	341.5	A	Saccharomyces cerevisiae chromosome XIII, complete chromosome
2779_s_at	599.2	A	Saccharomyces cerevisiae chromosome XIII, complete chromosome
2780_at	594	P	Saccharomyces cerevisiae chromosome XIII, complete chromosome
2781_at	422.9	A	Saccharomyces cerevisiae chromosome XIII, complete chromosome
2782_at	120.1	A	Saccharomyces cerevisiae chromosome XIII, complete chromosome
2783_g_at	889.7	M	Saccharomyces cerevisiae chromosome XIII, complete chromosome
2784_s_at	310.5	A	Saccharomyces cerevisiae chromosome XIII, complete chromosome
2785_s_at	492.5	A	Saccharomyces cerevisiae chromosome XIII, complete chromosome
2786_s_at	6502.5	P	Saccharomyces cerevisiae chromosome XIII, complete chromosome
2787_at	1405.6	P	Saccharomyces cerevisiae chromosome XIII, complete chromosome
2788_at	320.9	A	Saccharomyces cerevisiae chromosome XIII, complete chromosome
2703_g_at	48.9	A	Saccharomyces cerevisiae chromosome XIII, complete chromosome
2704_s_at	209.4	A	Saccharomyces cerevisiae chromosome XIII, complete chromosome
2705_s_at	16.2	A	Saccharomyces cerevisiae chromosome XIII, complete chromosome
2706_s_at	447.1	A	Saccharomyces cerevisiae chromosome XIII, complete chromosome
2707_s_at	41.4	A	Saccharomyces cerevisiae chromosome XIII, complete chromosome
2708_s_at	548	A	Saccharomyces cerevisiae chromosome XIII, complete chromosome
2709_s_at	865.4	A	Saccharomyces cerevisiae chromosome XIV, complete chromosome
2710_s_at	1754.5	P	Saccharomyces cerevisiae chromosome XIV, complete chromosome
2711_s_at	1765.7	A	Saccharomyces cerevisiae chromosome XIV, complete chromosome
2712_s_at	474	A	Saccharomyces cerevisiae chromosome XIV, complete chromosome
2713_s_at	2250.8	P	Saccharomyces cerevisiae chromosome XIV, complete chromosome
2714_s_at	18392.8	P	Saccharomyces cerevisiae chromosome XIV, complete chromosome
2715_at	76.1	A	Saccharomyces cerevisiae chromosome XIV, complete chromosome
2716_at	433.8	A	Saccharomyces cerevisiae chromosome XIV, complete chromosome
2717_at	909.3	A	Saccharomyces cerevisiae chromosome XIV, complete chromosome
2718_at	40	A	Saccharomyces cerevisiae chromosome XIV, complete chromosome
2719_at	50.7	A	Saccharomyces cerevisiae chromosome XIV, complete chromosome
2720_at	389.6	A	Saccharomyces cerevisiae chromosome XIV, complete chromosome
2721_at	26.2	A	Saccharomyces cerevisiae chromosome XIV, complete chromosome
2722_g_at	232.3	A	Saccharomyces cerevisiae chromosome XIV, complete chromosome
2723_s_at	13.8	A	Saccharomyces cerevisiae chromosome XIV, complete chromosome
2724_s_at	572.6	A	Saccharomyces cerevisiae chromosome XIV, complete chromosome
2725_s_at	36.3	A	Saccharomyces cerevisiae chromosome XIV, complete chromosome
2726_s_at	756.4	A	Saccharomyces cerevisiae chromosome XIV, complete chromosome
2727_s_at	964	P	Saccharomyces cerevisiae chromosome XIV, complete chromosome
2728_s_at	264.7	M	Saccharomyces cerevisiae chromosome XIV, complete chromosome
2729_at	787.2	A	Saccharomyces cerevisiae chromosome XIV, complete chromosome
2730_at	194.5	A	Saccharomyces cerevisiae chromosome XIV, complete chromosome
2731_at	183.1	A	Saccharomyces cerevisiae chromosome XIV, complete chromosome
2732_at	63.6	A	Saccharomyces cerevisiae chromosome XIV, complete chromosome
2733_g_at	768.8	P	Saccharomyces cerevisiae chromosome XIV, complete chromosome
2734_s_at	1267.9	P	Saccharomyces cerevisiae chromosome XIV, complete chromosome

2735_s_at	2657.3	P	Saccharomyces cerevisiae chromosome XIV, complete chromosome
2736_at	44.9	A	Saccharomyces cerevisiae chromosome XIV, complete chromosome
2737_at	207	A	Saccharomyces cerevisiae chromosome XIV, complete chromosome
2738_at	346.9	P	Saccharomyces cerevisiae chromosome XIV, complete chromosome
2739_g_at	56.7	A	Saccharomyces cerevisiae chromosome XIV, complete chromosome
2740_s_at	286.2	A	Saccharomyces cerevisiae chromosome XIV, complete chromosome
2741_s_at	152.5	A	Saccharomyces cerevisiae chromosome XIV, complete chromosome
2742_s_at	240.5	A	Saccharomyces cerevisiae chromosome XIV, complete chromosome
2743_at	36.1	A	Saccharomyces cerevisiae chromosome XIV, complete chromosome
2744_at	139.4	A	Saccharomyces cerevisiae chromosome XIV, complete chromosome
2745_g_at	283.8	A	Saccharomyces cerevisiae chromosome XIV, complete chromosome
2660_s_at	265.9	A	Saccharomyces cerevisiae chromosome XIV, complete chromosome
2661_s_at	46.4	A	Saccharomyces cerevisiae chromosome XIV, complete chromosome
2662_s_at	490.1	A	Saccharomyces cerevisiae chromosome XIV, complete chromosome
2663_s_at	1864.9	M	Saccharomyces cerevisiae chromosome XIV, complete chromosome
2664_at	315.2	P	Saccharomyces cerevisiae chromosome XIV, complete chromosome
2665_at	101.6	A	Saccharomyces cerevisiae chromosome XIV, complete chromosome
2666_s_at	264.4	A	Saccharomyces cerevisiae chromosome XIV, complete chromosome
2667_s_at	406.8	A	Saccharomyces cerevisiae chromosome XIV, complete chromosome
2668_s_at	734.7	A	Saccharomyces cerevisiae chromosome XIV, complete chromosome
2669_at	1669.4	A	Saccharomyces cerevisiae chromosome XIV, complete chromosome
2670_at	289.3	A	Saccharomyces cerevisiae chromosome XIV, complete chromosome
2671_at	11.1	A	Saccharomyces cerevisiae chromosome XIV, complete chromosome
2672_at	124.5	A	Saccharomyces cerevisiae chromosome XIV, complete chromosome
2673_at	152.9	A	Saccharomyces cerevisiae chromosome XIV, complete chromosome
2674_at	16.1	A	Saccharomyces cerevisiae chromosome XIV, complete chromosome
2675_at	790.2	A	Saccharomyces cerevisiae chromosome XIV, complete chromosome
2676_at	33.5	A	Saccharomyces cerevisiae chromosome XIV, complete chromosome
2677_at	126.7	A	Saccharomyces cerevisiae chromosome XIV, complete chromosome
2678_at	137.2	A	Saccharomyces cerevisiae chromosome XIV, complete chromosome
2679_at	229.4	A	Saccharomyces cerevisiae chromosome XIV, complete chromosome
2680_at	140.6	A	Saccharomyces cerevisiae chromosome XIV, complete chromosome
2681_g_at	2156.9	P	Saccharomyces cerevisiae chromosome XIV, complete chromosome
2682_s_at	2227.3	M	Saccharomyces cerevisiae chromosome XIV, complete chromosome
2683_at	229.6	A	Saccharomyces cerevisiae chromosome XIV, complete chromosome
2684_at	417.9	A	Saccharomyces cerevisiae chromosome XIV, complete chromosome
2685_at	609.1	A	Saccharomyces cerevisiae chromosome XIV, complete chromosome
2686_at	488.6	A	Saccharomyces cerevisiae chromosome XIV, complete chromosome
2687_g_at	92.4	A	Saccharomyces cerevisiae chromosome XIV, complete chromosome
2688_s_at	920.3	A	Saccharomyces cerevisiae chromosome XIV, complete chromosome
2689_s_at	137.1	A	Saccharomyces cerevisiae chromosome XIV, complete chromosome
2690_s_at	45.2	A	Saccharomyces cerevisiae chromosome XIV, complete chromosome
2691_s_at	102.5	A	Saccharomyces cerevisiae chromosome XIV, complete chromosome
2692_at	47.9	A	Saccharomyces cerevisiae chromosome XV, complete chromosome
2693_at	451.7	A	Saccharomyces cerevisiae chromosome XV, complete chromosome
2694_at	130.7	A	Saccharomyces cerevisiae chromosome XV, complete chromosome
2695_at	67.5	A	Saccharomyces cerevisiae chromosome XV, complete chromosome
2696_at	90.1	A	Saccharomyces cerevisiae chromosome XV, complete chromosome
2697_g_at	102.9	A	Saccharomyces cerevisiae chromosome XV, complete chromosome
2698_s_at	815	A	Saccharomyces cerevisiae chromosome XV, complete chromosome
2699_at	137.2	A	Saccharomyces cerevisiae chromosome XV, complete chromosome
2700_at	32.2	A	Saccharomyces cerevisiae chromosome XV, complete chromosome

2701_g_at	351.1	A	Saccharomyces cerevisiae chromosome XV, complete chromosome
2702_s_at	644.6	A	Saccharomyces cerevisiae chromosome XV, complete chromosome
2618_s_at	44.6	A	Saccharomyces cerevisiae chromosome XV, complete chromosome
2619_s_at	16.1	A	Saccharomyces cerevisiae chromosome XV, complete chromosome
2620_s_at	50.4	A	Saccharomyces cerevisiae chromosome XV, complete chromosome
2621_s_at	363.2	A	Saccharomyces cerevisiae chromosome XV, complete chromosome
2622_s_at	281.6	A	Saccharomyces cerevisiae chromosome XV, complete chromosome
2623_s_at	30.5	A	Saccharomyces cerevisiae chromosome XV, complete chromosome
2624_s_at	1012.5	P	Saccharomyces cerevisiae chromosome XV, complete chromosome
2625_at	267.9	A	Saccharomyces cerevisiae chromosome XV, complete chromosome
2626_at	1441.5	A	Saccharomyces cerevisiae chromosome XV, complete chromosome
2627_at	725.9	A	Saccharomyces cerevisiae chromosome XV, complete chromosome
2628_s_at	887.1	A	Saccharomyces cerevisiae chromosome XV, complete chromosome
2629_s_at	381.4	A	Saccharomyces cerevisiae chromosome XV, complete chromosome
2630_s_at	3651.5	P	Saccharomyces cerevisiae chromosome XV, complete chromosome
2631_s_at	2241.1	P	Saccharomyces cerevisiae chromosome XV, complete chromosome
2632_at	633.9	A	Saccharomyces cerevisiae chromosome XV, complete chromosome
2633_at	426.4	A	Saccharomyces cerevisiae chromosome XV, complete chromosome
2634_at	199.9	A	Saccharomyces cerevisiae chromosome XV, complete chromosome
2635_at	270.5	A	Saccharomyces cerevisiae chromosome XV, complete chromosome
2636_at	135.7	A	Saccharomyces cerevisiae chromosome XV, complete chromosome
2637_g_at	2567.6	P	Saccharomyces cerevisiae chromosome XV, complete chromosome
2638_s_at	11037.8	P	Saccharomyces cerevisiae chromosome XV, complete chromosome
2639_at	16.9	A	Saccharomyces cerevisiae chromosome XV, complete chromosome
2640_at	486.2	A	Saccharomyces cerevisiae chromosome XV, complete chromosome
2641_g_at	676.1	A	Saccharomyces cerevisiae chromosome XV, complete chromosome
2642_s_at	341.4	A	Saccharomyces cerevisiae chromosome XV, complete chromosome
2643_s_at	3896.3	P	Saccharomyces cerevisiae chromosome XV, complete chromosome
2644_s_at	2209.9	P	Saccharomyces cerevisiae chromosome XV, complete chromosome
2645_s_at	23717	P	Saccharomyces cerevisiae chromosome XV, complete chromosome
2646_at	75.2	A	Saccharomyces cerevisiae chromosome XV, complete chromosome
2647_at	379.2	A	Saccharomyces cerevisiae chromosome XV, complete chromosome
2648_at	14.8	A	Saccharomyces cerevisiae chromosome XV, complete chromosome
2649_at	71.8	A	Saccharomyces cerevisiae chromosome XV, complete chromosome
2650_g_at	52.7	A	Saccharomyces cerevisiae chromosome XV, complete chromosome
2651_s_at	658.2	M	Saccharomyces cerevisiae chromosome XV, complete chromosome
2652_s_at	1235.4	P	Saccharomyces cerevisiae chromosome XV, complete chromosome
2653_at	121.6	A	Saccharomyces cerevisiae chromosome XV, complete chromosome
2654_at	140.2	A	Saccharomyces cerevisiae chromosome XV, complete chromosome
2655_at	1106	A	Saccharomyces cerevisiae chromosome XV, complete chromosome
2656_at	1159	A	Saccharomyces cerevisiae chromosome XV, complete chromosome
2657_at	187.8	A	Saccharomyces cerevisiae chromosome XV, complete chromosome
2658_at	27.8	A	Saccharomyces cerevisiae chromosome XV, complete chromosome
2659_g_at	327.8	A	Saccharomyces cerevisiae chromosome XV, complete chromosome
2575_s_at	285.7	A	Saccharomyces cerevisiae chromosome XV, complete chromosome
2576_s_at	865	P	Saccharomyces cerevisiae chromosome XV, complete chromosome
2577_s_at	731.1	A	Saccharomyces cerevisiae chromosome XV, complete chromosome
2578_s_at	3272.7	P	Saccharomyces cerevisiae chromosome XV, complete chromosome
2579_at	1116.9	A	Saccharomyces cerevisiae chromosome XV, complete chromosome
2580_at	583.2	P	Saccharomyces cerevisiae chromosome XV, complete chromosome
2581_at	270.5	A	Saccharomyces cerevisiae chromosome XV, complete chromosome
2582_at	635.7	A	Saccharomyces cerevisiae chromosome XV, complete chromosome

2583_g_at	158.9	A	Saccharomyces cerevisiae chromosome XV, complete chromosome
2584_s_at	355.7	A	Saccharomyces cerevisiae chromosome XV, complete chromosome
2585_s_at	285.7	P	Saccharomyces cerevisiae chromosome XV, complete chromosome
2586_s_at	2591.6	P	Saccharomyces cerevisiae chromosome XV, complete chromosome
2587_at	240.3	A	Saccharomyces cerevisiae chromosome XV, complete chromosome
2588_at	569.6	P	Saccharomyces cerevisiae chromosome XV, complete chromosome
2589_g_at	812	A	Saccharomyces cerevisiae chromosome XV, complete chromosome
2590_s_at	1436.1	A	Saccharomyces cerevisiae chromosome XV, complete chromosome
2591_s_at	1125.3	P	Saccharomyces cerevisiae chromosome XV, complete chromosome
2592_s_at	5271.8	P	Saccharomyces cerevisiae chromosome XV, complete chromosome
2593_s_at	19126.7	P	Saccharomyces cerevisiae chromosome XV, complete chromosome
2594_at	309.8	A	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2595_at	2513.5	A	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2596_at	84.1	A	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2597_at	67.5	A	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2598_g_at	1144.5	P	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2599_s_at	8044.7	P	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2600_s_at	7139.7	P	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2601_at	845.9	A	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2602_g_at	1413.9	P	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2603_s_at	1276.8	P	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2604_s_at	2218.9	P	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2605_s_at	10565.8	P	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2606_s_at	13804.7	P	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2607_s_at	28798.4	P	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2608_at	334.8	A	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2609_at	716.7	A	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2610_at	35.7	A	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2611_at	987.1	P	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2612_g_at	46.4	A	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2613_s_at	198.3	A	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2614_s_at	124.8	A	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2615_s_at	279.4	P	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2616_at	15.8	A	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2617_at	394.9	M	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2532_g_at	5.9	A	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2533_s_at	336.9	A	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2534_s_at	215.2	A	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2535_s_at	678.4	A	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2536_s_at	851.5	A	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2537_s_at	4600.5	A	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2538_s_at	1946.9	P	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2539_at	695	A	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2540_at	1044.3	A	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2541_at	133.5	A	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2542_at	14.4	A	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2543_at	224.2	A	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2544_at	189.5	A	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2545_at	331.1	A	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2546_at	400.4	A	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2547_at	55.1	A	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2548_at	400.6	A	Saccharomyces cerevisiae chromosome XVI, complete chromosome

2549_at	158.4	A	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2550_at	36.3	A	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2551_at	40.3	A	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2552_at	12.2	A	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2553_at	291.2	P	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2554_at	663.6	P	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2555_at	407	P	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2556_at	163.4	A	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2557_at	23.2	A	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2558_at	288.6	A	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2559_at	1735.8	A	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2560_at	582.7	A	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2561_at	1007.6	A	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2562_g_at	182.9	A	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2563_s_at	922.9	M	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2564_s_at	1555.4	A	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2565_s_at	1022.2	P	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2566_s_at	4286.1	P	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2567_at	644.3	P	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2568_at	1536.3	A	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2569_at	138.5	A	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2570_at	451.3	A	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2571_s_at	1594.7	P	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2572_s_at	498.4	P	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2573_at	49.6	A	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2574_at	371.8	A	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2489_at	3.2	A	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2490_s_at	2776.5	P	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2491_s_at	1608.4	P	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2492_f_at	2437.8	P	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2493_at	422.9	A	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2494_at	411.4	A	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2495_at	227.6	A	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2496_g_at	63.8	A	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2497_s_at	27.2	A	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2498_s_at	1066.2	A	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2499_s_at	1215.7	A	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2500_at	480.6	P	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2501_g_at	216.9	A	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2502_s_at	633.2	A	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2503_s_at	112.5	A	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2504_s_at	678.5	A	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2505_s_at	840	P	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2506_s_at	1167.9	P	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2507_s_at	149.8	A	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2508_s_at	1174.5	P	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2509_at	2369.7	A	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2510_at	801.1	A	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2511_g_at	22.9	A	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2512_s_at	62.4	A	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2513_s_at	406.4	A	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2514_s_at	553.6	P	Saccharomyces cerevisiae chromosome XVI, complete chromosome

2515_s_at	84.4	A	Saccharomyces cerevisiae chromosome XVI, complete chromosome
2516_at	78.2	A	Saccharomyces cerevisiae chromosome II, complete chromosome s
2517_at	224.5	A	Saccharomyces cerevisiae chromosome II, complete chromosome s
2518_at	92.2	A	Saccharomyces cerevisiae chromosome II, complete chromosome s
2519_at	57.4	A	Saccharomyces cerevisiae chromosome II, complete chromosome s
2520_at	119.1	A	Saccharomyces cerevisiae chromosome II, complete chromosome s
2521_f_at	34.2	A	Saccharomyces cerevisiae chromosome II, complete chromosome s
2522_at	24.3	A	Saccharomyces cerevisiae chromosome II, complete chromosome s
2523_at	19.9	A	Saccharomyces cerevisiae chromosome II, complete chromosome s
2524_at	36.5	A	Saccharomyces cerevisiae chromosome II, complete chromosome s
2525_at	761.5	A	Saccharomyces cerevisiae chromosome II, complete chromosome s
2526_at	30.6	A	Saccharomyces cerevisiae chromosome II, complete chromosome s
2527_at	64.7	A	Saccharomyces cerevisiae chromosome II, complete chromosome s
2528_at	265.5	A	Saccharomyces cerevisiae chromosome II, complete chromosome s
2529_at	3.8	A	Saccharomyces cerevisiae chromosome II, complete chromosome s
2530_at	372.2	P	Saccharomyces cerevisiae chromosome II, complete chromosome s
2531_at	679	A	Saccharomyces cerevisiae chromosome II, complete chromosome s
2446_at	26.4	A	Saccharomyces cerevisiae chromosome II, complete chromosome s
2447_g_at	292.8	A	Saccharomyces cerevisiae chromosome II, complete chromosome s
2448_s_at	359.5	A	Saccharomyces cerevisiae chromosome II, complete chromosome s
2449_s_at	1878.4	P	Saccharomyces cerevisiae chromosome II, complete chromosome s
2450_s_at	873.7	A	Saccharomyces cerevisiae chromosome II, complete chromosome s
2451_s_at	6878.6	P	Saccharomyces cerevisiae chromosome II, complete chromosome s
2452_at	250.8	A	Saccharomyces cerevisiae chromosome II, complete chromosome s
2453_at	162.6	A	Saccharomyces cerevisiae chromosome II, complete chromosome s
2454_at	40.8	A	Saccharomyces cerevisiae chromosome II, complete chromosome s
2455_at	355.9	A	Saccharomyces cerevisiae chromosome II, complete chromosome s
2456_at	152.8	A	Saccharomyces cerevisiae chromosome II, complete chromosome s
2457_at	234.1	A	Saccharomyces cerevisiae chromosome II, complete chromosome s
2458_g_at	5180	P	Saccharomyces cerevisiae chromosome II, complete chromosome s
2459_at	1326.6	A	Saccharomyces cerevisiae chromosome II, complete chromosome s
2460_at	720.4	A	Saccharomyces cerevisiae chromosome II, complete chromosome s
2461_at	360.3	A	Saccharomyces cerevisiae chromosome II, complete chromosome s
2462_g_at	198.6	A	Saccharomyces cerevisiae chromosome II, complete chromosome s
2463_s_at	141.8	A	Saccharomyces cerevisiae chromosome II, complete chromosome s
2464_s_at	1557.3	P	Saccharomyces cerevisiae chromosome II, complete chromosome s
2465_s_at	1446	P	Saccharomyces cerevisiae chromosome II, complete chromosome s
2466_s_at	167.7	P	Saccharomyces cerevisiae chromosome II, complete chromosome s
2467_s_at	2001.9	A	Saccharomyces cerevisiae chromosome II, complete chromosome s
2468_s_at	3301.2	P	Saccharomyces cerevisiae chromosome II, complete chromosome s
2469_s_at	955.1	P	Saccharomyces cerevisiae chromosome II, complete chromosome s
2470_at	2116.1	P	Saccharomyces cerevisiae chromosome II, complete chromosome s
2471_g_at	189.4	A	Saccharomyces cerevisiae chromosome II, complete chromosome s
2472_s_at	130.1	A	Saccharomyces cerevisiae chromosome II, complete chromosome s
2473_s_at	531.8	A	Saccharomyces cerevisiae chromosome II, complete chromosome s
2474_s_at	229.3	A	Saccharomyces cerevisiae chromosome II, complete chromosome s
2475_s_at	184.3	A	Saccharomyces cerevisiae chromosome II, complete chromosome s
2476_s_at	814.4	A	Saccharomyces cerevisiae chromosome II, complete chromosome s
2477_s_at	1061.4	A	Saccharomyces cerevisiae chromosome II, complete chromosome s
2478_at	352.3	A	Saccharomyces cerevisiae chromosome II, complete chromosome s
2479_at	19.1	A	Saccharomyces cerevisiae chromosome II, complete chromosome s
2480_at	75.9	A	Saccharomyces cerevisiae chromosome II, complete chromosome s

2481_at	15.1	A	Saccharomyces cerevisiae chromosome II, complete chromosome s
2482_at	222.1	A	Saccharomyces cerevisiae chromosome II, complete chromosome s
2483_at	640	A	Saccharomyces cerevisiae chromosome II, complete chromosome s
2484_at	7	A	Saccharomyces cerevisiae chromosome II, complete chromosome s
2485_at	162.1	A	Saccharomyces cerevisiae chromosome II, complete chromosome s
2486_at	18.3	A	Saccharomyces cerevisiae chromosome II, complete chromosome s
2487_at	2096.9	P	Saccharomyces cerevisiae chromosome II, complete chromosome s
2488_at	406.3	A	Saccharomyces cerevisiae chromosome II, complete chromosome s
2421_at	62.1	A	Saccharomyces cerevisiae chromosome II, complete chromosome s
2422_at	451.9	A	Saccharomyces cerevisiae chromosome II, complete chromosome s
2423_at	448.7	A	Saccharomyces cerevisiae chromosome II, complete chromosome s
2424_at	424.4	M	Saccharomyces cerevisiae chromosome II, complete chromosome s
2425_at	106.7	A	Saccharomyces cerevisiae chromosome II, complete chromosome s
2426_at	1441.2	A	Saccharomyces cerevisiae chromosome II, complete chromosome s
2427_at	1078.5	A	Saccharomyces cerevisiae chromosome II, complete chromosome s
2428_at	23.6	A	Saccharomyces cerevisiae chromosome II, complete chromosome s
2429_at	27.8	A	Saccharomyces cerevisiae chromosome II, complete chromosome s
2430_at	30.1	A	Saccharomyces cerevisiae chromosome II, complete chromosome s
2431_at	96.3	A	Saccharomyces cerevisiae chromosome II, complete chromosome s
2432_at	3822.4	P	Saccharomyces cerevisiae chromosome III, complete chromosome s
2433_at	1517.2	A	Saccharomyces cerevisiae chromosome III, complete chromosome s
2434_at	86.3	A	Saccharomyces cerevisiae chromosome III, complete chromosome s
2435_at	200.2	A	Saccharomyces cerevisiae chromosome III, complete chromosome s
2436_g_at	264.5	A	Saccharomyces cerevisiae chromosome III, complete chromosome s
2437_s_at	4449.2	P	Saccharomyces cerevisiae chromosome III, complete chromosome s
2438_at	9.2	A	Saccharomyces cerevisiae chromosome III, complete chromosome s
2439_g_at	215.1	A	Saccharomyces cerevisiae chromosome III, complete chromosome s
2440_s_at	235.2	A	Saccharomyces cerevisiae chromosome III, complete chromosome s
2441_s_at	221.7	P	Saccharomyces cerevisiae chromosome III, complete chromosome s
2442_s_at	371.5	A	Saccharomyces cerevisiae chromosome III, complete chromosome s
2443_s_at	364.9	P	Saccharomyces cerevisiae chromosome III, complete chromosome s
2444_s_at	393.6	A	Saccharomyces cerevisiae chromosome III, complete chromosome s
2445_s_at	989.5	P	Saccharomyces cerevisiae chromosome III, complete chromosome s
2395_at	23.7	A	Saccharomyces cerevisiae chromosome III, complete chromosome s
2396_at	362.3	A	Saccharomyces cerevisiae chromosome III, complete chromosome s
2397_at	114.1	A	Saccharomyces cerevisiae chromosome III, complete chromosome s
2398_g_at	602	A	Saccharomyces cerevisiae chromosome III, complete chromosome s
2399_s_at	506.6	M	Saccharomyces cerevisiae chromosome III, complete chromosome s
2400_s_at	45.5	A	Saccharomyces cerevisiae chromosome III, complete chromosome s
2401_s_at	305.7	A	Saccharomyces cerevisiae chromosome III, complete chromosome s
2402_s_at	634.4	A	Saccharomyces cerevisiae chromosome III, complete chromosome s
2403_s_at	1282.4	P	Saccharomyces cerevisiae chromosome III, complete chromosome s
2404_s_at	2775.9	P	Saccharomyces cerevisiae chromosome III, complete chromosome s
2405_at	55.7	A	Saccharomyces cerevisiae chromosome IV, complete chromosome s
2406_at	19.2	A	Saccharomyces cerevisiae chromosome IV, complete chromosome s
2407_at	1712.5	A	Saccharomyces cerevisiae chromosome IV, complete chromosome s
2408_at	280.1	A	Saccharomyces cerevisiae chromosome IV, complete chromosome s
2409_at	187.9	A	Saccharomyces cerevisiae chromosome IV, complete chromosome s
2410_g_at	109.4	A	Saccharomyces cerevisiae chromosome IV, complete chromosome s
2411_s_at	1360.1	A	Saccharomyces cerevisiae chromosome IV, complete chromosome s
2412_at	1463.6	A	Saccharomyces cerevisiae chromosome IV, complete chromosome s
2413_at	573.7	A	Saccharomyces cerevisiae chromosome IV, complete chromosome s

2414_at	120.8	A	Saccharomyces cerevisiae chromosome IV, complete chromosome
2415_at	20.3	A	Saccharomyces cerevisiae chromosome IV, complete chromosome
2416_at	427	A	Saccharomyces cerevisiae chromosome IV, complete chromosome
2417_at	400.6	A	Saccharomyces cerevisiae chromosome IV, complete chromosome
2418_at	167.9	A	Saccharomyces cerevisiae chromosome IV, complete chromosome
2419_g_at	362.7	A	Saccharomyces cerevisiae chromosome IV, complete chromosome
2420_s_at	357	P	Saccharomyces cerevisiae chromosome IV, complete chromosome
2352_at	203.1	A	Saccharomyces cerevisiae chromosome IV, complete chromosome
2353_at	618.9	A	Saccharomyces cerevisiae chromosome IV, complete chromosome
2354_at	35.7	A	Saccharomyces cerevisiae chromosome IV, complete chromosome
2355_at	17.4	A	Saccharomyces cerevisiae chromosome IV, complete chromosome
2356_at	575.9	A	Saccharomyces cerevisiae chromosome IV, complete chromosome
2357_at	541.6	P	Saccharomyces cerevisiae chromosome IV, complete chromosome
2358_at	222.8	A	Saccharomyces cerevisiae chromosome IV, complete chromosome
2359_at	116.4	A	Saccharomyces cerevisiae chromosome IV, complete chromosome
2360_g_at	661	A	Saccharomyces cerevisiae chromosome IV, complete chromosome
2361_s_at	339	A	Saccharomyces cerevisiae chromosome IV, complete chromosome
2362_s_at	2090	A	Saccharomyces cerevisiae chromosome IV, complete chromosome
2363_s_at	1234.5	P	Saccharomyces cerevisiae chromosome IV, complete chromosome
2364_s_at	2480.8	P	Saccharomyces cerevisiae chromosome IV, complete chromosome
2365_at	143.6	A	Saccharomyces cerevisiae chromosome IV, complete chromosome
2366_s_at	83.4	A	Saccharomyces cerevisiae chromosome IV, complete chromosome
2367_s_at	545.9	P	Saccharomyces cerevisiae chromosome IV, complete chromosome
2368_s_at	70.3	A	Saccharomyces cerevisiae chromosome IV, complete chromosome
2369_s_at	476.6	P	Saccharomyces cerevisiae chromosome IV, complete chromosome
2370_s_at	211.4	A	Saccharomyces cerevisiae chromosome IV, complete chromosome
2371_at	17.3	A	Saccharomyces cerevisiae chromosome IV, complete chromosome
2372_at	2769.1	M	Saccharomyces cerevisiae chromosome IV, complete chromosome
2373_at	89	A	Saccharomyces cerevisiae chromosome IV, complete chromosome
2374_at	1183.1	A	Saccharomyces cerevisiae chromosome IV, complete chromosome
2375_s_at	173.5	A	Saccharomyces cerevisiae chromosome IV, complete chromosome
2376_s_at	815.3	A	Saccharomyces cerevisiae chromosome IV, complete chromosome
2377_at	276.5	A	Saccharomyces cerevisiae chromosome IV, complete chromosome
2378_g_at	1257.5	P	Saccharomyces cerevisiae chromosome IV, complete chromosome
2379_s_at	1258.7	P	Saccharomyces cerevisiae chromosome IV, complete chromosome
2380_s_at	770.2	P	Saccharomyces cerevisiae chromosome IV, complete chromosome
2381_s_at	1232.4	P	Saccharomyces cerevisiae chromosome IV, complete chromosome
2382_s_at	9696.7	M	Saccharomyces cerevisiae chromosome IV, complete chromosome
2383_at	174.3	A	Saccharomyces cerevisiae chromosome IV, complete chromosome
2384_at	117.5	A	Saccharomyces cerevisiae chromosome IV, complete chromosome
2385_at	7.2	A	Saccharomyces cerevisiae chromosome IV, complete chromosome
2386_at	49.5	A	Saccharomyces cerevisiae chromosome IV, complete chromosome
2387_at	240.5	A	Saccharomyces cerevisiae chromosome IV, complete chromosome
2388_s_at	166.6	A	Saccharomyces cerevisiae chromosome IV, complete chromosome
2389_s_at	6.8	A	Saccharomyces cerevisiae chromosome IV, complete chromosome
2390_s_at	21.7	A	Saccharomyces cerevisiae chromosome IV, complete chromosome
2391_s_at	15.2	A	Saccharomyces cerevisiae chromosome IV, complete chromosome
2392_s_at	116.6	A	Saccharomyces cerevisiae chromosome IV, complete chromosome
2393_s_at	427.6	M	Saccharomyces cerevisiae chromosome IV, complete chromosome
2394_s_at	669.9	P	Saccharomyces cerevisiae chromosome IV, complete chromosome
2309_at	68.6	A	Saccharomyces cerevisiae chromosome IV, complete chromosome
2310_at	170.6	A	Saccharomyces cerevisiae chromosome IV, complete chromosome

2311_at	5.5	A	Saccharomyces cerevisiae chromosome IV, complete chromosome
2312_at	578	A	Saccharomyces cerevisiae chromosome IV, complete chromosome
2313_at	807.9	A	Saccharomyces cerevisiae chromosome IV, complete chromosome
2314_at	1006.2	A	Saccharomyces cerevisiae chromosome IV, complete chromosome
2315_at	487.3	P	Saccharomyces cerevisiae chromosome IV, complete chromosome
2316_at	67.7	M	Saccharomyces cerevisiae chromosome IV, complete chromosome
2317_at	632.5	A	Saccharomyces cerevisiae chromosome IV, complete chromosome
2319_f_at	1343	M	Saccharomyces cerevisiae chromosome IV, complete chromosome
2320_at	64.3	A	Saccharomyces cerevisiae chromosome IV, complete chromosome
2321_at	364.2	P	Saccharomyces cerevisiae chromosome IV, complete chromosome
2322_at	418.5	M	Saccharomyces cerevisiae chromosome IV, complete chromosome
2323_g_at	649.5	P	Saccharomyces cerevisiae chromosome IV, complete chromosome
2324_s_at	165.5	A	Saccharomyces cerevisiae chromosome IV, complete chromosome
2325_s_at	430.1	A	Saccharomyces cerevisiae chromosome IV, complete chromosome
2326_s_at	354.9	P	Saccharomyces cerevisiae chromosome IV, complete chromosome
2327_s_at	505	P	Saccharomyces cerevisiae chromosome IV, complete chromosome
2328_at	363.2	A	Saccharomyces cerevisiae chromosome IV, complete chromosome
2329_at	303.4	A	Saccharomyces cerevisiae chromosome IV, complete chromosome
2330_g_at	529	A	Saccharomyces cerevisiae chromosome IV, complete chromosome
2331_s_at	1413.1	A	Saccharomyces cerevisiae chromosome IV, complete chromosome
2332_s_at	3400.1	P	Saccharomyces cerevisiae chromosome IV, complete chromosome
2333_s_at	1887.1	P	Saccharomyces cerevisiae chromosome IV, complete chromosome
2334_s_at	1520.3	P	Saccharomyces cerevisiae chromosome IV, complete chromosome
2335_s_at	2312.6	P	Saccharomyces cerevisiae chromosome IV, complete chromosome
2336_at	568.4	A	Saccharomyces cerevisiae chromosome IV, complete chromosome
2337_at	52.4	A	Saccharomyces cerevisiae chromosome IV, complete chromosome
2338_at	148.1	A	Saccharomyces cerevisiae chromosome IV, complete chromosome
2339_at	243.8	A	Saccharomyces cerevisiae chromosome IV, complete chromosome
2340_at	3881	A	Saccharomyces cerevisiae chromosome IV, complete chromosome
2341_g_at	1039.6	P	Saccharomyces cerevisiae chromosome IV, complete chromosome
2342_s_at	2613.8	M	Saccharomyces cerevisiae chromosome IV, complete chromosome
2343_at	1114.1	P	Saccharomyces cerevisiae chromosome IV, complete chromosome
2344_g_at	718.8	P	Saccharomyces cerevisiae chromosome IV, complete chromosome
2345_s_at	1655.9	A	Saccharomyces cerevisiae chromosome IV, complete chromosome
2346_s_at	50.2	A	Saccharomyces cerevisiae chromosome IV, complete chromosome
2347_s_at	74.7	A	Saccharomyces cerevisiae chromosome IV, complete chromosome
2348_s_at	422.9	A	Saccharomyces cerevisiae chromosome IV, complete chromosome
2349_s_at	42.2	A	Saccharomyces cerevisiae chromosome IV, complete chromosome
2350_s_at	1209.5	P	Saccharomyces cerevisiae chromosome IV, complete chromosome
2351_s_at	730.2	P	Saccharomyces cerevisiae chromosome IV, complete chromosome
2266_s_at	1128.4	P	Saccharomyces cerevisiae chromosome IV, complete chromosome
2267_s_at	1221.4	P	Saccharomyces cerevisiae chromosome IV, complete chromosome
2268_at	271.1	A	Saccharomyces cerevisiae chromosome V, complete chromosome s
2269_at	36.7	A	Saccharomyces cerevisiae chromosome V, complete chromosome s
2270_at	302.1	A	Saccharomyces cerevisiae chromosome V, complete chromosome s
2271_at	34.8	A	Saccharomyces cerevisiae chromosome V, complete chromosome s
2272_at	460.5	A	Saccharomyces cerevisiae chromosome V, complete chromosome s
2273_at	22.3	A	Saccharomyces cerevisiae chromosome V, complete chromosome s
2274_at	39.4	A	Saccharomyces cerevisiae chromosome V, complete chromosome s
2275_g_at	141.5	A	Saccharomyces cerevisiae chromosome V, complete chromosome s
2276_at	96.1	A	Saccharomyces cerevisiae chromosome V, complete chromosome s
2277_at	509.5	A	Saccharomyces cerevisiae chromosome V, complete chromosome s

2278_at	121.9	A	Saccharomyces cerevisiae chromosome V, complete chromosome s
2279_g_at	918.6	A	Saccharomyces cerevisiae chromosome V, complete chromosome s
2280_s_at	644.5	A	Saccharomyces cerevisiae chromosome V, complete chromosome s
2281_s_at	2026.8	A	Saccharomyces cerevisiae chromosome V, complete chromosome s
2282_s_at	2098.2	P	Saccharomyces cerevisiae chromosome V, complete chromosome s
2283_s_at	2670.6	P	Saccharomyces cerevisiae chromosome V, complete chromosome s
2284_at	189.3	A	Saccharomyces cerevisiae chromosome V, complete chromosome s
2285_at	22.6	A	Saccharomyces cerevisiae chromosome V, complete chromosome s
2286_at	157.3	A	Saccharomyces cerevisiae chromosome V, complete chromosome s
2287_at	420.5	A	Saccharomyces cerevisiae chromosome V, complete chromosome s
2288_at	513.8	A	Saccharomyces cerevisiae chromosome V, complete chromosome s
2289_at	44.2	A	Saccharomyces cerevisiae chromosome V, complete chromosome s
2290_at	367.8	A	Saccharomyces cerevisiae chromosome V, complete chromosome s
2291_g_at	706.5	A	Saccharomyces cerevisiae chromosome V, complete chromosome s
2294_f_at	8572.5	P	Saccharomyces cerevisiae chromosome V, complete chromosome s
2295_at	10.5	A	Saccharomyces cerevisiae chromosome V, complete chromosome s
2296_at	109.9	A	Saccharomyces cerevisiae chromosome V, complete chromosome s
2297_at	11.5	A	Saccharomyces cerevisiae chromosome V, complete chromosome s
2298_at	187.3	A	Saccharomyces cerevisiae chromosome V, complete chromosome s
2299_at	166.4	A	Saccharomyces cerevisiae chromosome V, complete chromosome s
2300_at	153.5	A	Saccharomyces cerevisiae chromosome V, complete chromosome s
2301_at	19.7	A	Saccharomyces cerevisiae chromosome V, complete chromosome s
2302_at	220.1	A	Saccharomyces cerevisiae chromosome V, complete chromosome s
2303_f_at	2285.9	M	Saccharomyces cerevisiae chromosome V, complete chromosome s
2306_at	962.5	P	Saccharomyces cerevisiae chromosome V, complete chromosome s
2307_at	489.2	A	Saccharomyces cerevisiae chromosome V, complete chromosome s
2308_at	15.7	A	Saccharomyces cerevisiae chromosome V, complete chromosome s
2223_at	280.9	A	Saccharomyces cerevisiae chromosome V, complete chromosome s
2224_at	29.2	A	Saccharomyces cerevisiae chromosome V, complete chromosome s
2225_at	298.5	A	Saccharomyces cerevisiae chromosome V, complete chromosome s
2226_at	461.2	P	Saccharomyces cerevisiae chromosome V, complete chromosome s
2227_at	68.3	A	Saccharomyces cerevisiae chromosome V, complete chromosome s
2228_at	37	A	Saccharomyces cerevisiae chromosome V, complete chromosome s
2229_at	145.4	A	Saccharomyces cerevisiae chromosome VI, complete chromosome
2230_at	1278	M	Saccharomyces cerevisiae chromosome VI, complete chromosome
2231_at	490.7	A	Saccharomyces cerevisiae chromosome VI, complete chromosome
2232_at	140.9	A	Saccharomyces cerevisiae chromosome VI, complete chromosome
2233_at	440.6	A	Saccharomyces cerevisiae chromosome VI, complete chromosome
2234_at	50.8	A	Saccharomyces cerevisiae chromosome VI, complete chromosome
2235_at	696.3	P	Saccharomyces cerevisiae chromosome VI, complete chromosome
2236_at	16.1	A	Saccharomyces cerevisiae chromosome VI, complete chromosome
2237_at	167.3	A	Saccharomyces cerevisiae chromosome VI, complete chromosome
2238_at	602.3	A	Saccharomyces cerevisiae chromosome VI, complete chromosome
2239_at	4622.8	P	Saccharomyces cerevisiae chromosome VI, complete chromosome
2240_at	90.5	A	Saccharomyces cerevisiae chromosome VI, complete chromosome
2241_s_at	1091.8	P	Saccharomyces cerevisiae chromosome VI, complete chromosome
2242_s_at	478.8	A	Saccharomyces cerevisiae chromosome VI, complete chromosome
2243_s_at	43.2	A	Saccharomyces cerevisiae chromosome VI, complete chromosome
2244_s_at	634.7	P	Saccharomyces cerevisiae chromosome VI, complete chromosome
2245_s_at	62.2	A	Saccharomyces cerevisiae chromosome VI, complete chromosome
2246_s_at	1363.7	P	Saccharomyces cerevisiae chromosome VI, complete chromosome
2247_at	432.2	A	Saccharomyces cerevisiae chromosome VII, complete chromosome

2248_at	344.8	A	Saccharomyces cerevisiae chromosome VII, complete chromosome
2249_at	152.5	A	Saccharomyces cerevisiae chromosome VII, complete chromosome
2250_at	1264.3	A	Saccharomyces cerevisiae chromosome VII, complete chromosome
2251_at	527.6	A	Saccharomyces cerevisiae chromosome VII, complete chromosome
2252_g_at	2273.1	P	Saccharomyces cerevisiae chromosome VII, complete chromosome
2253_s_at	1339.6	M	Saccharomyces cerevisiae chromosome VII, complete chromosome
2254_at	70.4	A	Saccharomyces cerevisiae chromosome VII, complete chromosome
2255_at	13.8	A	Saccharomyces cerevisiae chromosome VII, complete chromosome
2256_at	11.6	A	Saccharomyces cerevisiae chromosome VII, complete chromosome
2257_at	362.7	A	Saccharomyces cerevisiae chromosome VII, complete chromosome
2258_at	156.6	A	Saccharomyces cerevisiae chromosome VII, complete chromosome
2259_at	521.9	A	Saccharomyces cerevisiae chromosome VII, complete chromosome
2260_g_at	176.7	A	Saccharomyces cerevisiae chromosome VII, complete chromosome
2261_s_at	244.6	A	Saccharomyces cerevisiae chromosome VII, complete chromosome
2262_at	3023.2	A	Saccharomyces cerevisiae chromosome VII, complete chromosome
2263_g_at	401.6	A	Saccharomyces cerevisiae chromosome VII, complete chromosome
2264_s_at	493.9	P	Saccharomyces cerevisiae chromosome VII, complete chromosome
2265_s_at	618.5	A	Saccharomyces cerevisiae chromosome VII, complete chromosome
2180_s_at	749.9	P	Saccharomyces cerevisiae chromosome VII, complete chromosome
2181_s_at	912.9	M	Saccharomyces cerevisiae chromosome VII, complete chromosome
2182_s_at	1500.1	A	Saccharomyces cerevisiae chromosome VII, complete chromosome
2183_s_at	5930.9	P	Saccharomyces cerevisiae chromosome VII, complete chromosome
2184_s_at	6146.6	P	Saccharomyces cerevisiae chromosome VII, complete chromosome
2185_at	622.7	A	Saccharomyces cerevisiae chromosome VII, complete chromosome
2186_at	1129.3	A	Saccharomyces cerevisiae chromosome VII, complete chromosome
2187_at	328.8	A	Saccharomyces cerevisiae chromosome VII, complete chromosome
2188_at	60.9	A	Saccharomyces cerevisiae chromosome VII, complete chromosome
2189_at	364.8	P	Saccharomyces cerevisiae chromosome VII, complete chromosome
2190_g_at	1317	P	Saccharomyces cerevisiae chromosome VII, complete chromosome
2191_s_at	3577.6	P	Saccharomyces cerevisiae chromosome VII, complete chromosome
2192_at	45.1	A	Saccharomyces cerevisiae chromosome VII, complete chromosome
2193_at	244.1	A	Saccharomyces cerevisiae chromosome VII, complete chromosome
2194_at	109	A	Saccharomyces cerevisiae chromosome VII, complete chromosome
2195_at	1287.2	A	Saccharomyces cerevisiae chromosome VII, complete chromosome
2196_s_at	1833	P	Saccharomyces cerevisiae chromosome VII, complete chromosome
2197_s_at	5162.1	P	Saccharomyces cerevisiae chromosome VII, complete chromosome
2198_at	248.9	A	Saccharomyces cerevisiae chromosome VII, complete chromosome
2199_at	78.5	A	Saccharomyces cerevisiae chromosome VII, complete chromosome
2200_at	8.4	A	Saccharomyces cerevisiae chromosome VII, complete chromosome
2201_at	40.1	A	Saccharomyces cerevisiae chromosome VII, complete chromosome
2202_g_at	66.7	A	Saccharomyces cerevisiae chromosome VII, complete chromosome
2203_s_at	793.3	A	Saccharomyces cerevisiae chromosome VII, complete chromosome
2204_s_at	538.8	P	Saccharomyces cerevisiae chromosome VII, complete chromosome
2205_at	1411.5	P	Saccharomyces cerevisiae chromosome VII, complete chromosome
2206_g_at	26.5	A	Saccharomyces cerevisiae chromosome VII, complete chromosome
2207_s_at	750.7	A	Saccharomyces cerevisiae chromosome VII, complete chromosome
2208_s_at	92	A	Saccharomyces cerevisiae chromosome VII, complete chromosome
2209_s_at	422.2	A	Saccharomyces cerevisiae chromosome VII, complete chromosome
2210_s_at	2162.8	P	Saccharomyces cerevisiae chromosome VII, complete chromosome
2211_s_at	3507.7	P	Saccharomyces cerevisiae chromosome VII, complete chromosome
2212_at	771.5	P	Saccharomyces cerevisiae chromosome VII, complete chromosome
2213_at	137.2	A	Saccharomyces cerevisiae chromosome VII, complete chromosome

2214_at	636.6	P	Saccharomyces cerevisiae chromosome VII, complete chromosome
2215_g_at	894.6	M	Saccharomyces cerevisiae chromosome VII, complete chromosome
2216_s_at	249.5	A	Saccharomyces cerevisiae chromosome VII, complete chromosome
2217_s_at	562.1	M	Saccharomyces cerevisiae chromosome VII, complete chromosome
2218_s_at	2827	P	Saccharomyces cerevisiae chromosome VII, complete chromosome
2219_at	29.8	A	Saccharomyces cerevisiae chromosome VII, complete chromosome
2220_at	12.1	A	Saccharomyces cerevisiae chromosome VII, complete chromosome
2221_at	270.5	A	Saccharomyces cerevisiae chromosome VII, complete chromosome
2222_at	41.8	A	Saccharomyces cerevisiae chromosome VII, complete chromosome
2138_at	433.4	P	Saccharomyces cerevisiae chromosome VII, complete chromosome
2139_g_at	208.4	A	Saccharomyces cerevisiae chromosome VII, complete chromosome
2140_s_at	406.4	A	Saccharomyces cerevisiae chromosome VII, complete chromosome
2141_s_at	1607.3	P	Saccharomyces cerevisiae chromosome VII, complete chromosome
2142_at	385.5	A	Saccharomyces cerevisiae chromosome VII, complete chromosome
2143_at	18.5	A	Saccharomyces cerevisiae chromosome VII, complete chromosome
2144_at	17	A	Saccharomyces cerevisiae chromosome VII, complete chromosome
2145_at	5.7	A	Saccharomyces cerevisiae chromosome VII, complete chromosome
2146_at	406.6	A	Saccharomyces cerevisiae chromosome VII, complete chromosome
2147_at	832.1	A	Saccharomyces cerevisiae chromosome VII, complete chromosome
2148_at	90.8	A	Saccharomyces cerevisiae chromosome VII, complete chromosome
2149_at	102.8	A	Saccharomyces cerevisiae chromosome VII, complete chromosome
2150_g_at	681.7	A	Saccharomyces cerevisiae chromosome VII, complete chromosome
2151_s_at	46.8	A	Saccharomyces cerevisiae chromosome VII, complete chromosome
2152_s_at	401.7	A	Saccharomyces cerevisiae chromosome VII, complete chromosome
2153_s_at	807.9	A	Saccharomyces cerevisiae chromosome VII, complete chromosome
2154_s_at	738.1	A	Saccharomyces cerevisiae chromosome VII, complete chromosome
2155_s_at	604.8	P	Saccharomyces cerevisiae chromosome VII, complete chromosome
2156_s_at	1083.5	P	Saccharomyces cerevisiae chromosome VII, complete chromosome
2157_at	284.8	A	Saccharomyces cerevisiae chromosome VII, complete chromosome
2158_at	140.2	A	Saccharomyces cerevisiae chromosome VII, complete chromosome
2159_at	209.2	A	Saccharomyces cerevisiae chromosome VII, complete chromosome
2160_at	444	A	Saccharomyces cerevisiae chromosome VII, complete chromosome
2161_at	172.8	A	Saccharomyces cerevisiae chromosome VII, complete chromosome
2162_g_at	19020.6	P	Saccharomyces cerevisiae chromosome VII, complete chromosome
2163_s_at	27706	P	Saccharomyces cerevisiae chromosome VII, complete chromosome
2164_at	732.2	A	Saccharomyces cerevisiae chromosome VII, complete chromosome
2165_g_at	285.9	A	Saccharomyces cerevisiae chromosome VII, complete chromosome
2166_s_at	203.2	A	Saccharomyces cerevisiae chromosome VII, complete chromosome
2167_s_at	231	A	Saccharomyces cerevisiae chromosome VII, complete chromosome
2168_s_at	122.4	A	Saccharomyces cerevisiae chromosome VII, complete chromosome
2169_s_at	1197.9	P	Saccharomyces cerevisiae chromosome VII, complete chromosome
2170_s_at	1341.7	P	Saccharomyces cerevisiae chromosome VII, complete chromosome
2171_at	255.4	A	Saccharomyces cerevisiae chromosome VII, complete chromosome
2172_at	320.4	A	Saccharomyces cerevisiae chromosome VII, complete chromosome
2173_g_at	526.5	A	Saccharomyces cerevisiae chromosome VII, complete chromosome
2174_s_at	1335.2	P	Saccharomyces cerevisiae chromosome VII, complete chromosome
2175_s_at	613.3	P	Saccharomyces cerevisiae chromosome VII, complete chromosome
2176_s_at	996.6	P	Saccharomyces cerevisiae chromosome VII, complete chromosome
2177_s_at	6607.5	P	Saccharomyces cerevisiae chromosome VII, complete chromosome
2178_at	659.8	A	Saccharomyces cerevisiae chromosome VII, complete chromosome
2179_at	45	A	Saccharomyces cerevisiae chromosome VIII, complete chromosome
2100_g_at	1123.3	A	Saccharomyces cerevisiae chromosome VIII, complete chromosome

2101_s_at	39.5	A	Saccharomyces cerevisiae chromosome VIII, complete chromosome
2102_s_at	147.9	A	Saccharomyces cerevisiae chromosome VIII, complete chromosome
2103_s_at	1352.3	A	Saccharomyces cerevisiae chromosome VIII, complete chromosome
2104_s_at	4218.5	P	Saccharomyces cerevisiae chromosome VIII, complete chromosome
2105_s_at	2582.7	P	Saccharomyces cerevisiae chromosome VIII, complete chromosome
2106_at	202.6	A	Saccharomyces cerevisiae chromosome VIII, complete chromosome
2107_at	1094.7	A	Saccharomyces cerevisiae chromosome VIII, complete chromosome
2108_at	143.6	A	Saccharomyces cerevisiae chromosome VIII, complete chromosome
2109_g_at	46.9	A	Saccharomyces cerevisiae chromosome VIII, complete chromosome
2110_s_at	26.6	A	Saccharomyces cerevisiae chromosome VIII, complete chromosome
2111_s_at	13.8	A	Saccharomyces cerevisiae chromosome VIII, complete chromosome
2112_s_at	197.4	A	Saccharomyces cerevisiae chromosome VIII, complete chromosome
2113_s_at	151.2	A	Saccharomyces cerevisiae chromosome VIII, complete chromosome
2114_s_at	300.9	A	Saccharomyces cerevisiae chromosome VIII, complete chromosome
2115_at	30.7	A	Saccharomyces cerevisiae chromosome VIII, complete chromosome
2116_at	488.2	P	Saccharomyces cerevisiae chromosome VIII, complete chromosome
2117_at	204.7	A	Saccharomyces cerevisiae chromosome VIII, complete chromosome
2118_at	453.7	A	Saccharomyces cerevisiae chromosome VIII, complete chromosome
2119_g_at	131.2	A	Saccharomyces cerevisiae chromosome VIII, complete chromosome
2120_s_at	52.3	A	Saccharomyces cerevisiae chromosome VIII, complete chromosome
2121_s_at	1150.2	A	Saccharomyces cerevisiae chromosome VIII, complete chromosome
2122_s_at	65.9	A	Saccharomyces cerevisiae chromosome VIII, complete chromosome
2123_s_at	500.7	A	Saccharomyces cerevisiae chromosome VIII, complete chromosome
2124_s_at	75	A	Saccharomyces cerevisiae chromosome VIII, complete chromosome
2125_s_at	286.3	A	Saccharomyces cerevisiae chromosome VIII, complete chromosome
2126_s_at	282.8	P	Saccharomyces cerevisiae chromosome VIII, complete chromosome
2127_s_at	270.7	A	Saccharomyces cerevisiae chromosome VIII, complete chromosome
2128_s_at	78.7	A	Saccharomyces cerevisiae chromosome VIII, complete chromosome
2129_s_at	1194.8	P	Saccharomyces cerevisiae chromosome VIII, complete chromosome
2130_at	983.5	A	Saccharomyces cerevisiae chromosome VIII, complete chromosome
2131_at	17.8	A	Saccharomyces cerevisiae chromosome VIII, complete chromosome
2132_at	18.8	A	Saccharomyces cerevisiae chromosome VIII, complete chromosome
2133_at	39.3	A	Saccharomyces cerevisiae chromosome VIII, complete chromosome
2134_at	156.2	A	Saccharomyces cerevisiae chromosome VIII, complete chromosome
2135_at	22.6	A	Saccharomyces cerevisiae chromosome VIII, complete chromosome
2136_at	221.3	A	Saccharomyces cerevisiae chromosome VIII, complete chromosome
2137_at	186.5	A	Saccharomyces cerevisiae chromosome VIII, complete chromosome
11394_at	307.7	P	Saccharomyces cerevisiae chromosome VIII, complete chromosome
11395_at	492.4	A	Saccharomyces cerevisiae chromosome VIII, complete chromosome
11396_g_a	110.3	A	Saccharomyces cerevisiae chromosome VIII, complete chromosome
11397_f_at	400.8	A	Saccharomyces cerevisiae chromosome VIII, complete chromosome
11398_s_a	3425.4	A	Saccharomyces cerevisiae chromosome VIII, complete chromosome
11399_s_a	4885.3	P	Saccharomyces cerevisiae chromosome VIII, complete chromosome
11400_s_a	187.6	A	Saccharomyces cerevisiae chromosome VIII, complete chromosome
11401_at	75.6	A	Saccharomyces cerevisiae chromosome VIII, complete chromosome
11402_at	38.5	A	Saccharomyces cerevisiae chromosome VIII, complete chromosome
11403_at	121.8	A	Saccharomyces cerevisiae chromosome VIII, complete chromosome
11404_at	8.9	A	Saccharomyces cerevisiae chromosome VIII, complete chromosome
11405_at	7283.2	P	Saccharomyces cerevisiae chromosome VIII, complete chromosome
11406_f_at	205.9	A	Saccharomyces cerevisiae chromosome VIII, complete chromosome
11407_f_at	1002.9	P	Saccharomyces cerevisiae chromosome VIII, complete chromosome
11408_f_at	14466.3	P	Saccharomyces cerevisiae chromosome VIII, complete chromosome

11409_f_at	1046	A	Saccharomyces cerevisiae chromosome VIII, complete chromosome
11410_at	28.4	A	Saccharomyces cerevisiae chromosome VIII, complete chromosome
11411_at	131.8	A	Saccharomyces cerevisiae chromosome IX, complete chromosome s
11412_at	42.5	A	Saccharomyces cerevisiae chromosome IX, complete chromosome s
11413_s_a	115.1	A	Saccharomyces cerevisiae chromosome IX, complete chromosome s
11414_s_a	13	A	Saccharomyces cerevisiae chromosome IX, complete chromosome s
11415_f_at	241.9	A	Saccharomyces cerevisiae chromosome IX, complete chromosome s
11416_at	502.1	A	Saccharomyces cerevisiae chromosome IX, complete chromosome s
11417_at	31.6	A	Saccharomyces cerevisiae chromosome IX, complete chromosome s
11418_at	147.6	A	Saccharomyces cerevisiae chromosome IX, complete chromosome s
11419_at	85	A	Saccharomyces cerevisiae chromosome IX, complete chromosome s
11420_at	104.1	A	Saccharomyces cerevisiae chromosome IX, complete chromosome s
11421_at	30.3	A	Saccharomyces cerevisiae chromosome IX, complete chromosome s
11422_at	254.8	A	Saccharomyces cerevisiae chromosome IX, complete chromosome s
11423_at	30.9	A	Saccharomyces cerevisiae chromosome IX, complete chromosome s
11424_g_a	83.8	A	Saccharomyces cerevisiae chromosome IX, complete chromosome s
11425_s_a	1194.3	A	Saccharomyces cerevisiae chromosome IX, complete chromosome s
11426_s_a	477.5	M	Saccharomyces cerevisiae chromosome IX, complete chromosome s
11427_at	56.9	A	Saccharomyces cerevisiae chromosome IX, complete chromosome s
11428_at	211.8	A	Saccharomyces cerevisiae chromosome IX, complete chromosome s
11429_at	308.6	A	Saccharomyces cerevisiae chromosome IX, complete chromosome s
11430_at	13.7	A	Saccharomyces cerevisiae chromosome IX, complete chromosome s
11431_at	66.7	A	Saccharomyces cerevisiae chromosome IX, complete chromosome s
11432_at	336.1	A	Saccharomyces cerevisiae chromosome IX, complete chromosome s
11433_at	23.3	A	Saccharomyces cerevisiae chromosome IX, complete chromosome s
11434_g_a	534.7	A	Saccharomyces cerevisiae chromosome IX, complete chromosome s
11435_s_a	481.9	A	Saccharomyces cerevisiae chromosome IX, complete chromosome s
11436_s_a	84.6	A	Saccharomyces cerevisiae chromosome IX, complete chromosome s

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s 1358-3197 of L38424 (-5, -M, -3 represent transcript regions 5 prime, Middle, and 3 prime respectivel
s 1358-3197 of L38424 (-5, -M, -3 represent transcript regions 5 prime, Middle, and 3 prime respectivel
s 1358-3197 of L38424 (-5, -M, -3 represent transcript regions 5 prime, Middle, and 3 prime respectivel
sponding to nucleotides 350-1345 of X17013 (-5, -M, -3 represent transcript regions 5 prime, Middle, an
sponding to nucleotides 350-1345 of X17013 (-5, -M, -3 represent transcript regions 5 prime, Middle, an
sponding to nucleotides 350-1345 of X17013 (-5, -M, -3 represent transcript regions 5 prime, Middle, an
017-3334 of M24537 (-5, -M, -3 represent transcript regions 5 prime, Middle, and 3 prime respectively)
017-3334 of M24537 (-5, -M, -3 represent transcript regions 5 prime, Middle, and 3 prime respectively)
017-3334 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)
nding to nucleotides 1883-4400 of K01391 (-5, -M, -3 represent transcript regions 5 prime, Middle, and 3
nding to nucleotides 1883-4400 of K01391 (-5, -M, -3 represent transcript regions 5 prime, Middle, and 3
nding to nucleotides 1883-4400 of K01391 (-5, -M, -3 represent transcript regions 5 prime, Middle, and 3
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ase II holoenzyme/mediator complex (5, M, 3 represent transcript regions 5 prime, Middle and 3 prime
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esponds to 1-1799 in Z75578 (regions a-e represent transcript regions 5 prime to 3 prime respectively)
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esponds to complement of 4212-7605 in Z73326 (regions a-e represent transcript regions 5 prime to 3 p
esponds to complement of 4212-7605 in Z73326 (regions a-e represent transcript regions 5 prime to 3 p
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nsferase beta subunit
ction
rotein of the mitochondrial cytochrome bc1 complex .
MP decarboxylase

1w

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

dc42

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

sport (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.

A 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
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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

al 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)

rn6p 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)

x

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

csB

n S7

essing of the yeast a-factor precursor

rrin receptor protein

94_SCHPO) and Mrs11p (YHR005c-a)

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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.

R162c, YOR172w and YLR266c

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

nctional enzyme)

way
e b pre-mRNA

es type1 protein phosphatase

pment, 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
thetical 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

-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

rphogenesis

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

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73 and 94228 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yea
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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.

/lase\IMP cyclohydrolase

:rotubule ends at the spindle pole body

;AGA complex

ain 4

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

nteracts 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

ub4p-Spc98p-Spc97p complex may be part of the microtubule attachment site at the spindle pole body

with RPD3 gene product

rRNA

ɔrs

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.

acids

ad18

x

unction

chomosomes in spread meiotic nuclei but is excluded from the nucleolus

natography

coli

: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
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140 and 988277 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the
5773 and 1035940 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of th

erexpressed

ıg 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

hosphatase\; redundant with Cna1\; cytoplasmic

tein SPC25

6p and Rrn7p, which is required for rDNA transcription by RNA polymerase I eiosis during recombination

ains

efect.

n 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

KL132c
aM

tional machinery
tional machinery

ylase/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
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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

ce-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

ane

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

omolog of Rsc6p subunit of the RSC chromatin remodeling complex

ation

c domains\; homologous to Sol2p and Sol3p

ubunit 2

n, interacts with Sec1p
haropine reductase) (EC 1.5.1.10)

transporters

erase

YEL070w

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893 and 652045 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the
893 and 652045 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the

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

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

omologue 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
nary phase
a Yap recognition site

drial protein translocation complex, associates with Isp42p

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

complex

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
. elegans protein

of splicing

.21

ion

ases, the SWI2\/SNF2-like proteins

ted in secretion and nuclear segregation

pre-mRNA splicing mutation, prp8-1

ein

‹Da subunit

III)

n the 2-hybrid system

to half-bridges and interacts with KAR1

in the general control of amino acid biosynthesis

esis

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

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

mouse

sor of cobalt toxicity

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

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

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

escort protein)\; component of Rab geranylgeranyl transferase

atalogue number A5550, according to A. Blomberg)

83 and 33335 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yea
96 and 36175 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yea
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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

1

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

ɔtein

: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
the Fo-F1 ATP synthase

protein

p

-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

st-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)

cerevisiae)

ons when over-expressed

of 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

omatin

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
ıaliana

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

A0171 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

or thiamin metabolism

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

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.

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

n, and nuclear division

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

ation, 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

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

I) anchors to proteins
licase MSS116 / YDR194c

R010w

odulin, and a 35 kDa protein

to signal transducing adaptor from mouse and man proteins

required 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
n overexpressed
EC18 family of ATPases

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

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

ar to L23 family of ribosomal proteins

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

adaptor\/HAT (histone acetyltransferase)complexes

ar 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

equence), 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)

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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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
n overexpressed

hy

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

ɔn
ːrived transport vesicles

ɘ expression

ıse to starvation

ıl signals and thereby regulate meiosis
ᴧTP

protein

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

ɛnt 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

s 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

Vilms tumour proteins

osomes

omain type

mine cytidylyltransferase or phosphocholine cytidylyltransferase)

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

otransferase)
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

ration

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)

3AP37 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

93 and 34790 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yea

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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.
vith 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.
8122 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.

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

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

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

e sequence. Found reverse in NC_001148 between 437328 and 439490 with 100% identity.
e sequence. Found reverse in NC_001148 between 437328 and 439490 with 100% identity.
e 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.
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sequence. Found forward in NC_001142 between 714444 and 715443 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.
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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.
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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 416757 and 417146 with 100% identity.
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sequence. Found forward in NC_001143 between 536784 and 537783 with 100% identity.
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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.
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sequence. Found forward in NC_001143 between 621375 and 622374 with 100% identity.
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sequence. Found forward in NC_001143 between 624375 and 624566 with 100% identity.
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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.
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sequence. Found forward in NC_001143 between 648133 and 648994 with 100% identity.
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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.
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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.
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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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e sequence. Found forward in NC_001145 between 728433 and 729432 with 100% identity.
e sequence. Found forward in NC_001145 between 729433 and 730432 with 100% identity.
e sequence. Found forward in NC_001145 between 730433 and 731432 with 100% identity.
e sequence. Found forward in NC_001145 between 731433 and 731964 with 100% identity.
e sequence. Found forward in NC_001145 between 827528 and 828527 with 100% identity.
e sequence. Found forward in NC_001145 between 828528 and 829527 with 100% identity.
e sequence. Found forward in NC_001145 between 829528 and 830527 with 100% identity.
e sequence. Found forward in NC_001145 between 830528 and 831527 with 100% identity.
e sequence. Found forward in NC_001145 between 831528 and 832527 with 100% identity.
e sequence. Found forward in NC_001145 between 831528 and 832527 with 100% identity.
e sequence. Found forward in NC_001145 between 832528 and 832753 with 100% identity.
e sequence. Found forward in NC_001145 between 842936 and 843935 with 100% identity.
e sequence. Found forward in NC_001145 between 843936 and 844935 with 100% identity.
e sequence. Found forward in NC_001145 between 844936 and 845935 with 100% identity.
e sequence. Found forward in NC_001145 between 844936 and 845935 with 100% identity.
e sequence. Found forward in NC_001145 between 845936 and 846935 with 100% identity.
e sequence. Found forward in NC_001145 between 846936 and 847935 with 100% identity.
e sequence. Found forward in NC_001145 between 847936 and 847986 with 100% identity.
e sequence. Found forward in NC_001145 between 879563 and 880562 with 100% identity.
e sequence. Found forward in NC_001145 between 880563 and 881562 with 100% identity.
e sequence. Found forward in NC_001145 between 880563 and 881562 with 100% identity.
e sequence. Found forward in NC_001145 between 881563 and 882562 with 100% identity.
e sequence. Found forward in NC_001145 between 882563 and 883562 with 100% identity.
e sequence. Found forward in NC_001145 between 883563 and 884562 with 100% identity.
e sequence. Found forward in NC_001145 between 884563 and 885562 with 100% identity.
e sequence. Found forward in NC_001145 between 885563 and 886016 with 100% identity.
e sequence. Found forward in NC_001146 between 871 and 1870 with 100% identity.
e sequence. Found forward in NC_001146 between 1871 and 2870 with 100% identity.
e sequence. Found forward in NC_001146 between 2871 and 3870 with 100% identity.
e sequence. Found forward in NC_001146 between 3871 and 4870 with 100% identity.
e sequence. Found forward in NC_001146 between 4871 and 5870 with 100% identity.
e sequence. Found forward in NC_001146 between 5871 and 6080 with 100% identity.
e sequence. Found forward in NC_001146 between 130021 and 131020 with 100% identity.
e sequence. Found forward in NC_001146 between 131021 and 132020 with 100% identity.
e sequence. Found forward in NC_001146 between 132021 and 133020 with 100% identity.
e sequence. Found forward in NC_001146 between 133021 and 134020 with 100% identity.
e sequence. Found forward in NC_001146 between 134021 and 135020 with 100% identity.
e sequence. Found forward in NC_001146 between 135021 and 135939 with 100% identity.
e sequence. Found forward in NC_001146 between 147395 and 148394 with 100% identity.
e sequence. Found forward in NC_001146 between 147395 and 148394 with 100% identity.
e sequence. Found forward in NC_001146 between 148395 and 149394 with 100% identity.
e sequence. Found forward in NC_001146 between 149395 and 150394 with 100% identity.
e sequence. Found forward in NC_001146 between 150395 and 151394 with 100% identity.
e sequence. Found forward in NC_001146 between 151395 and 152394 with 100% identity.
e sequence. Found forward in NC_001146 between 152395 and 153394 with 100% identity.
e sequence. Found forward in NC_001146 between 153395 and 154379 with 100% identity.
e sequence. Found forward in NC_001146 between 161130 and 162129 with 100% identity.
e sequence. Found forward in NC_001146 between 162130 and 163129 with 100% identity.
e sequence. Found forward in NC_001146 between 163130 and 164129 with 100% identity.
e sequence. Found forward in NC_001146 between 164130 and 165129 with 100% identity.
e sequence. Found forward in NC_001146 between 164130 and 165129 with 100% identity.
e 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.
sequence. Found forward in NC_001147 between 618016 and 619015 with 100% identity.
sequence. Found forward in NC_001147 between 619016 and 620015 with 100% identity.
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.
sequence. Found forward in NC_001147 between 622016 and 623015 with 100% identity.
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.
sequence. Found forward in NC_001147 between 733506 and 734505 with 100% identity.
sequence. Found forward in NC_001147 between 734506 and 735505 with 100% identity.
sequence. Found forward in NC_001147 between 735506 and 735675 with 100% identity.
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sequence. Found forward in NC_001147 between 857642 and 858641 with 100% identity.
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.
sequence. Found forward in NC_001147 between 861642 and 862641 with 100% identity.
sequence. Found forward in NC_001147 between 862642 and 863641 with 100% identity.
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.
e sequence. Found forward in NC_001148 between 108147 and 109146 with 100% identity.
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.
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e sequence. Found forward in NC_001148 between 141119 and 142118 with 100% identity.
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.
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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.
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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.
e sequence. Found forward in NC_001148 between 399975 and 400974 with 100% identity.
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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e sequence. Found forward in NC_001148 between 439759 and 440758 with 100% identity.
e sequence. Found forward in NC_001148 between 440759 and 441758 with 100% identity.
e sequence. Found forward in NC_001148 between 441759 and 442758 with 100% identity.
e sequence. Found forward in NC_001148 between 442759 and 443758 with 100% identity.
e sequence. Found forward in NC_001148 between 443759 and 444574 with 100% identity.
e sequence. Found forward in NC_001148 between 446337 and 447336 with 100% identity.
e sequence. Found forward in NC_001148 between 447337 and 448336 with 100% identity.
e sequence. Found forward in NC_001148 between 448337 and 449336 with 100% identity.
e sequence. Found forward in NC_001148 between 449337 and 450336 with 100% identity.
e sequence. Found forward in NC_001148 between 450337 and 451336 with 100% identity.
e sequence. Found forward in NC_001148 between 451337 and 451904 with 100% identity.
e sequence. Found forward in NC_001148 between 519230 and 520229 with 100% identity.
e sequence. Found forward in NC_001148 between 520230 and 521229 with 100% identity.
e sequence. Found forward in NC_001148 between 520230 and 521229 with 100% identity.
e sequence. Found forward in NC_001148 between 521230 and 522229 with 100% identity.
e sequence. Found forward in NC_001148 between 522230 and 523229 with 100% identity.
e sequence. Found forward in NC_001148 between 523230 and 524229 with 100% identity.
e sequence. Found forward in NC_001148 between 524230 and 524453 with 100% identity.
e sequence. Found forward in NC_001148 between 536315 and 537314 with 100% identity.
e sequence. Found forward in NC_001148 between 537315 and 538314 with 100% identity.
e sequence. Found forward in NC_001148 between 538315 and 539314 with 100% identity.
e sequence. Found forward in NC_001148 between 539315 and 540314 with 100% identity.
e sequence. Found forward in NC_001148 between 540315 and 541314 with 100% identity.
e sequence. Found forward in NC_001148 between 541315 and 541465 with 100% identity.
e sequence. Found forward in NC_001148 between 542577 and 543576 with 100% identity.
e sequence. Found forward in NC_001148 between 543577 and 544576 with 100% identity.
e sequence. Found forward in NC_001148 between 544577 and 545576 with 100% identity.
e sequence. Found forward in NC_001148 between 545577 and 546576 with 100% identity.
e sequence. Found forward in NC_001148 between 546577 and 547576 with 100% identity.
e sequence. Found forward in NC_001148 between 547577 and 547638 with 100% identity.
e sequence. Found forward in NC_001148 between 624964 and 625963 with 100% identity.
e sequence. Found forward in NC_001148 between 625964 and 626963 with 100% identity.
e sequence. Found forward in NC_001148 between 626964 and 627963 with 100% identity.
e sequence. Found forward in NC_001148 between 626964 and 627963 with 100% identity.
e sequence. Found forward in NC_001148 between 627964 and 628963 with 100% identity.
e sequence. Found forward in NC_001148 between 628964 and 629963 with 100% identity.
e sequence. Found forward in NC_001148 between 629964 and 630740 with 100% identity.
e sequence. Found forward in NC_001148 between 759478 and 760477 with 100% identity.
e sequence. Found forward in NC_001148 between 759478 and 760477 with 100% identity.
e sequence. Found forward in NC_001148 between 760478 and 761477 with 100% identity.
e sequence. Found forward in NC_001148 between 761478 and 762477 with 100% identity.
e sequence. Found forward in NC_001148 between 762478 and 763477 with 100% identity.
e sequence. Found forward in NC_001148 between 763478 and 764477 with 100% identity.
e sequence. Found forward in NC_001148 between 764478 and 765477 with 100% identity.
e sequence. Found forward in NC_001148 between 765478 and 766477 with 100% identity.
e sequence. Found forward in NC_001148 between 766478 and 766991 with 100% identity.
e sequence. Found forward in NC_001148 between 869140 and 870139 with 100% identity.
e sequence. Found forward in NC_001148 between 870140 and 871139 with 100% identity.
e sequence. Found forward in NC_001148 between 870140 and 871139 with 100% identity.
e sequence. Found forward in NC_001148 between 871140 and 872139 with 100% identity.
e sequence. Found forward in NC_001148 between 872140 and 873139 with 100% identity.
e 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.
sequence. Found forward in NC_001134 between 25441 and 26440 with 100% identity.
sequence. Found forward in NC_001134 between 26441 and 27440 with 100% identity.
sequence. Found forward in NC_001134 between 27441 and 28440 with 100% identity.
sequence. Found forward in NC_001134 between 28441 and 29440 with 100% identity.
sequence. Found forward in NC_001134 between 29441 and 30440 with 100% identity.
sequence. Found forward in NC_001134 between 35441 and 35606 with 100% identity.
sequence. Found forward in NC_001134 between 51513 and 52512 with 100% identity.
sequence. Found forward in NC_001134 between 52513 and 53512 with 100% identity.
sequence. Found forward in NC_001134 between 53513 and 54512 with 100% identity.
sequence. Found forward in NC_001134 between 54513 and 55512 with 100% identity.
sequence. Found forward in NC_001134 between 55513 and 56512 with 100% identity.
sequence. Found forward in NC_001134 between 56513 and 57512 with 100% identity.
sequence. Found forward in NC_001134 between 57513 and 58512 with 100% identity.
sequence. Found forward in NC_001134 between 58513 and 59512 with 100% identity.
sequence. Found forward in NC_001134 between 59513 and 59815 with 100% identity.
sequence. Found forward in NC_001134 between 73564 and 74563 with 100% identity.
sequence. Found forward in NC_001134 between 74564 and 75563 with 100% identity.
sequence. Found forward in NC_001134 between 74564 and 75563 with 100% identity.
sequence. Found forward in NC_001134 between 75564 and 76563 with 100% identity.
sequence. Found forward in NC_001134 between 76564 and 77563 with 100% identity.
sequence. Found forward in NC_001134 between 77564 and 78563 with 100% identity.
sequence. Found forward in NC_001134 between 78564 and 79261 with 100% identity.
sequence. Found forward in NC_001134 between 187307 and 188306 with 100% identity.
sequence. Found forward in NC_001134 between 188307 and 189306 with 100% identity.
sequence. Found forward in NC_001134 between 189307 and 190306 with 100% identity.
sequence. Found forward in NC_001134 between 190307 and 191306 with 100% identity.
sequence. Found forward in NC_001134 between 191307 and 192306 with 100% identity.
sequence. Found forward in NC_001134 between 192307 and 192975 with 100% identity.
sequence. Found forward in NC_001134 between 192307 and 192975 with 100% identity.
sequence. Found forward in NC_001134 between 220363 and 221362 with 100% identity.
sequence. Found forward in NC_001134 between 226363 and 227362 with 100% identity.
sequence. Found forward in NC_001134 between 227363 and 228362 with 100% identity.
sequence. Found forward in NC_001134 between 227363 and 228362 with 100% identity.
sequence. Found forward in NC_001134 between 228363 and 229362 with 100% identity.
sequence. Found forward in NC_001134 between 229363 and 230362 with 100% identity.
sequence. Found forward in NC_001134 between 230363 and 231362 with 100% identity.
sequence. Found forward in NC_001134 between 231363 and 232362 with 100% identity.
sequence. Found forward in NC_001134 between 232363 and 233362 with 100% identity.
sequence. Found forward in NC_001134 between 233363 and 234362 with 100% identity.
sequence. Found forward in NC_001134 between 234363 and 234580 with 100% identity.
sequence. Found forward in NC_001134 between 505265 and 506264 with 100% identity.
sequence. Found forward in NC_001134 between 505265 and 506264 with 100% identity.
sequence. Found forward in NC_001134 between 506265 and 507264 with 100% identity.
sequence. Found forward in NC_001134 between 507265 and 508264 with 100% identity.
sequence. Found forward in NC_001134 between 508265 and 509264 with 100% identity.
sequence. Found forward in NC_001134 between 509265 and 510264 with 100% identity.
sequence. Found forward in NC_001134 between 510265 and 511264 with 100% identity.
sequence. Found forward in NC_001134 between 511265 and 512233 with 100% identity.
sequence. Found forward in NC_001134 between 517809 and 518808 with 100% identity.
sequence. Found forward in NC_001134 between 518809 and 519808 with 100% identity.
sequence. 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.
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sequence. Found forward in NC_001136 between 1307061 and 1308060 with 100% identity.
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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.
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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.
sequence. Found forward in NC_001136 between 1373375 and 1374374 with 100% identity.
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.
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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.
sequence. Found forward in NC_001137 between 113004 and 114003 with 100% identity.
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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.
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sequence. Found forward in NC_001137 between 442412 and 443411 with 100% identity.
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sequence. Found forward in NC_001137 between 479841 and 480840 with 100% identity.
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sequence. Found forward in NC_001137 between 482841 and 483321 with 100% identity.
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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.
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 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.
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 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.
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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.
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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.
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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.
sequence. Found forward in NC_001139 between 661764 and 662763 with 100% identity.
sequence. Found forward in NC_001139 between 662764 and 663763 with 100% identity.
sequence. Found forward in NC_001139 between 663764 and 664763 with 100% identity.
sequence. Found forward in NC_001139 between 664764 and 665565 with 100% identity.
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sequence. Found forward in NC_001139 between 684060 and 685059 with 100% identity.
sequence. Found forward in NC_001139 between 685060 and 686059 with 100% identity.
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.
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sequence. Found forward in NC_001139 between 860395 and 861394 with 100% identity.
sequence. Found forward in NC_001139 between 861395 and 862394 with 100% identity.
sequence. Found forward in NC_001139 between 862395 and 863394 with 100% identity.
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 955166 and 956165 with 100% identity.
sequence. Found forward in NC_001139 between 956166 and 957165 with 100% identity.
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sequence. Found forward in NC_001139 between 959166 and 960165 with 100% identity.
sequence. Found forward in NC_001139 between 960166 and 960596 with 100% identity.
sequence. Found forward in NC_001139 between 1031505 and 1032504 with 100% identity.
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sequence. Found forward in NC_001139 between 1034505 and 1035504 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 1052406 and 1053405 with 100% identity.
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sequence. Found forward in NC_001139 between 1053406 and 1054405 with 100% identity.
sequence. Found forward in NC_001139 between 1054406 and 1055405 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.
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sequence. Found forward in NC_001140 between 39533 and 40532 with 100% identity.

sequence. Found forward in NC_001140 between 40533 and 41532 with 100% identity.
sequence. Found forward in NC_001140 between 41533 and 42532 with 100% identity.
sequence. Found forward in NC_001140 between 42533 and 43532 with 100% identity.
sequence. Found forward in NC_001140 between 43533 and 44532 with 100% identity.
sequence. Found forward in NC_001140 between 44533 and 45188 with 100% identity.
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sequence. Found forward in NC_001140 between 311647 and 312646 with 100% identity.
sequence. Found forward in NC_001140 between 312647 and 313497 with 100% identity.
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sequence. Found forward in NC_001140 between 431206 and 432205 with 100% identity.
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sequence. Found forward in NC_001140 between 434206 and 435205 with 100% identity.
sequence. Found forward in NC_001140 between 435206 and 436205 with 100% identity.
sequence. Found forward in NC_001140 between 436206 and 437169 with 100% identity.
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sequence. Found forward in NC_001140 between 523872 and 524871 with 100% identity.
sequence. Found forward in NC_001140 between 524872 and 525871 with 100% identity.
sequence. Found forward in NC_001140 between 524872 and 525871 with 100% identity.
sequence. Found forward in NC_001140 between 525872 and 526871 with 100% identity.
sequence. Found forward in NC_001140 between 526872 and 527871 with 100% identity.
sequence. Found forward in NC_001140 between 527872 and 528114 with 100% identity.
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sequence. Found forward in NC_001140 between 533177 and 534176 with 100% identity.
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sequence. Found forward in NC_001140 between 535177 and 536176 with 100% identity.
sequence. Found forward in NC_001140 between 537177 and 537754 with 100% identity.
sequence. Found forward in NC_001140 between 543488 and 544487 with 100% identity.
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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.
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sequence. Found forward in NC_001141 between 113607 and 114606 with 100% identity.
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.
sequence. Found forward in NC_001141 between 366963 and 367962 with 100% identity.
sequence. Found forward in NC_001141 between 367963 and 368962 with 100% identity.
sequence. Found forward in NC_001141 between 368963 and 369962 with 100% identity.
sequence. Found forward in NC_001141 between 369963 and 370962 with 100% identity.
sequence. Found forward in NC_001141 between 369963 and 370962 with 100% identity.
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

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

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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 wild

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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 co 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 heptonate 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

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

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

lian type 1 phosphatase targeting subunit.

cdc24-4ts mutant

triglutamate homocysteine methyltransferase)

alysis\; 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

ediating 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

irs

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

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

ells

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

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

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.