

Table A1. 597 Periodic ORFs

feature	gene name	peak time	p value	chr	strand	start	stop	length	level	category	function
YKL116C	PRR1	0	6.40E-10	11	-	221016	222616	1601	2.72	ORF Verified	Serine/threonine protein kinase that inhibits pheromone induced signalling downstream of MAPK, possibly at the level of the Ste12p transcription factor
YKL164C	PIR1	0	1.28E-09	11	-	141776	142856	1081	5.51	ORF Verified	O-glycosylated protein required for cell wall stability; attached to the cell wall via beta-1,3-glucan; mediates mitochondrial translocation of Apn1p; expression regulated by the cell integrity pathway and by Swi5p during the cell cycle
YLR079W	SIC1	0	5.58E-10	12	+	286785	287761	977	3.15	ORF Verified	Inhibitor of Cdc28-Clb kinase complexes that controls G1/S phase transition, preventing premature S phase and ensuring genomic integrity; phosphorylation targets Sic1p for SCF(CDC4)-dependent turnover; functional homolog of mammalian Kip1
YNL078W	NIS1	0	5.95E-09	14	+	479737	481089	1353	3.29	ORF Verified	Protein localized in the bud neck at G2/M phase; physically interacts with septins; possibly involved in a mitotic signaling network
YNL327W	EGT2	0	5.49E-06	14	+	24065	27105	3041	4.79	ORF Verified	Glycosylphosphatidylinositol (GPI)-anchored cell wall endoglucanase required for proper cell separation after cytokinesis, expression is activated by Swi5p and tightly regulated in a
YIL009W	FAA3	1	2.71E-11	9	+	339305	341345	2041	2.28	ORF Verified	Long chain fatty acyl-CoA synthetase, has a preference for C16 and C18 fatty acids; green fluorescent protein (GFP)-fusion protein localizes to the cell periphery
YER158C		2	6.77E-06	5	-	487972	488877	906	-0.22	ORF Uncharacterized	Protein of unknown function, has similarity to Afr1p; potentially phosphorylated by Cdc28p
YNR067C	DSE4	2	1.09E-07	14	-	755782	759134	3353	3.37	ORF Verified	Daughter cell-specific secreted protein with similarity to glucanases, degrades cell wall from the daughter side causing daughter to separate from mother
YOL011W	PLB3	2	NA	15	+	304593	307617	3025	3.5	ORF Verified	Phospholipase B (lysophospholipase) involved in phospholipid metabolism; hydrolyzes phosphatidylinositol and phosphatidylserine and displays transacylase activity in vitro
YOR264W	DSE3	2	9.55E-09	15	+	818817	820089	1273	2.41	ORF Verified	Daughter cell-specific protein, may help establish daughter fate
YBR067C	TIP1	3	3.76E-08	2	-	372067	372787	721	4.9	ORF Verified	Major cell wall mannoprotein with possible lipase activity; transcription is induced by heat- and cold-shock; member of the Srp1p%2FTip1p family of serine-alanine-rich proteins
YBR158W	AMN1	3	7.97E-08	2	+	556264	558320	2057	4.54	ORF Verified	Protein required for daughter cell separation, multiple mitotic checkpoints, and chromosome stability; contains 12 degenerate leucine-rich repeat motifs; expression is
YDR055W	PST1	3	5.19E-10	4	+	563458	564850	1393	5.22	ORF Verified	Cell wall protein that contains a putative GPI-attachment site; secreted by regenerating protoplasts; up-regulated by activation of the cell integrity pathway, as mediated by Rlm1p; upregulated by cell wall damage via disruption of FKS1
YEL066W	HPA3	3	9.84E-07	5	+	26689	27049	361	2.6	ORF Verified	D-Amino acid N-acetyltransferase, catalyzes N-acetylation of D-amino acids through ordered bi-bi mechanism in which acetyl-CoA is first substrate bound and CoA is last product liberated; similar to Hpa2p, acetylates histones weakly in vitro
YGR044C	RME1	3	5.90E-09	7	-	583175	583967	793	3.41	ORF Verified	Zinc finger protein involved in control of meiosis; prevents meiosis by repressing IME1 expression and promotes mitosis by activating CLN2 expression; directly repressed by a1-a2 regulator; mediates cell type control of sporulation
YGR062C	COX18	3	3.18E-07	7	-	616327	617271	945	1.99	ORF Verified	Mitochondrial inner membrane protein, required for export of the Cox2p C terminus from the mitochondrial matrix to the intermembrane space during its assembly into cytochrome c
YJL218W		3	3.02E-06	10	+	21969	22505	537	0.81	ORF Uncharacterized	Putative protein of unknown function, similar to bacterial galactoside O-acetyltransferases; induced by oleate in an OAF1/PIP2-dependent manner; promoter contains an oleate response element consensus sequence; non-essential gene
YNL173C	MDG1	3	2.99E-07	14	-	309093	310069	977	2.49	ORF Verified	Plasma membrane protein involved in G-protein mediated pheromone signaling pathway; overproduction suppresses bem1 mutations

YCR098C	GIT1	4	1.47E-06	3-	298525	300677	2153	-0.27	ORF Verified	Plasma membrane permease, mediates uptake of the phosphatidylinositol metabolite glycerophosphoinositol as a source of the nutrients inositol and phosphate; expression and transport rate are regulated by phosphate and inositol availability
YNL192W	CHS1	4	9.60E-09	14+	276473	279505	3033	4.08	ORF Verified	Chitin synthase I, requires activation from zymogenic form in order to catalyze the transfer of N-acetylglucosamine (GlcNAc) to chitin; required for repairing the chitin septum during cytokinesis; transcription activated by mating factor
YOL006C	TOP1	4	2.08E-06	15-	313525	314933	1409	3.07	ORF Verified	Topoisomerase I, nuclear enzyme that relieves torsional strain in DNA by cleaving and re-sealing the phosphodiester backbone; relaxes both positively and negatively supercoiled DNA; functions in replication, transcription, and recombination
YOL159C-A		4	4.49E-08	15-	14725	15517	793	1.76	ORF Uncharacterized	Putative protein of unknown function; identified by sequence comparison with hemiascomycetous yeast species
YOR342C		4	2.47E-08	15-	966589	967717	1129	4.16	ORF Uncharacterized	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm and the nucleus
YGR289C	MAL11	5	NA	7-	1074070	1076086	2017	1.02	ORF Verified	Maltose permease, inducible high-affinity maltose transporter (alpha-glucoside transporter); encoded in the MAL1 complex locus; member of the 12 transmembrane
YLR194C		5	1.04E-05	12-	540789	541573	785	4.96	ORF Uncharacterized	Structural constituent of the cell wall attached to the plasma membrane by a GPI-anchor; expression is upregulated in response to cell wall stress
YMR251W-A	HOR7	5	1.08E-06	13+	774721	775105	385	4.63	ORF Verified	Protein of unknown function; overexpression suppresses Ca ²⁺ sensitivity of mutants lacking inositol phosphorylceramide mannosyltransferases Csg1p and Csh1p; transcription is induced under hyperosmotic stress and repressed by alpha factor
YGL055W	OLE1	6	2.09E-09	7+	398579	399755	1177	5.12	ORF Verified	Fatty acid desaturase, required for monounsaturated fatty acid synthesis and for normal
YLR049C		6	1.95E-12	12-	243781	245221	1441	2.35	ORF Uncharacterized	Putative protein of unknown function
YIL159W	BNR1	7	2.65E-06	9+	41977	44121	2145	0.65	ORF Verified	Formin, nucleates the formation of linear actin filaments, involved in cell processes such as budding and mitotic spindle orientation which require the formation of polarized actin
YOR374W	ALD4	7	3.44E-05	15+	1039833	1041257	1425	2.54	ORF Verified	Mitochondrial aldehyde dehydrogenase, required for growth on ethanol and conversion of acetaldehyde to acetate; phosphorylated; activity is K ⁺ dependent; utilizes NADP ⁺ or NAD ⁺ equally as coenzymes; expression is glucose repressed
YBR071W		8	3.31E-12	2+	380351	381271	921	4.13	ORF Uncharacterized	Putative protein of unknown function; (GFP)-fusion and epitope-tagged proteins localize to the cytoplasm; mRNA expression may be regulated by the cell cycle and/or cell wall stress
YER111C	SWI4	8	7.95E-12	5-	383733	385565	1833	2.35	ORF Verified	DNA binding component of the SBF complex (Swi4p-Swi6p), a transcriptional activator that in concert with MBF (Mbp1-Swi6p) regulates late G1-specific transcription of targets including cyclins and genes required for DNA synthesis and repair
YKL163W	PIR3	8	NA	11+	143604	144420	817	1.71	ORF Verified	O-glycosylated covalently-bound cell wall protein required for cell wall stability; expression is cell cycle regulated, peaking in M/G1 and also subject to regulation by the cell integrity
YOR347C	PYK2	8	2.11E-06	15-	985125	986533	1409	2.41	ORF Verified	Pyruvate kinase that appears to be modulated by phosphorylation; PYK2 transcription is repressed by glucose, and Pyk2p may be active under low glycolytic flux
YDL102W	POL3	9	1.22E-06	4+	276793	280185	3393	2.08	ORF Verified	Catalytic subunit of DNA polymerase delta; required for chromosomal DNA replication during mitosis and meiosis, intragenic recombination, repair of double strand DNA breaks, and DNA replication during nucleotide excision repair (NER)
YKR077W		9	1.96E-12	11+	583244	584172	929	3.12	ORF Uncharacterized	Putative transcriptional activator, identified by high-throughput two-hybrid experiments; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm and nucleus; YKR077W is not an essential gene
YPR018W	RLF2	9	9.30E-12	16+	594363	596291	1929	1.98	ORF Verified	Largest subunit (p90) of the Chromatin Assembly Complex (CAF-1) with Cac2p and Msi1p that assembles newly synthesized histones onto recently replicated DNA; involved in the

YDR309C	GIC2	10	1.82E-09	4-	1079039	1080263	1225	4.56	ORF Verified	Protein of unknown function involved in initiation of budding and cellular polarization, interacts with Cdc42p via the Cdc42/Rac-interactive binding (CRIB) domain
YGL028C	SCW11	10	7.46E-08	7-	441583	443087	1505	4.74	ORF Verified	Cell wall protein with similarity to glucanases; may play a role in conjugation during mating based on its regulation by Ste12p
YHR149C	SKG6	10	4.27E-08	8-	395493	396797	1305	3.01	ORF Verified	Integral membrane protein that localizes primarily to growing sites such as the bud tip or the cell periphery; potential Cdc28p substrate; Skg6p interacts with Zds1p and Zds2p
YHR189W	PTH1	10	NA	8+	484027	484795	769	1.46	ORF Verified	One of two (see also PTH2) mitochondrially-localized peptidyl-tRNA hydrolases; dispensable for cell growth and for mitochondrial respiration
YJL217W		10	8.58E-09	10+	23129	23561	433	4.3	ORF Uncharacterized	hypothetical protein
YLR457C	NBP1	10	3.21E-05	12-	1053163	1055891	2729	-0.72	ORF Verified	Spindle pole body (SPB) component, required for the insertion of the duplication plaque into the nuclear membrane during SPB duplication; essential for bipolar spindle formation;
YNL310C	ZIM17	10	8.65E-07	14-	51813	52461	649	2.49	ORF Verified	Heat shock protein with a zinc finger motif; essential for protein import into mitochondria; may act with Pam18p to facilitate recognition and folding of imported proteins by Ssc1p
YDL022W	GPD1	11	NA	4+	411785	412961	1177	3.83	ORF Verified	NAD-dependent glycerol-3-phosphate dehydrogenase, key enzyme of glycerol synthesis, essential for growth under osmotic stress; expression regulated by high-osmolarity glycerol
YDL103C	QRI1	11	5.44E-07	4-	275237	276637	1401	3.07	ORF Verified	UDP-N-acetylglucosamine pyrophosphorylase, catalyzes the formation of UDP-N-acetylglucosamine (UDP-GlcNAc), which is important in cell wall biosynthesis, protein N-
YDL127W	PCL2	11	5.83E-12	4+	234873	235769	897	3.14	ORF Verified	G1 cyclin, associates with Pho85p cyclin-dependent kinase (Cdk) to contribute to entry into the mitotic cell cycle, essential for cell morphogenesis; localizes to sites of polarized cell
YDL156W		11	1.48E-11	4+	174841	175953	1113	1.3	ORF Uncharacterized	Putative protein of unknown function; protein sequence contains three WD domains (WD-40 repeat); green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm and nucleus
YDR279W	RNH202	11	NA	4+	1019267	1020243	977	2.26	ORF Verified	Ribonuclease H2 subunit, required for RNase H2 activity
YDR528W	HLR1	11	9.24E-10	4+	1494299	1495891	1593	2.46	ORF Verified	Protein involved in regulation of cell wall composition and integrity and response to osmotic stress; overproduction suppresses a lysis sensitive PKC mutation; similar to Lre1p, which
YGL037C	PNC1	11	NA	7-	427199	427447	249	3.49	ORF Verified	Nicotinamidase that converts nicotinamide to nicotinic acid as part of the NAD(+) salvage pathway, required for life span extension by calorie restriction; PNC1 expression responds
YGR238C	KEL2	11	NA	7-	966086	968654	2569	0.95	ORF Verified	Protein that functions in a complex with Kel1p to negatively regulate mitotic exit, interacts with Tem1p and Lte1p; localizes to regions of polarized growth; potential Cdc28p substrate
YJL196C	ELO1	11	1.31E-07	10-	67869	68813	945	4.31	ORF Verified	Elongase I, medium-chain acyl elongase, catalyzes carboxy-terminal elongation of unsaturated C12-C16 fatty acyl-CoAs to C16-C18 fatty acids
YJR043C	POL32	11	NA	10-	516437	517453	1017	2.27	ORF Verified	Third subunit of DNA polymerase delta, involved in chromosomal DNA replication; required for error-prone DNA synthesis in the presence of DNA damage and processivity; interacts
YNL274C	GOR1	11	8.46E-06	14-	121325	122221	897	1.72	ORF Verified	Glyoxylate reductase; null mutation results in increased biomass after diauxic shift; the authentic, non-tagged protein is detected in highly purified mitochondria in high-throughput
YPL014W		11	3.05E-08	16+	527531	528611	1081	3.19	ORF Uncharacterized	uncharacterized ORF
YBL010C		12	NA	2-	205972	206972	1001	2.33	ORF Uncharacterized	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein colocalizes with clathrin-coated vesicles
YDL105W	NSE4	12	1.42E-10	4+	272385	273665	1281	0.98	ORF Verified	Nuclear protein that plays a role in the function of the Smc5p-Rhc18p complex
YFR027W	ECO1	12	3.62E-12	6+	207409	208313	905	0.96	ORF Verified	Acetyltransferase required for the establishment of sister chromatid cohesion during DNA replication, but not for its maintenance during G2 and M phases; also required for postreplicative double-strand break repair; interacts with Chl1p
YGL207W	SPT16	12	NA	7+	98899	102059	3161	3.78	ORF Verified	Subunit of the heterodimeric FACT complex (Spt16p-Pob3p), facilitates RNA Polymerase II transcription elongation through nucleosomes by destabilizing and then reassembling

YGR041W	BUD9	12	6.94E-11	7+	577179	578859	1681	2.44	ORF Verified	Protein involved in bud-site selection; diploid mutants display a unipolar budding pattern instead of the wild-type bipolar pattern, and bud at the distal pole
YJR057W	CDC8	12	NA	10+	543977	544425	449	2.81	ORF Verified	Thymidylate and uridylate kinase, functions in de novo biosynthesis of pyrimidine deoxyribonucleotides; converts dTMP to dTDP and dUMP to dUTP; essential for mitotic
YKL045W	PRI2	12	5.92E-10	11+	353548	354396	849	2.83	ORF Verified	Subunit of DNA primase, which is required for DNA synthesis and double-strand break
YKL108W	SLD2	12	5.80E-12	11+	234060	235324	1265	1.37	ORF Verified	Protein required for DNA replication, phosphorylated in S phase by S-phase cyclin-dependent kinases (Cdk), phosphorylation is essential for DNA replication and for
YLR233C	EST1	12	1.55E-05	12-	607461	609549	2089	1.47	ORF Verified	TLC1 RNA-associated factor involved in telomere length regulation as the recruitment subunit of the telomerase holoenzyme, has a possible role in activating Est2p-TLC1-RNA
YMR179W	SPT21	12	4.10E-12	13+	620449	622217	1769	2.15	ORF Verified	Protein required for normal transcription at several loci including HTA2-HTB2 and HHF2-HHT2, but not required at the other histone loci; functionally related to Spt10p; involved in
YNL082W	PMS1	12	2.28E-12	14+	473385	475993	2609	1.31	ORF Verified	ATP-binding protein required for mismatch repair in mitosis and meiosis; functions as a heterodimer with Mlh1p, binds double- and single-stranded DNA via its N-terminal domain,
YNL309W	STB1	12	2.18E-11	14+	52617	53977	1361	2.62	ORF Verified	Protein with a role in regulation of MBF-specific transcription at Start, phosphorylated by Cln-Cdc28p kinases in vitro; unphosphorylated form binds Swi6p and binding is required for Stb1p function; expression is cell-cycle regulated
YOR144C	ELG1	12	9.14E-11	15-	603069	605101	2033	2.02	ORF Verified	Protein required for S phase progression and telomere homeostasis, forms an alternative replication factor C complex important for DNA replication and genome integrity; involved in homologous recombination-mediated DNA repair
YBL035C	POL12	13	2.14E-12	2-	151523	153075	1553	2.24	ORF Verified	B subunit of DNA polymerase alpha-primase complex, required for initiation of DNA replication during mitotic and premeiotic DNA synthesis; also functions in telomere capping
YBR098W	MMS4	13	NA	2+	441495	443495	2001	0.87	ORF Verified	Subunit of the structure-specific Mms4p-Mus81p endonuclease that cleaves branched DNA; involved in recombination and DNA repair
YCL024W	KCC4	13	2.01E-12	3+	81913	82265	353	0.67	ORF Verified	Protein kinase of the bud neck involved in the septin checkpoint, associates with septin proteins, negatively regulates Swe1p by phosphorylation, shows structural homology to
YDL227C	HO	13	1.55E-09	4-	46285	48061	1777	1.5	ORF Verified	Site-specific endonuclease required for gene conversion at the MAT locus (homothallic switching) through the generation of a ds DNA break; expression restricted to mother cells in late G1 as controlled by Swi4p-Swi6p, Swi5p and Ash1p
YDR440W	DOT1	13	NA	4+	1342395	1344251	1857	1.5	ORF Verified	Nucleosomal histone H3-Lys79 methylase, associates with transcriptionally active genes, functions in gene silencing at telomeres, most likely by directly modulating chromatin
YGR109C	CLB6	13	5.84E-12	7-	705319	706575	1257	1.15	ORF Verified	B-type cyclin involved in DNA replication during S phase; activates Cdc28p to promote initiation of DNA synthesis; functions in formation of mitotic spindles along with Clb3p and
YGR151C		13	9.42E-12	7-	793095	794719	1625	-0.92	ORF Dubious	hypothetical protein immediately 5' of or overlapping of RSR1
YGR152C	RSR1	13	9.42E-12	7-	793095	794719	1625	-0.92	ORF Verified	GTP-binding protein of the ras superfamily required for bud site selection, morphological changes in response to mating pheromone, and efficient cell fusion; localized to the plasma membrane; significantly similar to mammalian Rap GTPases
YJL181W		13	3.62E-12	10+	86113	87441	1329	1.89	ORF Uncharacterized	Putative protein of unknown function; expression is cell-cycle regulated as shown by microarray analysis
YLR032W	RAD5	13	3.85E-12	12+	205001	208513	3513	1.61	ORF Verified	Single-stranded DNA-dependent ATPase, involved in postreplication repair; contains RING
YLR382C	NAM2	13	NA	12-	882203	884787	2585	2.23	ORF Verified	Mitochondrial leucyl-tRNA synthetase, also has a direct role in splicing of several mitochondrial group I introns; indirectly required for mitochondrial genome maintenance
YML020W		13	NA	13+	231017	233265	2249	1.51	ORF Uncharacterized	Putative protein of unknown function
YML102W	CAC2	13	6.17E-09	13+	68281	69745	1465	2.81	ORF Verified	Component of the chromatin assembly complex (with Rlf2p and Msi1p) that assembles newly synthesized histones onto recently replicated DNA, required for building functional
YNL273W	TOF1	13	6.70E-12	14+	122841	126233	3393	1.69	ORF Verified	Subunit of a replication-pausing checkpoint complex (Tof1p-Mrc1p-Csm3p) that acts at the stalled replication fork to promote sister chromatid cohesion after DNA damage, facilitating gap repair of damaged DNA; interacts with the MCM helicase

YNL304W	YPT11	13	6.08E-08	14+	60257	61633	1377	1.43	ORF Verified	Rab-type small GTPase that interacts with the C-terminal tail domain of Myo2p to mediate distribution of mitochondria to daughter cells
YOR033C	EXO1	13	4.01E-09	15-	392829	394629	1801	2.43	ORF Verified	5'-3' exonuclease and flap-endonuclease involved in recombination, double-strand break repair and DNA mismatch repair; member of the Rad2p nuclease family, with conserved N
YPL221W	FLC1	13	7.65E-08	16+	132801	135057	2257	3.97	ORF Verified	Putative FAD transporter; required for uptake of FAD into endoplasmic reticulum; involved
YPR175W	DPB2	13	2.06E-12	16+	888955	891003	2049	2.19	ORF Verified	Second largest subunit of DNA polymerase II (DNA polymerase epsilon), required for normal yeast chromosomal replication; expression peaks at the G1/S phase boundary;
YAR003W	SWD1	14	2.48E-05	1+	154943	156463	1521	2.68	ORF Verified	Subunit of the COMPASS (Set1C) complex, which methylates histone H3 on lysine 4 and is required in transcriptional silencing near telomeres; WD40 beta propeller superfamily member with similarity to mammalian Rbbp7
YAR008W	SEN34	14	1.31E-11	1+	158879	159847	969	2.35	ORF Verified	Subunit of the tRNA splicing endonuclease, which is composed of Sen2p, Sen15p, Sen34p, and Sen54p; Sen34p contains the active site for tRNA 3' splice site cleavage and has similarity to Sen2p and to Archaeal tRNA splicing endonuclease
YDL164C	CDC9	14	2.17E-12	4-	164869	167293	2425	2.72	ORF Verified	DNA ligase found in the nucleus and mitochondria, an essential enzyme that joins Okazaki fragments during DNA replication; also acts in nucleotide excision repair, base excision
YDR481C	PHO8	14	1.36E-06	4-	1418439	1420279	1841	4.39	ORF Verified	Repressible alkaline phosphatase, a glycoprotein localized to the vacuole; regulated by levels of inorganic phosphate and by a system consisting of Pho4p, Pho9p, Pho80p, Pho81p and Pho85p; dephosphorylates phosphotyrosyl peptides
YER153C	PET122	14	NA	5-	474101	474765	665	1.43	ORF Verified	Mitochondrial translational activator specific for the COX3 mRNA, acts together with Pet54p and Pet494p; located in the mitochondrial inner membrane
YFR026C		14	2.73E-11	6-	205869	207197	1329	0.69	ORF Uncharacterized	Putative protein of unknown function
YHR159W		14	2.99E-06	8+	417489	420017	2529	1.17	ORF Uncharacterized	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm; potential Cdc28p substrate
YIL101C	XBP1	14	NA	9-	176269	177421	1153	1.2	ORF Verified	Transcriptional repressor that binds to promoter sequences of the cyclin genes, CYS3, and SMF2; expression is induced by stress or starvation during mitosis, and late in meiosis; member of the Swi4p/Mbp1p family; potential Cdc28p substrate
YJL074C	SMC3	14	2.48E-12	10-	299125	302781	3657	1.18	ORF Verified	Subunit of the multiprotein cohesin complex required for sister chromatid cohesion in mitotic cells; also required, with Rec8p, for cohesion and recombination during meiosis; phylogenetically conserved SMC chromosomal ATPase family member
YJL078C	PRY3	14	2.26E-08	10-	293661	293989	329	2.06	ORF Verified	Protein of unknown function, has similarity to Pry1p and Pry2p and to the plant PR-1 class of pathogen related proteins
YNL233W	BNI4	14	7.36E-11	14+	211753	214521	2769	2.49	ORF Verified	Targeting subunit for Glc7p protein phosphatase, localized to the bud neck, required for localization of chitin synthase III to the bud neck via interaction with the chitin synthase III
YPR120C	CLB5	14	2.11E-12	16-	773903	775287	1385	1.96	ORF Verified	B-type cyclin involved in DNA replication during S phase; activates Cdc28p to promote initiation of DNA synthesis; functions in formation of mitotic spindles along with Clb3p and
YPR174C		14	1.43E-11	16-	887863	888727	865	2.73	ORF Uncharacterized	Protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the nuclear periphery; potential Cdc28p substrate
YPR184W	GDB1	14	NA	16+	902043	904195	2153	1.16	ORF Verified	Glycogen debranching enzyme containing glucanotransferase and alpha-1,6-amyloglucosidase activities, required for glycogen degradation; phosphorylated in
YDR097C	MSH6	15	1.65E-11	4-	640174	643862	3689	2.04	ORF Verified	Protein required for mismatch repair in mitosis and meiosis, forms a complex with Msh2p to repair both single-base & insertion-deletion mispairs; potentially phosphorylated by
YER124C	DSE1	15	4.46E-07	5-	407941	409093	1153	3.16	ORF Verified	Daughter cell-specific protein, may participate in pathways regulating cell wall metabolism; deletion affects cell separation after division and sensitivity to drugs targeted against the
YGL126W	SCS3	15	NA	7+	270947	272235	1289	3.36	ORF Verified	Protein required for inositol prototrophy, appears to be involved in the synthesis of inositol phospholipids from inositol but not in the control of inositol synthesis

YJL115W	ASF1	15	2.16E-12	10+	196137	196913	777	3.28	ORF Verified	Nucleosome assembly factor, involved in chromatin assembly and disassembly, anti-silencing protein that causes derepression of silent loci when overexpressed
YJR030C		15	8.20E-12	10-	484045	485693	1649	2.26	ORF Uncharacterized	Putative protein of unknown function; expression repressed in carbon limited vs carbon replete chemostat cultures; YJR030C is a non-essential gene
YJR154W		15	8.90E-11	10+	725473	726977	1505	1.18	ORF Uncharacterized	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm
YJR155W	AAD10	15	7.95E-10	10+	726985	727881	897	1.8	ORF Verified	Putative aryl-alcohol dehydrogenase with similarity to <i>P. chrysosporium</i> aryl-alcohol dehydrogenase; mutational analysis has not yet revealed a physiological role
YLL002W	RTT109	15	4.25E-09	12+	146273	147553	1281	2.13	ORF Verified	Histone acetyltransferase critical for cell survival in the presence of DNA damage during S phase, acetylates H3-K56; plays a role in regulation of Ty1 transposition
YLR212C	TUB4	15	4.96E-08	12-	564757	566285	1529	3.35	ORF Verified	Gamma-tubulin, involved in nucleating microtubules from both the cytoplasmic and nuclear faces of the spindle pole body
YMR011W	HXT2	15	2.57E-08	13+	288065	289561	1497	4.68	ORF Verified	High-affinity glucose transporter of the major facilitator superfamily, expression is induced by low levels of glucose and repressed by high levels of glucose
YNL015W	PBI2	15	1.10E-06	14+	605298	605722	425	3.38	ORF Verified	Cytosolic inhibitor of vacuolar proteinase B, required for efficient vacuole inheritance; with thioredoxin forms protein complex LMA1, which assists in priming SNARE molecules and
YNL077W	APJ1	15	1.69E-05	14+	481289	482833	1545	1.43	ORF Verified	Putative chaperone of the HSP40 (DNAJ) family; overexpression interferes with propagation of the [Psi+] prion; the authentic, non-tagged protein is detected in highly
YNL262W	POL2	15	7.47E-10	14+	148209	151657	3449	1.63	ORF Verified	Catalytic subunit of DNA polymerase (II) epsilon, one of the major chromosomal DNA replication polymerases characterized by processivity and proofreading exonuclease activity; also involved in DNA synthesis during DNA repair
YOR284W	HUA2	15	9.23E-11	15+	848433	849377	945	1.72	ORF Verified	Cytoplasmic protein of unknown function; computational analysis of large-scale protein-protein interaction data suggests a possible role in actin patch assembly
YPL267W	ACM1	15	1.99E-12	16+	38169	38785	617	1.93	ORF Verified	Cell cycle regulated protein of unknown function; associated with Cdh1p and may suppress the APC/C[Cdh1]-mediated proteolysis of mitotic cyclins
YPR135W	CTF4	15	5.97E-10	16+	800235	802035	1801	2.15	ORF Verified	Chromatin-associated protein, required for sister chromatid cohesion; interacts with DNA polymerase alpha (Pol1p) and may link DNA synthesis to sister chromatid cohesion
YAR007C	RFA1	16	2.07E-12	1-	156939	158675	1737	3.37	ORF Verified	Subunit of heterotrimeric Replication Protein A (RPA), which is a highly conserved single-stranded DNA binding protein involved in DNA replication, repair, and recombination
YBR073W	RDH54	16	5.85E-08	2+	383143	385991	2849	2.94	ORF Verified	DNA-dependent ATPase, stimulates strand exchange by modifying the topology of double-stranded DNA; involved in recombinational repair of DNA double-strand breaks during mitosis and meiosis; proposed to be involved in crossover interference
YCL061C	MRC1	16	3.07E-11	3-	18725	22141	3417	1.41	ORF Verified	S-phase checkpoint protein found at replication forks, required for DNA replication; also required for Rad53p activation during DNA replication stress, where it forms a replication-pausing complex with Tof1p and is phosphorylated by Mec1p
YDR307W		16	3.10E-05	4+	1076003	1077379	1377	3.26	ORF Uncharacterized	Putative protein of unknown function
YER170W	ADK2	16	NA						ORF Verified	Mitochondrial adenylate kinase, catalyzes the reversible synthesis of GTP and AMP from GDP and ADP; may serve as a back-up for synthesizing GTP or ADP depending on metabolic conditions; 3' sequence of ADK2 varies with strain background
YFL008W	SMC1	16	1.02E-09	6+	120993	123129	2137	1.78	ORF Verified	Subunit of the multiprotein cohesin complex, essential protein involved in chromosome segregation and in double-strand DNA break repair; SMC chromosomal ATPase family member, binds DNA with a preference for DNA with secondary structure
YFL054C		16	NA	6-	20901	22821	1921	1.17	ORF Uncharacterized	Putative channel-like protein; similar to Fps1p; mediates passive diffusion of glycerol in the presence of ethanol

YGL038C	OCH1	16	2.53E-10	7-	425111	426815	1705	3.87	ORF Verified	Mannosyltransferase of the cis-Golgi apparatus, initiates the polymannose outer chain elongation of N-linked oligosaccharides of glycoproteins
YGL089C	MF	16	6.57E-07	7-	344695	345199	505	1.33	ORF Verified	Mating pheromone alpha-factor, made by alpha cells; interacts with mating type a cells to induce cell cycle arrest and other responses leading to mating; also encoded by MF(ALPHA)1, which is more highly expressed than MF(ALPHA)2
YLR103C	CDC45	16	4.12E-12	12-	345581	346005	425	1.69	ORF Verified	DNA replication initiation factor; recruited to MCM pre-RC complexes at replication origins; promotes release of MCM from Mcm10p, recruits elongation machinery; mutants in human homolog may cause velocardiofacial and DiGeorge syndromes
YLR120C	YPS1	16	NA	12-	386197	388325	2129	4.73	ORF Verified	Aspartic protease, attached to the plasma membrane via a glycosylphosphatidylinositol
YLR286C	CTS1	16	4.28E-07	12-	708357	710365	2009	5.26	ORF Verified	Endochitinase, required for cell separation after mitosis; transcriptional activation during late G and early M cell cycle phases is mediated by transcription factor Ace2p
YLR312C-B		16	6.62E-12	12-	760413	762267	1855	1.46	ORF Verified	5' of or overlapping SPH1Protein involved in shmoo formation and bipolar bud site selection; homologous to Spa2p, localizes to sites of polarized growth in a cell cycle dependent- and Spa2p-dependent manner, interacts with MAPKKs Mkk1p, Mkk2p, and
YLR313C	SPH1	16	2.21E-12	12-	760413	762267	1855	1.46	ORF Verified	Protein involved in shmoo formation and bipolar bud site selection; homologous to Spa2p, localizes to sites of polarized growth in a cell cycle dependent- and Spa2p-dependent manner, interacts with MAPKKs Mkk1p, Mkk2p, and Ste7p
YMR048W	CSM3	16	3.61E-11	13+	366977	367921	945	1.52	ORF Verified	Protein required for accurate chromosome segregation during meiosis
YNL102W	POL1	16	4.10E-12	14+	430417	432769	2353	1.8	ORF Verified	Catalytic subunit of the DNA polymerase I alpha-primase complex, required for the initiation of DNA replication during mitotic DNA synthesis and premeiotic DNA synthesis
YOL017W	ESC8	16	1.24E-11	15+	292553	294505	1953	1.22	ORF Verified	Protein involved in telomeric and mating-type locus silencing, interacts with Sir2p and also interacts with the Gal11p, which is a component of the RNA pol II mediator complex
YOR288C	MPD1	16	1.93E-07	15-	852213	853133	921	2.94	ORF Verified	Member of the protein disulfide isomerase (PDI) family; interacts with and inhibits the chaperone activity of Cne1p; MPD1 overexpression in a pdi1 null mutant suppresses defects in Pdi1p functions such as carboxypeptidase Y maturation
YOR368W	RAD17	16	NA	15+	1026849	1027929	1081	1.22	ORF Verified	Checkpoint protein, involved in the activation of the DNA damage and meiotic pachytene checkpoints; with Mec3p and Ddc1p, forms a clamp that is loaded onto partial duplex DNA; homolog of human and S. pombe Rad1 and U. maydis Rec1 proteins
YPL153C	RAD53	16	2.17E-12	16-	261693	264325	2633	1.43	ORF Verified	Protein kinase, required for cell-cycle arrest in response to DNA damage; activated by trans autophosphorylation when interacting with hyperphosphorylated Rad9p; also interacts with ARS1 and plays a role in initiation of DNA replication
YBR088C	POL30	17	2.00E-12	2-	425003	425811	809	3.41	ORF Verified	Proliferating cell nuclear antigen (PCNA), functions as the sliding clamp for DNA polymerase delta; may function as a docking site for other proteins required for mitotic and
YCL027W	FUS1	17	NA	3+	71761	72985	1225	1.78	ORF Verified	Membrane protein localized to the shmoo tip, required for cell fusion; expression regulated by mating pheromone; proposed to coordinate signaling, fusion, and polarization events
YDL003W	MCD1	17	5.85E-12	4+	444561	446161	1601	2.96	ORF Verified	Essential protein required for sister chromatid cohesion in mitosis and meiosis; subunit of the cohesin complex; expression is cell cycle regulated and peaks in S phase
YDR507C	GIN4	17	7.11E-12	4-	1462791	1465887	3097	2.82	ORF Verified	Protein kinase involved in bud growth and assembly of the septin ring, proposed to have kinase-dependent and kinase-independent activities; undergoes autophosphorylation;
YDR517W	GRH1	17	NA	4+	1478107	1478443	337	3.21	ORF Verified	Acetylated, cis-golgi localized protein involved in ER to Golgi transport; homolog of human GRASP65; forms a complex with the coiled-coil protein Bug1p; mutants are compromised for the fusion of ER-derived vesicles with Golgi membranes
YER070W	RNR1	17	2.00E-12	5+	298881	301489	2609	4.41	ORF Verified	Ribonucleotide-diphosphate reductase (RNR), large subunit; the RNR complex catalyzes the rate-limiting step in dNTP synthesis and is regulated by DNA replication and DNA damage checkpoint pathways via localization of the small subunits
YER152C		17	1.94E-05	5-	472605	474093	1489	3.09	ORF Uncharacterized	Putative protein of unknown function; shares amino acid similarity with the aminotransferases Aro8p and Aro9p; YER152C is not an essential gene
YJL073W	JEM1	17	1.31E-06	10+	303009	304105	1097	2.18	ORF Verified	DnaJ-like chaperone required for nuclear membrane fusion during mating, localizes to the ER membrane; exhibits genetic interactions with KAR2

YKL113C	RAD27	17	4.18E-12	11	-	224432	225560	1129	3.01	ORF Verified	5' to 3' exonuclease, 5' flap endonuclease, required for Okazaki fragment processing and maturation as well as for long-patch base-excision repair; member of the S. pombe
YOL090W	MSH2	17	2.12E-11	15	+	147345	150017	2673	2.6	ORF Verified	Protein that forms heterodimers with Msh3p and Msh6p that bind to DNA mismatches to initiate the mismatch repair process; contains a Walker ATP-binding motif required for repair activity; Msh2p-Msh6p binds to and hydrolyzes ATP
YBR070C	ALG14	18	4.59E-12	2	-	379227	379971	745	2.8	ORF Verified	Component of UDP-GlcNAc transferase required for the second step of dolichyl-linked oligosaccharide synthesis; anchors the catalytic subunit Alg13p to the ER membrane;
YDL018C	ERP3	18	2.36E-12	4	-	423013	423565	553	3	ORF Verified	Protein with similarity to Emp24p and Erv25p, member of the p24 family involved in ER to
YEL064C	AVT2	18	1.23E-06	5	-	29973	31253	1281	2.43	ORF Verified	Putative transporter, member of a family of seven S. cerevisiae genes (AVT1-7) related to vesicular GABA-glycine transporters
YGR221C	TOS2	18	2.92E-11	7	-	937311	938463	1153	2.11	ORF Verified	Protein involved in localization of Cdc24p to the site of bud growth; may act as a membrane anchor; localizes to the bud neck and bud tip; potentially phosphorylated by
YHR127W		18	NA	8	+	360880	361840	961	2.6	ORF Verified	Protein of unknown function; localizes to the nucleus
YHR153C	SPO16	18	2.86E-11	8	-	401557	402677	1121	0.01	ORF Verified	Protein of unknown function, required for spore formation
YIL026C	IRR1	18	6.26E-12	9	-	304485	307229	2745	1.79	ORF Verified	Subunit of the cohesin complex, which is required for sister chromatid cohesion during mitosis and meiosis and interacts with centromeres and chromosome arms, essential for
YLR121C	YPS3	18	4.83E-12	12	-	388757	390285	1529	4.02	ORF Verified	Aspartic protease, attached to the plasma membrane via a glycosylphosphatidylinositol
YLR234W	TOP3	18	1.26E-08	12	+	609737	612297	2561	0.94	ORF Verified	DNA Topoisomerase III, conserved protein that functions in a complex with Sgs1p and Rmi1p to relax single-stranded negatively-supercoiled DNA preferentially, involved in telomere stability and regulation of mitotic recombination
YLR386W	VAC14	18	NA	12	+	894183	896367	2185	2.02	ORF Verified	Protein involved in regulated synthesis of PtdIns(3,5)P(2), in control of trafficking of some proteins to the vacuole lumen via the MVB, and in maintenance of vacuole size and acidity;
YML027W	YOX1	18	2.04E-12	13	+	221329	222641	1313	3.67	ORF Verified	Homeodomain-containing transcriptional repressor, binds to Mcm1p and to early cell cycle boxes (ECBs) in the promoters of cell cycle-regulated genes expressed in M/G1 phase; expression is cell cycle-regulated; potential Cdc28p substrate
YML060W	OGG1	18	4.03E-09	13	+	151809	152841	1033	2.32	ORF Verified	Mitochondrial glycosylase/lyase that specifically excises 7,8-dihydro-8-oxoguanine residues located opposite cytosine or thymine residues in DNA, repairs oxidative damage
YPL057C	SUR1	18	3.69E-10	16	-	451471	453223	1753	3.99	ORF Verified	Probable catalytic subunit of a mannosylinositol phosphorylceramide (MIPC) synthase, forms a complex with probable regulatory subunit Csg2p; function in sphingolipid
YPL255W	BBP1	18	NA	16	+	67681	68945	1265	1.9	ORF Verified	Protein required for the spindle pole body (SPB) duplication, localized at the central plaque periphery; forms a complex with a nuclear envelope protein Mps2p and SPB components Spc29p and Kar1p; required for mitotic functions of Cdc5p
YBR275C	RIF1	19	1.67E-05	2	-	753900	757212	3313	1.47	ORF Verified	Protein that binds to the Rap1p C-terminus and acts synergistically with Rif2p to help control telomere length and establish telomeric silencing; deletion results in telomere
YCL040W	GLK1	19	NA	3	+	50785	52217	1433	4.08	ORF Verified	Glucokinase, catalyzes the phosphorylation of glucose at C6 in the first irreversible step of glucose metabolism; one of three glucose phosphorylating enzymes; expression regulated
YCR065W	HCM1	19	5.81E-09	3	+	229801	231145	1345	3.52	ORF Verified	Forkhead transcription factor that drives S-phase specific expression of genes involved in chromosome segregation, spindle dynamics, and budding; suppressor of calmodulin mutants with specific SPB assembly defects; telomere maintenance role
YDR400W	URH1	19	6.00E-09	4	+	1270995	1271683	689	2.84	ORF Verified	Uridine nucleosidase (uridine-cytidine N-ribohydrolase), cleaves N-glycosidic bonds in nucleosides; involved in recycling pyrimidine deoxy- and ribonucleosides via the pyrimidine
YDR503C	LPP1	19	4.99E-11	4	-	1454951	1455895	945	2.14	ORF Verified	Lipid phosphate phosphatase, catalyzes Mg(2+)-independent dephosphorylation of phosphatidic acid (PA), lysophosphatidic acid, and diacylglycerol pyrophosphate; involved in control of the cellular levels of phosphatidylinositol and PA
YER095W	RAD51	19	1.08E-11	5	+	349921	351377	1457	3.68	ORF Verified	Strand exchange protein, forms a helical filament with DNA that searches for homology; involved in the recombinational repair of double-strand breaks in DNA during vegetative growth and meiosis; homolog of Dmc1p and bacterial RecA protein
YGR153W		19	6.87E-09	7	+	796083	796603	521	1.16	ORF Uncharacterized	Putative protein of unknown function

YHR143W	DSE2	19	4.52E-07	8+	385249	386529	1281	5.1	ORF Verified	Daughter cell-specific secreted protein with similarity to glucanases, degrades cell wall from the daughter side causing daughter to separate from mother; expression is repressed
YHR188C	GPI16	19	NA	8-	482439	483871	1433	4.22	ORF Verified	Transmembrane protein subunit of the glycosylphosphatidylinositol transamidase complex that adds GPIs to newly synthesized proteins; human PIG-Tp homolog
YJL019W	MPS3	19	NA	10+	403561	407201	3641	2.99	ORF Verified	Essential integral membrane protein required for spindle pole body duplication and for nuclear fusion, localizes to the spindle pole body half bridge, interacts with DnaJ-like
YJR054W		19	6.94E-08	10+	535945	537321	1377	2.76	ORF Uncharacterized	Vacuolar protein of unknown function; potential Cdc28p substrate
YLL022C	HIF1	19	1.78E-08	12-	99117	100189	1073	3.27	ORF Verified	Non-essential component of the HAT-B histone acetyltransferase complex (Hat1p-Hat2p-Hif1p), localized to the nucleus; has a role in telomeric silencing
YLR183C	TOS4	19	1.97E-12	12-	520469	522077	1609	2.89	ORF Verified	Transcription factor that binds to a number of promoter regions, particularly promoters of some genes involved in pheromone response and cell cycle; potential Cdc28p substrate;
YNL072W	RNH201	19	1.12E-09	14+	490305	491145	841	2.15	ORF Verified	Ribonuclease H2 catalytic subunit, removes RNA primers during Okazaki fragment synthesis; cooperates with Rad27p nuclease
YNL312W	RFA2	19	3.67E-12	14+	48417	49289	873	3.54	ORF Verified	Subunit of heterotrimeric Replication Factor A (RF-A), which is a highly conserved single-stranded DNA binding protein involved in DNA replication, repair, and recombination
YOL019W		19	7.00E-11	15+	289441	290521	1081	4.23	ORF Uncharacterized	Protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cell periphery and vacuole
YDR348C		20	NA	4-	1170263	1172039	1777	4.07	ORF Uncharacterized	Protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cell periphery and bud neck; potential Cdc28p substrate
YJL091C	GWT1	20	NA	10-	261317	262469	1153	3.34	ORF Verified	Protein involved in the inositol acylation of glucosaminyl phosphatidylinositol (GlcN-PI) to form glucosaminyl(acyl)phosphatidylinositol (GlcN(acyl)PI), an intermediate in the biosynthesis of glycosylphosphatidylinositol (GPI) anchors
YKL042W	SPC42	20	4.69E-11	11+	357988	359340	1353	1.4	ORF Verified	Central plaque component of spindle pole body (SPB); involved in SPB duplication, may facilitate attachment of the SPB to the nuclear membrane
YML021C	UNG1	20	2.84E-07	13-	229701	230781	1081	2.49	ORF Verified	Uracil-DNA glycosylase, required for repair of uracil in DNA formed by spontaneous cytosine deamination, not required for strand-specific mismatch repair, cell-cycle regulated, expressed in late G1, localizes to mitochondria and nucleus
YMR076C	PDS5	20	2.05E-12	13-	416197	419261	3065	2.13	ORF Verified	Protein required for establishment and maintenance of sister chromatid condensation and cohesion, colocalizes with cohesin on chromosomes in an interdependent manner, may
YNL289W	PCL1	20	4.00E-12	14+	87825	88801	977	2.86	ORF Verified	Pho85 cyclin of the Pcl1,2-like subfamily, involved in entry into the mitotic cell cycle and regulation of morphogenesis, localizes to sites of polarized cell growth
YOR074C	CDC21	20	2.03E-12	15-	466637	467629	993	2.5	ORF Verified	Thymidylate synthase, required for de novo biosynthesis of pyrimidine deoxyribonucleotides; expression is induced at G1%2FS
YPL208W	RKM1	20	2.75E-06	16+	157833	159129	1297	2.74	ORF Verified	SET-domain lysine-N-methyltransferase, catalyzes the formation of dimethyllysine residues on the large ribosomal subunit protein L23a (RPL23A and RPL23B)
YPL241C	CIN2	20	3.78E-11	16-	95437	96037	601	1.82	ORF Verified	Tubulin folding factor C (putative) involved in beta-tubulin (Tub2p) folding; isolated as mutant with increased chromosome loss and sensitivity to benomyl
YPL256C	CLN2	20	3.84E-11	16-	64773	66781	2009	4.35	ORF Verified	G1 cyclin involved in regulation of the cell cycle; activates Cdc28p kinase to promote the G1 to S phase transition; late G1 specific expression depends on transcription factor complexes, MBF (Swi6p-Mbp1p) and SBF (Swi6p-Swi4p)
YBR042C	CST26	21	NA	2-	320668	321652	985	2.94	ORF Verified	Protein of unknown function, affects chromosome stability when overexpressed
YDL010W		21	5.67E-09	4+	432329	433009	681	2.27	ORF Uncharacterized	Putative thiol oxidoreductase; green fluorescent protein (GFP)-fusion protein localizes to the vacuole; non-essential gene
YDL197C	ASF2	21	1.26E-09	4-	104781	106477	1697	2.09	ORF Verified	Anti-silencing protein that causes derepression of silent loci when overexpressed

YDL211C		21	2.47E-09	4-	79317	80469	1153	2.04	ORF Uncharacterized	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the vacuole
YER104W	RTT105	21	NA	5+	366785	367745	961	0.93	ORF Verified	Protein with a role in regulation of Ty1 transposition
YGR189C	CRH1	21	1.88E-07	7-	876615	878287	1673	5.99	ORF Verified	Cell wall protein that functions in the transfer of chitin to beta(1-6)glucan, putative chitin
YHR154W	RTT107	21	8.25E-12	8+	402929	405313	2385	2.24	ORF Verified	Protein implicated in Mms22-dependent DNA repair during S phase, DNA damage induces phosphorylation by Mec1p at one or more SQ/TQ motifs; interacts with Mms22p and Slx4p; has four BRCT domains; has a role in regulation of Ty1 transposition
YIL140W	AXL2	21	2.04E-12	9+	86289	87689	1401	3.84	ORF Verified	Integral plasma membrane protein required for axial budding in haploid cells, localizes to the incipient bud site and bud neck; glycosylated by Pmt4p; potential Cdc28p substrate
YIL141W		21	1.96E-12	9+	85233	86281	1049	3.18	ORF Dubious	3' region of AXL2 (Integral plasma membrane protein required for axial budding in haploid cells, localizes to the incipient bud site and bud neck; glycosylated by Pmt4p; potential
YJL187C	SWE1	21	2.06E-12	10-	76829	79333	2505	2.61	ORF Verified	Protein kinase that regulates the G2/M transition by inhibition of Cdc28p kinase activity; localizes to the nucleus and to the daughter side of the mother-bud neck; homolog of S.
YMR078C	CTF18	21	2.19E-10	13-	422445	424733	2289	1.9	ORF Verified	Subunit of a complex with Ctf8p that shares some subunits with Replication Factor C and is required for sister chromatid cohesion; may have overlapping functions with Rad24p in
YMR199W	CLN1	21	2.41E-11	13+	662449	664393	1945	3.83	ORF Verified	G1 cyclin involved in regulation of the cell cycle; activates Cdc28p kinase to promote the G1 to S phase transition; late G1 specific expression depends on transcription factor complexes, MBF (Swi6p-Mbp1p) and SBF (Swi6p-Swi4p)
YNL055C	POR1	21	NA	14-	517934	518910	977	5.29	ORF Verified	Mitochondrial porin (voltage-dependent anion channel), outer membrane protein required for the maintenance of mitochondrial osmotic stability and mitochondrial membrane
YNL165W		21	9.45E-06	14+	323769	325137	1369	2.29	ORF Uncharacterized	Putative protein of unknown function; YNL165W is not an essential gene
YOL007C	CSI2	21	2.00E-12	15-	311061	312445	1385	4.13	ORF Verified	Protein of unknown function; green fluorescent protein (GFP)- fusion protein localizes to the mother side of the bud neck and the vacuole; YOL007C is not an essential gene
YOR114W		21	2.35E-12	15+	537473	538433	961	0.71	ORF Uncharacterized	Hypothetical protein
YOR176W	HEM15	21	1.46E-06	15+	662305	663593	1289	3.73	ORF Verified	Ferrochelatase, a mitochondrial inner membrane protein, catalyzes the insertion of ferrous iron into protoporphyrin IX, the eighth and final step in the heme biosynthetic pathway
YOR321W	PMT3	21	4.12E-07	15+	915985	918313	2329	2.84	ORF Verified	Protein O-mannosyltransferase, transfers mannose residues from dolichyl phosphate-D-mannose to protein serine/threonine residues; acts in a complex with Pmt5p, can instead interact with Pmt1p in some conditions; target for new antifungals
YHR110W	ERP5	22	1.98E-11	8+	332264	332672	409	3.59	ORF Verified	Protein with similarity to Emp24p and Erv25p, member of the p24 family involved in ER to
YIL132C	CSM2	22	8.73E-07	9-	99453	100501	1049	0.89	ORF Verified	Protein required for accurate chromosome segregation during meiosis
YKL089W	MIF2	22	2.17E-08	11+	273012	274276	1265	1.74	ORF Verified	Kinetochore protein with homology to human CENP-C, required for structural integrity of the spindle during anaphase spindle elongation, interacts with histones H2A, H2B, and H4,
YKL092C	BUD2	22	NA	11-	265824	267880	2057	1.9	ORF Verified	GTPase activating factor for Rsr1p/Bud1p required for both axial and bipolar budding patterns; mutants exhibit random budding in all cell types
YKL165C	MCD4	22	1.36E-08	11-	139184	140760	1577	3.52	ORF Verified	Protein involved in glycosylphosphatidylinositol (GPI) anchor synthesis; multimembrane-spanning protein that localizes to the endoplasmic reticulum; highly conserved among
YML100W	TSL1	22	5.02E-07	13+	73713	74017	305	2.25	ORF Verified	Large subunit of trehalose 6-phosphate synthase (Tps1p)/phosphatase (Tps2p) complex, which converts uridine-5'-diphosphoglucose and glucose 6-phosphate to trehalose,
YPL124W	SPC29	22	2.72E-11	16+	316737	317513	777	1.27	ORF Verified	Inner plaque spindle pole body (SPB) component, links the central plaque component Spc42p to the inner plaque component Spc110p; required for SPB duplication
YBR161W	CSH1	23	8.15E-08	2+	561488	562832	1345	2.75	ORF Verified	Probable catalytic subunit of a mannosylinositol phosphorylceramide (MIPC) synthase, forms a complex with probable regulatory subunit Csg2p; function in sphingolipid

YDL101C	DUN1	23	3.67E-08	4-	280181	281845	1665	2.21	ORF Verified	Cell-cycle checkpoint serine-threonine kinase required for DNA damage-induced transcription of certain target genes, phosphorylation of Rad55p and Sml1p, and transient G2/M arrest after DNA damage; also regulates postreplicative DNA repair
YDR518W	EUG1	23	4.97E-06	4+	1478563	1479699	1137	3.57	ORF Verified	Protein disulfide isomerase of the endoplasmic reticulum lumen, function overlaps with that of Pdi1p; may interact with nascent polypeptides in the ER
YGL027C	CWH41	23	1.81E-07	7-	443919	446167	2249	3.41	ORF Verified	Processing alpha glucosidase I, ER type II integral membrane N-glycoprotein involved in assembly of cell wall beta 1,6 glucan and asparagine-linked protein glycosylation; also involved in ER protein quality control and sensing of ER stress
YJL173C	RFA3	23	1.35E-09	10-	96109	96533	425	2.8	ORF Verified	Subunit of heterotrimeric Replication Protein A (RPA), which is a highly conserved single-stranded DNA binding protein involved in DNA replication, repair, and recombination
YJR116W		23	NA	10+	640609	641697	1089	2.87	ORF Uncharacterized	Putative protein of unknown function
YLR383W	SMC6	23	5.54E-10	12+	885215	888695	3481	1.26	ORF Verified	Protein involved in structural maintenance of chromosomes; essential subunit of Mms21-Smc5-Smc6 complex; required for growth, DNA repair, interchromosomal and sister chromatid recombination; homologous to <i>S. pombe</i> rad18
YNL263C	YIF1	23	1.02E-05	14-	147045	147973	929	4.95	ORF Verified	Integral membrane protein required for the fusion of ER-derived COPII transport vesicles with the Golgi; interacts with Yip1p and Yos1p; localizes to the Golgi, the ER, and COPII
YOR008C	SLG1	23	NA	15-	341293	342461	1169	4.5	ORF Verified	Sensor-transducer of the stress-activated PKC1-MPK1 kinase pathway involved in maintenance of cell wall integrity; involved in organization of the actin cytoskeleton; secretory pathway Wsc1p is required for the arrest of secretion response
YEL047C		24	2.12E-11	5-	65829	66813	985	3.2	ORF Verified	Soluble fumarate reductase, required with isoenzyme Osm1p for anaerobic growth; may interact with ribosomes, based on co-purification experiments; authentic, non-tagged protein is detected in purified mitochondria in high-throughput studies
YKL101W	HSL1	24	2.52E-12	11+	249684	252740	3057	3.56	ORF Verified	Nim1p-related protein kinase that regulates the morphogenesis and septin checkpoints; associates with the assembled septin filament; required along with Hsl7p for bud neck recruitment, phosphorylation, and degradation of Swe1p
YKR013W	PRY2	24	2.26E-11	11+	463604	464196	593	5.83	ORF Verified	Protein of unknown function, has similarity to Pry1p and Pry3p and to the plant PR-1 class of pathogen related proteins
YLR042C		24	1.59E-07	12-	230029	230501	473	2.29	ORF Uncharacterized	Protein of unknown function; localizes to the cytoplasm; YLL042C is not an essential gene
YML061C	PIF1	24	1.98E-08	13-	148909	151661	2753	2.27	ORF Verified	DNA helicase involved in telomere formation and elongation; acts as a catalytic inhibitor of telomerase; also plays a role in repair and recombination of mitochondrial DNA
YDL093W	PMT5	25	3.31E-08	4+	289873	292313	2441	2.75	ORF Verified	Protein O-mannosyltransferase, transfers mannose residues from dolichyl phosphate-D-mannose to protein serine/threonine residues; acts in a complex with Pmt3p, can instead interact with Pmt2p in some conditions; target for new antifungals
YFL052W		25	NA	6+	28233	31617	3385	0.16	ORF Uncharacterized	Putative zinc cluster protein that contains a DNA binding domain; null mutant sensitive to calcofluor white, low osmolarity and heat, suggesting a role for YFL052Wp in cell wall integrity
YGL175C	SAE2	25	NA						ORF Verified	Protein with a role in accurate meiotic and mitotic double-strand break repair; phosphorylated in response to DNA damage and required for normal resistance to DNA-
YLR151C	PCD1	25	1.32E-06	12-	441725	442725	1001	1.21	ORF Verified	Peroxisomal nudix pyrophosphatase with specificity for coenzyme A and CoA derivatives, may function to remove potentially toxic oxidized CoA disulfide from peroxisomes to
YLR381W	CTF3	25	4.25E-08	12+	879687	881679	1993	2.22	ORF Verified	Outer kinetochore protein that forms a complex with Mcm16p and Mcm22p; may bind the kinetochore to spindle microtubules
YPL163C	SVS1	25	1.14E-11	16-	241765	242733	969	5.5	ORF Verified	Cell wall and vacuolar protein, required for wild-type resistance to vanadate
YAL034W-A	MTW1	26	5.02E-07	1+	79719	80519	801	0.97	ORF Verified	Essential component of the MIND kinetochore complex (Mtw1p including Nnf1p-Nsl1p-Dsn1p) which joins kinetochore subunits contacting DNA to those contacting microtubules;
YAL053W	FLC2	26	NA	1+	45761	48305	2538	4.01	ORF Verified	Putative FAD transporter; required for uptake of FAD into endoplasmic reticulum; involved

YDR263C	DIN7	26	NA	4-	994159	995759	1601	1.18	ORF Verified	Mitochondrial nuclease functioning in DNA repair and replication, modulates the stability of the mitochondrial genome, induced by exposure to mutagens, also induced during meiosis at a time nearly coincident with commitment to recombination
YDR501W	PLM2	26	3.03E-12	4+	1451299	1452971	1673	0.7	ORF Verified	Protein required for partitioning of the 2-micron plasmid
YER001W	MNN1	26	6.64E-12	5+	153473	155769	2297	4.03	ORF Verified	Alpha-1,3-mannosyltransferase, integral membrane glycoprotein of the Golgi complex, required for addition of alpha1,3-mannose linkages to N-linked and O-linked oligosaccharides, one of five <i>S. cerevisiae</i> proteins of the MNN1 family
YFR053C	HXK1	26	6.88E-06	6-	253485	255133	1649	3.01	ORF Verified	Hexokinase isoenzyme 1, a cytosolic protein that catalyzes phosphorylation of glucose during glucose metabolism; expression is highest during growth on non-glucose carbon sources; glucose-induced repression involves the hexokinase Hxk2p
YKL067W	YNK1	26	1.06E-06	11+	314348	315108	761	4.71	ORF Verified	Nucleoside diphosphate kinase, catalyzes the transfer of gamma phosphates from nucleoside triphosphates, usually ATP, to nucleoside diphosphates by a mechanism that involves formation of an autophosphorylated enzyme intermediate
YLR050C		26	2.23E-08	12-	245629	246141	513	2.93	ORF Uncharacterized	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the endoplasmic reticulum; YLR050C is not an essential gene
YNL300W		26	1.96E-12	14+	65665	66281	617	4.35	ORF Uncharacterized	Glycosylphosphatidylinositol-dependent cell wall protein, expression is periodic and decreases in response to ergosterol perturbation or upon entry into stationary phase; depletion increases resistance to lactic acid
YPR183W	DPM1	26	NA	16+	900723	901619	897	5.03	ORF Verified	Dolichol phosphate mannose (Dol-P-Man) synthase of the ER membrane, catalyzes the formation of Dol-P-Man from Dol-P and GDP-Man; required for glycosyl phosphatidylinositol membrane anchoring, O mannosylation, and protein glycosylation
YGL061C	DUO1	27	NA	7-	389039	389775	737	1.94	ORF Verified	Essential subunit of the Dam1 complex (aka DASH complex), couples kinetochores to the force produced by MT depolymerization thereby aiding in chromosome segregation; is
YJL042W	MHP1	27	NA	10+	361097	364865	3769	2.63	ORF Verified	Microtubule-associated protein involved in assembly and stabilization of microtubules; overproduction results in cell cycle arrest at G2 phase; similar to <i>Drosophila</i> protein MAP
YBR241C		28	NA	2-	703036	704108	1073	2.75	ORF Uncharacterized	Putative transporter, member of the sugar porter family; green fluorescent protein (GFP)-fusion protein localizes to the vacuolar membrane; YBR241C is not an essential gene
YER118C	SHO1	28	NA	5-	398005	399221	1217	3.65	ORF Verified	Transmembrane osmosensor, participates in activation of both the Cdc42p- and MAP kinase-dependent filamentous growth pathway and the high-osmolarity glycerol response
YGL094C	PAN2	28	NA	7-	331167	334639	3473	3.06	ORF Verified	Essential subunit of the Pan2p-Pan3p poly(A)-ribonuclease complex, which acts to control poly(A) tail length and regulate the stoichiometry and activity of postreplication repair
YLR343W	GAS2	28	1.31E-08	12+	815903	817695	1793	0.86	ORF Verified	Putative 1,3-beta-glucanosyltransferase, has similarity to Gas1p
YOR195W	SLK19	28	6.82E-09	15+	712809	714689	1881	1.75	ORF Verified	Kinetochores-associated protein required for normal segregation of chromosomes in meiosis and mitosis; component of the FEAR regulatory network, which promotes Cdc14p release from the nucleolus during anaphase; potential Cdc28p substrate
YPR075C	OPY2	28	6.56E-07	16-	695823	696863	1041	3.51	ORF Verified	Integral membrane protein that functions in the signaling branch of the high-osmolarity glycerol (HOG) pathway; interacts with Ste50p; overproduction blocks cell cycle arrest in
YDR480W	DIG2	29	9.99E-08	4+	1417331	1418139	809	2.47	ORF Verified	Regulatory protein of unknown function, pheromone-inducible, involved in the regulation of mating-specific genes and the invasive growth pathway, required for MAP-kinase imposed repression, inhibits pheromone-responsive transcription
YLR326W		29	3.35E-08	12+	782175	782935	761	2.85	ORF Uncharacterized	Hypothetical protein
YDL095W	PMT1	30	NA	4+	287617	289465	1849	5.12	ORF Verified	Protein O-mannosyltransferase, transfers mannose residues from dolichyl phosphate-D-mannose to protein serine/threonine residues; acts in a complex with Pmt2p, can instead interact with Pmt3p in some conditions; target for new antifungals

YDR297W	SUR2	30	7.29E-08	4+	1056475	1057643	1169	4.92	ORF Verified	Sphinganine C4-hydroxylase, catalyses the conversion of sphinganine to phytosphingosine in sphingolipid biosynthesis
YDR488C	PAC11	30	4.54E-08	4-	1429047	1430767	1721	2	ORF Verified	Dynein intermediate chain, acts in the cytoplasmic dynein pathway, forms cortical cytoplasmic microtubule capture site with Num1p; null mutant is defective in nuclear
YER016W	BIM1	30	NA	5+	188257	189073	817	3.14	ORF Verified	Microtubule-binding protein that together with Kar9p makes up the cortical microtubule capture site and delays the exit from mitosis when the spindle is oriented abnormally
YGR188C	BUB1	30	2.08E-08	7-	872279	875151	2873	0.75	ORF Verified	Protein kinase that forms a complex with Mad1p and Bub3p that is crucial in the checkpoint mechanism required to prevent cell cycle progression into anaphase in the presence of spindle damage, associates with centromere DNA via Skp1p
YHR092C	HXT4	30	7.32E-06	8-	287292	288212	921	3.89	ORF Verified	High-affinity glucose transporter of the major facilitator superfamily, expression is induced by low levels of glucose and repressed by high levels of glucose
YKL008C	LAC1	30	1.63E-10	11-	426816	428312	1497	3.92	ORF Verified	Ceramide synthase component, involved in synthesis of ceramide from C26(acyl)-coenzyme A and dihydrosphingosine or phytosphingosine, functionally equivalent to Lag1p
YMR304C-A		30	9.22E-10	13-	879069	880381	1313	6.05	ORF Dubious	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; partially overlaps the verified gene SCW10
YPR106W	ISR1	31	1.71E-09	16+	740035	741419	1385	1.93	ORF Verified	Predicted protein kinase, overexpression causes sensitivity to staurosporine, which is a potent inhibitor of protein kinase C
YDR113C	PDS1	32	2.51E-12	4-	680470	681702	1233	1.67	ORF Verified	Securin that inhibits anaphase by binding separin Esp1p, also blocks cyclin destruction and mitotic exit, essential for cell cycle arrest in mitosis in the presence of DNA damage or
YER003C		32	1.13E-10	5-	155693	157741	2049	-0.59	ORF Verified	PMI40Mannose-6-phosphate isomerase, catalyzes the interconversion of fructose-6-P and mannose-6-P; required for early steps in protein mannosylation
YMR305C	SCW10	32	5.47E-08						ORF Verified	Cell wall protein with similarity to glucanases; may play a role in conjugation during mating based on mutant phenotype and its regulation by Ste12p
YBR015C	MNN2	33	NA	2-	267972	269628	1657	4.03	ORF Verified	Alpha-1,2-mannosyltransferase, responsible for addition of the first alpha-1,2-linked mannose to form the branches on the mannan backbone of oligosaccharides, localizes to
YLR342W	FKS1	33	NA	12+	809751	815607	5857	5.64	ORF Verified	Catalytic subunit of 1,3-beta-D-glucan synthase, functionally redundant with alternate catalytic subunit Gsc2p; binds to regulatory subunit Rho1p; involved in cell wall synthesis and maintenance; localizes to sites of cell wall remodeling
YAL007C	ERP2	34	NA	1-	137723	138443	721	4.28	ORF Verified	Protein that forms a heterotrimeric complex with Erp1p, Emp24p, and Erv25p; member, along with Emp24p and Erv25p, of the p24 family involved in ER to Golgi transport and
YGL093W	SPC10 5	34	8.20E-10	7+	334851	337571	2721	1.93	ORF Verified	Protein required for accurate chromosome segregation, localizes to the nuclear side of the spindle pole body; forms a complex with Ydr532cp
YMR144W		34	6.55E-08	13+	553249	554449	1201	1.9	ORF Uncharacterized	uncharacterized ORF
YNL088W	TOP2	34	5.59E-07	14+	457657	459857	2201	2.37	ORF Verified	Essential type II topoisomerase, relieves torsional strain in DNA by cleaving and re-sealing the phosphodiester backbone of both positively and negatively supercoiled DNA; cleaves complementary strands; localizes to axial cores in meiosis
YOR081C	STC2	34	NA	15-	476885	479221	2337	2.67	ORF Verified	Triacylglycerol lipase involved in TAG mobilization; localizes to lipid particles; potential
YOR083W	WHI5	34	1.75E-09	15+	479465	481825	2361	1.74	ORF Verified	Repressor of G1 transcription that binds to SCB binding factor (SBF) at SCB target promoters in early G1; phosphorylation of Whi5p by the CDK, Cln3p/Cdc28p relieves repression and promoter binding by Whi5; periodically expressed in G1
YOR084W		34	5.24E-09						ORF Verified	Putative lipase of the peroxisomal matrix; transcriptionally activated by Yrm1p along with genes involved in multidrug resistance
YDR356W	SPC11 0	35	2.23E-08	4+	1186083	1188491	2409	0.73	ORF Verified	Inner plaque spindle pole body (SPB) component, ortholog of human kendrin; involved in connecting nuclear microtubules to SPB; interacts with Tub4p-complex and calmodulin; phosphorylated by Mps1p in cell cycle-dependent manner
YFL025C	BST1	35	NA	6-	85229	87301	2073	2.51	ORF Verified	GPI inositol deacylase of the ER that negatively regulates COPII vesicle formation, prevents production of vesicles with defective subunits, required for proper discrimination between resident ER proteins and Golgi-bound cargo molecules

YGR014W	MSB2	35	2.87E-10	7+	516683	519051	2369	4.46	ORF Verified	Mucin family member involved in the Cdc42p- and MAP kinase-dependent filamentous growth signaling pathway; also functions as an osmosensor in parallel to the Sho1p-
YLL021W	SPA2	35	6.79E-09	12+	103473	105305	1833	3.27	ORF Verified	Component of the polarisome, which functions in actin cytoskeletal organization during polarized growth; acts as a scaffold for Mkk1p and Mpk1p cell wall integrity signaling
YBL009W	ALK2	36	2.62E-08	2+	207176	209048	1873	2.81	ORF Verified	Protein kinase; accumulation and phosphorylation are periodic during the cell cycle; phosphorylated in response to DNA damage; contains characteristic motifs for degradation via the APC pathway; similar to Alk1p and to mammalian haspins
YGL200C	EMP24	36	NA	7-	122631	123359	729	5.09	ORF Verified	Integral membrane component of endoplasmic reticulum-derived COPII-coated vesicles, which function in ER to Golgi transport
YGR140W	CBF2	36	2.92E-08	7+	767483	769091	1609	1.95	ORF Verified	Essential kinetochore protein, component of the CBF3 multisubunit complex that binds to the CDEIII region of the centromere; Cbf2p also binds to the CDEII region possibly forming a different multimeric complex, ubiquitinated in vivo
YNL283C	WSC2	36	2.34E-10	14-	105461	106725	1265	4.78	ORF Verified	Partially redundant sensor-transducer of the stress-activated PKC1-MPK1 signaling pathway involved in maintenance of cell wall integrity and recovery from heat shock; secretory pathway Wsc2p is required for the arrest of secretion response
YOR373W	NUD1	36	4.81E-08	15+	1036793	1038665	1873	1.89	ORF Verified	Component of the spindle pole body outer plaque, required for exit from mitosis
YHR061C	GIC1	37	3.11E-11	8-	221404	222588	1185	2.01	ORF Verified	Protein of unknown function involved in initiation of budding and cellular polarization, interacts with Cdc42p via the Cdc42/Rac-interactive binding (CRIB) domain
YHR172W	SPC97	37	5.08E-09	8+	448225	451241	3017	1.74	ORF Verified	Component of the microtubule-nucleating Tub4p (gamma-tubulin) complex; interacts with Spc110p at the spindle pole body (SPB) inner plaque and with Spc72p at the SPB outer
YNL030W	HHF2	37	3.21E-10	14+	576706	577074	369	4.94	ORF Verified	One of two identical histone H4 proteins (see also HHF1); core histone required for chromatin assembly and chromosome function; contributes to telomeric silencing; N-
YNL166C	BNI5	37	1.21E-07	14-	322557	323581	1025	3.08	ORF Verified	Protein involved in organization of septins at the mother-bud neck, may interact directly with the Cdc11p septin, localizes to bud neck in a septin-dependent manner
YPL127C	HHO1	37	3.29E-12	16-	308821	309637	817	4.04	ORF Verified	Histone H1, a linker histone required for nucleosome packaging at restricted sites; suppresses DNA repair involving homologous recombination; not required for telomeric silencing, basal transcriptional repression, or efficient sporulation
YBL002W	HTB2	38	8.22E-12	2+	236384	237016	633	5.1	ORF Verified	One of two nearly identical (see HTB1) histone H2B subtypes required for chromatin assembly and chromosome function; Rad6p-Bre1p-Lge1p mediated ubiquitination regulates transcriptional activation, meiotic DSB formation and H3 methylation
YDR225W	HTA1	38	7.71E-12	4+	915427	916067	641	5.06	ORF Verified	One of two nearly identical (see also HTA2) histone H2A subtypes; core histone required for chromatin assembly and chromosome function; DNA damage-dependent phosphorylation by Mec1p facilitates DNA repair; acetylated by Nat4p
YER019W	ISC1	38	2.57E-07	5+	192289	192849	561	0.71	ORF Verified	Mitochondrial membrane localized inositol phosphosphingolipid phospholipase C, hydrolyzes complex sphingolipids to produce ceramide; activated by phosphatidylserine, cardiolipin, and phosphatidylglycerol; mediates Na+ and Li+ halotolerance
YBL031W	SHE1	39	1.61E-09	2+	161695	162471	777	2.24	ORF Verified	Cytoskeletal protein of unknown function; overexpression causes growth arrest
YBR010W	HHT1	39	3.24E-11	2+	256312	256824	513	4.94	ORF Verified	One of two identical histone H3 proteins (see also HHT2); core histone required for chromatin assembly, involved in heterochromatin-mediated telomeric and HM silencing; regulated by acetylation, methylation, and mitotic phosphorylation
YDR224C	HTB1	39	3.42E-11	4-	914295	914791	497	4.71	ORF Verified	One of two nearly identical (see HTB2) histone H2B subtypes required for chromatin assembly and chromosome function; Rad6p-Bre1p-Lge1p mediated ubiquitination regulates transcriptional activation, meiotic DSB formation and H3 methylation
YJL118W		39	7.66E-12	10+	191601	192313	713	3.19	ORF Verified	Putative protein of unknown function; may interact with ribosomes, based on co-purification experiments; YJL18W is a non-essential gene; deletion enhances the toxicity of
YNL031C	HHT2	39	6.45E-10	14-	575396	576061	666	5.52	ORF Verified	One of two identical histone H3 proteins (see also HHT1); core histone required for chromatin assembly, involved in heterochromatin-mediated telomeric and HM silencing; regulated by acetylation, methylation, and mitotic phosphorylation
YMR117C	SPC24	40	3.14E-06	13-	500709	501917	1209	1.88	ORF Verified	Component of the evolutionarily conserved kinetochore-associated Ndc80 complex (Ndc80p-Nuf2p-Spc24p-Spc25p); involved in chromosome segregation, spindle checkpoint

YPR141C	KAR3	40	3.24E-11	16-	816751	818039	1289	0.91	ORF Verified	Minus-end-directed microtubule motor that functions in mitosis and meiosis, localizes to the spindle pole body and localization is dependent on functional Cik1p, required for
YBL003C	HTA2	41	2.08E-12	2-	235276	235828	553	4.37	ORF Verified	One of two nearly identical (see also HTA1) histone H2A subtypes; core histone required for chromatin assembly and chromosome function; DNA damage-dependent phosphorylation by Mec1p facilitates DNA repair; acetylated by Nat4p
YEL061C	CIN8	41	9.88E-12	5-	36405	38157	1753	1.01	ORF Verified	Kinesin motor protein involved in mitotic spindle assembly and chromosome segregation
YJR146W		41	1.12E-09	10+	704065	705297	1233	3.1	ORF Dubious	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; partially overlaps the verified gene HMS2
YNL014W	HEF3	41	NA	14+	606594	608778	2185	0.57	ORF Verified	Translational elongation factor EF-3; paralog of YEF3 and member of the ABC superfamily; stimulates EF-1 alpha-dependent binding of aminoacyl-tRNA by the ribosome; normally
YNL126W	SPC98	41	3.63E-12	14+	387201	389809	2609	1.73	ORF Verified	Component of the microtubule-nucleating Tub4p (gamma-tubulin) complex; interacts with Spc110p at the spindle pole body (SPB) inner plaque and with Spc72p at the SPB outer
YER018C	SPC25	42	5.70E-07	5-	191629	192661	1033	2.35	ORF Verified	Component of the evolutionarily conserved kinetochore-associated Ndc80 complex (Ndc80p-Nuf2p-Spc24p-Spc25p); involved in chromosome segregation, spindle checkpoint
YHR086W	NAM8	42	5.98E-07	8+	277944	279728	1785	2.84	ORF Verified	RNA binding protein, component of the U1 snRNP protein; mutants are defective in meiotic recombination and in formation of viable spores, involved in the formation of DSBs through
YBR162C	TOS1	43	NA	2-	562932	564780	1849	5.48	ORF Verified	Covalently-bound cell wall protein of unknown function; identified as a cell cycle regulated SBF target gene; deletion mutants are highly resistant to treatment with beta-1,3-
YGR099W	TEL2	43	3.97E-11	7+	687843	689843	2001	2.16	ORF Verified	Essential DNA-binding protein specific to single-stranded yeast telomeric DNA repeats, required for telomere length regulation and telomere position effect
YJR147W	HMS2	43	3.62E-05	10+	704065	705297	1233	3.1	ORF Verified	Protein with similarity to heat shock transcription factors; overexpression suppresses the pseudohyphal filamentation defect of a diploid mep1 mep2 homozygous null mutant
YLR045C	STU2	43	1.10E-10	12-	235021	237709	2689	2.3	ORF Verified	Microtubule-associated protein (MAP) of the XMAP215/Dis1 family; regulates microtubule dynamics during spindle orientation and metaphase chromosome alignment; interacts with
YNR009W	NRM1	43	2.23E-12	14+	642658	643530	873	3.29	ORF Verified	Transcriptional co-repressor of MBF (MCB binding factor)-regulated gene expression; Nrm1p associates stably with promoters via MBF to repress transcription upon exit from
YBL063W	KIP1	44	2.45E-10	2+	101895	105175	1810	1.55	ORF Verified	Kinesin-related motor protein required for mitotic spindle assembly and chromosome segregation; functionally redundant with Cin8p
YBR009C	HHF1	44	3.16E-09	2-	255260	255716	457	5.29	ORF Verified	One of two identical histone H4 proteins (see also HHF2); core histone required for chromatin assembly and chromosome function; contributes to telomeric silencing; N-
YIR034C	LYS1	44	NA	9-	419581	420757	1177	3.6	ORF Verified	Saccharopine dehydrogenase (NAD ⁺ , L-lysine-forming), catalyzes the conversion of saccharopine to L-lysine, which is the final step in the lysine biosynthesis pathway
YBR184W		45	1.16E-06	2+	598008	598920	913	0.23	ORF Uncharacterized	Putative protein of unknown function; YBR184W is not an essential gene
YMR006C	PLB2	45	3.34E-10	13-	277557	279429	1873	3.41	ORF Verified	Phospholipase B (lysophospholipase) involved in phospholipid metabolism; displays transacylase activity in vitro; overproduction confers resistance to lysophosphatidylcholine
YOR372C	NDD1	45	2.29E-09	15-	1035069	1036533	1465	3.46	ORF Verified	Transcriptional activator essential for nuclear division; localized to the nucleus; essential component of the mechanism that activates the expression of a set of late-S-phase-
YDR302W	GPI11	46	NA	4+	1067675	1068219	545	3.59	ORF Verified	ER membrane protein involved in a late step of glycosylphosphatidylinositol (GPI) anchor assembly; involved in the addition of phosphoethanolamine to the multiply mannosylated GPI intermediate; human PIG-Fp is a functional homolog
YJR053W	BFA1	46	4.87E-10	10+	533913	535937	2025	1.01	ORF Verified	Component of the GTPase-activating Bfa1p-Bub2p complex involved in multiple cell cycle checkpoint pathways that control exit from mitosis
YKL096W	CWP1	46	5.36E-11	11+	260740	260860	121	3.61	ORF Verified	Cell wall mannoprotein, linked to a beta-1,3- and beta-1,6-glucan heteropolymer through a phosphodiester bond; involved in cell wall organization
YPL269W	KAR9	46	2.23E-07	16+	33017	34993	1977	0.81	ORF Verified	Karyogamy protein required for correct positioning of the mitotic spindle and for orienting cytoplasmic microtubules, localizes at the shmoo tip in mating cells and at the tip of the
YDR451C	YHP1	47	5.04E-12	4-	1360959	1362215	1257	3.01	ORF Verified	One of two homeobox transcriptional repressors (see also Yox1p), that bind to Mcm1p and to early cell cycle box (ECB) elements of cell cycle regulated genes, thereby restricting

YLR455W		48	3.20E-09	12+	1053391	1054791	1401	2.47	ORF Uncharacterized	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the nucleus; deletion confers sensitivity to 4-(N-(S-glutathionylacetyl)amino) phenylarsenoxide (GSAO)
YMR215W	GAS3	48	3.22E-12	13+	696737	698337	1601	4.45	ORF Verified	Putative 1,3-beta-glucanosyltransferase, has similarity to Gas1p; localizes to the cell wall
YPL116W	HOS3	48	1.41E-11	16+	329433	331457	2025	2.54	ORF Verified	Trichostatin A-insensitive homodimeric histone deacetylase (HDAC) with specificity in vitro for histones H3, H4, H2A, and H2B; similar to Hda1p, Rpd3p, Hos1p, and Hos2p; deletion results in increased histone acetylation at rDNA repeats
YCR086W	CSM1	49	5.81E-11	3+	263361	263929	569	1.16	ORF Verified	Nucleolar protein that forms a complex with Lrs4p which binds Mam1p at kinetochores during meiosis I to mediate accurate chromosome segregation, may be involved in premeiotic DNA replication; possible role in telomere maintenance
YGR113W	DAM1	49	1.31E-06	7+	718843	720139	1297	2.81	ORF Verified	Essential subunit of the Dam1 complex (aka DASH complex), couples kinetochores to the force produced by MT depolymerization thereby aiding in chromosome segregation; Ipl1p
YOR073W	SGO1	49	5.16E-11	15+	464713	466241	1529	2.25	ORF Verified	Component of the spindle checkpoint, involved in sensing lack of tension on mitotic chromosomes; protects centromeric Rec8p at meiosis I; required for accurate chromosomal segregation at meiosis II and for mitotic chromosome stability
YBR008C	FLR1	50	3.17E-09	2-	253276	254884	1609	2.44	ORF Verified	Plasma membrane multidrug transporter of the major facilitator superfamily, involved in efflux of fluconazole, diazaborine, benomyl, methotrexate, and other drugs
YDR219C	MFB1	50	4.26E-07	4-	905327	907015	1689	1.96	ORF Verified	Mitochondria-associated F-box protein involved in maintenance of normal mitochondrial morphology; interacts with Skp1p through the F-box motif; preferentially localizes to the
YKR010C	TOF2	50	1.69E-09	11-	458456	460984	2529	1.26	ORF Verified	Nonessential mitochondrial protein of unknown function with sequence similarity to Net1p; identified as a topoisomerase I (Top1p) binding protein; displays synthetic genetic
YLR209C	PNP1	50	2.48E-07	12-	560909	561757	849	3.06	ORF Verified	Purine nucleoside phosphorylase, specifically metabolizes inosine and guanosine
YMR163C	INP2	50	5.56E-10	13-	584469	586517	2049	1.27	ORF Verified	Peroxisome-specific receptor important for peroxisome inheritance; co-fractionates with peroxisome membranes and co-localizes with peroxisomes in vivo; physically interacts with the myosin V motor Myo2p; INP2 is not an essential gene
YEL017W	GTT3	51	3.61E-08	5+	123641	124369	729	3.35	ORF Verified	Protein of unknown function with a possible role in glutathione metabolism, as suggested by computational analysis of large-scale protein-protein interaction data; GFP-fusion protein localizes to the nuclear periphery
YGL216W	KIP3	51	1.34E-06	7+	84626	87346	2721	2.31	ORF Verified	Kinesin-related motor protein involved in mitotic spindle positioning
YLR288C	MEC3	51	1.98E-05	12-	714893	717189	2297	-0.78	ORF Verified	DNA damage and meiotic pachytene checkpoint protein; subunit of a heterotrimeric complex (Rad17p-Mec3p-Ddc1p) that forms a sliding clamp, loaded onto partial duplex DNA by a clamp loader complex; homolog of human and <i>S. pombe</i> Hus1
YER011W	TIR1	52	5.52E-07	5+	175209	176001	793	3.33	ORF Verified	Cell wall mannoprotein of the Srp1p/Tip1p family of serine-alanine-rich proteins; expression is downregulated at acidic pH and induced by cold shock and anaerobiosis;
YIR010W	DSN1	52	4.66E-09	9+	375377	376657	1281	2.24	ORF Verified	Essential component of the MIND kinetochore complex (Mtw1p including Nnf1p-Nsl1p-Dsn1p) which joins kinetochore subunits contacting DNA to those contacting microtubules;
YJL105W	SET4	52	1.87E-07	10+	223673	227217	3545	-0.18	ORF Verified	Protein of unknown function, contains a SET domain
YKL052C	ASK1	52	8.47E-07	11-	339464	340208	745	3.38	ORF Verified	Component of the DASH complex that binds to microtubules and kinetochores and is essential for chromosome segregation; phosphorylated during the cell cycle by cyclin-
YLR210W	CLB4	52	2.68E-10	12+	562393	563501	1109	2.94	ORF Verified	B-type cyclin involved in cell cycle progression; activates Cdc28p to promote the G2/M transition; may be involved in DNA replication and spindle assembly; accumulates during S phase and G2, then targeted for ubiquitin-mediated degradation
YMR003W		52	2.06E-12	13+	273081	273705	625	1.99	ORF Uncharacterized	Protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the mitochondria; YMR003W is not an essential gene
YNL176C		52	2.03E-08	14-	305869	307157	1289	4.3	ORF Uncharacterized	hypothetical protein; has FKH1 TFBS
YOL012C	HTZ1	52	2.74E-11	15-	303381	304093	713	3.3	ORF Verified	Histone variant H2AZ, exchanged for histone H2A in nucleosomes by the SWR1 complex; involved in transcriptional regulation through prevention of the spread of silent

YMR198W	CIK1	53	9.26E-08	13+	659473	661937	2465	1.78	ORF Verified	Kinesin-associated protein required for both karyogamy and mitotic spindle organization, interacts stably and specifically with Kar3p and may function to target this kinesin to a
YPL253C	VIK1	53	1.16E-10	16-	70973	73045	2073	1.3	ORF Verified	Protein that forms a complex with Kar3p at the spindle pole body, possible regulator of Kar3p function in microtubule-mediated processes; required for sister chromatid cohesion;
YER032W	FIR1	54	7.19E-12	5+	214993	217801	2809	2.34	ORF Verified	Protein involved in 3' mRNA processing, interacts with Ref2p; potential Cdc28p substrate
YIL131C	FKH1	54	2.55E-12	9-	100733	102285	1553	2.98	ORF Verified	Forkhead family transcription factor with a minor role in the expression of G2/M phase genes; negatively regulates transcriptional elongation; positive role in chromatin silencing at HML and HMR; regulates donor preference during switching
YLR437C		54	2.57E-07	12-	1011619	1012075	457	3.78	ORF Uncharacterized	Putative protein of unknown function; epitope tagged protein localizes to the cytoplasm
YBL097W	BRN1	55	5.07E-07	2+	42729	43233	505	0.95	ORF Verified	Essential protein required for chromosome condensation, likely to function as an intrinsic component of the condensation machinery, may influence multiple aspects of chromosome
YDR179W-A		55	1.42E-09	4+	819362	820635	1274	2.01	ORF Uncharacterized	Putative protein of unknown function
YGL101W		55	5.00E-10	7+	312195	312947	753	2.91	ORF Uncharacterized	Putative protein of unknown function; non-essential gene with similarity to YBR242W; interacts with the DNA helicase Hpr5p
YJR076C	CDC11	55	9.02E-07	10-	572885	575269	2385	-0.29	ORF Verified	Component of the septin ring of the mother-bud neck that is required for cytokinesis; septins recruit proteins to the neck and can act as a barrier to diffusion at the membrane,
YKL048C	ELM1	55	4.57E-06	11-	347000	348856	1857	1.54	ORF Verified	Serine/threonine protein kinase that regulates cellular morphogenesis, septin behavior, and cytokinesis; required for the regulation of other kinases; forms part of the bud neck ring
YKL069W		55	1.15E-08	11+	306932	307428	497	2.63	ORF Uncharacterized	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm and nucleus
YMR190C	SGS1	55	7.51E-07	13-	640789	645413	4625	1.18	ORF Verified	Nucleolar DNA helicase of the RecQ family involved in maintenance of genome integrity, regulates chromosome synapsis and meiotic crossing over; has similarity to human BLM and WRN helicases implicated in Bloom and Werner syndromes
YDL028C	MPS1	56	2.32E-06	4-	400925	403405	2481	1.64	ORF Verified	Dual-specificity kinase required for spindle pole body (SPB) duplication and spindle checkpoint function; substrates include SPB proteins Spc42p, Spc110p, and Spc98p, mitotic exit network protein Mob1p, and checkpoint protein Mad1p
YDR130C	FIN1	56	1.60E-09	4-	715590	716606	1017	2.23	ORF Verified	Spindle pole body-related intermediate filament protein, forms cell cycle-specific filaments between spindle pole bodies in mother and daughter cells, able to self-assemble, expression induced during S/G2, localization cell-cycle dependent
YDR227W	SIR4	56	NA	4+	917451	919779	2329	1.17	ORF Verified	Silent information regulator that, together with SIR2 and SIR3, is involved in assembly of silent chromatin domains at telomeres and the silent mating-type loci; potentially phosphorylated by Cdc28p; some alleles of SIR4 prolong lifespan
YEL016C	NPP2	56	4.30E-07	5-	124773	126389	1617	2.52	ORF Verified	Nucleotide pyrophosphatase/phosphodiesterase family member; mediates extracellular nucleotide phosphate hydrolysis along with Npp1p and Pho5p; activity and expression enhanced during conditions of phosphate starvation
YHR031C	RRM3	56	6.68E-09	8-	170837	172981	2145	1.53	ORF Verified	DNA helicase involved in rDNA replication and Ty1 transposition; relieves replication fork pauses at telomeric regions; structurally and functionally related to Pif1p
YHR146W	CRP1	56	2.00E-07	8+	390297	391601	1305	3.24	ORF Verified	Protein that binds to cruciform DNA structures
YJL137C	GLG2	56	8.57E-08	10-	154885	156061	1177	2.02	ORF Verified	Self-glucosylating initiator of glycogen synthesis, also glucosylates n-dodecyl-beta-D-maltoside; similar to mammalian glycogenin
YPR004C		56	3.75E-06	16-	564199	565079	881	3.65	ORF Verified	Protein with homology to mammalian electron transfer flavoprotein complex subunit ETF-alpha; has an FAD binding domain; interacts with yeast frataxin homolog Yfh1p; associates with a large complex containing several dehydrogenases

YIL050W	PCL7	57	4.47E-08	9+	258849	259361	513	2.71	ORF Verified	Pho85p cyclin of the Pho80p subfamily, forms a functional kinase complex with Pho85p which phosphorylates Mmr1p and is regulated by Pho81p; involved in glycogen
YBL032W	HEK2	58	2.08E-09	2+	160103	161359	1257	3.7	ORF Verified	RNA binding protein with similarity to hnRNP-K that localizes to the cytoplasm and to subtelomeric DNA; required for the proper localization of ASH1 mRNA; involved in the
YDR325W	YCG1	58	6.23E-08	4+	1117115	1120227	3113	2.05	ORF Verified	Non-SMC subunit of the condensin complex (Smc2p-Smc4p-Ycs4p-Brn1p-Ycg1p); required for establishment and maintenance of chromosome condensation, chromosome segregation and for chromatin binding of the condensin complex
YBR130C	SHE3	59	4.13E-07	2-	495572	496916	1345	2.62	ORF Verified	Protein that acts as an adaptor between Myo4p and the She2p-mRNA complex; part of the mRNA localization machinery that restricts accumulation of certain proteins to the bud;
YDR326C	YSP2	59	7.37E-06	4-	1121967	1125095	3129	3.81	ORF Verified	Protein involved in programmed cell death; mutant shows resistance to cell death induced by amiodarone or intracellular acidification
YKR041W		59	5.57E-09	11+	517852	518948	1097	0.57	ORF Uncharacterized	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm and nucleus
YML072C	TCB3	59	9.80E-08	13-	124813	128101	3289	3.74	ORF Verified	Contains three calcium and lipid binding domains; localized to the bud; green fluorescent protein (GFP)-fusion protein localizes to the cell periphery; mRNA is targeted to the bud via the mRNA transport system involving She2p; C-terminal portion of Tcb1p, Tcb2p and
YDR089W		60	1.53E-11	4+	622210	624410	2201	1.98	ORF Uncharacterized	Protein of unknown function; deletion confers resistance to Nickel
YBL052C	SAS3	61	9.60E-07	2-	119427	121787	2361	2.42	ORF Verified	Histone acetyltransferase catalytic subunit of NuA3 complex that acetylates histone H3, involved in transcriptional silencing; homolog of the mammalian MOZ proto-oncogene;
YBL068W-A		61	1.05E-09	2+	90673	92113	1441	2.2	ORF Dubious	dubious ORF; part of AST1
YBL069W	AST1	61	1.05E-09	2+	90673	92113	1441	2.2	ORF Verified	Peripheral membrane protein that interacts with the plasma membrane ATPase Pma1p and has a role in its targeting to the plasma membrane, possibly by influencing its
YFL017C	GNA1	61	7.68E-07	6-	103997	104477	481	2.57	ORF Verified	Evolutionarily conserved glucosamine-6-phosphate acetyltransferase required for multiple cell cycle events including passage through START, DNA synthesis, and mitosis; involved in UDP-N-acetylglucosamine synthesis, forms GlcNAc6P from AcCoA
YML065W	ORC1	61	1.00E-07	13+	142129	144929	2801	1.61	ORF Verified	Largest subunit of the origin recognition complex, which directs DNA replication by binding to replication origins and is also involved in transcriptional silencing; exhibits ATPase
YML125C	PGA3	61	9.50E-07	13-	20693	21725	1033	4.89	ORF Uncharacterized	Essential protein required for maturation of Gas1p and Pho8p, protein trafficking; GFP-fusion protein localizes to the endoplasmic reticulum; null mutants have a cell separation defect
YCL014W	BUD3	62	8.04E-12	3+	96193	99073	2881	1.95	ORF Verified	Protein involved in bud-site selection and required for axial budding pattern; localizes with septins to bud neck in mitosis and may constitute an axial landmark for next round of
YCL063W	VAC17	62	1.54E-11	3+	17257	18393	1137	3.13	ORF Verified	Protein involved in vacuole inheritance; acts as a vacuole-specific receptor for myosin Myo2p
YER114C	BOI2	62	3.54E-07	5-	390605	394005	3401	2.66	ORF Verified	Protein implicated in polar growth, functionally redundant with Boi1p; interacts with bud-emergence protein Bem1p; contains an SH3 (src homology 3) domain and a PH (pleckstrin homology) domain
YLL032C		62	2.61E-11	12-	74157	76821	2665	1.81	ORF Verified	Protein of unknown function that may interact with ribosomes, based on co-purification experiments; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm;
YML052W	SUR7	62	2.66E-12	13+	170377	171361	985	4.97	ORF Verified	Putative integral membrane protein; component of eisosomes; associated with endocytosis, along with Pil1p and Lsp1p; sporulation and plasma membrane sphingolipid
YNL068C	FKH2	62	3.84E-10	14-	496061	497509	1449	2.81	ORF Verified	Forkhead family transcription factor with a major role in the expression of G2/M phase genes; positively regulates transcriptional elongation; negative role in chromatin silencing at HML and HMR; substrate of the Cdc28p/Clb5p kinase
YBR086C	IST2	63	4.13E-07	2-	420219	423227	3009	4.81	ORF Verified	Plasma membrane protein that may be involved in osmotolerance, localizes to the mother cell in small-budded cells and to the bud in medium- and large-budded cells; mRNA is transported to the bud tip by an actomyosin-driven process

YML058W	SML1	63	2.40E-09	13+	159329	159977	649	5.49	ORF Verified	Ribonucleotide reductase inhibitor involved in regulating dNTP production; regulated by Mec1p and Rad53p during DNA damage and S phase
YMR299C	DYN3	63	1.53E-07	13-	864301	865341	1041	2.03	ORF Verified	Dynein light intermediate chain (LIC); localizes with dynein, null mutant is defective in
YDR147W	EK1	64	1.62E-06	4+	753154	755562	2409	-0.67	ORF Verified	Ethanolamine kinase, primarily responsible for phosphatidylethanolamine synthesis via the CDP-ethanolamine pathway; also exhibits choline kinase activity
YDR346C	SVF1	64	1.08E-05	4-	1166943	1168799	1857	4.58	ORF Verified	Protein with a potential role in cell survival pathways, required for the diauxic growth shift; expression in mammalian cells increases survival under conditions inducing apoptosis
YOR129C		64	5.24E-07	15-	566693	569613	2921	2.23	ORF Verified	Putative component of the outer plaque of the spindle pole body; may be involved in cation homeostasis or multidrug resistance
YBR123C	TFC1	65	2.44E-08	2-	484868	486724	1857	2.17	ORF Verified	One of six subunits of the RNA polymerase III transcription initiation factor complex (TFIIIC); part of the TauA globular domain of TFIIIC that binds DNA at the BoxA promoter
YGL021W	ALK1	65	2.06E-12	7+	454827	457035	2209	3.76	ORF Verified	Protein kinase; accumulation and phosphorylation are periodic during the cell cycle; phosphorylated in response to DNA damage; contains characteristic motifs for degradation via the APC pathway; similar to Alk2p and to mammalian haspins
YIL011W	TIR3	65	8.43E-07	9+	333681	334273	593	2.71	ORF Verified	Cell wall mannoprotein of the Srp1p%2FTip1p family of serine-alanine-rich proteins; expressed under anaerobic conditions and required for anaerobic growth
YJR092W	BUD4	65	2.08E-12	10+	598649	602977	4329	2.34	ORF Verified	Protein involved in bud-site selection and required for axial budding pattern; localizes with septins to bud neck in mitosis and may constitute an axial landmark for next round of
YKL183W	LOT5	65	1.39E-06	11+	98580	99436	857	2.77	ORF Verified	Protein of unknown function; gene expression increases in cultures shifted to a lower
YOL069W	NUF2	65	1.59E-11	15+	198937	200393	1457	1.34	ORF Verified	Component of the evolutionarily conserved kinetochore-associated Ndc80 complex (Ndc80p-Nuf2p-Spc24p-Spc25p); involved in chromosome segregation, spindle checkpoint
YPR111W	DBF20	65	2.79E-05	16+	747275	749107	1833	1.29	ORF Verified	Ser/Thr kinase involved in late nuclear division, one of the mitotic exit network (MEN) proteins; necessary for the execution of cytokinesis
YDR146C	SWI5	66	1.99E-12	4-	748830	750342	1513	2.98	ORF Verified	Transcription factor that activates transcription of genes expressed at the M/G1 phase boundary and in G1 phase; localization to the nucleus occurs during G1 and appears to be
YDR389W	SAC7	66	NA	4+	1252003	1254467	2465	3.41	ORF Verified	GTPase activating protein (GAP) for Rho1p, involved in signaling to the actin cytoskeleton, null mutations suppress tor2 mutations and temperature sensitive mutations in actin;
YGR108W	CLB1	66	2.00E-12	7+	703395	705179	1785	3.19	ORF Verified	B-type cyclin involved in cell cycle progression; activates Cdc28p to promote the transition from G2 to M phase; accumulates during G2 and M, then targeted via a destruction box motif for ubiquitin-mediated degradation by the proteasome
YIL158W		66	2.00E-12	9+	46201	46881	681	3.28	ORF Uncharacterized	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the vacuole
YLR063W		66	6.11E-06	12+	264241	265449	1209	2.39	ORF Uncharacterized	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm; YLR063W is not an essential gene
YLR353W	BUD8	66	4.59E-12	12+	833879	836151	2273	2.84	ORF Verified	Protein involved in bud-site selection; diploid mutants display a unipolar budding pattern instead of the wild-type bipolar pattern, and bud at the proximal pole
YOR315W	SFG1	66	2.00E-12	15+	904761	905785	1025	3.85	ORF Verified	Nuclear protein, putative transcription factor required for growth of superficial pseudohyphae (which do not invade the agar substrate) but not for invasive pseudohyphal growth; may act together with Phd1p; potential Cdc28p substrate
YPL155C	KIP2	66	5.12E-11	16-	257693	259365	1673	2.82	ORF Verified	Kinesin-related motor protein involved in mitotic spindle positioning, stabilizes microtubules by targeting Bik1p to the plus end; Kip2p levels are controlled during the cell cycle
YBL029W		67	1.08E-06	2+	166135	167327	1193	1.32	ORF Uncharacterized	hypothetical protein
YBR138C		67	8.92E-12	2-	513636	515380	1745	1.41	ORF Uncharacterized	Cytoplasmic protein of unknown function, potentially phosphorylated by Cdc28p; YBR138C is not an essential gene

YBR242W		67	2.76E-07	2+	704512	705240	729	3.42	ORF Uncharacterized	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm and nucleus; YBR242W is not an essential gene
YFR039C		67	2.09E-07	6-	232013	233653	1641	3.16	ORF Uncharacterized	Putative protein of unknown function; YFR039C is not an essential gene
YLR131C	ACE2	67	2.31E-12	12-	405573	407021	1449	2.23	ORF Verified	Transcription factor that activates expression of early G1-specific genes, localizes to daughter cell nuclei after cytokinesis and delays G1 progression in daughters, localization is regulated by phosphorylation; potential Cdc28p substrate
YML034W	SRC1	67	2.92E-12	13+	210121	211417	1297	2.75	ORF Verified	Protein with a putative role in sister chromatid segregation, potentially phosphorylated by Cdc28p; green fluorescent protein (GFP)-fusion protein localizes to the nuclear periphery
YMR001C	CDC5	67	2.07E-12	13-	268885	271325	2441	3.51	ORF Verified	Polo-like kinase with similarity to Xenopus Plx1 and S. pombe Plp1p; found at bud neck, nucleus and SPBs; has multiple functions in mitosis and cytokinesis through
YMR001C-A		67	9.74E-12	13-	271357	271517	161	2.98	ORF Uncharacterized	Putative protein of unknown function
YPR119W	CLB2	67	2.06E-12	16+	771259	773443	2185	3.86	ORF Verified	B-type cyclin involved in cell cycle progression; activates Cdc28p to promote the transition from G2 to M phase; accumulates during G2 and M, then targeted via a destruction box motif for ubiquitin-mediated degradation by the proteasome
YDL074C	BRE1	68	NA	4-	324005	326221	2217	2.64	ORF Verified	E3 ubiquitin ligase for Rad6p, required for the ubiquitination of histone H2B, recruitment of Rad6p to promoter chromatin and subsequent methylation of histone H3 (on K4 and K79),
YMR132C	JLP2	68	2.80E-07	13-	534741	535605	865	1.2	ORF Uncharacterized	Protein of unknown function, contains sequence that closely resembles a J domain (typified by the E. coli DnaJ protein)
YMR183C	SSO2	68	2.83E-08	13-	626701	627869	1169	4.16	ORF Verified	Plasma membrane t-SNARE involved in fusion of secretory vesicles at the plasma membrane; syntaxin homolog that is functionally redundant with Sso1p
YOR025W	HST3	68	4.16E-12	15+	378201	379561	1361	2.83	ORF Verified	Member of the Sir2 family of NAD(+)-dependent protein deacetylases; involved along with Hst4p in telomeric silencing, cell cycle progression, radiation resistance, genomic stability
YPL141C		68	5.79E-12	16-	283517	285357	1841	3.4	ORF Uncharacterized	Putative protein kinase; similar to Kin4p; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm; YPL141C is not an essential gene
YHR023W	MYO1	69	5.84E-11	8+	151641	155521	3881	1.9	ORF Verified	Type II myosin heavy chain, required for wild-type cytokinesis and cell separation; localizes to the actomyosin ring; binds to myosin light chains Mlc1p and Mlc2p through its IQ1 and
YJL051W		69	1.95E-12	10+	340113	342169	2057	2.97	ORF Uncharacterized	Bud tip localized protein of unknown function; mRNA is targeted to the bud by a She2p dependent transport system; mRNA is cell cycle regulated via Fkh2p, peaking in G2/M phase; null mutant displays increased levels of spontaneous Rad52 foci
YOR058C	ASE1	69	4.77E-12	15-	434573	436437	1865	1.71	ORF Verified	Mitotic spindle midzone localized microtubule-associated protein (MAP) family member; required for spindle elongation and stabilization; undergoes cell cycle-regulated degradation by anaphase promoting complex; potential Cdc28p substrate
YOR104W	PIN2	69	9.09E-07	15+	517625	518857	1233	2.97	ORF Verified	Protein that induces appearance of %5BPIN+%5D prion when overproduced
YOR105W		69	1.32E-06	15+	517625	518857	1233	2.97	ORF Dubious	hypothetical protein (adjacent to YOR104W)
YOR346W	REV1	69	1.73E-09	15+	981665	984889	3225	2.32	ORF Verified	Deoxycytidyl transferase, forms a complex with the subunits of DNA polymerase zeta, Rev3p and Rev7p; involved in repair of abasic sites in damaged DNA
YBL005W	PDR3	70	5.60E-09	2+	217512	220608	3097	2.06	ORF Verified	Transcriptional activator of the pleiotropic drug resistance network, regulates expression of ATP-binding cassette (ABC) transporters through binding to cis-acting sites known as
YIL106W	MOB1	70	5.09E-11	9+	166521	167497	977	2.77	ORF Verified	Component of the mitotic exit network; associates with and is required for the activation and Cdc15p-dependent phosphorylation of the Dbf2p kinase; required for cytokinesis and cell separation; component of the CCR4 transcriptional complex
YKL130C	SHE2	70	1.35E-10	11-	195464	196056	593	2.68	ORF Verified	RNA-binding protein that binds specific mRNAs and interacts with She3p; part of the mRNA localization machinery that restricts accumulation of certain proteins to the bud

YLR190W	MMR1	70	2.05E-12	12+	534961	536953	1993	3.91	ORF Verified	Phosphorylated protein of the mitochondrial outer membrane, localizes only to mitochondria of the bud; interacts with Myo2p to mediate mitochondrial distribution to buds; mRNA is targeted to the bud via the transport system involving She2p
YMR102C		70	3.90E-08	13-	469741	472605	2865	2.73	ORF Uncharacterized	Protein of unknown function; transcription is activated by paralogous transcription factors Yrm1p and Yrr1p along with genes involved in multidrug resistance; mutant shows increased resistance to azoles; YMR102C is not an essential gene
YOR056C	NOB1	70	5.15E-07	15-	430285	431701	1417	3.5	ORF Verified	Essential nuclear protein involved in proteasome maturation and synthesis of 40S ribosomal subunits; required for cleavage of the 20S pre-rRNA to generate the mature 18S
YOR064C	YNG1	70	1.31E-06	15-	446005	446757	753	2.13	ORF Verified	Subunit of the NuA3 histone acetyltransferase complex that acetylates histone H3; contains PHD finger domain that interacts with methylated histone H3, has similarity to the
YDR514C		71	1.46E-06	4-	1471511	1473023	1513	2.3	ORF Uncharacterized	hypothetical protein
YHL028W	WSC4	71	6.27E-11	8+	48729	50273	1545	2.94	ORF Verified	ER membrane protein involved in the translocation of soluble secretory proteins and insertion of membrane proteins into the ER membrane; exhibits functional overlap with
YNL172W	APC1	71	3.01E-08	14+	311241	316081	4841	1.99	ORF Verified	Largest subunit of the Anaphase-Promoting Complex/Cyclosome (APC/C), which is a ubiquitin-protein ligase required for degradation of anaphase inhibitors, including mitotic
YOL124C	TRM11	71	6.53E-08	15-	85477	86781	1305	3.3	ORF Verified	Catalytic subunit of an adoMet-dependent tRNA methyltransferase complex (Trm11p-Trm112p), required for the methylation of the guanosine nucleotide at position 10 (m2G10) in tRNAs; contains a THUMP domain and a methyltransferase domain
YBR267W	REI1	72	3.54E-07	2+	739832	741120	1289	3.74	ORF Verified	Protein of unknown function involved in bud growth in the mitotic signaling network; proposed negative regulator of Swe1p and Gin4p; contains dispersed C2H2 zinc finger
YGR145W	ENP2	72	9.63E-07	7+	781731	783723	1993	2.73	ORF Verified	Essential nucleolar protein of unknown function; contains WD repeats, interacts with Mpp10p and Bfr2p, and has homology to Spb1p
YKL078W	DHR2	72	1.29E-06	11+	288468	290668	2201	1.62	ORF Verified	Predominantly nucleolar DEAH-box RNA helicase, required for 18S rRNA synthesis
YLL028W	TPO1	72	5.37E-11	12+	84681	86913	2233	4.41	ORF Verified	Polyamine transporter that recognizes spermine, putrescine, and spermidine; catalyzes uptake of polyamines at alkaline pH and excretion at acidic pH; phosphorylation enhances
YML064C	TEM1	72	2.07E-09	13-	145181	145957	777	3.21	ORF Verified	GTP-binding protein of the ras superfamily involved in termination of M-phase; controls actomyosin and septin dynamics during cytokinesis
YMR032W	HOF1	72	5.84E-12	13+	335209	337177	1969	1.52	ORF Verified	Bud neck-localized, SH3 domain-containing protein required for cytokinesis; regulates actomyosin ring dynamics and septin localization; interacts with the formins, Bni1p and
YNL024C		72	2.33E-06	14-	587246	587854	609	1.55	ORF Uncharacterized	Putative protein of unknown function with seven beta-strand methyltransferase motif; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm; YNL024C is not an essential gene
YNL151C	RPC31	72	1.49E-06	14-	347669	348581	913	3.79	ORF Verified	RNA polymerase III subunit C31; contains HMG-like C-terminal domain
YOR313C	SPS4	72	4.97E-10	15-	901741	903397	1657	0.61	ORF Verified	Protein whose expression is induced during sporulation; not required for sporulation; heterologous expression in E. coli induces the SOS response that senses DNA damage
YPR156C	TPO3	72	1.62E-11	16-	839447	840071	625	4.05	ORF Verified	Polyamine transport protein specific for spermine; localizes to the plasma membrane; member of the major facilitator superfamily
YCR024C-A	PMP1	73	2.75E-07	3-	162653	163261	609	5.58	ORF Verified	May regulate plasma membrane H(+)-ATPase; Proteolipid associated with plasma
YCR024C-B		73	4.40E-07	3-	162653	163261	609	5.58	ORF Uncharacterized	Putative protein of unknown function; identified by expression profiling and mass spectrometry
YDL063C		73	4.76E-07	4-	338469	340221	1753	2.85	ORF Uncharacterized	hypothetical protein
YIL122W	POG1	73	5.15E-08	9+	130489	131737	1249	1.61	ORF Verified	Putative transcriptional activator that promotes recovery from pheromone induced arrest; inhibits both alpha-factor induced G1 arrest and repression of CLN1 and CLN2 via SCB/MCB promoter elements; potential Cdc28p substrate; SBF regulated

YJR003C		73	3.09E-08	10	-	440869	442461	1593	3.01	ORF Uncharacterized	Putative protein of unknown function; the authentic, non-tagged protein is detected in highly purified mitochondria in high-throughput studies
YKR021W	ALY1	73	4.79E-09	11	+	478820	481748	2929	2.57	ORF Uncharacterized	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm
YKR081C	RPF2	73	9.06E-08	11	-	591136	592200	1065	3.31	ORF Verified	Essential protein involved in the processing of pre-rRNA and the assembly of the 60S ribosomal subunit; interacts with ribosomal protein L11; localizes predominantly to the
YLR003C		73	2.37E-08	12	-	156765	157757	993	3.25	ORF Uncharacterized	Putative protein of unknown function that may participate in DNA replication; green fluorescent protein (GFP)-fusion protein is localized to the nucleus; YLR003C is not an essential gene
YNR004W		73	5.19E-07	14	+	635930	636746	817	1.02	ORF Uncharacterized	Putative protein of unknown function; haploid disruptant exhibits slow growth rate on glucose-minimal medium at 15 C
YPR157W		73	1.98E-11	16	+	841211	842491	1281	1	ORF Uncharacterized	Putative protein of unknown function
YDR020C		74	2.75E-06	4	-	485405	486557	1153	2.71	ORF Uncharacterized	Predicted protein shares weak similarity with uridine kinases and with phosphoribokinases; null mutant suppresses <i>dst1</i> delta sensitivity for 6-azauracil
YHR148W	IMP3	74	6.59E-07	8	+	393521	394321	801	2.55	ORF Verified	Component of the SSU processome, which is required for pre-18S rRNA processing, essential protein that interacts with Mpp10p and mediates interactions of Imp4p and
YLR057W		74	2.95E-09	12	+	255265	257889	2625	3.01	ORF Uncharacterized	Putative protein of unknown function; YLR050C is not an essential gene
YNL056W	OCA2	74	2.17E-07	14	+	517234	517866	633	3.54	ORF Verified	Putative protein with similarity to predicted tyrosine phosphatases Oca1p and Siw14p; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm; YNL056W is not
YNL058C		74	4.58E-10	14	-	516070	516766	697	4.11	ORF Uncharacterized	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the vacuole; YNL058C is not an essential gene
YNL141W	AAH1	74	7.73E-07	14	+	359601	360361	761	4.12	ORF Verified	Adenine deaminase (adenine aminohydrolase), involved in purine salvage and nitrogen
YNL308C	KRI1	74	1.10E-06	14	-	54141	55925	1785	2.96	ORF Verified	Essential nucleolar protein required for 40S ribosome biogenesis; physically and
YOR101W	RAS1	74	1.23E-06	15	+	515145	516345	1201	3.36	ORF Verified	GTPase involved in G-protein signaling in the adenylate cyclase activating pathway, plays a role in cell proliferation; localized to the plasma membrane; homolog of mammalian RAS
YPL058C	PDR12	74	1.06E-08	16	-	445695	450455	4761	4.74	ORF Verified	Plasma membrane ATP-binding cassette (ABC) transporter, weak-acid-inducible multidrug transporter required for weak organic acid resistance; induced by sorbate and benzoate and regulated by War1p; mutants exhibit sorbate hypersensitivity
YBR255W		75	NA	2	+	724472	726576	2105	1.8	ORF Uncharacterized	Protein of unknown function, required for normal growth rate at 15 degrees C; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm in a punctate pattern
YER031C	YPT31	75	9.11E-07	5	-	213917	214773	857	4.37	ORF Verified	GTPase of the Ypt/Rab family, very similar to Ypt32p; involved in the exocytic pathway; mediates intra-Golgi traffic or the budding of post-Golgi vesicles from the trans-Golgi
YER140W		75	2.35E-08	5	+	451529	453137	1609	2.04	ORF Uncharacterized	Putative protein of unknown function; the authentic, non-tagged protein is detected in highly purified mitochondria in high-throughput studies
YGL116W	CDC20	75	2.20E-11	7	+	289675	291707	2033	2.48	ORF Verified	Cell-cycle regulated activator of anaphase-promoting complex/cyclosome (APC/C), which is required for metaphase/anaphase transition; directs ubiquitination of mitotic cyclins, Pds1p, and other anaphase inhibitors; potential Cdc28p substrate

YIL092W		75	2.93E-06	9+	190881	193425	2545	-0.64	ORF Uncharacterized	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm and to the nucleus
YLR363W-A		75	2.75E-07	12+	853447	854015	569	2.35	ORF Uncharacterized	hypothetical protein
YML119W		75	8.73E-12	13+	30561	31393	833	3.48	ORF Uncharacterized	Putative protein of unknown function; YML119W is not an essential gene; potential Cdc28p substrate
YOL014W		75	1.30E-09	15+	299497	300217	721	2.37	ORF Uncharacterized	Putative protein of unknown function
YOL158C	ENB1	75	5.95E-06	15-	19853	21109	1257	2.8	ORF Verified	Endosomal ferric enterobactin transporter, expressed under conditions of iron deprivation; member of the major facilitator superfamily; expression is regulated by Rcs1p and affected
YBL004W	UTP20	76	2.45E-07	2+	233672	234768	1097	3.6	ORF Verified	Component of the small-subunit (SSU) processome, which is involved in the biogenesis of
YDR324C	UTP4	76	3.19E-07	4-	1114655	1116711	2057	3.8	ORF Verified	Nucleolar protein, component of the small subunit (SSU) processome containing the U3 snoRNA that is involved in processing of pre-18S rRNA
YGR177C	ATF2	76	2.03E-11	7-	848815	850495	1681	2.83	ORF Verified	Alcohol acetyltransferase, may play a role in steroid detoxification; forms volatile esters during fermentation, which is important in brewing
YLR276C	DBP9	76	1.61E-07	12-	695221	696917	1697	3.61	ORF Verified	ATP-dependent RNA helicase of the DEAD-box family involved in biogenesis of the 60S
YMR009W	ADI1	76	4.36E-07	13+	284057	284585	529	2.8	ORF Verified	Acireductone dioxygenase involved in the methionine salvage pathway; ortholog of human MTCBP-1; transcribed with YMR010W and regulated post-transcriptionally by RNase III (Rnt1p) cleavage; ADI1 mRNA is induced in heat shock conditions
YMR294W	JNM1	76	1.21E-06	13+	856961	858081	1121	1.41	ORF Verified	Component of the yeast dynactin complex, consisting of Nip100p, Jnm1p, and Arp1p; required for proper nuclear migration and spindle partitioning during mitotic anaphase B
YOL144W	NOP8	76	1.09E-06	15+	53057	54481	1425	2.19	ORF Verified	Nucleolar protein required for 60S ribosomal subunit biogenesis
YOR023C	AHC1	76	NA	15-	376013	376229	217	2.05	ORF Verified	Subunit of the Ada histone acetyltransferase complex, required for structural integrity of the
YOR319W	HSH49	76	9.40E-07	15+	912793	913569	777	2.49	ORF Verified	U2-snRNP associated splicing factor with similarity to the mammalian splicing factor SAP49; proposed to function as a U2-snRNP assembly factor along with Hsh155p and binding partner Cus1p; contains two RNA recognition motifs (RRM)
YPR149W	NCE102	76	1.08E-09	16+	829731	830507	777	5.78	ORF Verified	Protein of unknown function; contains transmembrane domains; involved in secretion of proteins that lack classical secretory signal sequences; component of the detergent-
YAL025C	MAK16	77	8.86E-07	1-	100059	101171	1113	3.83	ORF Verified	Essential nuclear protein, constituent of 66S pre-ribosomal particles; required for normal concentration of free 60S ribosomal subunits; required for maintenance of M1 satellite double-stranded RNA of the L-A virus
YAL059W	ECM1	77	1.76E-07	1+	36545	37097	553	2.77	ORF Verified	Protein of unknown function, localized in the nucleoplasm and the nucleolus, genetically interacts with MTR2 in 60S ribosomal protein subunit export
YFR001W	LOC1	77	1.54E-06	6+	149097	149561	465	2.53	ORF Verified	Nuclear protein involved in asymmetric localization of ASH1 mRNA; binds double-stranded RNA in vitro; constituent of 66S pre-ribosomal particles
YGR068C		77	6.15E-06	7-	624983	627119	2137	2.09	ORF Uncharacterized	Putative protein of unknown function; YGR068C is not an essential gene.
YLR297W		77	2.27E-09	12+	723921	724545	625	3.73	ORF Uncharacterized	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the vacuole; YLR297W is not an essential gene
YOL070C		77	9.79E-09	15-	197509	198477	969	3.77	ORF Verified	Protein of unknown function; may interact with ribosomes, based on co-purification experiments; green fluorescent protein (GFP)-fusion protein localizes to the cell periphery,
YPL183C		77	NA	16-	199773	201357	1585	3.24	ORF Uncharacterized	Cytoplasmic protein of unknown function

YPR112C	MRD1	77	5.95E-08	16-	749359	751951	2593	3.14	ORF Verified	Essential conserved protein that associates with 35S precursor rRNA and is required for its initial processing at the A(0)-A(2) cleavage sites, shows partial nucleolar localization,
YDL153C	SAS10	78	2.34E-07	4-	181405	183037	1633	3.37	ORF Verified	Component of the small (ribosomal) subunit (SSU) processosome required for pre-18S rRNA processing; essential nucleolar protein that, when overproduced, disrupts silencing
YDR083W	RRP8	78	2.96E-07	4+	613178	617482	4305	-0.38	ORF Verified	Protein involved in rRNA processing; involved in pre-rRNA cleavage at site A2; mutation is synthetically lethal with a gar1 mutation
YDR183C-A		78	1.10E-06	4-	827367	830407	3041	-0.73	ORF Dubious	hypothetical protein overlapping with ATC1
YER139C		78	2.37E-08	5-	450005	451333	1329	1.79	ORF Uncharacterized	Putative protein of unknown function; YER139C has been shown to be required for growth at high temperatures; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm
YHR046C	INM1	78	NA	8-	197477	198333	857	2.89	ORF Verified	Inositol monophosphatase, involved in biosynthesis of inositol and in phosphoinositide second messenger signaling; INM1 expression increases in the presence of inositol and decreases upon exposure to antibipolar drugs lithium and valproate
YNL110C	NOP15	78	1.40E-06	14-	417877	418525	649	3.07	ORF Verified	Constituent of 66S pre-ribosomal particles, involved in 60S ribosomal subunit biogenesis; localizes to both nucleolus and cytoplasm
YOR262W		78	6.78E-07	15+	817241	818361	1121	2.73	ORF Uncharacterized	Cytoplasmic protein of unknown function; essential gene with similarity to YLR243W; contains an ATP/GTP binding site motif
YOR274W	MOD5	78	7.41E-08	15+	837665	838881	1217	2.2	ORF Verified	Delta 2-isopentenyl pyrophosphate:tRNA isopentenyl transferase, required for biosynthesis of the modified base isopentenyladenosine in mitochondrial and cytoplasmic tRNAs; gene
YAR018C	KIN3	79	5.85E-11	1-	170403	171707	1305	2.15	ORF Verified	Nonessential protein kinase with unknown cellular role
YDR033W	MRH1	79	2.77E-08	4+	507810	509578	1769	5.95	ORF Verified	Protein that localizes primarily to the plasma membrane, also found at the nuclear envelope; the authentic, non-tagged protein is detected in mitochondria in a
YGR143W	SKN1	79	2.54E-12	7+	774947	777627	2681	3.05	ORF Verified	Protein involved in sphingolipid biosynthesis; type II membrane protein with similarity to
YHR151C		79	3.50E-07	8-	399349	401005	1657	2.42	ORF Uncharacterized	Putative protein of unknown function
YHR152W	SPO12	79	1.27E-10	8+	401337	402049	713	3.2	ORF Verified	Nucleolar protein of unknown function, positive regulator of exit from mitosis; involved in regulating the release of Cdc14p from the nucleolus in early anaphase; proposed to play
YKL129C	MYO3	79	9.43E-08	11-	196360	199960	3601	1.42	ORF Verified	One of two type I myosins; localizes to actin cortical patches; deletion of MYO3 has little effect on growth, but myo3 myo5 double deletion causes severe defects in growth and
YOR001W	RRP6	79	1.56E-06	15+	326809	328985	2177	2.86	ORF Verified	Exonuclease component of the nuclear exosome; contributes to the quality-control system that retains and degrades aberrant mRNAs in the nucleus
YBL067C	UBP13	80	1.82E-05	2-	89493	93645	4153	-0.49	ORF Verified	Putative ubiquitin carboxyl-terminal hydrolase, ubiquitin-specific protease that cleaves
YBR092C	PHO3	80	2.13E-10	2-	427659	429115	1457	5.23	ORF Verified	Constitutively expressed acid phosphatase similar to Pho5p; brought to the cell surface by transport vesicles; hydrolyzes thiamin phosphates in the periplasmic space, increasing cellular thiamin uptake; expression is repressed by thiamin
YBR139W		80	1.23E-06	2+	515656	516992	1337	3.7	ORF Verified	hypothetical protein
YCR090C		80	7.62E-07	3-	272293	272877	585	2.94	ORF Uncharacterized	hypothetical protein
YDR308C	SRB7	80	6.47E-07	4-	1077911	1078463	553	2.45	ORF Verified	RNA polymerase II holoenzyme component
YGL162W	SUT1	80	NA	7+	198019	199059	1041	1.79	ORF Verified	Transcription factor of the Zn[II]2Cys6 family involved in sterol uptake; involved in induction of hypoxic gene expression
YGR092W	DBF2	80	9.32E-10	7+	668147	670051	1905	2.91	ORF Verified	Ser/Thr kinase involved in transcription and stress response; functions as part of a network of genes in exit from mitosis; localization is cell cycle regulated; activated by Cdc15p

YMR031C		80	1.80E-11	13-	332381	334805	2425	2.54	ORF Uncharacterized	Protein of unknown function with similarity to Ykl050cp and Uso1p; the authentic, non-tagged protein is detected in a phosphorylated state in highly purified mitochondria in high-throughput studies; YMR031C is not an essential gene
YDR465C	RMT2	81	3.12E-07	4-	1393303	1394615	1313	4.06	ORF Verified	Arginine methyltransferase; ribosomal protein L12 is a substrate
YGR070W	ROM1	81	4.07E-07	7+	627795	630891	3097	1.7	ORF Verified	GDP/GTP exchange protein (GEP) for Rho1p; mutations are synthetically lethal with mutations in rom2, which also encodes a GEP
YOR229W	WTM2	81	3.77E-11	15+	768337	769985	1649	2.29	ORF Verified	Transcriptional repressor involved in regulation of meiosis and silencing; contains WD
YOR273C	TPO4	81	1.09E-06	15-	834349	836493	2145	2.86	ORF Verified	Polyamine transport protein, recognizes spermine, putrescine, and spermidine; localizes to the plasma membrane; member of the major facilitator superfamily
YPL148C	PPT2	81	7.33E-07	16-	272157	272909	753	1.23	ORF Verified	Phosphopantetheine:protein transferase (PPTase), activates mitochondrial acyl carrier protein (Acp1p) by phosphopantetheinylation
YDR198C	RKM2	82	2.72E-07	4-	852671	853975	1305	2.49	ORF Verified	Ribosomal protein lysine methyltransferase, responsible for epsilon-trimethylation of the lysine residue at position 10 of Rpl12Ap and Rpl12Bp
YGR230W	BNS1	82	8.14E-12	7+	951771	952395	625	2.19	ORF Verified	Protein with some similarity to Spo12p; overexpression bypasses need for Spo12p, but not
YJL077W-B		82	3.59E-07	10+	293545	294729	1185	2.41	ORF Uncharacterized	Putative protein of unknown function; identified by gene-trapping, microarray-based expression analysis, and genome-wide homology searching
YNL032W	SIW14	82	1.37E-06	14+	574377	575297	921	3.01	ORF Verified	Tyrosine phosphatase that plays a role in actin filament organization and endocytosis;
YOR049C	RCB1	82	1.07E-07	15-	422557	423933	1377	1.79	ORF Verified	Suppressor of sphingoid long chain base (LCB) sensitivity of an LCB-lyase mutation; putative integral membrane transporter or flippase that may transport LCBs from the cytoplasmic side toward the extracytoplasmic side of the membrane
YAL022C	FUN26	83	1.39E-06	1-	108859	110451	1593	3.93	ORF Verified	Nucleoside transporter with broad nucleoside selectivity; localized to intracellular
YCR095W-A		83	3.79E-08	3+	289545	291057	1513	0.63	ORF Uncharacterized	Putative protein of unknown function
YER053C-A		83	4.85E-08	5-	260733	261077	345	2.82	ORF Uncharacterized	hypothetical protein
YHL026C		83	2.52E-12	8-	53133	54237	1105	2.17	ORF Uncharacterized	Putative protein of unknown function; YHL026C is not an essential gene; in 2005 the start site was moved 141 nt upstream (see Locus History)
YCR042C	TAF2	84	5.67E-12	3-	201101	205405	4305	2.21	ORF Verified	TFIID subunit (150 kDa), involved in RNA polymerase II transcription initiation
YLR254C	NDL1	84	2.14E-10	12-	644357	645061	705	1.78	ORF Verified	Homolog of nuclear distribution factor NudE, NUDEL; interacts with Pac1p and regulates dynein targeting to microtubule plus ends
YDL039C	PRM1	85	1.26E-06	4-	381981	384845	2865	2.62	ORF Verified	Pheromone-regulated protein, predicted to have one transmembrane segment; promoter contains Gcn4p binding elements
YER037W	PHM8	85	6.39E-07	5+	225825	227001	1177	2.82	ORF Verified	Protein of unknown function, expression is induced by low phosphate levels and by
YFL050C	ALR2	85	9.56E-09	6-	33149	35845	2697	1.27	ORF Verified	Probable Mg(2+) transporter; overexpression confers increased tolerance to Al(3+) and
YJL079C	PRY1	85	8.15E-08	10-	289645	290845	1201	4.44	ORF Verified	Protein of unknown function, has similarity to Pry2p and Pry3p and to the plant PR-1 class of pathogen related proteins
YMR253C		85	1.29E-07	13-	775789	777229	1441	2.06	ORF Uncharacterized	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm in a punctate pattern; YMR253C is not an essential gene
YNL298W	CLA4	85	7.30E-07	14+	69225	71065	1841	3.29	ORF Verified	Cdc42p activated signal transducing kinase of the PAK (p21-activated kinase) family, involved in septin ring assembly and cytokinesis; directly phosphorylates septins Cdc3p and Cdc10p; other yeast PAK family members are Ste20p and Skm1p

YAL040C	CLN3	86	7.85E-08	1-	65611	67843	2233	4.59	ORF Verified	G1 cyclin involved in cell cycle progression; activates Cdc28p kinase to promote the G1 to S phase transition; plays a role in regulating transcription of the other G1 cyclins, CLN1 and CLN2; regulated by phosphorylation and proteolysis
YBR200W	BEM1	86	9.93E-09	2+	620816	622680	1865	2.91	ORF Verified	Protein containing SH3-domains, involved in establishing cell polarity and morphogenesis; functions as a scaffold protein for complexes that include Cdc24p, Ste5p, Ste20p, and
YDL138W	RGT2	86	6.39E-11	4+	213185	215129	1945	2.37	ORF Verified	Plasma membrane glucose receptor, highly similar to Snf3p; both Rgt2p and Snf3p serve as transmembrane glucose sensors generating an intracellular signal that induces
YIL167W	SDL1	86	4.81E-07	9+	28961	30177	1217	1.18	pseudogene	hypothetical protein; constitutes an ORF with YIL168W
YBR202W	MCM7	87	1.37E-11	2+	625704	627288	1585	2.76	ORF Verified	Component of the hexameric MCM complex, which is important for priming origins of DNA replication in G1 and becomes an active ATP-dependent helicase that promotes DNA melting and elongation when activated by Cdc7p-Dbf4p in S-phase
YIL168W		87	6.49E-07	9+	28961	30177	1217	1.18	pseudogene	L-serine dehydratase goes together with SDL1
YMR233W		87	1.56E-06	13+	739169	740009	841	1.75	ORF Verified	uncharacterized ORF
YNL160W	YGP1	87	3.36E-12	14+	336497	337825	1329	5.52	ORF Verified	Cell wall-related secretory glycoprotein; induced by nutrient deprivation-associated growth arrest and upon entry into stationary phase; may be involved in adaptation prior to
YBR085C-A		88	4.99E-07	2-	418715	419251	537	4.04	ORF Uncharacterized	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm and to the nucleus
YGL201C	MCM6	88	4.90E-09	7-	118031	120967	2937	2.57	ORF Verified	Protein involved in DNA replication; component of the Mcm2-7 hexameric complex that binds chromatin as a part of the pre-replicative complex
YJL084C	ALY2	88	5.84E-07	10-	275237	278029	2793	2.12	ORF Verified	Cytoplasmic protein of unknown function that interacts with the cyclin Pcl7p; phosphorylated in vitro by the cyclin-CDK complex, Pcl7p-Pho85p; identified as a potential Cdc28p substrate; mRNA is cell cycle regulated, peaking in M phase
YLR237W	THI7	88	2.61E-07	12+	612305	614145	1841	2.91	ORF Verified	Plasma membrane transporter responsible for the uptake of thiamine, member of the major facilitator superfamily of transporters; mutation of human ortholog causes thiamine-
YOR127W	RGA1	88	1.54E-07	15+	561529	563905	2377	3.01	ORF Verified	GTPase-activating protein for the polarity-establishment protein Cdc42p; implicated in control of septin organization, pheromone response, and haploid invasive growth
YOR228C		88	7.59E-07	15-	766741	767997	1257	1.79	ORF Verified	Protein of unknown function, localized to the mitochondrial outer membrane
YDR493W	FMP36	89	5.43E-07	4+	1436139	1436523	385	2.22	ORF Uncharacterized	The authentic, non-tagged protein was localized to the mitochondria
YJL044C	GYP6	89	7.88E-09	10-	358093	359141	1049	2.95	ORF Verified	GTPase-activating protein (GAP) for the yeast Rab family member, Ypt6p; involved in vesicle mediated protein transport
YDL044C	MTF2	90	3.05E-07	4-	374077	375629	1553	0.91	ORF Verified	Mitochondrial matrix protein that interacts with an N-terminal region of mitochondrial RNA polymerase (Rpo41p) and couples RNA processing and translation to transcription
YJL157C	FAR1	90	6.61E-09	10-	123773	126277	2505	3.06	ORF Verified	Cyclin-dependent kinase inhibitor that mediates cell cycle arrest in response to pheromone; also forms a complex with Cdc24p, Ste4p, and Ste18p that may specify the direction of polarized growth during mating; potential Cdc28p substrate
YKL209C	STE6	90	2.63E-07	11-	42421	45261	2841	2.31	ORF Verified	ATP-binding cassette (ABC) transporter required for the export of a-factor, catalyzes ATP hydrolysis coupled to a-factor transport, contains 12 transmembrane domains and two ATP
YNL329C	PEX6	90	3.56E-05	14-	19525	22621	3097	2.45	ORF Verified	AAA-peroxin that heterodimerizes with AAA-peroxin Pex6p and participates in the recycling of peroxisomal signal receptor Pex5p from the peroxisomal membrane to the cytosol
YBL023C	MCM2	91	1.24E-10	2-	174939	177579	2641	2.55	ORF Verified	Protein involved in DNA replication; component of the Mcm2-7 hexameric complex that binds chromatin as a part of the pre-replicative complex
YDR191W	HST4	92	6.81E-12	4+	842315	843219	905	1.29	ORF Verified	Member of the Sir2 family of NAD(+)-dependent protein deacetylases; involved along with Hst3p in silencing at telomeres, cell cycle progression, radiation resistance, genomic
YHR005C	GPA1	92	6.40E-10	8-	113421	114997	1577	3.2	ORF Verified	GTP-binding alpha subunit of the heterotrimeric G protein that couples to pheromone receptors; negatively regulates the mating pathway by sequestering G(beta)gamma and by triggering an adaptive response; activates Vps34p at the endosome

YOL154W	ZPS1	92	1.13E-06	15+	34449	35417	969	1.81	ORF Verified	Putative GPI-anchored protein; transcription is induced under low-zinc conditions, as mediated by the Zap1p transcription factor, and at alkaline pH
YEL032W	MCM3	93	5.87E-11	5+	86889	89393	2505	2.88	ORF Verified	Protein involved in DNA replication; component of the Mcm2-7 hexameric complex that binds chromatin as a part of the pre-replicative complex
YLR274W	MCM5	93	3.00E-12	12+	691529	693857	2329	2.78	ORF Verified	Component of the hexameric MCM complex, which is important for priming origins of DNA replication in G1 and becomes an active ATP-dependent helicase that promotes DNA melting and elongation when activated by Cdc7p-Dbf4p in S-phase
YNL146C-A		93	2.93E-06	14-	351157	351757	601	0.27	ORF Uncharacterized	Putative protein of unknown function
YOR066W		93	2.27E-12	15+	450097	451145	1049	3.5	ORF Uncharacterized	Protein of unknown function; potential Cdc28p substrate; YOR066W is not an essential gene
YHR075C	PPE1	94	NA	8-	248460	249684	1225	1.37	ORF Verified	Protein with carboxyl methyl esterase activity that may have a role in demethylation of the phosphoprotein phosphatase catalytic subunit; also identified as a small subunit
YOR126C	IAH1	94	1.45E-08	15-	559917	560709	793	1.13	ORF Verified	Isoamyl acetate-hydrolyzing esterase, required in balance with alcohol acetyltransferase to maintain optimal amounts of isoamyl acetate, which is particularly important in sake
YDL117W	CYK3	95	1.42E-10	4+	248305	251137	2833	2.94	ORF Verified	SH3-domain protein located in the mother-bud neck and the cytokinetic actin ring; mutant phenotype and genetic interactions suggest a role in cytokinesis
YKL185W	ASH1	95	2.40E-10	11+	94324	95940	1617	4.23	ORF Verified	Zinc-finger inhibitor of HO transcription; mRNA is localized and translated in the distal tip of anaphase cells, resulting in accumulation of Ash1p in daughter cell nuclei and inhibition of
YNL188W	KAR1	95	1.15E-06	14+	286297	287497	1201	2.03	ORF Verified	Essential protein involved in karyogamy during mating and in spindle pole body duplication during mitosis, localizes to the half-bridge of the spindle pole body, interacts with Spc72p
YPL061W	ALD6	95	2.14E-08	16+	432547	434147	1601	4.99	ORF Verified	Cytosolic aldehyde dehydrogenase, activated by Mg2+ and utilizes NADP+ as the preferred coenzyme; required for conversion of acetaldehyde to acetate; constitutively expressed; locates to the mitochondrial outer surface upon oxidative stress
YPL158C		95	1.23E-09	16-	252853	254365	1513	2.59	ORF Uncharacterized	Hypothetical protein
YBR054W	YRO2	96	2.14E-12	2+	342768	344312	1545	4.44	ORF Verified	Putative protein of unknown function; the authentic, non-tagged protein is detected in a phosphorylated state in highly purified mitochondria in high-throughput studies;
YJL159W	HSP150	96	1.87E-07	10+	120409	121833	1425	6.05	ORF Verified	O-mannosylated heat shock protein that is secreted and covalently attached to the cell wall via beta-1,3-glucan and disulfide bridges; required for cell wall stability; induced by heat
YOR018W	ROD1	96	1.33E-07	15+	366817	366993	177	0.77	ORF Verified	Membrane protein; overexpression confers resistance to the GST substrate o-dinitrobenzene as well as to zinc and calcium; contains 2 PY motifs, which are required for
YDL179W	PCL9	97	5.06E-09	4+	138217	139225	1009	2.68	ORF Verified	Cyclin, forms a functional kinase complex with Pho85p cyclin-dependent kinase (Cdk), expressed in late M/early G1 phase, activated by Swi5p
YGR042W		98	NA						ORF Uncharacterized	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to both the cytoplasm and the nucleus
YJL194W	CDC6	98	3.39E-12	10+	69313	70289	977	2.32	ORF Verified	Essential ATP-binding protein required for DNA replication, component of the pre-replicative complex (pre-RC) which requires ORC to associate with chromatin and is in turn required for Mcm2-7p DNA association; homologous to <i>S. pombe</i> Cdc18p
YLR273C	PIG1	98	4.29E-12	12-	689085	691253	2169	1.63	ORF Verified	Putative targeting subunit for the type-1 protein phosphatase Glc7p that tethers it to the
YBR083W	TEC1	99	1.86E-08	2+	409127	410679	1553	2.89	ORF Verified	Transcription factor required for full Ty1 expression, Ty1-mediated gene activation, and haploid invasive and diploid pseudohyphal growth; TEA%2FATTS DNA-binding domain
YBR157C	ICS2	99	4.31E-10	2-	553644	554428	785	2.83	ORF Verified	Protein of unknown function; null mutation does not confer any obvious defects in growth, spore germination, viability, or carbohydrate utilization
YDR180W	SCC2	99	NA	4+	825243	825747	505	1.27	ORF Verified	Subunit of cohesin loading factor (Scc2p-Scc4p), a complex required for the loading of cohesin complexes onto chromosomes; involved in establishing sister chromatid cohesion

YER150W	SPI1	99	8.84E-10	5+	468345	468841	497	2.63	ORF Verified	GPI-anchored, serine/threonine rich cell wall protein of unknown function; basal expression requires Msn2p/Msn4p; expression is induced under conditions of stress and during the
YGR222W	PET54	99	NA	7+	939675	939955	281	0.69	ORF Verified	Mitochondrial translational activator specific for the COX3 mRNA, acts together with Pet122p and Pet494p; also required for splicing of the COX1 intron AI5 beta; located in the
YKL062W	MSN4	99	4.22E-07	11+	322876	324572	1697	3.38	ORF Verified	Transcriptional activator related to Msn2p; activated in stress conditions, which results in translocation from the cytoplasm to the nucleus; binds DNA at stress response elements of responsive genes, inducing gene expression
YNL046W		99	4.12E-08	14+	542594	542954	361	1.91	ORF Uncharacterized	uncharacterized ORF
YNL328C	MDJ2	99	3.24E-08						ORF Verified	Constituent of the mitochondrial import motor associated with the presequence translocase; function overlaps with that of Pam18p; stimulates the ATPase activity of
YOL101C	IZH4	99	1.07E-07	15-	126949	127965	1017	1.58	ORF Verified	Membrane protein involved in zinc metabolism, member of the four-protein IZH family, expression induced by fatty acids and altered zinc levels; deletion reduces sensitivity to excess zinc; possible role in sterol metabolism
YBR038W	CHS2	NA	NA	2+	311856	313120	1265	3.51	ORF Verified	Chitin synthase II, requires activation from zymogenic form in order to catalyze the transfer of N-acetylglucosamine (GlcNAc) to chitin; required for the synthesis of chitin in the primary
YDR150W	NUM1	NA	NA	4+	759786	761458	1673	2.61	ORF Verified	Protein required for nuclear migration, localizes to the mother cell cortex and the bud tip; may mediate interactions of dynein and cytoplasmic microtubules with the cell cortex
YGR098C	ESP1	NA	NA	7-	683655	685991	2337	1.98	ORF Verified	Separase with cysteine protease activity (related to caspases) that promotes sister chromatid separation by mediating dissociation of the cohesin Scc1p from chromatin;
YIR019C	MUC1	NA	NA	9-	393157	393669	513	0.26	ORF Verified	GPI-anchored cell surface glycoprotein (flocculin) required for pseudohyphal formation, invasive growth, flocculation, and biofilms; transcriptionally regulated by the MAPK pathway (via Ste12p and Tec1p) and the cAMP pathway (via Flo8p)
YJL092W	HPR5	NA	NA	10+	257145	259097	1953	1.35	ORF Verified	DNA helicase and DNA-dependent ATPase involved in DNA repair, needed for proper timing of commitment to meiotic recombination and transition from Meiosis I to II; affects genome stability by suppressing unscheduled homologous recombination
YKR054C	DYN1	NA	NA	11-	542336	547616	5281	0.47	ORF Verified	Cytoplasmic heavy chain dynein, microtubule motor protein, required for anaphase spindle elongation; involved in spindle assembly, chromosome movement, and spindle orientation during cell division, targeted to microtubule tips by Pac1p
YPL032C	SVL3	NA	NA	16-	488885	491362	2478	4.01	ORF Verified	Protein of unknown function, mutant phenotype suggests a potential role in vacuolar function; green fluorescent protein (GFP)-fusion protein localizes to the cell periphery,
YPL162C		NA	NA	16-	242741	243613	873	3.01	ORF Uncharacterized	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the membrane of vacuole with cell cycle-correlated morphology
YPL230W		NA	NA	16+	115313	115865	553	1.35	ORF Verified	Putative transcription factor containing a C2H2 zinc finger; mutation affects transcriptional regulation of genes involved in protein folding, ATP binding, and cell wall biosynthesis
YPL242C	IQG1	NA	NA	16-	93517	95149	1633	1.82	ORF Verified	Essential protein required for determination of budding pattern, promotes localization of axial markers Bud4p and Cdc12p and functionally interacts with Sec3p, localizes to the contractile ring during anaphase, member of the IQGAP family
YPR019W	cdc54	NA	NA	16+	598083	599323	1241	3.2	ORF Verified	Essential helicase component of heterohexameric MCM2-7 complexes which bind pre-replication complexes on DNA and melt the DNA prior to replication; accumulates in the