systematic	institution	name	description	ORF Description
	Stephanie Schroeder			Putative glycoside hydrolase of the mitochondrial intermembrane space
YBR056W	Webster University			
	John Carmen			Protein of unknown function that interacts with Msb2p; may play a role in
	Northern Kentucky			activation of the filamentous growth pathway
YBR062C	University			
				GPI-anchored protein of unknown function; possible role in apical bud
	Devid Meriling add Ohio			growth; GPI-anchoring on the plasma membrane crucial to function;
	David Markwardt Ohio	E 0 M 00	ExtraCellular	phosphorylated in mitochondria; similar to Sps2p; ECM33 has a paralog,
YBR078W	Wesleyan University	ECM33	Mutant P-BodY	PST1, that arose from the whole genome duplication
	Susan Parrish McDaniel			Putative tubulin tyrosine ligase associated with P-bodies; may have a role
YBR094W		PBY1	associated protein	in mRNA metabolism; yeast knockout collection strain identified as a pby1
101(03400	College	r DTT	protein	null mutant is actually wild-type for PBY1 and deleted for mms4
	Ellen France Georgia			Putative protein of unknown function; green fluorescent protein (GFP)- fusion protein localizes to the Golgi apparatus; YCR043C is not an
YCR043C	College			essential gene
	David Markwardt Ohio			Protein of unknown function; involved in invasive and pseudohyphal
YDL024C	Wesleyan University	DIA3	Digs Into Agar	growth
		2	2.ge inte / igai	Putative RNA binding protein of unknown function; localizes to stress
	Susan Parrish McDaniel		N (asparagine)-	granules induced by glucose deprivation; predicted to be involved in
YDL167C	College	NRP1	Rich Protein	ribosome biogenesis
YDL199C	of Mary Washington			Putative transporter; member of the sugar porter family
1021000	of Mary Washington			Putative protein of unknown function; YDL218W transcription is regulated
	David Markwardt Ohio			by Azf1p and induced by starvation and aerobic conditions; expression
YDL218W	Wesleyan			also induced in cells treated with the mycotoxin patulin
				Protein of unknown function; overexpression suppresses the growth
	La marca la miliari salis			defect of mutants lacking protein kinase A activity; involved in cAMP-
VEBAAAA	Jenny Lenkowski	001/4	Suppressor Of	mediated signaling; localized to the nucleus; similar to the mouse testis-
YDR006C	Goucher College	SOK1	Kinase	specific protein PBS13
				Protein of unknown function; protein increases in abundance and relative
	Bernadette Connors			distribution to the nucleus increases upon DNA replication stress;
YDR132C	Dominican College			YDR132C has a paralog, YLR108C, that arose from the whole genome duplication
	Dominican concec			Predicted tail-anchored plasma membrane protein; contains a conserved
				CYSTM module; related proteins in other organisms may be involved in
	David Markwardt Ohio			response to stress; green fluorescent protein (GFP)-fusion protein
YDR210W	Wesleyan			localizes to the cell periphery
				Subunit of a kinetochore-microtubule binding complex; complex bridges
	purchased for Michael			centromeric heterochromatin and kinetochore MAPs and motors; required
	Wolyniak, Hampden-			for sister chromatid bi-orientation and kinetochore binding of SAC
YDR532C		KRE28		components; complex also includes Spc105p; modified by sumoylation
101(3320	Syndey College, VA	NNL20	Muc1 expressed	The second time to second stars of the second stars when the second stars with the second stars of the second stars at the sec
			Independent of	Transcriptional regulator of pseudohyphal growth; protein with sequence similarity to S. pombe gti1+ (gluconate transport inducer 1) and C.
YEL007W	Rhodes College	MIT1	TEC1	albicans Wor1
			-	Protein with ubiguitin-like N terminus; subunit of Nuclear Excision Repair
				Factor 2 (NEF2) with Rad4p that binds damaged DNA; enhances protein
				deglycosylation activity of Png1p; also involved, with Rad4p, in
				ubiquitylated protein turnover; Rad4p-Rad23p heterodimer binds to
	Bernadette Connors		RADiation	promoters of DNA damage response genes to repress their transcription
YEL037C	Dominican College	RAD23	sensitive	in the absence of DNA damage
	lill Koonov, lunista		Regulator of	Putative protein of unknown function; non-essential gene identified in a
YER066W	Jill Keeney, Juniata	RRT13	rDNA Transcription	screen for mutants with decreased levels of rDNA transcription
	College	1113	Tanscription	
				Coiled-coil protein involved in spindle-assembly checkpoint; required for inhibition of karyopherin/importin Pse1p (aka Kap121p) upon spindle
				assembly checkpoint arrest; phosphorylated by Mps1p upon checkpoint
	Michael Wolyniak,			activation which leads to inhibition of anaphase promoting complex
	Hampden-Sydney		Mitotic Arrest-	activity; forms a complex with Mad2p; gene dosage imbalance between
YGL086W	College	MAD1	Deficient	MAD1 and MAD2 leads to chromosome instability
	Gavin McStay		Maintenance of	Protein of unknown function; green fluorescent protein (GFP)-fusion
	New York Institute of		Telomere	protein localizes to the mitochondrion; mtc3 is synthetically sick with
YGL226W	Technology	МТС3	Capping	cdc13-1
YGL226W	Technology	IVITC3	Capping	

YGL247W	Michael Wolyniak, Hampden-Sydney College	BRR6	Bad Response to Refrigeration	Essential nuclear envelope integral membrane protein; interacts and functions with Apq12p and Brl1p in lipid homeostasis; mutants are defective in nuclear pore complex biogenesis, nuclear envelope morphology, mRNA nuclear export, and are sensitive to sterol biosynthesis inhibitors and membrane fluidizing agents; exhibits synthetic lethal genetic interactions with genes involved in lipid metabolism; homeoscare brl1p.
YGR035C	Stephanie Schroeder Webster University	DIRICO	to Kenigeration	homologous to Brl1p Putative protein of unknown function, potential Cdc28p substrate; transcription is activated by paralogous transcription factors Yrm1p and Yrr1p along with genes involved in multidrug resistance; YGR035C has a paralog, YLR346C, that arose from the whole genome duplication
YGR089W	Joanna Haye/Shuba Ireland Xavier University of Louisiana	NNF2		Protein that exhibits physical and genetic interactions with Rpb8p; Rpb8p is a subunit of RNA polymerases I, II, and III; computational analysis of large-scale protein-protein interaction data suggests a role in chromosome segregation
YGR161C	Rhodes College	RTS3		Putative component of the protein phosphatase type 2A complex
YHL010C	Jenny Lenkowski Goucher College Stephanie Schroeder	ETP1	Ethanol Tolerance Protein	Protein of unknown function required for growth on ethanol; contains a zinc finger region and has homology to human BRAP2, which is a cytoplasmic protein that binds nuclear localization sequences Putative protein of unknown function; YHR022C is not an essential gene
YHR022C	Webster University			
YHR036W	Michael Wolyniak, Hampden-Sydney College	BRL1	BRr6 Like protein	Essential nuclear envelope/ER integral membrane protein; interacts and functions with Apq12p and Brr6p in lipid homeostasis; mutants are defective in nuclear pore complex biogenesis, mRNA nuclear export and are sensitive to sterol biosynthesis inhibitors and membrane fluidizing agents; identified as a dosage suppressor of a temperature sensitive mutation in the major karyopherin, CRM1; homologous to Brr6p
YHR087W	Stephanie Schroeder Webster University	RTC3	Restriction of Telomere Capping	Protein of unknown function involved in RNA metabolism; has structural similarity to SBDS, the human protein mutated in Shwachman-Diamond Syndrome (the yeast SBDS ortholog = SDO1); null mutation suppresses cdc13-1 temperature sensitivity; protein abundance increases in response to DNA replication stress
YHR125W	Stephanie Schroeder Webster University			Putative protein of unknown function; conserved across S. cerevisiae strains
YHR129C	Bernadette Connors Dominican College	ARP1	Actin-Related Protein	Actin-related protein of the dynactin complex; required for spindle orientation and nuclear migration; forms actin-like short filament composed of 9 or 10 Arp1p monomers; putative ortholog of mammalian centractin
YIL040W	Michael Wolyniak, Hampden-Sydney College	APQ12	APical growth revealed by Quantitative morphological analysis	Nuclear envelope/ER integral membrane protein; interacts and functions with Brr6p and Brl1p in lipid homeostasis; mutants are defective in nuclear pore complex biogenesis, nuclear envelope morphology, mRNA export from the nucleus and are sensitive to sterol biosynthesis inhibitors and membrane fluidizing agents; exhibits synthetic lethal genetic interactions with genes involved in lipid metabolism
YIL089W	David Aiello Austin College			Protein of unknown function found in the ER and vacuole lumen; overexpression of YIL089W affects endocytic protein trafficking
YIL105C	Bernadette Connors Dominican College	SLM1	Synthetic Lethal with Mss4	Phosphoinositide PI4,5P(2) binding protein, forms a complex with SIm2p; acts downstream of Mss4p in a pathway regulating actin cytoskeleton organization in response to stress; TORC2 complex substrate and effector; protein abundance increases in response to DNA replication stress; SLM1 has a paralog, SLM2, that arose from the whole genome duplication
YIL140W	Dale Beach, Longwood University	AXL2	AXiaL 2 bud site selection	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
YIL156W	Crystal Goldyn Mount Aloysius College	UBP7	UBiquitin- specific Protease	Ubiquitin-specific protease that cleaves ubiquitin-protein fusions; UBP7 has a paralog, UBP11, that arose from the whole genome duplication
YIL158W	Deborah Zies Univeristy of Mary Washington	, AIM20	Altered Inheritance rate of Mitochondria	Protein of unknown function; overexpression causes cell cycle delay or arrest; green fluorescent protein (GFP)-fusion protein localizes to vacuole; null mutant displays elevated frequency of mitochondrial genome loss; relocalizes from nucleus to cytoplasm upon DNA replication stress; AIM20 has a paralog, SKG1, that arose from the whole genome duplication

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YIR003W	Indrani Bose Western Carolina Univeristy	AIM21	Altered Inheritance rate of Mitochondria	Subunit of a complex that associates with actin filaments; forms a complex with Tda2p that inhibits barbed end F-actin assembly; elevates actin monomer pools to increase endocytotic efficiency and to regulate the distribution of actin between cables and patches; Aim21p/Tda2p forms a larger complex with actin capping proteins Cap1p and Cap2p; involved in mitochondrial migration along actin filaments; recruited to cortical actin patches by SH3 domain-containing proteins Bbc1p and Abp1p
YIR030C	William Alexander Truman State University	DCG1	Dal80p- Controlled Gene	Protein of unknown function; expression is sensitive to nitrogen catabolite repression and regulated by Dal80p; contains transmembrane domain
YJL030W	Dale Beach, Longwood University	MAD2	Mitotic Arrest- Deficient	Component of the spindle-assembly checkpoint complex; delays onset of anaphase in cells with defects in mitotic spindle assembly; forms a complex with Mad1p; regulates APC/C activity during prometaphase and metaphase of meiosis I; gene dosage imbalance between MAD1 and MAD2 leads to chromosome instability
YJL107C	Jenny Lenkowski Goucher College			Putative protein of unknown function; expression is induced by activation of the HOG1 mitogen-activated signaling pathway and this induction is Hog1p/Pbs2p dependent; YJL107C and adjacent ORF, YJL108C are merged in related fungi
V II 4740	David Markwardt Ohio	TOUM	TOS One	GPI-anchored cell wall protein of unknown function; induced in response to cell wall damaging agents and by mutations in genes involved in cell wall biogenesis; sequence similarity to YBR162C/TOS1, a covalently bound cell wall protein; protein abundance increases in response to DNA
YJL171C	Wesleyan University John Carmen Northern Kentucky	TOH1	Homolog Increased Loss of Mitochondrial	replication stress Protein of unknown function; may be involved in mitochondrial DNA maintenance; required for slowed DNA synthesis-induced filamentous growth
YJR118C YJR126C	University Jenny Lenkowski Goucher College	ILM1 VPS70	DNA Vacuolar Protein Sorting	Protein of unknown function involved in vacuolar protein sorting; SWAT- GFP and mCherry fusion proteins localize to the endoplasmic reticulum
YKL023W	Susan Parrish McDaniel College			Putative protein of unknown function; predicted by computational methods to be involved in mRNA degradation; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm
YKL142W	Bhadas Callaga	MRP8	Mitochondrial Ribosomal Protein	Protein of unknown function; undergoes sumoylation; transcription induced under cell wall stress; protein levels are reduced under anaerobic conditions; protein abundance increases in response to DNA replication stress; originally thought to be a mitochondrial ribosomal protein based on
YKL222C	Rhodes College Rhodes College			sequence analysis Protein of unknown function; may interact with ribosomes, based on co- purification experiments; similar to transcriptional regulators from the zinc cluster (binuclear cluster) family; null mutant is sensitive to caffeine
YKR095W	Bernadette Connors Dominican College	MLP1	Myosin-Like Protein	Myosin-like protein associated with the nuclear envelope; nuclear basket protein that connects the nuclear pore complex with the nuclear interior; involved with Tel1p in telomere length control; involved with Pml1p and Pml39p in nuclear retention of unspliced mRNAs; MLP1 has a paralog, MLP2, that arose from the whole genome duplication
YKR098C	Crystal Goldyn Mount Aloysius College	UBP11	UBiquitin- specific Protease	Ubiquitin-specific protease; cleaves ubiquitin from ubiquitinated proteins; UBP11 has a paralog, UBP7, that arose from the whole genome duplication
YLL049W	Dale Beach, Longwood University	LDB18	Low Dye Binding	
YLR001C	Jill Keeney, Juniata College			Putative protein of unknown function; the authentic, non-tagged protein is detected in highly purified mitochondria in high-throughput studies; predicted to be palmitoylated
YLR036C	David Aiello Austin College			Putative protein predicted to have transmembrane domains; interacts with HSP90 by yeast two-hybrid analysis; YLR036C is not an essential protein
YLR108C	Bernadette Connors Dominican College			Protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the nucleus; YLR108C is not an esssential gene; protein abundance increases in response to DNA replication stress; YLR108C has a paralog, YDR132C, that arose from the whole genome duplication
YLR346C	Stephanie Schroeder Webster University	CIS1	Cltrinin Sensitive knockout	Protein of unknown function found in mitochondria; expression is regulated by transcription factors involved in pleiotropic drug resistance, Pdr1p and Yrr1p; not an essential gene; YLR346C has a paralog, YGR035C, that arose from the whole genome duplication

	Joanna Haye/Shuba			Putative protein of unknown function; null mutant displays elongated buds
	Ireland Xavier			and a large fraction of budded cells have only one nucleus
YLR407W	University of Louisiana			
YML018C	Michael Wolyniak, Hampden-Sydney College Indrani Bose Western		Altered	Protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the membrane of the vacuole; physical interaction with Atg27p suggests a possible role in autophagy; YML018C is not an essential gene; relative distribution to the vacuolar membrane decreases upon DNA replication stress; YML018C has a paralog, THI74, that arose from the whole genome duplication Protein of unknown function; GFP-fusion protein localizes to the
YMR003W	Carolina Univeristy	AIM34	Inheritance rate of Mitochondria	mitochondria; null mutant is viable and displays reduced frequency of mitochondrial genome loss
YMR107W	Stephanie Schroeder Webster University	SPG4	Stationary Phase Gene	Protein required for high temperature survival during stationary phase; not required for growth on nonfermentable carbon sources
YMR295C YMR316W	Dale Beach, Longwood University John Carmen Northern Kentucky University	DIA1	Ilm1p BInding	Protein of unknown function that associates with ribosomes; green fluorescent protein (GFP)-fusion protein localizes to the cell periphery and bud; not an essential gene; protein abundance increases in response to DNA replication stress; YMR295C has a paralog, YGR273C, that arose from the whole genome duplication Protein of unknown function; involved in invasive and pseudohyphal growth; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm in a punctate pattern
YNL209W	Bernadette Connors Dominican College	SSB2	Stress-Seventy subfamily B	Cytoplasmic ATPase that is a ribosome-associated molecular chaperone; functions with J-protein partner Zuo1p; may be involved in the folding of newly-synthesized polypeptide chains; member of the HSP70 family; SSB2 has a paralog, SSB1, that arose from the whole genome duplication
YNL213C	Rhodes College	RRG9	Required for Respiratory Growth	Protein of unknown function; null mutant lacks mitochondrial DNA and cannot grow on glycerol; the authentic, non-tagged protein is detected in highly purified mitochondria in high-throughput studies
YNL234W	Jenny Lenkowski Goucher College			Protein of unknown function with similarity to globins; has a functional heme-binding domain; mutant has aneuploidy tolerance; transcription induced by stress conditions; may be involved in glucose signaling or metabolism; regulated by Rgt1
YNL298W	Bernadette Connors Dominican College	CLA4	CLn Activity dependant	Cdc42p-activated signal transducing kinase; member of the PAK (p21- activated kinase) family, along with Ste20p and Skm1p; involved in septin ring assembly, vacuole inheritance, cytokinesis, sterol uptake regulation; phosphorylates Cdc3p and Cdc10p; CLA4 has a paralog, SKM1, that arose from the whole genome duplication
YNL307C	Dale Beach, Longwood University	MCK1	Meiosis and Centromere regulatory Kinase	Dual-specificity ser/thr and tyrosine protein kinase; roles in chromosome segregation, meiotic entry, genome stability, phosphorylation-dependent protein degradation (Rcn1p and Cdc6p), inhibition of protein kinase A, transcriptional regulation, inhibition of RNA pol III, calcium stress and inhibition of Clb2p-Cdc28p after nuclear division; MCK1 has a paralog, YGK3, that arose from the whole genome duplication
YOL154W	David Markwardt Ohio Wesleyan University	ZPS1	Zinc- and pH- regulated Surface protein	Putative GPI-anchored protein; transcription is induced under low-zinc conditions, as mediated by the Zap1p transcription factor, and at alkaline pH
YOR092W	Jenny Lenkowski Goucher College	ECM3	ExtraCellular Mutant	Non-essential protein of unknown function; involved in signal transduction and the genotoxic response; induced rapidly in response to treatment with 8-methoxypsoralen and UVA irradiation; relocalizes from ER to cytoplasm upon DNA replication stress; ECM3 has a paralog, YNL095C, that arose from the whole genome duplication
YOR324C	Jenny Lenkowski Goucher College	FRT1	Functionally Related to TCP1	Tail-anchored ER membrane protein of unknown function; substrate of the phosphatase calcineurin; interacts with homolog Frt2p; promotes cell growth in stress conditions, possibly via a role in posttranslational translocation; FRT1 has a paralog, FRT2, that arose from the whole genome duplication
YPL018W	Bernadette Connors Dominican College	CTF19	Chromosome Transmission Fidelity	Outer kinetochore protein, needed for accurate chromosome segregation; component of kinetochore sub-complex COMA (Ctf19p, Okp1p, Mcm21p, Ame1p) that functions as platform for kinetochore assembly; required for spindle assembly checkpoint; minimizes potentially deleterious centromere-proximal crossovers by preventing meiotic DNA break formation proximal to centromere; homolog of human centromere constitutive-associated network (CCAN) subunit CENP-P and fission yeast fta2

YPL031C	Bernadette Connors Dominican College	PHO85	PHOsphate metabolism	Cyclin-dependent kinase; has ten cyclin partners; involved in regulating the cellular response to nutrient levels and environmental conditions and progression through the cell cycle; human lissencephaly-associated homolog CDK5 functionally complements null mutation
YPL055C	Candice Jones Lane College	LGE1	LarGE cells	Protein of unknown function; null mutant forms abnormally large cells, and homozygous diploid null mutant displays delayed premeiotic DNA synthesis and reduced efficiency of meiotic nuclear division
YPL158C	Dale Beach, Longwood University	AIM44	Altered Inheritance rate of Mitochondria	Protein that regulates Cdc42p and Rho1p; functions in the late steps of cytokinesis and cell separation; sustains Rho1p at the cell division site after actomyosin ring contraction; inhibits the activation of Cdc42-Cla4 at the cell division site to prevent budding inside the old bud neck; transcription is regulated by Swi5p; null mutant displays elevated frequency of mitochondrial genome loss; relocalizes from bud neck to cytoplasm upon DNA replication stress
YPL174C	Dale Beach, Longwood University	NIP100	Nuclear ImPort	Large subunit of the dynactin complex; dynactin is involved in partitioning the mitotic spindle between mother and daughter cells; putative ortholog of mammalian p150(glued)
YPL257W	Ellen France Georgia College			Putative protein of unknown function; homozygous diploid deletion strain exhibits low budding index; physically interacts with Hsp82p; YPL257W is not an essential gene
YPL269W	Dale Beach, Longwood University	KAR9	KARyogamy	Spindle positioning factor; orients astral microtubules, connecting them to actin cables at the cortex with Bim1p and Myo2, resulting in proper spindle positioning; targeted for StuBL-dependent degradation at kinetochores by Slx5p-Slx8p, ensuring chromosome transmission fidelity and correct spindle positioning; role in karyogamy; localizes to the shmoo tip, the growing bud-tip, the nucleus, the kinetochore, the spindle and microtubules; homolog of adenomatous polyposis coli
YPR149W	Jenny Lenkowski Goucher College	NCE102	NonClassical Export	Protein of unknown function; contains transmembrane domains; involved in secretion of proteins that lack classical secretory signal sequences; component of the detergent-insoluble glycolipid-enriched complexes (DIGs); NCE102 has a paralog, FHN1, that arose from the whole genome duplication