

# SUPPLEMENTAL TABLES

## Details of modularized genes from yeast cell cycling data\*

Module	Gene #	Systematic name	Common name	Gene Ontology			Linked gene(s)	Assigned color
				Molecular Function	Biological Process	Cellular Component		
Module 1	1	YBL037W	APL3	vesicle-mediated transport	molecular_function unknown	AP-2 adaptor complex	2 3 4 5	Red
	2	YBL051C	PIN4	biological_process unknown	molecular_function unknown	cytoplasm	1 3 4 5	Gray10
	3	YBR108W		biological_process unknown	molecular_function unknown	cellular_component unknown	1 2 4 5 6	Gray10
	4	YBR110W	ALG1	N-linked glycosylation	beta-1,4-mannosyltransferase activity	integral to membrane	1 2 3 5 6	Red
	5	YBR124W					1 2 3 4	Gray10
Module 2	6	YDL239C	ADY3	protein complex assembly	protein binding	spindle	3 4	Red
	7	YBL099W	ATP1	ATP synthesis coupled proton transport	hydrogen-transporting ATP synthase activity, rotational mechanism	proton-transporting ATP synthase, catalytic core (sensu Eukarya)	10	Lavender
	8	YOR108W	LEU9	leucine biosynthesis	2-isopropylmalate synthase activity	mitochondrion	10	Red
	9	YDR134C		biological_process unknown	molecular_function unknown	cell wall (sensu Fungi)	10	Gray10
	10	YDR158W	HOM2	methionine metabolism	aspartate-semialdehyde dehydrogenase activity	cytoplasm	7 9 8	Red
Module 3	11	YBR018C	GAL7	galactose metabolism	UTP-hexose-1-phosphate uridylyltransferase activity	cytoplasm	12 13 15	Red
	12	YBR019C	GAL10	galactose metabolism	molecular_function unknown	cellular_component unknown	11 15 14	Red
	13	YBR020W	GAL1	galactose metabolism	galactokinase activity	cellular_component unknown	11	Red
	14	YLR081W	GAL2	galactose metabolism	glucose transporter activity	plasma membrane	12 15	Red
	15	YDR009W	GAL3	regulation of transcription, DNA-dependent	protein binding	cytoplasm	11 12 14	Red
Module 4	16	YFL037W	TUB2	mitotic chromosome segregation	structural constituent of cytoskeleton	spindle pole body	21 25 22 23	Yellow
	17	YFL045C	SEC53	protein-ER targeting	phosphomannomutase activity	cytosol	27 20 18 19 28	Red
	18	YGL012W	ERG4	ergosterol biosynthesis	delta24(24-1) sterol reductase activity	endoplasmic reticulum	17	LimeGreen
	19	YGL225W	VRG4	N-linked glycosylation	nucleotide-sugar transporter activity	Golgi apparatus	20 17 28 29	Red
	20	YAL023C	PMT2	O-linked glycosylation	dolichyl-phosphate-mannose-protein mannosyltransferase activity	endoplasmic reticulum	17 19 29	Red
	21	YBR078W	ECM33	cell wall organization and biogenesis	molecular_function unknown	plasma membrane	16 22 23	Yellow
	22	YIL123W	SIM1	microtubule cytoskeleton organization and biogenesis	molecular_function unknown	cell wall (sensu Fungi)	21 25 16 23 26	Yellow
	23	YJL158C	CIS3	cell wall organization and biogenesis	structural constituent of cell wall	plasma membrane	21 25 16 22 29	Yellow
	24	YJR143C	PMT4	O-linked glycosylation	dolichyl-phosphate-mannose-protein mannosyltransferase activity	endoplasmic reticulum	29 30	Red
	25	YBR243C	ALG7	N-linked glycosylation	UDP-N-acetylglucosamine-dolichyl-phosphate N-acetylglucosaminophosphotransferase activity	endoplasmic reticulum	16 22 23	Red
	26	YMR215W	GAS3	biological_process unknown	molecular_function unknown	cell wall (sensu Fungi)	22	Yellow
	27	YAL007C	ERP2	ER to Golgi transport	molecular_function unknown	COPII-coated vesicle	17 28	Red
	28	YOR099W	KTR1	O-linked glycosylation	alpha-1,2-mannosyltransferase activity	Golgi apparatus	27 17 19 31	Red
	29	YOR247W	SRL1	nucleobase, nucleoside, nucleotide and nucleic acid metabolism	molecular_function unknown	cytoplasm	20 19 23 24 30	LimeGreen
	30	YOR248W					24 29	Gray10
Module 5	31	YPL067C		biological_process unknown	molecular_function unknown	cytoplasm	28	Gray10
	32	YDR274C					38	Gray10
	33	YKR039W	GAP1	amino acid transport	general amino acid permease activity	integral to plasma membrane	37 34 36	Red
	34	YKR093W	PTR2	peptide transport	peptide transporter activity	plasma membrane	37 33	Red
	35	YLL041C	SDH2	tricarboxylic acid cycle	succinate dehydrogenase (ubiquinone) activity	respiratory chain complex II (sensu Eukarya)	36	Lavender
	36	YML120C	ND1	mitochondrial electron transport, NADH to ubiquinone	oxidoreductase activity, acting on NADH or NADPH, quinone or similar compound as acceptor	mitochondrial inner membrane	33 35	Lavender
	37	YCL025C	AGP1	amino acid transport	amino acid transporter activity	plasma membrane	39 33 34 38	Red
	38	YOL101C		biological_process unknown	molecular_function unknown	integral to membrane	37 32	Red
	39	YCLX09W					37	Gray10
	40	YLR452C	SST2	signal transduction	GTPase activator activity	plasma membrane	41 43 42	Red
Module 6	41	YCL027W	FUS1	conjugation with cellular fusion	molecular_function unknown	plasma membrane	44 40	Red
	42	YNR044W	AGA1	agglutination during conjugation with cellular fusion	cell adhesion receptor activity	cell wall (sensu Fungi)	43 40	Red
	43	YCL055W	KAR4	meiosis	transcription regulator activity	nucleus	40 42	Red
	44	YCLX07W					41	Gray10
	45	YGR192C	TDH3	gluconeogenesis	glyceraldehyde-3-phosphate dehydrogenase (phosphorylating) activity	cytoplasm	49 50 47	Red
	46	YHR174W	ENO2	gluconeogenesis	phosphopyruvate hydratase activity	soluble fraction	50 47	Red
	47	YJR009C	TDH2	gluconeogenesis	glyceraldehyde-3-phosphate dehydrogenase (phosphorylating) activity	cytoplasm	49 50 45 46	Red
	48	YKL153W					49	Gray10
	49	YCR012W	PGK1	gluconeogenesis	phosphoglycerate kinase activity	cytoplasm	50 45 47 48	Red
	50	YCR013C					49 51 45 46 47	Gray10
Module 8	51	YDR050C	TP11	gluconeogenesis	triose-phosphate isomerase activity	cytoplasm	50	Red
	52	YDL037C	BSC1	biological_process unknown	molecular_function unknown	cellular_component unknown	53 54	Gray10
	53	YDL038C		biological_process unknown	molecular_function unknown	cellular_component unknown	52 54	Gray10
	54	YDL039C	PRM7	conjugation with cellular fusion	molecular_function unknown	integral to membrane	52 53	Gray10
	55	YDR279W	RNH202	biological_process unknown	molecular_function unknown	nucleus	95 140	Gray10
Module 9	56	YDR297W	SUR2	sphingolipid biosynthesis	sphingosine hydroxylase activity	endoplasmic reticulum	69 158	LimeGreen
	57	YDR400W	URH1	pyrimidine salvage	hydrolase activity, acting on glycosyl bonds	cytoplasm	193	LimeGreen
	58	YDR451C	YHP1	negative regulation of transcription from Pol II promoter	specific RNA polymerase II transcription factor activity	nuclear chromosome	143	Red
	59	YBL035C	POL12	DNA replication initiation	alpha DNA polymerase activity	alpha DNA polymerase:primase complex	224 225 112 185 187 91 127 147 194 198 205	Red
	60	YDR503C	LPP1	phospholipid metabolism	phosphatidate phosphatase activity	membrane	223	LimeGreen
	61	YEL032W	MCM3	DNA replication initiation	chromatin binding	cytoplasm	136 105 155	Red
	62	YEL042W	GDA1	protein amino acid glycosylation	guanosine-diphosphatase activity	Golgi apparatus	76 124 190	LimeGreen
	63	YEL075C		biological_process unknown	molecular_function unknown	cellular_component unknown	64 70 71 103 113 161 163	Purple
	64	YEL076C		biological_process unknown	molecular_function unknown	cellular_component unknown	80 63 70 73 113 161	Purple
	65	YEL077C		biological_process unknown	molecular_function unknown	cellular_component unknown	71 120 129 141 165 220	Purple
	66	YER001W	MNN1	O-linked glycosylation	alpha-1,3-mannosyltransferase activity	Golgi apparatus	117 193 210	LimeGreen
	67	YER016W	BIM1	mitotic spindle checkpoint	structural constituent of cytoskeleton	spindle pole body	77	Red
	68	YER095W	RAD51	chromatin remodeling	recombinase activity	nuclear chromosome	224 111 112 221 91 117 131 133 134 139 162 163 189 193 205 210	Red
	69	YER118C	SHO1	pseudohyphal growth	osmosensor activity	plasma membrane	221 56 86 117	Lavender
	70	YER189W		biological_process unknown	molecular_function unknown	cellular_component unknown	80 63 64 73 103 113 161 163 218	Purple
	71	YER190W	YRF1-2	telomerase-independent telomere maintenance	DNA helicase activity	cellular_component unknown	80 63 65 83 100 104 113 120 129 141 139 162 163 165 192 218 219 220	Purple
	72	YFL008W	SMC1	mitotic chromosome segregation	ATPase activity	nuclear cohesin complex	147 157 170 205	Red
	73	YFL064C		biological_process unknown	molecular_function unknown	cellular_component unknown	80 64 70 103 113 161	Purple
	74	YGL008C	PMA1	regulation of pH	hydrogen-exporting ATPase activity, phosphorylative mechanism	plasma membrane	114 207 152	LimeGreen
	75	YGL021W	ALK1	mitosis	protein serine/threonine kinase activity	nucleus	236 90 106 119 121 149	Red

							152 167 168 171 172 174 197 213	
76	YGL022W	STT3	N-linked glycosylation	dolichyl-diphosphooligosaccharide-protein glycotransferase activity	oligosaccharyl transferase complex		62 124 146	LimeGreen
77	YGL027C	CWH41	cell wall organization and biogenesis	mannosyl-oligosaccharide glucosidase activity	endoplasmic reticulum membrane		228 67 126 132 134 140 151 196	LimeGreen
78	YGL038C	OCH1	N-linked glycoprotein maturation	alpha-1,6-mannosyltransferase activity	Golgi cis cisterna		91 214	LimeGreen
79	YGL116W	CDC20	ubiquitin-dependent protein catabolism	enzyme activator activity	anaphase-promoting complex		227 93 116 152 171 172 174 184	Red
80	YBL111C		biological_process unknown	molecular_function unknown	cellular_component unknown		82 64 70 71 73 103 104 113 161	Purple
81	YBL112C		biological_process unknown	molecular_function unknown	cellular_component unknown		82	Purple
82	YBL113C		biological_process unknown	molecular_function unknown	cellular_component unknown		80 81 100 113 129 142	Purple
83	YGL207W	SPT16	chromatin remodeling	Pol II transcription elongation factor activity	nuclear chromatin		234 71	Red
84	YBR009C	HHF1	chromatin assembly/disassembly	DNA binding	nuclear nucleosome		237 238 85 240 241 179 180	Yellow
85	YBR010W	HHT1	chromatin assembly/disassembly	DNA binding	nucleus		237 238 84 226 240 241 179 180 204	Yellow
86	YGR014W	MSB2	establishment of cell polarity (sensu Saccharomyces)	osmosensor activity	integral to plasma membrane		69	Lavender
87	YGR041W	BUD9	bud site selection	molecular_function unknown	bud neck		144	Lavender
88	YGR086C	PLI1	biological_process unknown	molecular_function unknown	cytoplasm		145	Gray10
89	YGR092W	DBF2	protein amino acid phosphorylation	protein kinase activity	bud neck		227 136 184	Red
90	YGR108W	CLB1	G2/M transition of mitotic cell cycle	cyclin-dependent protein kinase regulator activity	nucleus		236 75 106 149 152 167 168 172 174 213	Red
91	YGR109C	CLB6	G1/S transition of mitotic cell cycle	cyclin-dependent protein kinase regulator activity	cellular_component unknown		59 111 112 187 199 222 234 68 78 98 131 137 147 166 170 175 194 205 214	Red
92	YBR038W	CHS2	response to osmotic stress	chitin synthase activity	contractile ring (sensu Saccharomyces)		149 152 172 184 197 213	Lavender
93	YGR143W	SKN1	cell wall organization and biogenesis	glucosidase activity	integral to membrane		79 117 171 173 193	LimeGreen
94	YGR151C						224 111 222 234 95 97 131 140 150 151 166 188 191 194 196 217	Gray10
95	YGR152C	RSR1	polar budding	signal transducer activity	plasma membrane		224 111 185 187 199 222 234 55 94 97 108 131 134 140 151 166 188 191 193 194 196 210 214 216 217	Lavender
96	YBR054W	YRO2	biological_process unknown	molecular_function unknown	bud		114 136 233 186	Gray10
97	YGR189C	CRH1	biological_process unknown	molecular_function unknown	cell wall (sensu Fungi)		111 94 95 134 151 166 193 195 196 210	Gray10
98	YGR221C	TOS2	biological_process unknown	molecular_function unknown	bud neck		224 111 112 222 234 91 117 118 122 139 147 151 157 166 193 194 205	Gray10
99	YGR230W	BNS1	meiosis	molecular_function unknown	cellular_component unknown		227	Red
100	YGR296W	YRF1-3	telomerase-independent telomere maintenance	DNA helicase activity	cellular_component unknown		82 71 103 113 120 129 141 161 162 163 164 165 192 211 218 219 220	Purple
101	YBR070C		biological_process unknown	molecular_function unknown	cellular_component unknown		154 157 170 205	Gray10
102	YBR071W		biological_process unknown	molecular_function unknown	cytoplasm		111 222 137 144	Gray10
103	YHL049C		biological_process unknown	molecular_function unknown	cellular_component unknown		80 63 70 73 100 113 161 163 218	Purple
104	YHL050C		biological_process unknown	helicase activity	cellular_component unknown		80 71 113 120 163 165 218 219 220	Purple
105	YHR005C	GPA1	signal transduction during conjugation with cellular fusion	heterotrimeric G-protein GTPase activity	plasma membrane		239 61 155 200	Lavender
106	YHR023W	MYO1	response to osmotic stress	microfilament motor activity	contractile ring (sensu Saccharomyces)		236 75 90 121 152 171 172 174 184 213	Red
107	YHR098C	SFB3	ER to Golgi transport	molecular_function unknown	endoplasmic reticulum		190	Gray10
108	YHR110W	ERP5	secretory pathway	molecular_function unknown	integral to membrane		224 111 222 223 95 194 196	Black
109	YHR149C		biological_process unknown	molecular_function unknown	bud neck		221	Gray10
110	YHR153C	SPO16	sporulation (sensu Saccharomyces)	molecular_function unknown	cellular_component unknown		232 147	Red
111	YBR088C	POL30	lagging strand elongation	DNA polymerase processivity factor activity	replication fork		224 102 112 187 199 221 222 234 68 91 94 95 97 98 108 115 117 122 131 133 134 139 140 147 151 166 175 176 188 189 193 194 195 196 205 208 210 214 216 217	Red
112	YBR089W						224 59 111 185 187 199 234 68 91 98 122 194 205	Gray10
113	YHR218W		biological_process unknown	molecular_function unknown	cellular_component unknown		80 82 63 64 70 71 73 100 103 104 120 161 162 163 218 219	Purple
114	YBR092C	PHO3	thiamin transport	acid phosphatase activity	periplasmic space (sensu Fungi)		96 207 233 74 152 215	LimeGreen
115	YIL066C	RNR3	DNA replication	ribonucleoside-diphosphate reductase activity	cytoplasm		111 222 234 166 193 210	Red
116	YIL106W	MOB1	protein amino acid phosphorylation	kinase regulator activity	bud neck		79 149 167 168 171 172 174 197	Red
117	YIL140W	AXL2	bud site selection	molecular_function unknown	bud neck		111 221 222 66 68 69 93 98 128 132 133 134 151 166 176 193 208 210	Lavender
118	YIL141W						98	Gray10
119	YIL158W		biological_process unknown	molecular_function unknown	vacuole (sensu Fungi)		75 149 167 168 172 174	Gray10
120	YIL177C		biological_process unknown	helicase activity	cellular_component unknown		65 71 100 104 113 129 141 144 161 162 164 165 192 218 219 220	Purple
121	YIL051W		biological_process unknown	molecular_function unknown	bud tip		75 106 152 167 172 174 213	Gray10
122	YIL074C	SMC3	sporulation (sensu Saccharomyces)	ATPase activity	nuclear cohesin complex		224 111 112 199 222 234 98 128 139 147 151 157 166 175 188 193 194 196 205 208 210 216 217	Red
123	YJL079C	PRY1	biological_process unknown	molecular_function unknown	endoplasmic reticulum		186	Red
124	YJL080C	SCP160	chromosome segregation	RNA binding	endoplasmic reticulum membrane		62 76	Red
125	YJL115W	ASF1	DNA damage response, signal transduction resulting in induction of apoptosis	histone binding	chromatin assembly complex		131	Lavender
126	YJL173C	RFA3	DNA recombination	DNA binding	DNA replication factor A complex		235 77 140	Red
127	YJL181W		biological_process unknown	molecular_function unknown	cellular_component unknown		224 59 185 187 147 205	Gray10
128	YJL187C	SWE1	G2/M transition of mitotic cell cycle	protein kinase activity	nucleus		221 222 234 117 122 132 134 139 140 147 151 160 166 193 203 210	Red
129	YJL225C		biological_process unknown	helicase activity	cellular_component unknown		82 65 71 100 120 141 142 161 165 211 220	Purple
130	YJR043C	POL32	lagging strand elongation	delta DNA polymerase activity	nucleus		150	Red
131	YKL045W	PR12	DNA replication initiation	alpha DNA polymerase activity	alpha DNA polymerase/primase complex		224 111 187 199 222 230 234 68 91 94 95 125 147 151 166 175 188 193 194	Red

	132	YKL101W	HSL1	protein amino acid phosphorylation	protein kinase activity	bud neck	196 205 210 214 216 217	Red
	133	YKR012C					222 77 117 128 138 151 193 195	Gray10
	134	YKR013W	PRY2	biological_process unknown	molecular_function unknown	vacuole (sensu Fungi)	111 222 68 117 134 166 193 210	Gray10
	135	YBR200W	BEM1	establishment of cell polarity (sensu Saccharomyces)	protein binding	bud neck	136	Red
	136	YBR202W	CDC47	DNA replication initiation	chromatin binding	cytoplasm	227 96 135 61 89 155	Red
	137	YKR077W		biological_process unknown	molecular_function unknown	cytoplasm	102 185 187 91 144	Gray10
	138	YKR090W	PXL1	biological_process unknown	molecular_function unknown	cytoplasm	132 151	Gray10
	139	YLL002W	RTT109	negative regulation of DNA transposition	molecular_function unknown	nucleus	224 111 199 222 234 68 98 122 128 140 147 151 166 194 196 205 209	Red
	140	YLL022C	HIF1	biological_process unknown	molecular_function unknown	nucleus	224 111 199 222 231 234 55 77 94 95 126 128 134 139 147 151 153 160 166 191 193 194 196 210 214 217	Gray10
	141	YLL066C		biological_process unknown	molecular_function unknown	cellular_component unknown	65 71 100 120 129 142 165 192 218 219 220	Purple
	142	YLL067C		biological_process unknown	molecular_function unknown	cellular_component unknown	82 129 141 165	Purple
	143	YLR045C	STU2	microtubule nucleation	structural constituent of cytoskeleton	spindle pole body	237 58 201	Red
	144	YLR049C		biological_process unknown	molecular_function unknown	cellular_component unknown	102 234 87 120 137 145	Gray10
	145	YLR079W	SIC1	G1/S transition of mitotic cell cycle	protein binding	cytoplasm	88 144	Red
	146	YLR088W	GAA1	attachment of GPI anchor to protein	GPI-anchor transamidase activity	integral to endoplasmic reticulum membrane	76	LimeGreen
	147	YLR103C	CDC45	DNA replication initiation	DNA binding	replication fork	224 59 111 222 234 72 91 98 110 122 127 128 131 139 140 151 157 160 166 175 188 193 194 205 214 217	Red
	148	YLR121C	YPS3	protein metabolism	aspartic-type endopeptidase activity	plasma membrane	222 152 166 193	LimeGreen
	149	YLR131C	ACE2	G1-specific transcription in mitotic cell cycle	transcriptional activator activity	nucleus	92 75 90 116 119 168 172 197 213	Red
	150	YLR154C	RNH203	biological_process unknown	molecular_function unknown	cytoplasm	94 130	Gray10
	151	YLR183C	TOS4	biological_process unknown	transcription factor activity	cytoplasm	224 111 199 221 222 234 68 77 94 95 97 98 117 122 128 131 132 134 138 139 140 147 160 166 176 188 193 194 195 196 208 210 214 216 217	Gray10
	152	YLR190W	MMR1	biological_process unknown	molecular_function unknown	bud neck	92 114 236 74 75 79 90 106 121 148 167 171 172 174 184 197 213	Gray10
	153	YLR234W	TOP3	meiotic recombination	DNA topoisomerase type I activity	nucleus	140	Red
	154	YLR236C					101	Gray10
	155	YLR274W	CDC46	DNA replication initiation	chromatin binding	cytoplasm	136 239 61 105 200	Red
	156	YLR300W	EXG1	cell wall organization and biogenesis	glucan 1,3-beta-glucosidase activity	cell wall (sensu Fungi)	195	Lavender
	157	YLR313C	SPH1	establishment of cell polarity (sensu Saccharomyces)	cytoskeletal regulatory protein binding	bud neck	101 72 98 122 147 160 188 205 212	Lavender
	158	YLR342W	FKS1	cell wall organization and biogenesis	1,3-beta-glucan synthase activity	actin cap (sensu Saccharomyces)	56 190	LimeGreen
	159	YLR353W	BUD8	pseudohyphal growth	molecular_function unknown	bud tip	197	Red
	160	YLR383W	RHC18	DNA repair	molecular_function unknown	nucleus	128 140 147 151 157 193 208	Red
	161	YLR462W		biological_process unknown	molecular_function unknown	cellular_component unknown	80 63 64 70 71 73 100 103 113 120 129 162 163 165 218 219	Purple
	162	YLR463C					71 100 113 120 161 163 165 218 219	Purple
	163	YLR464W		biological_process unknown	molecular_function unknown	cellular_component unknown	63 70 71 100 103 104 113 161 162 218 219	Purple
	164	YLR466W	YRF1-4	telomerase-independent telomere maintenance	DNA helicase activity	cellular_component unknown	100 120 165 218 219 220	Purple
	165	YLR467W	YRF1-5	telomerase-independent telomere maintenance	DNA helicase activity	cellular_component unknown	65 71 100 104 120 129 141 142 161 162 164 192 218 219 220	Purple
	166	YML027W	YOX1	negative regulation of transcription from Pol II promoter, mitotic	DNA binding	nucleus	224 111 221 222 234 68 91 94 95 97 98 115 117 122 128 131 133 134 139 140 147 148 151 175 176 188 193 194 196 210 214 216 217	Red
	167	YML033W					236 75 90 116 119 121 152 168 171 172 174 197 213	Lavender
	168	YML034W	SRC1	mitotic sister chromatid separation	molecular_function unknown	cellular_component unknown	75 90 116 119 149 167 172 174 197	Red
	169	YML064C	TEM1	signal transduction	protein binding	spindle pole body	171	Red
	170	YML102W	CAC2	DNA repair	molecular_function unknown	chromatin assembly complex	101 72 91 205	Red
	171	YML119W		biological_process unknown	molecular_function unknown	cellular_component unknown	227 236 75 79 93 106 116 152 167 169 172 174 184 213	Gray10
	172	YMR001C	CDC5	protein amino acid phosphorylation	protein serine/threonine kinase activity	nucleus	92 236 75 79 90 106 116 119 121 149 152 167 168 171 174 197 213	Red
	173	YMR031C		biological_process unknown	molecular_function unknown	cytoplasm	93	Gray10
	174	YMR032W	HOF1	cytokinesis	cytoskeletal protein binding	contractile ring (sensu Saccharomyces)	236 75 79 90 106 116 119 121 152 167 168 171 172 184 197	Red
	175	YMR179W	SPT21	regulation of transcription from Pol II promoter	molecular_function unknown	nucleus	111 187 199 222 234 91 122 131 147 166 188 194 214 217	Yellow
	176	YMR199W	CLN1	regulation of CDK activity	cyclin-dependent protein kinase regulator activity	cytoplasm	111 117 151 166 193 210	Red
	177	YMR238W	DFG5	pseudohyphal growth	molecular_function unknown	extrinsic to plasma membrane, GPI-anchored	190	Lavender
	178	YCL012W					181 182	Gray10
	179	YNL030W	HHP2	chromatin assembly/disassembly	DNA binding	nuclear nucleosome	237 238 84 85 226 240 241 180 204	Yellow
	180	YNL031C	HHT2	chromatin assembly/disassembly	DNA binding	nuclear nucleosome	237 238 84 85 226 240 241 179 204	Yellow
	181	YCL013W					178 206	Gray10
	182	YCL014W	BUD3	cytokinesis	molecular_function unknown	contractile ring (sensu Saccharomyces)	178 197	Lavender
	183	YNL057W					184	Gray10
	184	YNL058C		biological_process unknown	molecular_function unknown	vacuole (sensu Fungi)	227 92 233 79 89 106 152	Gray10

	185	YCL022C					171 174 183	
	186	YNL160W	YGP1	response to stress	molecular_function unknown	cell wall (sensu Fungi)	224 59 112 187 234 95 127 137 194 217	Gray10
	187	YCL024W	KCC4	protein amino acid phosphorylation	protein kinase activity	bud neck	96 123	Black
	188	YNL233W	BN14	cytokinesis	protein binding	contractile ring (sensu Saccharomyces)	224 59 111 112 185 199 222 234 91 95 127 131 137 175 188 191 194 196 205 216 217	Red
	189	YNL262W	POL2	lagging strand elongation	epsilon DNA polymerase activity	replication fork	224 111 187 199 222 234	Lavender
	190	YNL283C	WSC2	cell wall organization and biogenesis	transmembrane receptor activity	cytoplasm	224 111 187 199 222 234 94 95 122 131 147 151 157 166 175 191 193 194 196 198 205 210 214 216 217	Red
	191	YNL309W	STB1	G1/S transition of mitotic cell cycle	transcriptional activator activity	cytoplasm	240 241 62 107 158 177 202	LimeGreen
	192	YNL339C	YRF1-6	telomerase-independent telomere maintenance	DNA helicase activity	cellular_component unknown	187 94 95 140 188 216 217	Red
	193	YOL007C		biological_process unknown	molecular_function unknown	vacuole (sensu Fungi)	71 100 120 141 165 211 218 219 220	Purple
	194	YOL017W	ESC8	chromatin silencing	molecular_function unknown	nucleus	224 111 221 222 234 235 57 66 68 93 95 97 98 115 117 122 128 131 132 133 134 140 147 148 151 160 166 176 188 194 196 208 210 214 216 217	Gray10
	195	YOL019W		biological_process unknown	molecular_function unknown	vacuole (sensu Fungi)	224 59 111 112 185 187 199 222 234 91 94 95 98 108 122 131 139 140 147 151 166 175 188 193 196 205 214 216 217	Gray10
	196	YOL090W	MSH2	DNA recombination	ATPase activity	nuclear chromosome	111 222 97 132 151 156 196	Gray10
	197	YOR025W	HST3	chromatin silencing at telomere	DNA binding	nucleus	224 111 187 199 222 234 77 94 95 97 108 122 131 134 139 140 151 166 188 189 193 194 195 208 210 216 217	Red
	198	YOR033C	EXO1	mismatch repair	exonuclease activity	nucleus	92 182 236 75 116 149 152 159 167 168 172 174 213	Red
	199	YCL060C					59 188 214	Red
	200	YOR066W		biological_process unknown	molecular_function unknown	cellular_component unknown	224 111 112 187 222 234 91 95 122 131 139 140 151 175 188 194 196 217	Gray10
	201	YOR073W	SGO1	biological_process unknown	molecular_function unknown	nucleus	105 155	Gray10
	202	YOR112W		biological_process unknown	molecular_function unknown	cytoplasm	143	Red
	203	YOR195W	SLK19	meiosis	molecular_function unknown	condensed nuclear chromosome kinetochore	190	Gray10
	204	YPL127C	HHO1	regulation of transcription, DNA-dependent	DNA binding	nucleus	235 128	Red
	205	YPL153C	RAD53	DNA repair	protein threonine/tyrosine kinase activity	nucleus	237 238 85 235 240 241 179 180	Yellow
	206	YPL155C	KIP2	nuclear migration (sensu Saccharomyces)	microtubule motor activity	cytoplasmic microtubule	224 59 101 111 112 187 234 68 72 91 98 122 127 131 139 147 157 170 188 194 214 216 217	Red
	207	YCR024C-A	PMP1	cation transport	enzyme regulator activity	plasma membrane	181	Red
	208	YPL208W		biological_process unknown	molecular_function unknown	cytoplasm	114 74 215	LimeGreen
	209	YPL241C	CIN2	microtubule-based process	molecular_function unknown	cellular_component unknown	111 222 117 122 134 151 160 193 196 210	Gray10
	210	YPL256C	CLN2	regulation of CDK activity	cyclin-dependent protein kinase regulator activity	cytoplasm	139	Red
	211	YPL283C	YRF1-7	telomerase-independent telomere maintenance	DNA helicase activity	cellular_component unknown	224 111 221 222 234 66 68 95 97 115 117 122 128 131 133 134 140 151 166 176 188 193 196 208 214 216	Red
	212	YPR018W	RLF2	nucleosome assembly	molecular_function unknown	nucleus	100 129 192	Purple
	213	YPR119W	CLB2	G2/M transition of mitotic cell cycle	cyclin-dependent protein kinase regulator activity	cytoplasm	92 236 75 90 106 121 149 152 167 171 172 197	Red
	214	YPR120C	CLB5	G1/S transition of mitotic cell cycle	cyclin-dependent protein kinase regulator activity	nucleus	224 111 221 222 234 78 91 95 131 140 147 151 166 175 188 193 194 198 205 210 217	Red
	215	YPR149W	NCE102	protein secretion	molecular_function unknown	cytoplasm	114 207	Black
	216	YPR174C		biological_process unknown	molecular_function unknown	cellular_component unknown	224 111 187 222 234 95 122 131 134 151 166 188 191 193 194 196 205 210 217	Gray10
	217	YPR175W	DPB2	lagging strand elongation	epsilon DNA polymerase activity	replication fork	224 111 185 187 199 222 234 94 95 122 131 140 147 151 166 175 188 189 191 193 194 196 205 214 216	Red
	218	YPR202W		biological_process unknown	molecular_function unknown	cellular_component unknown	70 71 100 103 104 113 120 141 161 162 163 164 165 192 219 220	Purple
	219	YPR203W		biological_process unknown	molecular_function unknown	cellular_component unknown	71 100 104 113 120 141 161 162 163 164 165 192 218 220	Purple
	220	YPR204W		biological_process unknown	DNA helicase activity	cellular_component unknown	65 71 100 104 120 129 141 164 165 192 218 219	Purple
	221	YCR065W	HCM1	transcription initiation from Pol II promoter	specific RNA polymerase II transcription factor activity	nucleus	111 222 229 234 68 69 109 117 128 151 166 193 210 214	Red
	222	YDL003W	MCD1	mitotic chromosome condensation	molecular_function unknown	nuclear cohesin complex	224 102 111 187 199 221 230 234 91 94 95 98 108 115 117 122 128 131 132 133 134 139 140 147 148 151 166 175 188 193 194 195 196 208 210 214 216 217	Red
	223	YDL018C	ERP3	secretory pathway	molecular_function unknown	integral to membrane	224 60 108	Black
	224	YAR007C	RFA1	DNA recombination	damaged DNA binding	DNA replication factor A complex	59 111 112 185 187 199 222 223 234 68 94 95 98 108 122 127 131 139 140 147 151 166 188 189 193 194 196 205 210 214 216 217	Red

	225	YAR008W	SEN34	tRNA splicing	tRNA-intron endonuclease activity	nuclear inner membrane	59	Black
	226	YDL055C	PSA1	protein amino acid glycosylation	mannose-1-phosphate guanylyltransferase activity	cytoplasm	237 238 85 240 241 179 180	LimeGreen
	227	YAR018C	KIN3	chromosome segregation	protein kinase activity	cellular_component unknown	136 79 89 99 171 184	Red
	228	YDL095W	PMT1	O-linked glycosylation	dolichyl-phosphate-mannose-protein mannosyltransferase activity	endoplasmic reticulum membrane	77	LimeGreen
	229	YDL101C	DUN1	protein amino acid phosphorylation	protein kinase activity	nucleus	221 234	Red
	230	YDL103C	QRI1	UDP-N-acetylglucosamine biosynthesis	UDP-N-acetylglucosamine diphosphorylase activity	cytoplasm	222 234 131	LimeGreen
	231	YDL157C		biological_process unknown	molecular_function unknown	mitochondrion	140	Gray10
	232	YDL227C	HO	mating-type switching/recombination	endonuclease activity	nucleus	110	Lavender
	233	YDR033W	MRH1	biological_process unknown	molecular_function unknown	plasma membrane	96 114 184	Gray10
	234	YDR097C	MSH6	mismatch repair	DNA binding	nucleus	224 111 112 185 187 199 221 222 229 230 83 91 94 95 98 115 122 128 131 139 140 144 147 151 166 175 188 189 193 194 196 205 210 214 216 217	Red
	235	YDR113C	PDS1	protein-nucleus import	protein binding	nucleus	126 193 203 204	Red
	236	YDR146C	SWI5	G1-specific transcription in mitotic cell cycle	transcriptional activator activity	cytoplasm	75 90 106 152 167 171 172 174 197 213	Lavender
	237	YBL002W	HTB2	chromatin assembly/disassembly	DNA binding	nuclear nucleosome	238 84 85 226 240 241 143 179 180 204	Yellow
	238	YBL003C	HTA2	chromatin assembly/disassembly	DNA binding	nuclear nucleosome	237 84 85 226 240 241 179 180 204	Yellow
	239	YDR191W	HST4	chromatin silencing at telomere	DNA binding	cytoplasm	105 155	Lavender
	240	YDR224C	HTB1	chromatin assembly/disassembly	DNA binding	nuclear nucleosome	237 238 84 85 226 241 179 180 190 204	Yellow
	241	YDR225W	HTA1	chromatin assembly/disassembly	DNA binding	nuclear nucleosome	237 238 84 85 226 240 179 180 190 204	Yellow
Module 10	242	YEL049W	PAU2	biological_process unknown	molecular_function unknown	cellular_component unknown	243 244	Red
	243	YLL064C		biological_process unknown	molecular_function unknown	cellular_component unknown	242 244	Gray10
	244	YLR461W	PAU4	biological_process unknown	molecular_function unknown	cellular_component unknown	242 243	Red
Module 11	245	YGL089C	MF(ALPHA)2	response to pheromone during conjugation with cellular fusion	pheromone activity	extracellular	246 247 248	Red
	246	YGL090W	LIF1	double-strand break repair via nonhomologous end-joining	structural molecule activity	nucleus	245 247	Red
	247	YJR004C	SAG1	agglutination during conjugation with cellular fusion	cell adhesion receptor activity	cell wall (sensu Fungi)	245 246	Red
	248	YKL177W					245	Gray10
Module 12	249	YGR214W	RPS0A	protein biosynthesis	structural constituent of ribosome	cytosolic small ribosomal subunit (sensu Eukarya)	251	Red
	250	YOR063W	RPL3	protein biosynthesis	structural constituent of ribosome	cytosolic large ribosomal subunit (sensu Eukarya)	251 252	Red
	251	YPL131W	RPL5	protein biosynthesis	structural constituent of ribosome	cytosolic large ribosomal subunit (sensu Eukarya)	249 250 252	Red
	252	YPR080W	TEF1	translational elongation	translation elongation factor activity	ribosome	250 251	Red
Module 13	253	YER124C	DSE1	cell wall organization and biogenesis	molecular_function unknown	bud neck	254 256 264	Red
	254	YGL028C	SCW11	cytokinesis, completion of separation	glucan 1,3-beta-glucosidase activity	cell wall (sensu Fungi)	260 253 256 258 264 267	Red
	255	YGR044C	RME1	meiosis	specific transcriptional repressor activity	nucleus	260	Lavender
	256	YHR143W	DSE2	cell wall organization and biogenesis	glucan 1,3-beta-glucosidase activity	cell wall (sensu Fungi)	253 254 258 264	Red
	257	YIL009W	FAA3	lipid metabolism	long-chain-fatty-acid-CoA ligase activity	cellular_component unknown	262	LimeGreen
	258	YJL078C	PRY3	biological_process unknown	molecular_function unknown	cell wall (sensu Fungi)	254 256	Red
	259	YJL159W	HSP150	cell wall organization and biogenesis	structural constituent of cell wall	cell wall (sensu Fungi)	261 262	Red
	260	YBR158W	AMN1	negative regulation of exit from mitosis	protein binding	cytoplasm	254 255	Lavender
	261	YKL163W	PIR3	cell wall organization and biogenesis	structural constituent of cell wall	cell wall (sensu Fungi)	259 262 263	Red
	262	YKL164C	PIR1	cell wall organization and biogenesis	structural constituent of cell wall	cell wall (sensu Fungi)	257 259 261 263 265 266	Red
	263	YKL185W	ASH1	pseudohyphal growth	specific transcriptional repressor activity	nucleus	261 262 265 268	Lavender
	264	YLR286C	CTS1	cytokinesis, completion of separation	chitinase activity	endoplasmic reticulum	253 254 256	Lavender
	265	YNL078W	NIS1	regulation of mitosis	molecular_function unknown	nucleus	269 262 263 266 267	Lavender
	266	YNL327W	EGT2	cytokinesis	cellulase activity	cell wall (sensu Fungi)	270 262 265 267 268	Red
	267	YNR067C	DSE4	cytokinesis, completion of separation	glucan 1,3-beta-glucosidase activity	cell wall (sensu Fungi)	254 265 266	Red
	268	YPL158C		biological_process unknown	molecular_function unknown	bud neck	263 266	Gray10
	269	YDL117W	CYK3	cytokinesis	molecular_function unknown	cytoplasm	265	Gray10
	270	YDR055W	PST1	biological_process unknown	molecular_function unknown	cell wall (sensu Fungi)	266	Red
Module 14	271	YDR380W	ARO10	leucine catabolism	carboxyl-lyase activity	cytoplasm	272	Red
	272	YHR137W	ARO9	aromatic amino acid family metabolism	aromatic-amino-acid transaminase activity	cytoplasm	271 276 277 279	Red
	273	YOR048W	CYC1	electron transport	electron carrier activity	mitochondrial intermembrane space	274 276	Red
	274	YKL085W	MDH1	tricarboxylic acid cycle	L-malate dehydrogenase activity	mitochondrial matrix	273	Red
	275	YLR304C	ACO1	tricarboxylic acid cycle	aconitate hydratase activity	cytosol	277 278	Red
	276	YOR065W	CYT1	mitochondrial electron transport, ubiquinol to cytochrome c	electron transporter, transferring electrons within CoQH2-cytochrome c reductase complex activity	mitochondrial inner membrane	272 273	Red
	277	YOR135C					272 275 278	Gray10
	278	YOR136W	IDH2	tricarboxylic acid cycle	isocitrate dehydrogenase (NAD+) activity	mitochondrion	275 277	Red
	279	YPL265W	DIP5	amino acid transport	amino acid transporter activity	plasma membrane	272	Red
Module 15	280	YDR312W	SSF2	ribosomal large subunit assembly and maintenance	rRNA binding	nucleolus	683 717 781 799 283 410 433 474 551 564 576 618 674	Red
	281	YDR358W	GGA1	Golgi to vacuole transport	molecular_function unknown	Golgi trans face	723	Purple
	282	YDR361C	BCP1	biological_process unknown	molecular_function unknown	cytoplasm	283 312 322 350 386 389 539 671 674 716 737	Gray10
	283	YDR365C		rRNA processing	molecular_function unknown	nucleus	687 796 280 282 355 386 389 409 410 474 492 502 516 568 576 597 611 618 671	Red
	284	YDR368W	YPR1	arabinose metabolism	oxidoreductase activity	cytoplasm	472	LimeGreen
	285	YDR382W	RPP2B	protein biosynthesis	structural constituent of ribosome	cytosolic large ribosomal subunit (sensu Eukarya)	384 454 782 785 299 480 584	Yellow
	286	YDR385W	EFT2	translational elongation	translation elongation factor activity	ribosome	696	Yellow
	287	YDR394W	RPT3	ubiquitin-dependent protein catabolism	ATPase activity	proteasome regulatory particle (sensu Eukarya)	346 456 605	Purple
	288	YDR398W	UTP5	processing of 20S pre-rRNA	snRNA binding	small nucleolar ribonucleoprotein complex	573 775 802 355 359 492 533 576 611 622	Red
	289	YDR403W	DIT1	spore wall assembly (sensu Saccharomycetes)	catalytic activity	cellular_component unknown	304	LightCyan
	290	YDR410C	STE14	peptide pheromone maturation	protein-S-isoprenylcysteine O-methyltransferase activity	endoplasmic reticulum membrane	631	LimeGreen
	291	YDR412W		rRNA processing	molecular_function unknown	cytoplasm	683 422 432 433 437 524	Red
	292	YDR413C					683 312 334	Gray10
	293	YBL027W	RPL19B	protein biosynthesis	structural constituent of ribosome	cytosolic large ribosomal subunit (sensu Eukarya)	429 500	Yellow
	294	YDR417C					362 374 477 552 753	Gray10
	295	YDR418W	RPL12B	protein biosynthesis	structural constituent of ribosome	cytosolic large ribosomal subunit (sensu Eukarya)	454 511 514 741 789 317 324 344 357 391 418 548 558 582 585 595 670 680 701 733	Yellow
	296	YBL028C		biological_process unknown	molecular_function unknown	nucleus	413 474 671 674	Gray10
	297	YDR429C	TIF35	translational initiation	translation initiation factor activity	eukaryotic translation initiation factor 3	311	Yellow

298	YDR449C	UTP6	processing of 20S pre-rRNA	snRNA binding	complex small nucleolar ribonucleoprotein complex	796 312 370 389 406 426 450 470 501 504 533 539 611 622 653 666 671 674 675 697 707 739 757	Red
299	YDR450W	RPS18A	protein biosynthesis	structural constituent of ribosome	cytosolic small ribosomal subunit (sensu Eukarya)	401 454 511 514 782 285 418 480 546 693	Yellow
300	YDR494W	RSM28	biological_process unknown	molecular_function unknown	cellular_component unknown	801 365 405 518 656 700	Gray10
301	YDR513W	TTR1	response to oxidative stress	thiol-disulfide exchange intermediate activity	mitochondrion	438	LimeGreen
302	YDR516C	EMI2	biological_process unknown	molecular_function unknown	cytoplasm	599 312 612	LimeGreen
303	YBL039C	URA7	phospholipid biosynthesis	CTP synthase activity	cytosol	467 392 651 679 721	LimeGreen
304	YEL010W					289 321 335 340 353 404	Gray10
305	YEL011W	GLC3	glycogen metabolism	1,4-alpha-glucan branching enzyme activity	cytoplasm	402 339 414 475 501 523	LimeGreen
306	YEL015W	EDC3	biological_process unknown	molecular_function unknown	cytoplasm	769 342 617 750	Gray10
307	YEL027W	CUP5	protein-vacuolar targeting	hydrogen ion transporter activity	hydrogen-transporting ATPase V0 domain	615 337 338	Purple
308	YEL035C	UTR5	biological_process unknown	molecular_function unknown	cellular_component unknown	767 351 462 463	Gray10
309	YEL054C	RPL12A	protein biosynthesis	structural constituent of ribosome	cytosolic large ribosomal subunit (sensu Eukarya)	319	Yellow
310	YEL059W					335	Gray10
311	YER002W	NOP16	ribosomal large subunit biogenesis	molecular_function unknown	nucleus	687 717 297 410 474 516 568	Red
312	YER006W	NUG1	rRNA processing	GTPase activity	nucleus	599 681 683 687 703 717 779 780 781 797 282 292 298 302 322 334 343 350 355 358 359 370 386 389 393 406 410 422 450 474 539 559 564 576 611 622 653 671 674 707 739 756	Red
313	YER012W	PRE1	ubiquitin-dependent protein catabolism	endopeptidase activity	nucleus	786 354	Purple
314	YER029C	SMB1	nuclear mRNA splicing, via spliceosome	pre-mRNA splicing factor activity	small nuclear ribonucleoprotein complex	483	Lavender
315	YER050C	RSM18	protein biosynthesis	structural constituent of ribosome	mitochondrial small ribosomal subunit	695 751 330	Tan
316	YER066W		biological_process unknown	molecular_function unknown	cellular_component unknown	353	Gray10
317	YER102W	RPS8B	protein biosynthesis	structural constituent of ribosome	cytosolic small ribosomal subunit (sensu Eukarya)	741 295 324 344 357 362 372 391 418 548 558 582 585 595 670 680	Yellow
318	YER103W	SSA4	response to stress	chaperone activity	cytoplasm	738	Purple
319	YER117W	RPL23B	protein biosynthesis	structural constituent of ribosome	cytosolic large ribosomal subunit (sensu Eukarya)	309 473 587 613 724	Yellow
320	YER119C	AVT6	amino acid transport	amino acid transporter activity	vacuole	325	LimeGreen
321	YER121W					304	Gray10
322	YER126C	NSA2	ribosomal large subunit biogenesis	molecular_function unknown	nucleus	726 599 681 797 282 312 343 370 386 392 393 539 594 653 671 674 698 707 737 756	Red
323	YER127W	LCP5	rRNA modification	RNA binding	small nucleolar ribonucleoprotein complex	370	Red
324	YER131W	RPS26B	protein biosynthesis	structural constituent of ribosome	cytosolic small ribosomal subunit (sensu Eukarya)	295 317 344 357 372 391 418 548 558 582 585 595 680	Yellow
325	YER141W	COX15	cytochrome c oxidase biogenesis	molecular_function unknown	mitochondrial inner membrane	320 352 355 389 443	LimeGreen
326	YER148W	SPT15	transcription initiation from Pol II promoter	DNA binding	nucleus	399 483 516 638	Red
327	YBL078C	ATG8	protein-vacuolar targeting	microtubule binding	microtubule associated complex	672 688 723	Purple
328	YER156C		biological_process unknown	molecular_function unknown	cytoplasm	367 539 559 743	Gray10
329	YER171W	RAD3	transcription initiation from Pol II promoter	general RNA polymerase II transcription factor activity	transcription factor TFIIB complex	406 576 611 671 707	LightCyan
330	YER182W	FMP10	biological_process unknown	molecular_function unknown	mitochondrion	695 776 315 375 380 709	Tan
331	YBL082C	RHK1	protein amino acid glycosylation	alpha-1,3-mannosyltransferase activity	endoplasmic reticulum	553	LimeGreen
332	YER185W		biological_process unknown	molecular_function unknown	integral to membrane	333	Gray10
333	YER187W		biological_process unknown	molecular_function unknown	cellular_component unknown	332 340 353	Gray10
334	YFL002C	SPB4	35S primary transcript processing	ATP dependent RNA helicase activity	nucleolus	681 687 703 779 797 292 312 355 359 386 389 410 450 539 622 671 674	Red
335	YFL015C					304 310	Gray10
336	YFL016C	MDJ1	protein folding	co-chaperone activity	mitochondrial inner membrane	636	Purple
337	YFL039C	ACT1	cell wall organization and biogenesis	structural constituent of cytoskeleton	actin cortical patch (sensu Saccharomyces)	307 338	LightCyan
338	YFL041W	FET5	iron ion transport	ferroxidase activity	membrane fraction	307 337	LimeGreen
339	YFR015C	GSY1	glycogen metabolism	glycogen (starch) synthase activity	cytoplasm	402 305	LimeGreen
340	YFR020W					769 304 333 403 436 706	Gray10
341	YFR022W		biological_process unknown	molecular_function unknown	cellular_component unknown	367	LimeGreen
342	YFR037C	RSC8	chromatin remodeling	molecular_function unknown	nucleus	769 306 345 361 371 436 442	LightCyan
343	YGL029W	CGR1	rRNA processing	molecular_function unknown	nucleolus	413 687 717 796 312 322 350 370 386 409 410 474 516 539 576 594 597 611 638 645 671 674 725 737	Red
344	YGL031C	RPL24A	protein biosynthesis	structural constituent of ribosome	cytosolic large ribosomal subunit (sensu Eukarya)	295 317 324 357 372 391 418 548 558 582 585 595 670 680 705	Yellow
345	YGL044C	RNA15	mRNA polyadenylation	cleavage/polyadenylation specificity factor activity	mRNA cleavage factor complex	791 342 368 617	Lavender
346	YGL048C	RPT6	ubiquitin-dependent protein catabolism	ATPase activity	nucleus	287 456 512 754	Purple
347	YGL049C	TIF4632	translational initiation	translational initiation factor activity	ribosome	526	Yellow
348	YGL068W		biological_process unknown	molecular_function unknown	mitochondrion	508	Tan
349	YGL076C	RPL7A	protein biosynthesis	structural constituent of ribosome	cytosolic large ribosomal subunit (sensu Eukarya)	356	Yellow
350	YGL078C	DBP3	35S primary transcript processing	ATP dependent RNA helicase activity	nucleolus	413 520 573 683 282 312 343 355 359 370 386 389 390 406 410 455 460 468 474 482 492 504 531 533 539 559 563 576 611 618 622 639 645 653 671 674 676 707 716 725 732 739 757	Red
351	YGL081W		biological_process unknown	molecular_function unknown	cellular_component unknown	308	Gray10
352	YGL084C	GUP1	glycerol catabolism	glycerol transporter activity	membrane	325	LimeGreen
353	YGL088W					304 316 333 377 379	Gray10
354	YGL095C	VPS45	protein complex assembly	chaperone activity	cytosol	313 485	Purple
355	YGL099W	LSG1	sporulation (sensu Saccharomyces)	GTPase activity	cytoplasm	573 683 283 288 312 325 334 350 359 370 386 389 390 406 410 460 482 492 502 504 516 531 533 539 541 556 576 591 611 622 671 676 707 739	Red
356	YGL102C					349 374 383 549 608 753	Gray10
357	YGL103W	RPL28	protein biosynthesis	structural constituent of ribosome	nucleus	741 295 317 324 344 362 372 391 418 548 558 582 585 595 670 680 693	Yellow
358	YGL111W	NSA1	ribosomal large subunit biogenesis	molecular_function unknown	nucleus	599 703 780 797 312 359 386 389 410 455 460	Red

	359	YGL120C	PRP43	U2-type spliceosome dissembly	pre-mRNA splicing factor activity	spliceosome complex	520 573 683 687 775 797 288 312 334 350 355 358 370 386 389 390 406 410 433 450 460 468 474 482 492 504 516 531 533 539 559 562 563 564 568 569 576 590 611 620 621 622 645 647 653 657 660 661 671 674 676 697 698 707 716 739 756 757	Lavender
	360	YGL121C	GP61	signal transduction	signal transducer activity	cellular_component unknown	767 415	Gray10
	361	YGL122C	NAB2	mRNA polyadenylation	poly(A) binding	cytoplasm	342	Lavender
	362	YGL123W	RPS2	protein biosynthesis	structural constituent of ribosome	cytosolic small ribosomal subunit (sensu Eukarya)	294 317 357 366 490 552 582	Yellow
	363	YGL128C	CWC23	biological_process unknown	molecular_function unknown	spliceosome complex	773 403 436	Gray10
	364	YGL135W	RPL1B	protein biosynthesis	structural constituent of ribosome	cytosolic large ribosomal subunit (sensu Eukarya)	528 583	Yellow
	365	YGL143C	MRF1	protein biosynthesis	translation release factor activity	mitochondrion	300 380 405 518	Tan
	366	YGL147C	RPL9A	protein biosynthesis	structural constituent of ribosome	cytosolic large ribosomal subunit (sensu Eukarya)	362 753	Yellow
	367	YGL148W	ARO2	aromatic amino acid family biosynthesis	chorismate synthase activity	cytoplasm	328 341 427 740 743	LimeGreen
	368	YGL164C	YRB30	biological_process unknown	protein binding	cytoplasm	345 491	Gray10
	369	YGL169W	SUA5	cell growth and/or maintenance	molecular_function unknown	cytoplasm	783	Yellow
	370	YGL171W	ROK1	35S primary transcript processing	ATPase activity	nucleolus	413 573 599 683 687 703 784 298 312 322 323 343 350 355 359 386 389 390 406 409 410 426 433 450 458 460 474 482 492 504 516 524 531 533 539 569 576 594 611 618 622 638 643 645 653 657 666 671 674 697 698 707 725 737 739 756 761	Red
	371	YGL172W	NUP49	mRNA-nucleus export	structural_molecule activity	nuclear pore	769 342	Red
	372	YGL189C	RPS26A	protein biosynthesis	structural constituent of ribosome	cytosolic small ribosomal subunit (sensu Eukarya)	317 324 344 357 391 548 558 582 585 595 670 680	Yellow
	373	YGL204C					377 379 416 462 463	Gray10
	374	YGR027C	RPS25A	protein biosynthesis	structural constituent of ribosome	cytosolic small ribosomal subunit (sensu Eukarya)	294 356 387 596 608	Yellow
	375	YGR028W	MSP1	protein-mitochondrial targeting	ATPase activity	mitochondrial outer membrane	330 509 600 709	Tan
	376	YGR034W	RPL26B	protein biosynthesis	structural constituent of ribosome	cytosolic large ribosomal subunit (sensu Eukarya)	440 552	Yellow
	377	YGR039W					353 373 379 463	Gray10
	378	YGR043C		biological_process unknown	transaldolase activity	nucleus	415	Gray10
	379	YGR059W	SPR3	cell wall organization and biogenesis	structural constituent of cytoskeleton	prosopore membrane	353 373 377	LightCyan
	380	YGR076C	MRPL25	protein biosynthesis	structural constituent of ribosome	mitochondrial large ribosomal subunit	695 330 365 518	Tan
	381	YGR081C	SLX9	DNA metabolism	molecular_function unknown	nucleus	542	Gray10
	382	YGR083C	GCD2	translational initiation	translation initiation factor activity	ribosome	618	Yellow
	383	YGR085C	RPL11B	protein biosynthesis	structural constituent of ribosome	cytosolic large ribosomal subunit (sensu Eukarya)	356 440 608 753	Yellow
	384	YBR031W	RPL4A	protein biosynthesis	structural constituent of ribosome	cytosolic large ribosomal subunit (sensu Eukarya)	401 454 514 782 785 285 503 584	Yellow
	385	YGR095C	RRP46	35S primary transcript processing	3'-5' exoribonuclease activity	nuclear exosome (RNase complex)	386 611 638 658	Red
	386	YGR103W	NOP7	processing of 20S pre-rRNA	molecular_function unknown	nucleus	520 573 683 687 768 780 282 283 312 322 334 343 350 355 358 359 370 385 389 390 406 410 412 450 460 474 482 492 516 531 539 551 559 562 564 568 576 597 611 622 629 658 661 671 674 676 707 712 739 756 757 764	Red
	387	YGR118W	RPS23A	protein biosynthesis	structural constituent of ribosome	cytosolic small ribosomal subunit (sensu Eukarya)	374 440 753	Yellow
	388	YGR123C	PPT1	protein amino acid phosphorylation	protein serine/threonine phosphatase activity	cytoplasm	606 775 390 423 468 492 533 562 576 611 647 739	Gray10
	389	YGR128C	UTP8	processing of 20S pre-rRNA	snRNA binding	small nucleolar ribonucleoprotein complex	413 573 683 796 282 283 298 312 325 334 350 355 358 359 370 386 390 406 410 433 443 450 455 460 468 470 474 482 492 501 504 516 523 531 533 539 562 576 588 591 611 621 622 647 649 657 671 674 675 676 707 716 739 747 757	Red
	390	YGR145W	ENP2	rRNA processing	molecular_function unknown	nucleolus	413 573 606 683 703 775 350 355 359 370 386 388 389 406 410 423 455 460 468 474 482 492 494 497 502 504 516 531 533 539 551 562 576 590 611 618 622 645 647 657 660 671 676 698 699 707 716 725 739 757	Red
	391	YGR148C	RPL24B	protein biosynthesis	structural constituent of ribosome	cytosolic large ribosomal subunit (sensu Eukarya)	295 317 324 344 357 372 548 558 582 585 595 670 680	Yellow
	392	YGR159C	NSR1	rRNA processing	RNA binding	nucleus	726 303 467 784 797 322 393 432 453 563 569 620 632 644 653 679 698 721	Red
	393	YGR160W					681 703 784 797 312 322 392 406 453 465 517 539 620 632 644 646 653 662 674 692 730	Gray10
	394	YGR167W	CLC1	vesicle-mediated transport	structural_molecule activity	clathrin vesicle coat	801 398 435 452 484 488 491 518 522 633 754	Black
	395	YBR048W	RPS11B	protein biosynthesis	structural constituent of ribosome	cytosolic small ribosomal subunit (sensu Eukarya)	500 527 586 678	Yellow
	396	YGR173W	GIR1	biological_process unknown	molecular_function unknown	cytoplasm	474 492 516 576 739	Gray10
	397	YGR187C	HGH1	biological_process unknown	molecular_function unknown	cytoplasm	437 594 684	Gray10
	398	YGR193C	PDX1	acetyl-CoA biosynthesis from pyruvate	protein binding	mitochondrion	394 434 633 689	Tan
	399	YGR195W	SKI6	35S primary transcript processing	3'-5' exoribonuclease activity	nuclear exosome (RNase complex)	769 326 412 450 474 492 496 507 516 540 576 592 593 597 603 611 617 625 629 652 699 739 750 757	Red
	400	YGR200C	ELP2	regulation of transcription from Pol II promoter	Pol II transcription elongation factor activity	transcription elongation factor complex	455	LightCyan

401	YAL003W	EFB1	translational elongation	translation elongation factor activity	ribosome	545 384 454 511 514 299 480 546	Yellow
402	YBR056W		biological_process unknown	molecular_function unknown	cytoplasm	472 305 339 414 449	Gray10
403	YGR201C		biological_process unknown	molecular_function unknown	cellular_component unknown	340 363 436	Gray10
404	YGR212W		biological_process unknown	molecular_function unknown	cellular_component unknown	304	Gray10
405	YGR220C	MRPL9	protein biosynthesis	structural constituent of ribosome	mitochondrial large ribosomal subunit	300 365 614	Tan
406	YGR245C	SDA1	actin cytoskeleton organization and biogenesis	molecular_function unknown	nucleus	573 599 683 703 770 784 797 298 312 329 350 355 359 370 386 389 390 393 410 433 437 453 455 458 460 465 468 474 482 492 501 504 523 531 533 539 556 562 563 569 576 588 590 611 618 620 621 622 632 637 646 647 653 657 660 666 671 674 675 676 698 707 716 730 732 739 757	LightCyan
407	YGR248W	SOL4	biological_process unknown	6-phosphogluconolactonase activity	cytoplasm	627	Gray10
408	YGR267C	FOL2	folic acid and derivative biosynthesis	GTP cyclohydrolase 1 activity	cytoplasm	791 529	LightGreen
409	YGR272C		processing of 20S pre-rRNA	molecular_function unknown	cytoplasm	413 796 283 343 370 410 426 474 502 504 516 594 611 638 671 725	Red
410	YGR280C	PXR1	35S primary transcript processing	RNA binding	nucleolus	413 476 573 683 687 703 717 796 799 280 283 311 312 334 343 350 355 358 359 370 386 389 390 406 409 426 433 450 460 474 482 492 502 504 516 524 531 533 539 547 551 559 564 568 576 594 597 611 618 622 638 643 645 653 657 671 674 697 707 725 739 757 761 764	Red
411	YGR282C	BGL2	cell wall organization and biogenesis	glucan 1,3-beta-glucosidase activity	cell wall (sensu Fungi)	598 624 667	LightGreen
412	YGR285C	ZUO1	protein folding	chaperone activity	cytoplasm	386 399 457 492 495 496 559 564 576 597 611 658 661 739 750	Red
413	YAL025C	MAK16	ribosomal large subunit biogenesis	molecular_function unknown	nucleolus	296 476 573 683 687 796 343 350 370 389 390 409 410 433 450 460 474 482 492 502 504 516 531 539 576 611 643 645 653 671 674 707 725	Red
414	YHL021C	FMP12	biological_process unknown	molecular_function unknown	mitochondrion	402 664 305 438 449 523 535 557 723	Gray10
415	YBR072W	HSP26	response to stress	chaperone activity	cytoplasm	360 378	Purple
416	YHL037C					373	Gray10
417	YHR006W	STP2	positive regulation of transcription from Pol II promoter	specific RNA polymerase II transcription factor activity	nucleus	673 752	Lavender
418	YHR010W	RPL27A	protein biosynthesis	structural constituent of ribosome	cytosolic large ribosomal subunit (sensu Eukarya)	295 299 317 324 344 357 558 582 595 680 693	Yellow
419	YHR013C	ARD1	protein amino acid acetylation	peptide alpha-N-acetyltransferase activity	cytoplasm	758	LightGreen
420	YHR014W	SPO13	positive regulation of sister chromatid cohesion	protein binding	nucleus	448 463 571 619	LightCyan
421	YHR016C	YSC84	actin filament organization	molecular_function unknown	actin cortical patch (sensu Saccharomyces)	475	LightCyan
422	YHR052W	CICI	protein catabolism	protein binding, bridging	nucleolus	291 312	Gray10
423	YHR065C	RRP3	35S primary transcript processing	ATP dependent RNA helicase activity	nucleolus	388 390 458 468 482 591	Red
424	YHR069C	RRP4	35S primary transcript processing	3'-5' exoribonuclease activity	nuclear exosome (RNase complex)	450 576 611	Red
425	YHR085W	IP1	rRNA processing	molecular_function unknown	nucleus	775 802 524	Red
426	YHR088W	RPF1	ribosomal large subunit assembly and maintenance	rRNA primary transcript binding	nucleolus	298 370 409 410 450 474 492 504 539 622 671 697 707	Red
427	YHR096C	HXT5	hexose transport	glucose transporter activity	plasma membrane	367	LightGreen
428	YHR116W		aerobic respiration	molecular_function unknown	cytoplasm	513	Gray10
429	YBR084C-A	RPL19A	protein biosynthesis	structural constituent of ribosome	cytosolic large ribosomal subunit (sensu Eukarya)	293 711	Yellow
430	YHR148W	IMP3	rRNA modification	snRNA binding	small nucleolar ribonucleoprotein complex	524	Red
431	YHR169W	DBP8	35S primary transcript processing	ATP dependent RNA helicase activity	nucleolus	599 432 465 523 569 610 653	Red
432	YHR170W	NMD3	ribosomal large subunit assembly and maintenance	protein binding	cytosol	291 392 431 433 468 563 569 632 653 698 730	Red
433	YHR196W	UTP9	processing of 20S pre-rRNA	snRNA binding	nucleus	413 573 599 683 703 781 784 280 291 359 370 389 406 410 432 453 460 465 468 531 539 563 569 618 620 632 639 646 653 671 674 698 707 716 730 732	Red
434	YHR200W	RPN10	ubiquitin-dependent protein catabolism	endopeptidase activity	proteasome regulatory particle (sensu Eukarya)	398 754	Purple
435	YHR201C	PPX1	polyphosphate metabolism	exopolyphosphatase activity	cytoplasm	394	LightGreen
436	YIL001W		biological_process unknown	molecular_function unknown	cytoplasm	340 342 363 403	Gray10
437	YIL019W		biological_process unknown	molecular_function unknown	cytoplasm	599 291 397 406 446	Gray10
438	YIL034C	CAP2	cell wall organization and biogenesis	F-actin capping activity	actin cortical patch (sensu Saccharomyces)	777 301 414	LightCyan
439	YIL035C	CKA1	protein amino acid phosphorylation	protein kinase CK2 activity	protein kinase CK2 complex	617	LightCyan
440	YIL052C	RPL34B	protein biosynthesis	structural constituent of ribosome	cytosolic large ribosomal subunit (sensu Eukarya)	376 383 387 552 580 753	Yellow
441	YIL062C	ARC15	actin cortical patch assembly	structural molecule activity	mitochondrial membrane	461 600	Tan
442	YIL063C	YRB2	mRNA-nucleus export	structural molecule activity	nuclear pore	342	Red
443	YIL064W		biological_process unknown	S-adenosylmethionine-dependent methyltransferase activity	cytoplasm	325 389 455	Gray10
444	YIL070C	MAM33	aerobic respiration	molecular_function unknown	mitochondrial matrix	550	Tan
445	YIL093C	RSM25	protein biosynthesis	structural constituent of ribosome	mitochondrial small ribosomal subunit	464 550	Tan
446	YIL096C		biological_process unknown	molecular_function unknown	nucleus	437	Gray10
447	YIL098C	FMC1	protein complex assembly	molecular_function unknown	mitochondrion	508 513	Tan
448	YIL100W					420 571	Gray10
449	YIL124W	AYR1	phosphatidic acid biosynthesis	acylglycerone-phosphate reductase activity	cytoplasm	402 664 414 575	LightGreen
450	YIL127C		biological_process unknown	molecular_function unknown	nucleolus	413 796 298 312 334 359 370 386 389 399 410 424 426 460 474 482 492 502 504 516 539 568 576 611 622 638 649 671 674 707 739 757	Gray10
451	YIL133C	RPL16A	protein biosynthesis	structural constituent of ribosome	cytosolic large ribosomal subunit (sensu Eukarya)	490	Yellow
452	YIR003W		biological_process unknown	molecular_function unknown	actin cytoskeleton	394 491 593	Gray10
453	YIR012W	SQT1	ribosomal large subunit assembly and maintenance	molecular_function unknown	cytoplasm	797 392 393 406 433 465 563 569 620 632 644 646	Red

	454	YBR118W	TEF2	translational elongation	translation elongation factor activity	ribosome	653 662 692 698 401 384 511 514 285 295 299 480	Yellow
	455	YIR026C	YVH1	meiosis	protein-tyrosine-phosphatase activity	cytoplasm	772 784 350 358 389 390 400 406 443 460 501 523 590 591 637 647 657 707 716	LightCyan
	456	YJL001W	PRE3	ubiquitin-dependent protein catabolism	endopeptidase activity	proteasome core complex (sensu Eukarya)	287 346 605	Purple
	457	YJL009W					412	Gray10
	458	YJL010C		rRNA processing	RNA binding	nucleus	573 703 784 370 406 423 460 523 707	Red
	459	YJL011C	RPC17	transcription initiation from Pol III promoter	DNA-directed RNA polymerase activity	DNA-directed RNA polymerase III complex	576 611	Lavender
	460	YJL033W	HCA4	35S primary transcript processing	ATP dependent RNA helicase activity	nucleolus	413 573 683 703 770 775 784 350 355 358 359 370 386 389 390 406 410 433 450 455 458 468 470 474 482 492 501 504 516 523 531 533 539 556 562 563 576 588 590 591 611 618 621 622 637 646 647 649 660 671 674 675 676 697 698 707 716 739 757	Red
	461	YJL036W	SNX4	transport	lipid binding	membrane	441	Purple
	462	YJL037W		biological_process unknown	molecular_function unknown	cellular_component unknown	308 373 463 487	Gray10
	463	YJL038C		biological_process unknown	molecular_function unknown	cellular_component unknown	308 373 377 420 462 749	Gray10
	464	YJL063C	MRPL8	protein biosynthesis	structural constituent of ribosome	mitochondrial large ribosomal subunit	445 550 654	Tan
	465	YJL069C	UTP18	processing of 20S pre-rRNA	snRNA binding	nucleolus	703 797 393 406 431 433 453 523 539 621 632 646 653 657	Red
	466	YJL104W	PAM16	biological_process unknown	molecular_function unknown	mitochondrion	700 710	Tan
	467	YBR142W	MAK5	rRNA processing	ATP dependent RNA helicase activity	nucleus	726 303 392 651 679	Red
	468	YJL122W		biological_process unknown	molecular_function unknown	nucleus	573 683 703 350 359 388 389 390 406 423 432 433 460 504 523 531 533 539 563 569 576 588 591 620 622 632 639 642 645 653 698 707 716 730 732 739	Gray10
	469	YJL124C	LSM1	rRNA processing	RNA cap binding	cytoplasmic mRNA processing body	522 710	Red
	470	YJL125C	GCD14	tRNA methylation	tRNA methyltransferase activity	nucleus	298 389 460 482 501 504 523 533 539 675 676 707	Yellow
	471	YJL136C	RPS21B	protein biosynthesis	structural constituent of ribosome	cytosolic small ribosomal subunit (sensu Eukarya)	711	Yellow
	472	YBR149W	ARA1	carbohydrate metabolism	aldo-keto reductase activity	cytosol	402 664 284 627	LimeGreen
	473	YJL138C	TIF2	translational initiation	translation initiation factor activity	cytoplasm	319 480 528	Yellow
	474	YJL148W	RPA34	transcription from Pol I promoter	DNA-directed RNA polymerase activity	nucleus	413 296 683 687 717 796 280 283 311 312 343 350 359 370 386 389 390 396 399 406 409 410 426 450 460 482 492 502 504 516 531 539 559 564 568 576 590 594 597 611 618 622 629 638 643 645 652 661 666 671 674 697 707 725 739 756 757 761 764	Red
	475	YJL164C	TPK1	protein amino acid phosphorylation	protein serine/threonine kinase activity	cytoplasm	305 421	Red
	476	YBR155W	CNS1	protein folding	chaperone activity	cytoplasm	413 687 410 516 611	Purple
	477	YJL177W	RPL17B	protein biosynthesis	structural constituent of ribosome	cytosolic large ribosomal subunit (sensu Eukarya)	294 552 580 753	Yellow
	478	YJL180C	ATP12	protein complex assembly	chaperone activity	mitochondrial matrix	714 605 700	Tan
	479	YJL183W	MNN11	protein amino acid glycosylation	alpha-1,6-mannosyltransferase activity	mannosyltransferase complex	553	LimeGreen
	480	YJL190C	RPS22A	protein biosynthesis	structural constituent of ribosome	cytosolic small ribosomal subunit (sensu Eukarya)	401 454 514 782 785 285 299 473 546 574 584 693 733	Yellow
	481	YJL200C		biological_process unknown	aconitate hydratase activity	mitochondrion	730	Tan
	482	YJR002W	MPP10	rRNA modification	molecular_function unknown	nucleus	413 573 683 350 355 359 370 386 389 390 406 410 423 450 460 470 474 492 504 516 533 539 551 562 576 590 597 611 618 622 645 649 671 674 676 707 725 739 757	Red
	483	YJR014W		biological_process unknown	RNA binding	cytoplasm	314 326 597 609 629	Gray10
	484	YJR049C	UTR1	iron ion homeostasis	NAD+ kinase activity	cytoplasm	394 617	LimeGreen
	485	YJR050W	ISY1	nuclear mRNA splicing, via spliceosome	pre-mRNA splicing factor activity	spliceosome complex	354 734	Lavender
	486	YJR101W	RSM26	protein biosynthesis	structural constituent of ribosome	mitochondrial small ribosomal subunit	710	Tan
	487	YJR108W	ABM1	microtubule cytoskeleton organization and biogenesis	molecular_function unknown	cellular_component unknown	462	Gray10
	488	YKL002W	DID4	late endosome to vacuole transport	protein binding	cytoplasm	801 394 522	Purple
	489	YKL003C	MRP17	protein biosynthesis	structural constituent of ribosome	mitochondrial small ribosomal subunit	714	Tan
	490	YKL006W	RPL14A	protein biosynthesis	structural constituent of ribosome	cytosolic large ribosomal subunit (sensu Eukarya)	362 451 499	Yellow
	491	YKL007W	CAP1	cell wall organization and biogenesis	F-actin capping activity	actin cortical patch (sensu Saccharomyces)	368 394 452	LightCyan
	492	YKL009W	MRT4	rRNA processing	molecular_function unknown	nucleus	413 520 573 798 283 288 350 355 359 370 386 388 389 390 396 399 406 410 412 426 450 460 474 482 496 502 504 516 531 533 539 541 559 562 564 568 576 597 611 622 645 661 671 674 697 702 707 712 725 739 756 757 761 764	Red
	493	YKL014C	URB1	biological_process unknown	molecular_function unknown	nucleolus	563 646	Gray10
	494	YKL021C	MAK11	ribosomal large subunit biogenesis	molecular_function unknown	membrane fraction	683 390 504	Red
	495	YKL024C	URA6	nucleobase, nucleoside, nucleotide and nucleic acid metabolism	uridine kinase activity	cytoplasm	412 541 712	LimeGreen
	496	YKL027W		biological_process unknown	molecular_function unknown	mitochondrion	399 412 492 502 576 611	Tan
	497	YKL029C	MAE1	pyruvate metabolism	malate dehydrogenase (oxaloacetate-decarboxylating) activity	mitochondrion	390 498 533	Tan
	498	YKL030W					497	Gray10
	499	YKL056C		biological_process unknown	molecular_function unknown	cytoplasm	490 604 669	Yellow
	500	YBR181C	RPS6B	protein biosynthesis	structural constituent of ribosome	cytoplasm	293 395	Yellow
	501	YKL078W	DHR2	ribosome biogenesis	RNA helicase activity	nucleolus	770 772 784 298 305 389 406 455 460 470 523 533 539 620 621 637 646 647 676 697 707 762	Red
	502	YKL082C	RRP14	establishment of cell polarity (sensu Saccharomyces)	molecular_function unknown	nucleolus	413 796 283 355 390 409 410 450 474 492 496 504 516 576 597 611 643 645	Red

	503	YKL096W-A	CWP2	cell wall organization and biogenesis	structural constituent of cell wall	cell wall (sensu Fungi)	690 725 739 757 384	LightCyan
	504	YKL099C	UTP11	processing of 20S pre-rRNA	snRNA binding	small nucleolar ribonucleoprotein complex	413 298 350 355 359 370 389 390 406 409 410 426 450 460 468 470 474 482 492 494 502 516 531 533 539 541 576 611 622 645 653 697 707 739 757	Red
	505	YAL005C	SSA1	protein folding	chaperone activity	cytoplasm	804 534	Purple
	506	YKL117W	SBA1	protein folding	co-chaperone activity	cytoplasm	755	Purple
	507	YKL122C	SRP21	protein-ER targeting	signal sequence binding	nucleus	399 597 609 617 750	Purple
	508	YKL138C	MRPL31	protein biosynthesis	structural constituent of ribosome	mitochondrial large ribosomal subunit	348 447 532	Tan
	509	YKL142W	MRP8	protein biosynthesis	structural constituent of ribosome	mitochondrial ribosome	375 572 709	Tan
	510	YKL144C	RPC25	transcription from Pol III promoter	DNA-directed RNA polymerase activity	DNA-directed RNA polymerase III complex	576	Red
	511	YBR189W	RPS9B	protein biosynthesis	structural constituent of ribosome	cytosolic small ribosomal subunit (sensu Eukarya)	401 454 514 295 299	Yellow
	512	YKL145W	RPT1	ubiquitin-dependent protein catabolism	ATPase activity	proteasome regulatory particle (sensu Eukarya)	786 346	Purple
	513	YKL167C	MRP49	protein biosynthesis	structural constituent of ribosome	mitochondrial large ribosomal subunit	428 447 515	Tan
	514	YBR191W	RPL21A	protein biosynthesis	structural constituent of ribosome	cytosolic large ribosomal subunit (sensu Eukarya)	401 384 454 511 782 295 299 480	Yellow
	515	YKL169C					513	Gray10
	516	YKL172W	EBP2	rRNA processing	molecular_function unknown	nucleolus	413 476 687 717 796 798 283 311 326 343 355 359 370 386 389 390 396 399 409 410 450 460 474 482 492 502 504 533 547 551 568 576 597 603 609 611 622 629 638 643 645 652 671 674 707 725 728 739 757 761	Red
	517	YKL181W	PRS1	histidine biosynthesis	ribose-phosphate diphosphokinase activity	cytoplasm	393	LimeGreen
	518	YKL195W	FMP15	protein targeting	molecular_function unknown	mitochondrion	801 300 365 380 394 521	Tan
	519	YKL216W	URA1	pyrimidine base biosynthesis	dihydroorotate dehydrogenase activity	cytoplasm	661	LimeGreen
	520	YAL036C	FUN11	biological_process unknown	molecular_function unknown	cytoplasm	573 350 359 386 492 531 562 588 647	Gray10
	521	YKR006C	MRPL13	protein biosynthesis	structural constituent of ribosome	mitochondrial large ribosomal subunit	518 532	Tan
	522	YKR016W	FMP13	biological_process unknown	molecular_function unknown	mitochondrion	394 469 488 543	Tan
	523	YKR024C	DBP7	35S primary transcript processing	ATP dependent RNA helicase activity	nucleolus	573 770 772 784 305 389 406 414 431 455 458 460 465 468 470 501 531 533 539 563 620 621 646 653 732	Red
	524	YKR025W	RPC37	transcription from Pol III promoter	DNA-directed RNA polymerase activity	DNA-directed RNA polymerase III complex	802 291 370 410 425 430 551 671	Lavender
	525	YKR047W					617	Gray10
	526	YKR048C	NAP1	bud growth	protein binding	cytoplasm	347 537 581	Yellow
	527	YKR057W	RPS21A	protein biosynthesis	structural constituent of ribosome	cytosolic small ribosomal subunit (sensu Eukarya)	395 586 678	Yellow
	528	YKR059W	TIF1	translational initiation	translation initiation factor activity	ribosome	364 473 613 641	Yellow
	529	YKR071C	DRE2	biological_process unknown	molecular_function unknown	cytoplasm	408 538	Gray10
	530	YKR081C	RPF2	ribosomal large subunit assembly and maintenance	rRNA binding	nucleolus	563 569 639 663 679	Red
	531	YLL008W	DRS1	35S primary transcript processing	ATP dependent RNA helicase activity	nucleolus	413 520 573 683 784 350 355 359 370 386 389 390 406 410 433 460 468 474 492 504 523 533 539 559 563 569 591 611 620 622 632 645 646 653 660 662 671 674 697 698 707 716 730 732 757	Red
	532	YLL009C	COX17	cytochrome c oxidase biogenesis	copper chaperone activity	cytosol	714 774 508 521 544 605 659 685	Tan
	533	YLL011W	SOF1	rRNA modification	snRNA binding	small nucleolar ribonucleoprotein complex	573 606 683 771 775 288 298 350 355 359 370 388 389 390 406 410 460 468 470 482 492 497 501 504 516 523 531 539 562 576 611 621 622 647 649 653 660 671 674 676 697 707 739 757	Red
	534	YLL024C	SSA2	protein folding	heat shock protein activity	cytoplasm	505 804 623 636	Purple
	535	YLL026W	HSP104	response to stress	heat shock protein activity	cytoplasm	787 800 414 623 636 686 738	Purple
	536	YLL027W	ISA1	iron ion transport	molecular_function unknown	mitochondrial matrix	538	Tan
	537	YLL036C	PRP19	nuclear mRNA splicing, via spliceosome	pre-mRNA splicing factor activity	cytoplasm	526 579	Lavender
	538	YLL037W					769 791 529 536 673 722 748 750	Gray10
	539	YLR009W	RLP24	ribosomal large subunit biogenesis	molecular_function unknown	nucleolus	413 573 683 703 784 795 282 298 312 322 328 334 343 350 355 359 370 386 389 390 393 406 410 426 433 450 460 465 468 470 474 482 492 501 504 523 531 533 559 564 576 591 611 620 621 622 632 643 646 653 657 666 671 674 675 676 697 707 732 739 756 757 762 764	Red
	540	YLR016C		biological_process unknown	molecular_function unknown	cytoplasm	399 699	Gray10
	541	YLR017W	MEU1	glutamate biosynthesis	molecular_function unknown	cytoplasm	355 492 495 504	LimeGreen
	542	YLR022C		35S primary transcript processing	molecular_function unknown	cytoplasm	381 547	Red
	543	YLR025W	SNF7	late endosome to vacuole transport	molecular_function unknown	cytoplasm	522	Purple
	544	YLR038C	COX12	cytochrome c oxidase biogenesis	cytochrome-c oxidase activity	respiratory chain complex IV (sensu Eukarya)	532 605 710 718	Tan
	545	YAL038W	CDC19	glycolysis	pyruvate kinase activity	cytosol	401	LimeGreen
	546	YLR048W	RPS0B	protein biosynthesis	structural constituent of ribosome	cytosolic small ribosomal subunit (sensu Eukarya)	401 299 480 584 693	Yellow
	547	YLR051C		biological_process unknown	molecular_function unknown	nucleus	410 516 542	Gray10
	548	YLR061W	RPL22A	protein biosynthesis	structural constituent of ribosome	cytosolic large ribosomal subunit (sensu Eukarya)	295 317 324 344 357 372 391 558 582 585 595 670 680 705	Yellow
	549	YLR062C	BUD28	bud site selection	molecular_function unknown	cellular_component unknown	356 608 711	Gray10
	550	YLR069C	MEF1	translational elongation	translation elongation factor activity	mitochondrion	444 445 464	Tan
	551	YLR074C	BUD20	bud site selection	molecular_function unknown	nucleus	573 280 386 390 410 482 516 524 576 611 661 739 757 764	Gray10

552	YLR075W	RPL10	protein biosynthesis	structural constituent of ribosome	cytosolic large ribosomal subunit (sensu Eukarya)	294 362 376 440 477 580 715 753	Yellow
553	YLR083C	EMP70	transport	transporter activity	membrane fraction	331 745 479 667	Black
554	YLR090W	XDJ1	biological_process unknown	chaperone regulator activity	nucleus	763 614	Gray10
555	YLR093C	NYV1	nonselective vesicle fusion	v-SNARE activity	vacuolar membrane	709	Purple
556	YLR129W	DIP2	processing of 20S pre-rRNA	snRNA binding	small nucleolar ribonucleoprotein complex	573 770 355 406 460 621	Red
557	YLR149C		biological_process unknown	molecular_function unknown	cellular_component unknown	803 414	Gray10
558	YLR167W	RPS31	protein biosynthesis	structural constituent of ribosome	cytoplasm	295 317 324 344 357 372 391 418 548 582 585 595 670 680	Yellow
559	YLR175W	CBF5	rRNA modification	pseudouridylylase activity	small nucleolar ribonucleoprotein complex	312 328 350 359 386 410 412 474 492 531 539 564 565 568 576 597 611 620 622 674 677 702 756 764	Red
560	YLR178C	TFS1	regulation of proteolysis and peptidolysis	lipid binding	soluble fraction	627 704	Purple
561	YLR185W	RPL37A	protein biosynthesis	structural constituent of ribosome	cytosolic large ribosomal subunit (sensu Eukarya)	711	Yellow
562	YLR186W	EMG1	processing of 20S pre-rRNA	snRNA binding	cytoplasm	520 573 359 386 388 389 390 406 460 482 492 533 576 588 611 647 676 707 739 757	Red
563	YLR196W	PWP1	biological_process unknown	molecular_function unknown	cytoplasm	726 573 599 683 703 780 781 784 797 350 359 392 406 432 433 453 460 468 493 523 530 531 569 588 618 620 632 639 646 674 679 698 707 716 721 730 732	Gray10
564	YLR197W	SIK1	rRNA modification	molecular_function unknown	nucleus	687 280 312 359 386 410 412 474 492 539 559 565 568 576 577 597 674 677 756 764	Red
565	YLR198C					559 564 735 736	Gray10
566	YLR216C	CPR6	protein folding	chaperone activity	cytoplasm	804 567 636 686 738	Purple
567	YLR217W					566	Gray10
568	YLR221C	RSA3	biological_process unknown	molecular_function unknown	nucleolus	687 796 283 311 359 386 410 450 474 492 516 559 564 576 597 609 611 629 671 674 729	Gray10
569	YLR222C	UTP13	processing of 20S pre-rRNA	snRNA binding	small nucleolar ribonucleoprotein complex	726 573 781 784 359 370 392 406 431 432 433 453 468 530 531 563 620 632 639 646 653 662 679 697 698 707 721 730 732	Red
570	YLR226W	BUR2	transcription	cyclin-dependent protein kinase regulator activity	nucleus	625 728	LightCyan
571	YLR255C					420 448	Gray10
572	YLR257W		biological_process unknown	molecular_function unknown	cytoplasm	509	Gray10
573	YBR247C	ENP1	processing of 20S pre-rRNA	snRNA binding	nucleus	413 520 606 683 703 781 288 350 355 359 370 386 389 390 406 410 433 458 460 468 482 492 523 531 533 539 551 556 562 563 569 576 588 591 611 618 621 622 639 642 653 660 671 698 707 716 730 739	Red
574	YLR264W	RPS28B	protein biosynthesis	structural constituent of ribosome	cytosolic small ribosomal subunit (sensu Eukarya)	480 587 746	Yellow
575	YLR270W	DCS1	deadenylation-dependent decapping	hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides	cytoplasm	449	Gray10
576	YLR276C	DBP9	35S primary transcript processing	ATP dependent RNA helicase activity	nucleolus	413 573 683 687 717 775 796 798 280 283 288 312 329 343 350 355 359 370 386 388 389 390 396 399 406 410 412 424 450 459 460 468 474 482 492 496 502 504 510 516 533 539 551 559 562 564 568 597 609 611 618 622 626 629 645 647 649 652 661 671 674 676 694 699 707 716 725 739 757	Red
577	YLR293C	GSP1	rRNA processing	RAN small monomeric GTPase activity	cytoplasm	564	Red
578	YBR251W	MRP55	protein biosynthesis	structural constituent of ribosome	mitochondrial small ribosomal subunit	700	Tan
579	YLR321C	SFH1	chromatin remodeling	protein binding	nucleosome remodeling complex	537 589	LightCyan
580	YLR325C	RPL38	protein biosynthesis	structural constituent of ribosome	cytosolic large ribosomal subunit (sensu Eukarya)	440 477 552 608 715 753	Yellow
581	YLR330W	CHS5	conjugation with cellular fusion	molecular_function unknown	cytoplasm	526 750	LimeGreen
582	YLR333C	RPS25B	protein biosynthesis	structural constituent of ribosome	cytosolic small ribosomal subunit (sensu Eukarya)	295 317 324 344 357 362 372 391 418 548 558 595 670 680 693	Yellow
583	YLR339C					364 696	Gray10
584	YLR340W	RPP0	protein biosynthesis	structural constituent of ribosome	cytosolic large ribosomal subunit (sensu Eukarya)	384 782 785 789 285 480 546 733	Yellow
585	YLR344W	RPL26A	protein biosynthesis	structural constituent of ribosome	cytosolic large ribosomal subunit (sensu Eukarya)	295 317 324 344 357 372 391 548 558 595 670 701 705	Yellow
586	YLR367W	RPS22B	protein biosynthesis	structural constituent of ribosome	cytosolic small ribosomal subunit (sensu Eukarya)	395 527	Yellow
587	YLR388W	RPS29A	protein biosynthesis	structural constituent of ribosome	cytosolic small ribosomal subunit (sensu Eukarya)	319 574 746	Yellow
588	YLR397C	AFG2	response to drug	ATPase activity	intracellular	520 573 389 406 460 468 562 563 591 647	Gray10
589	YLR399C	BDF1	sporulation (sensu Saccharomycetes)	transcription regulator activity	nucleus	579	LightCyan
590	YLR400W					359 390 406 455 460 474 482 611 622 676 707 757	Gray10
591	YLR401C	DUS3	tRNA modification	tRNA dihydrouridine synthase activity	cytoplasm	573 355 389 423 455 460 468 531 539 588 622 646 732	Lavender
592	YLR418C	CDC73	RNA elongation from Pol II promoter	Pol II transcription elongation factor activity	transcription elongation factor complex	399 625	LightCyan
593	YLR420W	URA4	pyrimidine nucleotide biosynthesis	dihydroorotase activity	cytoplasm	399 452	LimeGreen
594	YLR435W	TSR2	processing of 20S pre-rRNA	molecular_function unknown	cytoplasm	687 796 322 343 370 397 409 410 474 643 671 674	Red
595	YLR441C	RPS1A	protein biosynthesis	structural constituent of ribosome	cytosolic small ribosomal subunit (sensu Eukarya)	295 317 324 344 357 372 391 418 548 558 582 585 670 680 682 705	Yellow
596	YLR448W	RPL6B	protein biosynthesis	structural constituent of ribosome	cytosolic large ribosomal subunit (sensu Eukarya)	374	Yellow
597	YLR449W	FPR4	biological_process unknown	peptidyl-prolyl cis-trans isomerase activity	nucleus	687 717 798 283 343 386	Gray10

							399 410 412 474 482 483 492 502 507 516 559 564 568 576 609 611 629 661 671 702 712 725 729 739 757 761	
598	YLR459W	CDC91	attachment of GPI anchor to protein	GPI-anchor transamidase activity	cellular_component unknown	411		Black
599	YBR266C					681 683 703 784 797 302 312 322 358 370 406 431 433 437 563 653 671 698 716		Gray10
600	YML004C	GLO1	glutathione metabolism	lactoylglutathione lyase activity	cytoplasm	375 441		LimeGreen
601	YBR268W	MRPL37	protein biosynthesis	structural constituent of ribosome	mitochondrial large ribosomal subunit	774		Tan
602	YML007W	YAP1	transcription	transcription factor activity	cytoplasm	754		LightCyan
603	YML015C	TAF11	transcription initiation from Pol II promoter	general RNA polymerase II transcription factor activity	transcription factor TFIID complex	796 399 516 638		LightCyan
604	YML022W	APT1	AMP biosynthesis	adenine phosphoribosyltransferase activity	cytoplasm	499		LimeGreen
605	YML030W		biological_process unknown	molecular_function unknown	mitochondrion	790 287 456 478 532 544 614 700		Tan
606	YBR271W		biological_process unknown	S-adenosylmethionine-dependent methyltransferase activity	cytoplasm	573 771 775 388 390 533 739		Gray10
607	YML058W	SML1	mitochondrion organization and biogenesis	enzyme inhibitor activity	cytoplasm	667		LimeGreen
608	YML063W	RPS1B	protein biosynthesis	structural constituent of ribosome	cytosolic small ribosomal subunit (sensu Eukarya)	356 374 383 549 580 682 753		Yellow
609	YML074C	FPR3	biological_process unknown	peptidyl-prolyl cis-trans isomerase activity	nucleolus	798 483 507 516 568 576 597 617 629		Gray10
610	YML080W	DUS1	rRNA modification	rRNA dihydrouridine synthase activity	nucleus	431		Lavender
611	YML093W	UTP14	processing of 20S pre-rRNA	snRNA binding	small nucleolar ribonucleoprotein complex	413 476 573 683 687 796 798 283 288 298 312 329 343 350 355 359 370 385 386 388 389 390 399 406 409 410 412 424 450 459 460 474 482 492 496 502 504 516 531 533 539 551 559 562 568 576 590 597 618 621 622 629 638 645 647 649 657 661 671 674 676 694 699 707 725 739 757		Red
612	YML100W	TSL1	response to stress	enzyme regulator activity	alpha.alpha-trehalose-phosphate synthase complex (UDP-forming)	783 784 302		LimeGreen
613	YML106W	URA5	pyrimidine base biosynthesis	orotate phosphoribosyltransferase activity	cytoplasm	615 319 528 624 641 724		LimeGreen
614	YML110C	COQ5	aerobic respiration	ubiquinone biosynthesis methyltransferase activity	mitochondrion	405 554 605		Tan
615	YBR283C	SSH1	cotranslational membrane targeting	protein transporter activity	endoplasmic reticulum membrane	631 307 613		Yellow
616	YML128C	MSC1	meiotic recombination	molecular_function unknown	endoplasmic reticulum	627		Gray10
617	YMR005W	TAF4	transcription from Pol II promoter	RNA polymerase II transcription factor activity	transcription factor TFIID complex	791 306 345 399 439 484 507 525 609 648 750 758 765		Yellow
618	YMR014W	BUD22	bud site selection	molecular_function unknown	nucleus	573 683 687 717 781 280 283 350 370 382 390 406 410 433 460 474 482 563 576 611 645 657 671 707 725		Gray10
619	YMR017W	SPO20	nonselective vesicle fusion	t-SNARE activity	prospore membrane	420		Black
620	YMR049C	ERB1	rRNA processing	molecular_function unknown	nucleus	784 797 359 392 393 406 433 453 468 501 523 531 539 559 563 569 632 640 644 646 653 662 674 679 692 698 721 730 732		Red
621	YMR093W	UTP15	processing of 20S pre-rRNA	snRNA binding	small nucleolar ribonucleoprotein complex	573 770 772 784 359 389 406 460 465 501 523 533 539 556 611 637 646 675		Red
622	YMR128W	ECM16	processing of 20S pre-rRNA	RNA helicase activity	nucleolus	573 683 288 298 312 334 350 355 359 370 386 389 390 406 410 426 450 460 468 474 482 492 504 516 531 533 539 559 576 590 591 611 649 653 671 674 676 707 725 731 739 757		Red
623	YMR186W	HSC82	response to stress	chaperone activity	cytoplasm	534 535 636 686		Purple
624	YMR202W	ERG2	ergosterol biosynthesis	C-8 sterol isomerase activity	endoplasmic reticulum	411 613		LimeGreen
625	YMR213W	CEF1	nuclear mRNA splicing, via spliceosome	pre-mRNA splicing factor activity	spliceosome complex	399 570 592 699		Lavender
626	YMR235C	RNA1	protein-nucleus import	Ran GTPase activator activity	nucleus	576		Red
627	YMR250W	GAD1	response to oxidative stress	glutamate decarboxylase activity	cytoplasm	472 787 407 560 616		LimeGreen
628	YMR267W	PPA2	aerobic respiration	inorganic diphosphatase activity	mitochondrion	714 791 630 656		Tan
629	YMR269W		biological_process unknown	molecular_function unknown	nucleolus	386 399 474 483 516 568 576 597 609 611 635 652 708		Gray10
630	YMR276W	DSK2	spindle pole body duplication (sensu Saccharomyces)	protein degradation tagging activity	nucleus	628		Purple
631	YCL005W		biological_process unknown	molecular_function unknown	lipid particle	615 713 290		Gray10
632	YMR290C	HAS1	biological_process unknown	molecular_function unknown	nucleolus	703 784 797 392 393 406 432 433 453 465 468 531 539 563 569 620 639 644 646 653 662 674 692 698 707 721 730 732		Gray10
633	YMR302C	PRP12	rRNA processing	exonuclease activity	mitochondrial inner membrane	801 394 398 691		Tan
634	YMR311C	GLC8	glycogen biosynthesis	enzyme activator activity	cytoplasm	709		LimeGreen
635	YNL001W	DOM34	protein biosynthesis	molecular_function unknown	cytoplasm	629		Yellow
636	YNL007C	SIS1	translational initiation	chaperone activity	cytosolic small ribosomal subunit (sensu Eukarya)	804 336 534 535 566 623 686 738		Purple
637	YNL023C	FAP1	biological_process unknown	transcription factor activity	cellular_component unknown	406 455 460 501 621		Gray10
638	YNL050C		biological_process unknown	molecular_function unknown	cellular_component unknown	326 343 370 385 409 410 450 474 516 603 611 671 737		Gray10
639	YNL061W	NOP2	rRNA processing	RNA methyltransferase activity	nucleolus	573 703 350 433 468 530 563 569 632 716 732		Red
640	YNL062C	GCD10	translational initiation	rRNA methyltransferase activity	nucleus	620		Lavender
641	YNL069C	RPL16B	protein biosynthesis	structural constituent of ribosome	cytosolic large ribosomal subunit (sensu Eukarya)	528 613 724		Yellow
642	YNL075W	IMP4	rRNA modification	rRNA primary transcript binding	small nucleolar ribonucleoprotein complex	573 468		Red
643	YNL110C	NOP15	ribosomal large subunit biogenesis	molecular_function unknown	nucleus	413 687 717 796 370 410 474 502 516 539 594 653 671 674		Red
644	YNL112W	DBP2	mRNA catabolism, nonsense-mediated	RNA helicase activity	cytoplasm	392 393 453 620 632 646 653 721		Red
645	YNL113W	RPC19	transcription from Pol I promoter	DNA-directed RNA polymerase activity	DNA-directed RNA polymerase III complex	413 683 343 350 359 370 390 410 468 474 482 492 502 504 516 531 576 611		Red

	646	YNL132W	KRE33	biological_process unknown	molecular_function unknown	nucleolus	618 725 739 757 683 784 797 393 406 433 453 460 465 493 501 523 531 539 563 569 591 620 621 632 644 653 657 674 692 730 732	Gray10
	647	YNL141W	AAH1	adenine catabolism	adenine deaminase activity	cytoplasm	520 775 784 359 388 389 390 406 455 460 501 533 562 576 588 611 698 707	LimeGreen
	648	YNL147W	LSM7	nuclear mRNA splicing, via spliceosome	U6 snRNA binding	snRNP U6	617	Red
	649	YNL163C	RIA1	ribosome biogenesis	translation elongation factor activity	cytoplasm	389 450 460 482 533 576 611 622 676 739 757	Red
	650	YNL174W					674	Gray10
	651	YNL175C	NOP13	biological_process unknown	RNA binding	nucleolus	303 467 663 679	Gray10
	652	YNL232W	CSL4	35S primary transcript processing	3'-5' exoribonuclease activity	nuclear exosome (RNase complex)	399 474 516 576 629 739	Red
	653	YNL248C	RPA49	transcription from Pol I promoter	DNA-directed RNA polymerase activity	DNA-directed RNA polymerase I complex	413 573 599 683 703 770 784 797 298 312 322 350 359 370 392 393 406 410 431 432 433 453 465 468 504 523 531 533 539 569 620 622 632 643 644 646 662 671 674 692 697 698 707 721 730 732 756	Red
	654	YNL252C	MRPL17	protein biosynthesis	structural constituent of ribosome	mitochondrial large ribosomal subunit	790 464 656	Tan
	655	YNL255C	GIS2	intracellular signaling cascade	transcription factor activity	cytoplasm	766	Yellow
	656	YNL315C	ATP11	protein complex assembly	chaperone activity	mitochondrial matrix	714 790 801 300 628 654	Tan
	657	YNR003C	RPC34	transcription from Pol III promoter	DNA-directed RNA polymerase activity	cytoplasm	703 784 796 359 370 389 390 406 410 455 465 539 611 618 646 666 671 674 675 697 707 716	Red
	658	YNR018W		biological_process unknown	molecular_function unknown	mitochondrion	385 386 412 661	Tan
	659	YNR037C	RSM19	protein biosynthesis	structural constituent of ribosome	mitochondrial small ribosomal subunit	532	Tan
	660	YNR038W	DBP6	35S primary transcript processing	ATP dependent RNA helicase activity	nucleolus	573 775 784 359 390 406 460 531 533	Red
	661	YNR046W		biological_process unknown	molecular_function unknown	cytoplasm	359 386 412 474 492 519 551 576 597 611 658 757	Gray10
	662	YNR053C	NOG2	ribosomal large subunit-nucleus export	GTPase activity	nucleus	393 453 531 569 620 632 653 721	Red
	663	YNR054C		biological_process unknown	transcription regulator activity	cytoplasm	530 651 679	Gray10
	664	YCL040W	GLK1	carbohydrate metabolism	glucokinase activity	cytosol	472 665 414 449	LimeGreen
	665	YCL042W		biological_process unknown	molecular_function unknown	cytoplasm	664	Gray10
	666	YOL022C		biological_process unknown	molecular_function unknown	cytoplasm	795 298 370 406 474 539 657 671 674 675 697 707	Gray10
	667	YOL030W	GAS5	biological_process unknown	molecular_function unknown	cell wall (sensu Fungi)	411 553 607	Gray10
	668	YOL032W		biological_process unknown	molecular_function unknown	cytoplasm	709	Gray10
	669	YOL039W	RPP2A	protein biosynthesis	structural constituent of ribosome	cytosolic large ribosomal subunit (sensu Eukarya)	499	Yellow
	670	YOL040C	RPS15	protein biosynthesis	structural constituent of ribosome	cytosolic small ribosomal subunit (sensu Eukarya)	741 295 317 344 357 372 391 548 558 582 585 595 680 701	Yellow
	671	YOL041C	NOP12	rRNA metabolism	RNA binding	nucleolus	413 296 573 599 683 687 703 717 796 282 283 298 312 322 329 334 343 350 355 359 370 386 389 390 406 409 410 426 433 450 460 474 482 492 516 524 531 533 539 568 576 594 597 611 618 622 638 643 653 657 666 674 697 707 725 737 739 756 757 760 761 764	Red
	672	YOL048C		biological_process unknown	molecular_function unknown	lipid particle	327 723	Gray10
	673	YOL056W	GPM3	gluconeogenesis	NOT phosphoglycerate mutase activity	cytosol	417 538 750	LimeGreen
	674	YOL077C	BRX1	ribosomal large subunit assembly and maintenance	rRNA primary transcript binding	nucleolus	413 296 683 687 703 717 780 784 797 799 280 282 298 312 322 334 343 350 359 370 386 389 393 406 410 433 450 460 474 482 492 516 531 533 539 559 563 564 568 576 594 611 620 622 632 643 646 650 653 657 666 671 677 692 697 707 739 756 757 761	Red
	675	YOL079W					703 298 389 406 460 470 539 621 657 666 707 747	Gray10
	676	YOL080C	REX4	rRNA processing	3'-5' exonuclease activity	nucleus	350 355 359 386 389 390 406 460 470 482 501 533 539 562 576 590 611 622 649 707 739 757	Red
	677	YOL097C	WRS1	tryptophanyl-tRNA aminoacylation	tryptophan-tRNA ligase activity	cytoplasm	559 564 674 756	Yellow
	678	YOL120C	RPL18A	protein biosynthesis	structural constituent of ribosome	cytosolic large ribosomal subunit (sensu Eukarya)	395 527	Yellow
	679	YOL124C		biological_process unknown	S-adenosylmethionine-dependent methyltransferase activity	cytoplasm	303 467 392 530 563 569 620 651 663 698 721	Gray10
	680	YOL127W	RPL25	protein biosynthesis	structural constituent of ribosome	cytosolic large ribosomal subunit (sensu Eukarya)	295 317 324 344 357 372 391 418 548 558 582 595 670 705	Yellow
	681	YCL053C					599 703 780 797 312 322 334 393	Gray10
	682	YOL139C	CDC33	translational initiation	translation initiation factor activity	cytoplasm	595 608 753	Yellow
	683	YCL054W	SPB1	rRNA processing	RNA methyltransferase activity	nucleus	413 573 599 687 703 717 781 799 280 291 292 312 350 355 359 370 386 389 390 406 410 433 460 468 474 482 494 531 533 539 563 576 611 618 622 645 646 653 671 674 707 716 725 732 739 757	Red
	684	YOL144W	NOP8	rRNA processing	molecular_function unknown	nucleolus	397	Red
	685	YOR020C	HSP10	protein folding	chaperone activity	mitochondrial matrix	532 754	Tan
	686	YOR027W	STI1	protein folding	chaperone activity	cytoplasm	535 566 623 636 738	Purple
	687	YCL059C	KRR1	rRNA processing	molecular_function unknown	nucleolus	413 476 683 703 717 780 788 796 799 283 311 312 334 343 359 370 386 410 474 516 564 568 576 594 597 611 618 643 671 674	Purple
	688	YOR036W	PEP12	Golgi to vacuole transport	t-SNARE activity	Golgi apparatus	327 723	Purple
	689	YOR042W	CUE5	biological_process unknown	molecular_function unknown	cytoplasm	398	Gray10

690	YOR051C		biological_process unknown	molecular_function unknown	nucleus	502	Gray10
691	YOR090C	PTC5	biological_process unknown	protein phosphatase type 2C activity	cellular_component unknown	633	Gray10
692	YOR095C	RK11	pentose-phosphate shunt	ribose-5-phosphate isomerase activity	cytoplasm	393 453 620 632 646 653 674	LimeGreen
693	YOR096W	RPS7A	protein biosynthesis	structural constituent of ribosome	cytosolic small ribosomal subunit (sensu Eukarya)	299 357 418 480 546 582	Yellow
694	YOR106W	VAM3	nonselective vesicle fusion	t-SNARE activity	vacuolar membrane	576 611 699 750	Purple
695	YCL067C	HMLALPHA2	regulation of transcription from Pol II promoter	transcription corepressor activity	nucleus	751 776 315 530 380 709	LightCyan
696	YOR133W	EFT1	translational elongation	translation elongation factor activity	ribosome	286 583	Yellow
697	YOR145C	PNO1	rRNA processing	chaperone activity	nucleus	775 784 298 359 370 410 426 460 474 492 501 504 531 533 539 569 653 657 666 671 674 698 707 739 756	Red
698	YOR146W					726 573 599 775 784 322 359 370 390 392 406 432 433 453 460 468 531 563 569 620 632 647 653 679 697 707 721	Gray10
699	YOR154W		biological_process unknown	molecular_function unknown	cellular_component unknown	390 399 540 576 611 625 694 707 728 739 757	Gray10
700	YOR158W	PET123	protein biosynthesis	structural constituent of ribosome	mitochondrial small ribosomal subunit	578 801 300 466 478 605	Tan
701	YOR167C	RPS28A	protein biosynthesis	structural constituent of ribosome	cytosolic small ribosomal subunit (sensu Eukarya)	741 782 295 585 670 733	Yellow
702	YOR169C					492 559 597 764	Gray10
703	YCLX02C					573 599 681 683 687 781 784 797 312 334 358 370 390 393 406 410 433 458 460 465 468 539 563 632 639 653 657 671 674 675 716	Gray10
704	YOR173W	DCS2	biological_process unknown	molecular_function unknown	cytoplasm	560	Gray10
705	YOR182C	RPS30B	protein biosynthesis	structural constituent of ribosome	cytosolic small ribosomal subunit (sensu Eukarya)	344 548 585 595 680	Yellow
706	YOR183W	FYV12	biological_process unknown	molecular_function unknown	cellular_component unknown	340	Gray10
707	YOR206W	NOC2	ribosome-nucleus export	molecular_function unknown	nucleus	413 573 683 784 298 312 322 329 350 355 359 370 386 389 390 406 410 426 433 450 455 458 460 468 470 474 482 492 501 504 516 531 533 539 562 563 569 576 590 611 618 622 632 647 653 657 666 671 674 675 676 697 698 699 716 725 739 747 756 757 759	Red
708	YOR210W	RPB10	transcription from Pol II promoter	DNA-directed RNA polymerase activity	DNA-directed RNA polymerase III complex	629	Red
709	YOR215C		biological_process unknown	molecular_function unknown	mitochondrion	695 300 375 509 555 634 668	Tan
710	YOR232W	MGE1	mitochondrial matrix protein import	chaperone activity	mitochondrion	466 469 486 544 754	Tan
711	YOR234C	RPL33B	protein biosynthesis	structural constituent of ribosome	cytosolic large ribosomal subunit (sensu Eukarya)	429 471 549 561 727	Yellow
712	YOR277C					386 492 495 597	Gray10
713	YCLX12W					631	Gray10
714	YCR003W	MRPL32	protein biosynthesis	structural constituent of ribosome	mitochondrial large ribosomal subunit	478 489 532 628 656	Tan
715	YPL037C	EGD1	nascent polypeptide association	chaperone activity	nascent polypeptide-associated complex	552 580 735 753	Yellow
716	YPL044C					573 599 683 703 784 282 350 359 389 390 406 433 455 460 468 531 563 576 639 657 707	Gray10
717	YCR016W		biological_process unknown	molecular_function unknown	nucleus	683 687 780 799 280 311 312 343 410 474 516 576 597 618 643 671 674	Gray10
718	YPL078C	ATP4	ATP synthesis coupled proton transport	structural molecule activity	proton-transporting ATP synthase, stator stalk (sensu Eukarya)	544	Tan
719	YPL079W	RPL21B	protein biosynthesis	structural constituent of ribosome	cytosolic large ribosomal subunit (sensu Eukarya)	720 753	Yellow
720	YPL081W	RPS9A	protein biosynthesis	structural constituent of ribosome	cytoplasm	719 753	Yellow
721	YPL093W	NOG1	ribosome-nucleus export	GTPase activity	nucleolus	303 784 392 563 569 620 632 644 653 662 679 698 732	Red
722	YPL105C		biological_process unknown	molecular_function unknown	cytoplasm	769 538 750	Gray10
723	YPL123C	RNY1	cellular morphogenesis	endoribonuclease activity	extracellular	327 281 414 672 688	Purple
724	YPL142C					319 613 641	Gray10
725	YPL146C		biological_process unknown	molecular_function unknown	nucleus	413 683 343 350 370 390 409 410 474 482 492 502 516 576 597 611 618 622 645 671 707 760 761 764	Gray10
726	YAL059W	ECM1	cell wall organization and biogenesis	molecular_function unknown	nucleus	467 322 392 563 569 698 732	Red
727	YPL198W	RPL7B	protein biosynthesis	structural constituent of ribosome	cytosolic large ribosomal subunit (sensu Eukarya)	793 711	Yellow
728	YPL202C	AFT2	transcription initiation from Pol II promoter	specific RNA polymerase II transcription factor activity	nucleus	516 570 699 739	Gray10
729	YPL206C		biological_process unknown	molecular_function unknown	cytoplasm	568 597	Gray10
730	YPL207W		biological_process unknown	molecular_function unknown	endoplasmic reticulum	573 797 393 406 432 433 468 481 531 563 569 620 632 646 653 732	Gray10
731	YPL212C	PUS1	tRNA modification	pseudouridylylase activity	nucleus	622	Lavender
732	YPL217C	BMS1	rRNA processing	GTP binding	cytoplasm	726 683 795 350 406 433 468 523 531 539 563 569 591 620 632 639 646 653 721 730	Red
733	YPL220W	RPL1A	protein biosynthesis	structural constituent of ribosome	cytosolic large ribosomal subunit (sensu Eukarya)	789 295 480 584 701	Yellow
734	YPL225W		biological_process unknown	molecular_function unknown	cytoplasm	485 755	Gray10
735	YPL237W	SUI3	translational initiation	translation initiation factor activity	ribosome	565 715 753	Yellow
736	YPL238C					565 766	Gray10
737	YPL239W	YAR1	biological_process unknown	molecular_function unknown	cytoplasm	282 322 343 370 638 671	Gray10
738	YPL240C	HSP82	response to stress	ATPase activity, coupled	cytoplasm	318 535 566 636 686	Purple
739	YPL266W	DIM1	rRNA modification	rRNA (adenine-N6,N6)-dimethyltransferase activity	nucleolus	573 606 683 775 298 312 350 355 359 370 386 388 389 390 396 399 406 410 412 450 460 468 474 482 492 502 504 516 533 539 551 562 576 597 611 622 645 649 652 671 674 676	Red

	740	YPL273W	SAM4	sulfur amino acid metabolism	homocysteine S-methyltransferase activity	cytoplasm	697 699 707 728 750 757	
	741	YCR031C	RPS14A	protein biosynthesis	structural constituent of ribosome	cytosolic small ribosomal subunit (sensu Eukarya)	367 782 295 317 357 670 701	Gray10 Yellow
	742	YPR015C		biological_process unknown	molecular_function unknown	cellular_component unknown	749	Gray10
	743	YPR033C	HTS1	histidyl-tRNA aminoacylation	histidine-tRNA ligase activity	cytoplasm	328 367	Yellow
	744	YPR037C	ERV2	protein thiol-disulfide exchange	thiol oxidase activity	microsome	769 750	Tan
	745	YCR034W	FEN1	sphingolipid biosynthesis	fatty acid elongase activity	endoplasmic reticulum	553	LimeGreen
	746	YPR045W	RPL43A	protein biosynthesis	structural constituent of ribosome	cytosolic large ribosomal subunit (sensu Eukarya)	574 587	Yellow
	747	YPR048W	TAH18	biological_process unknown	molecular_function unknown	cellular_component unknown	784 389 675 707	Gray10
	748	YPR062W	FCY1	cytosine metabolism	cytosine deaminase activity	cytoplasm	538	LimeGreen
	749	YPR077C					463 742	Gray10
	750	YPR087W	VPS69	protein-vacuolar targeting	molecular_function unknown	cellular_component unknown	769 791 306 399 412 507 538 581 617 673 694 722 739 744 765	Gray10
	751	YCR039C	MATALPHA2	regulation of transcription from Pol II promoter	transcription corepressor activity	nucleus	695 776 315	LightCyan
	752	YPR101W	SNT309	nuclear mRNA splicing, via spliceosome	molecular_function unknown	spliceosome complex	417	Lavender
	753	YPR102C	RPL11A	protein biosynthesis	structural constituent of ribosome	cytosolic large ribosomal subunit (sensu Eukarya)	294 356 366 383 387 440 477 552 580 608 682 715 719 720 735	Yellow
	754	YPR103W	PRE2	ubiquitin-dependent protein catabolism	endopeptidase activity	proteasome core complex (sensu Eukarya)	346 394 434 602 685 710	Purple
	755	YPR108W	RPN7	ubiquitin-dependent protein catabolism	endopeptidase activity	proteasome regulatory particle (sensu Eukarya)	506 734	Purple
	756	YPR110C	RPC40	transcription from Pol I promoter	DNA-directed RNA polymerase activity	DNA-directed RNA polymerase III complex	312 322 359 370 386 474 492 539 559 564 653 671 674 677 697 707 764	Red
	757	YPR112C	MRD1	35S primary transcript processing	snRNA binding	nucleolus	683 298 350 359 386 389 390 399 406 410 450 460 474 482 492 502 504 516 531 533 539 551 562 576 590 597 611 622 645 649 661 671 674 676 699 707 739	Red
	758	YPR125W		biological_process unknown	molecular_function unknown	mitochondrion	769 419 617 765	Tan
	759	YPR136C					707	Gray10
	760	YPR142C					671 725	Gray10
	761	YPR143W		biological_process unknown	molecular_function unknown	nucleus	370 410 474 492 516 597 671 674 725 764	Gray10
	762	YPR144C	NOC4	processing of 20S pre-rRNA	snRNA binding	nucleus	770 501 539	Red
	763	YCR046C	IMG1	protein biosynthesis	structural constituent of ribosome	mitochondrial ribosome	554	Tan
	764	YPR169W	JIP5	protein monoubiquitination	molecular_function unknown	nucleus	386 410 474 492 539 551 559 564 671 702 725 756 761	Gray10
	765	YPR173C	VPS4	late endosome to vacuole transport	ATPase activity	cytoplasm	769 617 750 758	Purple
	766	YPR187W	RPO26	transcription from Pol II promoter	DNA-directed RNA polymerase activity	DNA-directed RNA polymerase III complex	655 736	Red
	767	YAL062W	GDH3	glutamate biosynthesis	glutamate dehydrogenase activity	nucleus	308 360	LimeGreen
	768	YCR051W		biological_process unknown	molecular_function unknown	cytoplasm	386	Gray10
	769	YCR052W	RSC6	chromatin remodeling	molecular_function unknown	nucleosome remodeling complex	791 306 340 342 371 399 538 722 744 750 758 765 772 406 460 501 523 556 621 653 762	LightCyan Gray10
	770	YCR055C					606 533	Gray10
	771	YCR056W					406 533	Gray10
	772	YCR057C	PWP2	establishment of cell polarity (sensu Saccharomycetes)	snRNA binding	cytoplasm	770 784 455 501 523 621	Red
	773	YCR068W	ATG15	autophagy	lipase activity	integral to membrane	794 363	Gray10
	774	YCR071C	IMG2	protein biosynthesis	structural constituent of ribosome	mitochondrial large ribosomal subunit	601 532	Tan
	775	YCR072C		biological_process unknown	molecular_function unknown	cellular_component unknown	606 802 288 359 388 390 425 460 533 576 647 660 697 698 739	Gray10
	776	YCR096C	HMRA2	biological_process unknown	molecular_function unknown	cellular_component unknown	695 751 330	Gray10
	777	YDL022W	GPD1	intracellular accumulation of glycerol	glycerol-3-phosphate dehydrogenase (NAD+) activity	cytoplasm	778 438	LimeGreen
	778	YDL023C	SRF4	biological_process unknown	molecular_function unknown	cellular_component unknown	777	Gray10
	779	YDL031W	DBP10	35S primary transcript processing	ATP dependent RNA helicase activity	nucleolus	780 797 312 334	Red
	780	YDL051W	LHP1	tRNA processing	RNA binding	nucleus	681 687 717 779 781 797 799 312 358 386 563 674	Lavender
	781	YDL060W	TSR1	rRNA processing	molecular_function unknown	nucleolus	573 683 703 780 280 312 433 563 569 618	Red
	782	YDL061C	RPS29B	protein biosynthesis	structural constituent of ribosome	cytosolic small ribosomal subunit (sensu Eukarya)	384 514 741 785 285 299 480 584 701	Yellow
	783	YDL062W					784 369 612	Gray10
	784	YDL063C		biological_process unknown	molecular_function unknown	cytoplasm	599 703 772 783 797 370 392 393 406 433 455 488 460 501 523 531 539 563 569 612 620 621 632 646 647 653 657 660 674 697 698 707 716 721 747	Gray10
	785	YDL081C	RPP1A	protein biosynthesis	structural constituent of ribosome	cytosolic large ribosomal subunit (sensu Eukarya)	384 782 285 480 584	Yellow
	786	YDL097C	RPN6	ubiquitin-dependent protein catabolism	structural molecule activity	proteasome regulatory particle (sensu Eukarya)	313 512	Purple
	787	YDL124W		biological_process unknown	molecular_function unknown	cytoplasm	535 627	LimeGreen
	788	YDL213C	NOP6	rRNA processing	molecular_function unknown	nucleolus	687	Red
	789	YDR012W	RPL4B	protein biosynthesis	structural constituent of ribosome	cytoplasm	295 584 733	Yellow
	790	YDR041W	RSM10	protein biosynthesis	structural constituent of ribosome	mitochondrial small ribosomal subunit	605 654 656	Tan
	791	YDR054C	CDC34	ubiquitin-dependent protein catabolism	ubiquitin-protein ligase activity	cytoplasm	769 792 345 408 538 617 628 750	LimeGreen
	792	YDR056C		biological_process unknown	molecular_function unknown	endoplasmic reticulum	791	Gray10
	793	YDR064W	RPS13	protein biosynthesis	structural constituent of ribosome	cytosolic small ribosomal subunit (sensu Eukarya)	727	Yellow
	794	YDR076W	RAD55	DNA recombinase assembly	protein binding	nucleus	773	Lavender
	795	YDR083W	RRP8	rRNA processing	methyltransferase activity	nucleolus	539 666 732	Red
	796	YDR087C	RRP1	rRNA processing	molecular_function unknown	nucleus	413 687 283 298 343 389 409 410 450 474 502 516 568 576 594 603 611 643 657 671	Red
	797	YDR101C	ARX1	ribosomal large subunit biogenesis	molecular_function unknown	cytoplasm	599 681 703 779 780 784 799 312 322 334 358 359 392 393 406 453 465 563 620 632 646 653 674 730	Red
	798	YDR152W	GIR2	biological_process unknown	molecular_function unknown	cytoplasm	492 516 576 597 609 611	Gray10
	799	YDR165W	TRM82	tRNA methylation	protein binding	nucleus	683 687 717 780 797 280 410 674	Lavender
	800	YDR171W	HSP42	response to stress	chaperone activity	cytoplasm	535	Purple
	801	YDR175C	RSM24	protein biosynthesis	structural constituent of ribosome	mitochondrial small ribosomal subunit	300 394 488 518 633 656	Tan

							700	
802	YDR184C	ATC1	response to stress	molecular_function unknown	nucleus		775 288 425 524	Black
803	YDR204W	COQ4	ubiquinone metabolism	molecular_function unknown	mitochondrial inner membrane		557	LimeGreen
804	YDR214W	AHA1	response to stress	chaperone activator activity	cytoplasm		505 534 566 636	Purple

\* Colors were assigned to nodes according to their functional categories: Red represents the major functional category of each module while purple, yellow and tan represent other functional categories, which are often clustered into sub-modules. Genes in Lavender participate in processes closely related to genes in red. White nodes are unknown genes while black nodes are genes whose functional links to other genes are not currently understood. Green nodes are genes in metabolic processes, which are influenced by many biological processes.