Afu1g00310	chitinase activity
Afu1g00310	cell wall chitin catabolic process
Afu1g00310	cell wall organization
Afu1g00310	fungal-type cell wall
Afu1g00350	ferric-chelate reductase activity
Afu1g00420	serine-type carboxypeptidase activity
Afu1g00420	proteolysis
Afu1g00440	integral to membrane
Afu1g00450	amino sugar metabolic process
Afu1g00450	N-acetylglucosamine catabolic process
Afu1g00450	N-acetylglucosamine-6-phosphate deacetylase activity
Afu1g00470	3-chloroallyl aldehyde dehydrogenase activity
Afu1g00470	cytoplasm
Afu1g00470	polyamine catabolic process
Afu1g00470	response to stress
Afu1g00470	response to osmotic stress
Afu1g00470	beta-alanine biosynthetic process
Afu1g00480	glucosamine-6-phosphate deaminase activity
Afu1g00480	N-acetylglucosamine catabolic process
Afu1g00490	mitochondrial matrix
Afu1g00490	tricarboxylic acid cycle
Afu1g00490	2-oxoglutarate metabolic process
Afu1g00500	L-lactate dehydrogenase (cytochrome) activity
Afu1g00500	mitochondrial intermembrane space
Afu1g00500	electron transport
Afu1g00510	D-lactate dehydrogenase (cytochrome) activity
Afu1g00510	mitochondrial inner membrane
Afu1g00510	carbohydrate metabolic process
Afu1g00510	aerobic respiration
Afu1g00530	cytoplasm
Afu1g00630	nucleus
Afu1g00630	chromatin assembly or disassembly
Afu1g00630	mating type switching
Afu1g00630	DNA-dependent ATPase activity
Afu1g00650	hydrolase activity, hydrolyzing O-glycosyl compounds
Afu1g00650	cellular glucan metabolic process
Afu1g00650	fungal-type cell wall
Afu1g00730	protein binding
Afu1g00730	protein folding
Afu1g00750	biological process unknown
Afu1g00750	molecular function unknown
Afu1g00750	mitochondrion
Afu1g00790	molecular function unknown
Afu1g00970	transporter activity
Afu1g00970	transport
Afu1g00990	metabolic process
Afu1g00990	oxidoreductase activity
Afu1g01000	metabolic process
Afu1g01000	oxidoreductase activity
Afu1g01010	polyketide synthase activity

Afu1g01020	nucleotide binding
Afu1g01020	purine-nucleoside phosphorylase activity
Afu1g01020	protein binding
Afu1g01020	cellular component unknown
Afu1g01180	FAD binding
Afu1g01240	transcription factor activity
Afu1g01240	nucleus
Afu1g01240	zinc ion binding
Afu1g01240	regulation of transcription
Afu1g01260	transporter activity
Afu1g01260	plasma membrane
Afu1g01260	transport
Afu1g01270	metabolic process
Afu1g01270	oxidoreductase activity
Afu1g01330	nucleus
Afu1g01330	cytoplasm
Afu1g01330	L-serine metabolic process
Afu1g01330	oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acc
Afu1g01370	glutathione transferase activity
Afu1g01370	endoplasmic reticulum
Afu1g01370	glutathione metabolic process
Afu1g01380	alpha-1,6-mannosyltransferase activity
Afu1g01380	cell wall mannoprotein biosynthetic process
Afu1g01380	alpha-1,6-mannosyltransferase complex
Afu1g01380	substituted mannan metabolic process
Afu1g01380	N-glycan processing
Afu1g01380	transferase activity, transferring glycosyl groups
Afu1g01480	plasma membrane
Afu1g01480	peptide transporter activity
Afu1g01480	peptide transport
Afu1g01550	high affinity zinc uptake transmembrane transporter activity
Afu1g01550	integral to plasma membrane
Afu1g01550	high-affinity zinc ion transport
Afu1g01560	zinc ion binding
Afu1g01590	transcription factor activity
Afu1g01590	nucleus
Afu1g01590	zinc ion binding
Afu1g01590	regulation of transcription
Afu1g01600	photoreactive repair
Afu1g01600	deoxyribodipyrimidine photo-lyase activity
Afu1g01600	nucleus
Afu1g01600	DNA repair
Afu1g01640	mitotic anaphase B
Afu1g01640	microtubule motor activity
Afu1g01640	structural constituent of cytoskeleton
Afu1g01640	spindle pole body
Afu1g01640	kinesin complex
Afu1g01640	spindle microtubule
Afu1g01640	microtubule nucleation
Afu1g01670	formaldehyde dehydrogenase (glutathione) activity

Afu1g01670	cytoplasm
Afu1g01670	zinc ion binding
Afu1g01670	formaldehyde assimilation
Afu1g01680	branched-chain-amino-acid transaminase activity
Afu1g01680	nucleus
Afu1g01680	cytoplasm
Afu1g01680	cellular amino acid catabolic process
Afu1g01680	branched chain family amino acid biosynthetic process
Afu1g01690	metabolic process
Afu1g01690	oxidoreductase activity
Afu1g01720	endoribonuclease activity
Afu1g01720	protein serine/threonine kinase activity
Afu1g01720	nuclear envelope
Afu1g01720	endoplasmic reticulum membrane
Afu1g01720	inositol metabolic process
Afu1g01720	protein amino acid phosphorylation
Afu1g01720	activation of signaling protein activity involved in unfolded protein response
Afu1g01720	unfolded protein response, cleavage of primary transcript encoding UFP-specific transcriptic
Afu1g01730	membrane fraction
Afu1g01730	fungal-type cell wall biogenesis
Afu1g01730	anchored to plasma membrane
Afu1g01740	chaperone activity
Afu1g01740	cytoplasm
Afu1g01740	cytoskeleton
Afu1g01740	protein folding
Afu1g01740	cytoskeleton organization
Afu1g01750	biological process unknown
Afu1g01750	peptidyl-prolyl cis-trans isomerase activity
Afu1g01750	cytoplasm
Afu1g01750	endoplasmic reticulum
Afu1g01770	nucleus
Afu1g01770	cytoplasm
Afu1g01770	L-serine metabolic process
Afu1g01770	metabolic process
Afu1g01770	oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acc
Afu1g01780	soluble fraction
Afu1g01780	alcohol metabolic process
Afu1g01780	alcohol dehydrogenase (NADP+) activity
Afu1g01812	integral to plasma membrane
Afu1g01812	nicotinamide mononucleotide permease activity
Afu1g01812	nicotinamide mononucleotide transport
Afu1g01830	metabolic process
Afu1g01830	cellular component unknown
Afu1g01830	hydrolase activity
Afu1g01870	biological process unknown
Afu1g01870	molecular function unknown
Afu1g01870	integral to membrane
Afu1g01890	pathogenesis
Afu1g01900	biological process unknown
Afu1g01900	molecular function unknown

Afu1g01900	cytoplasm
Afu1g01930	integral to plasma membrane
Afu1g01930	response to toxin
Afu1g01930	multidrug transporter activity
Afu1g01990	biological process unknown
Afu1g01990	molecular function unknown
Afu1g01990	cellular component unknown
Afu1g02000	nuclear chromosome
Afu1g02000	DNA binding
Afu1g02000	catalytic activity
Afu1g02000	DNA repair
Afu1g02000	reciprocal meiotic recombination
Afu1g02010	biological process unknown
Afu1g02010	DNA binding
Afu1g02010	nucleus
Afu1g02010	zinc ion binding
Afu1g02020	biological process unknown
Afu1g02020	molecular function unknown
Afu1g02020	nucleus
Afu1g02020	nucleolus
Afu1g02020	cytoplasm
Afu1g02030	translation initiation factor activity
Afu1g02030	cytoplasm
Afu1g02030	eukaryotic translation initiation factor 3 complex
Afu1g02030	translational initiation
Afu1g02050	site of polarized growth (sensu Saccharomyces)
Afu1g02050	protein binding
Afu1g02050	endocytosis
Afu1g02060	nucleolus
Afu1g02060	regulation of meiosis
Afu1g02070	mitochondrial inner membrane
Afu1g02070	mitochondrial respiratory chain
Afu1g02070	mitochondrial respiratory chain complex III
Afu1g02070	oxidative phosphorylation
Afu1g02070	mitochondrial electron transport, ubiquinol to cytochrome c
Afu1g02070	electron transporter, transferring electrons within CoQH2-cytochrome c reductase complex
Afu1g02090	nucleus
Afu1g02090	cytoplasm
Afu1g02090	metabolic process
Afu1g02090	zinc ion binding
Afu1g02090	oxidoreductase activity
Afu1g02110	3-deoxy-7-phosphoheptulonate synthase activity
Afu1g02110	nucleus
Afu1g02110	cytoplasm
Afu1g02110	aromatic amino acid family biosynthetic process
Afu1g02130	biological process unknown
Afu1g02130	molecular function unknown
Afu1g02130	cellular component unknown
Afu1g02140	4-alpha-glucanotransferase activity
Afu1g02140	amylo-alpha-1,6-glucosidase activity

Afu1g02140	cytoplasm
Afu1g02140	glycogen catabolic process
Afu1g02150	glycerol-3-phosphate dehydrogenase (NAD+) activity
Afu1g02150	cytosol
Afu1g02150	glycerol metabolic process
Afu1g02170	biological process unknown
Afu1g02170	chaperone activity
Afu1g02170	ATP binding
Afu1g02170	mitochondrial matrix
Afu1g02190	GTPase activity
Afu1g02190	Golgi apparatus
Afu1g02190	exocytosis
Afu1g02190	vesicle-mediated transport
Afu1g02210	ribosomal large subunit assembly
Afu1g02210	nucleolus
Afu1g02210	5S rRNA binding
Afu1g02210	rRNA primary transcript binding
Afu1g02350	integral to plasma membrane
Afu1g02350	transport
Afu1g02350	response to toxin
Afu1g02350	multidrug transporter activity
Afu1g02370	biological process unknown
Afu1g02370	catalytic activity
Afu1g02370	molecular function unknown
Afu1g02370	mitochondrion
Afu1g02370	metabolic process
Afu1g02390	mitochondrion
Afu1g02390	metabolic process
Afu1g02390	hydrolase activity
Afu1g02410	nucleus
Afu1g02410	regulation of transcription from RNA polymerase II promoter
Afu1g02410	35S primary transcript processing
Afu1g02410	snoRNA metabolic process
Afu1g02410	chromatin remodeling complex
Afu1g02410	ATPase activity
Afu1g02430	protein binding
Afu1g02430	endoplasmic reticulum
Afu1g02430	mRNA processing
Afu1g02430	ubiquitin-dependent protein catabolic process
Afu1g02430	protein transport
Afu1g02460	DNA-directed RNA polymerase activity
Afu1g02460	DNA-directed RNA polymerase III complex
Afu1g02460	transcription from RNA polymerase III promoter
Afu1g02480	fungal-type vacuole
Afu1g02480	endoplasmic reticulum
Afu1g02480	plasma membrane
Afu1g02480	regulation of pH
Afu1g02480	hydrogen-exporting ATPase activity, phosphorylative mechanism
Afu1g02480	proton transport
Afu1g02510	nuclear-transcribed mRNA catabolic process, deadenylation-dependent decay

Afu1g02510	loss of chromatin silencing during replicative cell aging
Afu1g02510	mRNA binding
Afu1g02510	cytoplasm
Afu1g02510	protein targeting
Afu1g02530	plasma membrane
Afu1g02540	molecular function unknown
Afu1g02540	actin cortical patch (sensu Saccharomyces)
Afu1g02540	cellular bud tip
Afu1g02540	cellular bud neck
Afu1g02540	endocytosis
Afu1g02550	nuclear migration (sensu Saccharomyces)
Afu1g02550	mitotic sister chromatid segregation
Afu1g02550	nuclear migration during conjugation with cellular fusion
Afu1g02550	structural constituent of cytoskeleton
Afu1g02550	spindle pole body
Afu1g02550	polar microtubule
Afu1g02550	kinetochore microtubule
Afu1g02550	nuclear microtubule
Afu1g02550	cytoplasmic microtubule
Afu1g02550	homologous chromosome segregation
Afu1g02570	aspartate-tRNA ligase activity
Afu1g02570	cytoplasm
Afu1g02570	translation
Afu1g02590	RNA polymerase I transcription factor complex
Afu1g02590	RNA polymerase I transcription factor activity
Afu1g02590	transcription from RNA polymerase I promoter
Afu1g02610	molecular function unknown
Afu1g02610	mitochondrion
Afu1g02610	rRNA processing
Afu1g02610	maturation of SSU-rRNA
Afu1g02630	nucleus
Afu1g02630	nucleolus
Afu1g02630	cytoplasm
Afu1g02630	rRNA processing
Afu1g02670	structural molecule activity
Afu1g02670	Arp2/3 protein complex
Afu1g02670	cell growth and/or maintenance
Afu1g02680	small nucleolar ribonucleoprotein complex
Afu1g02680	maturation of SSU-rRNA
Afu1g02680	snoRNA binding
Afu1g02700	molecular function unknown
Afu1g02700	cellular component unknown
Afu1g02700	protein sumoylation
Afu1g02730	inorganic phosphate transmembrane transporter activity
Afu1g02730	mitochondrion
Afu1g02730	mitochondrial envelope
Afu1g02730	phosphate transport
Afu1g02780	asparaginase activity
Afu1g02780	nuclear envelope
Afu1g02780	endoplasmic reticulum

Afu1g02780	asparagine catabolic process
Afu1g02780	cellular response to nitrogen starvation
Afu1g02780	cell wall-bounded periplasmic space
Afu1g02800	chitinase activity
Afu1g02800	chitin catabolic process
Afu1g02810	mRNA cleavage and polyadenylation specificity factor complex
Afu1g02810	mRNA polyadenylation
Afu1g02810	mRNA cleavage
Afu1g02810	cleavage and polyadenylylation specificity factor activity
Afu1g02820	electron transporter activity
Afu1g02820	cytoplasm
Afu1g02820	electron transport
Afu1g02830	endoplasmic reticulum
Afu1g02830	ER-associated protein catabolic process
Afu1g02830	nuclear envelope-endoplasmic reticulum network
Afu1g02850	L-cystine transmembrane transporter activity
Afu1g02850	L-cystine transport
Afu1g02850	integral to membrane
Afu1g02860	transcription factor activity
Afu1g02860	nucleus
Afu1g02860	regulation of transcription, DNA-dependent
Afu1g02860	zinc ion binding
Afu1g02880	transferase activity, transferring phosphorus-containing groups
Afu1g02890	dUTP diphosphatase activity
Afu1g02890	nucleus
Afu1g02890	cytoplasm
Afu1g02890	pyrimidine deoxyribonucleoside triphosphate catabolic process
Afu1g02900	cellular bud site selection
Afu1g02900	nucleus
Afu1g02900	cytoplasm
Afu1g02900	pyridoxal kinase activity
Afu1g02900	pyridoxal 5'-phosphate salvage
Afu1g02930	calcium ion binding
Afu1g02940	GTPase activator activity
Afu1g02940	spindle pole body
Afu1g02940	mitotic cell cycle spindle assembly checkpoint
Afu1g02980	nucleus
Afu1g02980	cytoplasm
Afu1g02980	tRNA processing
Afu1g02980	6-phosphogluconolactonase activity
Afu1g03010	nuclear mRNA splicing, via spliceosome
Afu1g03010	molecular function unknown
Afu1g03010	spliceosomal complex
Afu1g03050	RNA helicase activity
Afu1g03050	nucleus
Afu1g03050	DNA repair
Afu1g03060	F-actin capping activity
Afu1g03060	endocytosis
Afu1g03060	response to osmotic stress
Afu1g03060	actin filament organization

Afu1g03060	cell wall organization
Afu1g03060	F-actin capping protein complex
Afu1g03070	regulation of transcription involved in G1 phase of mitotic cell cycle
Afu1g03070	SAGA complex
Afu1g03070	transcription factor TFIID complex
Afu1g03070	chromatin organization
Afu1g03070	transcription initiation from RNA polymerase II promoter
Afu1g03070	protein amino acid acetylation
Afu1g03070	general RNA polymerase II transcription factor activity
Afu1g03070	chromatin modification
Afu1g03070	histone acetylation
Afu1g03080	protein modification process
Afu1g03080	cellular component unknown
Afu1g03080	carboxylic ester hydrolase activity
Afu1g03090	biological process unknown
Afu1g03090	fungal-type vacuole
Afu1g03090	molecular function unknown
Afu1g03100	mitochondrial proton-transporting ATP synthase, central stalk
Afu1g03100	ATP synthesis coupled proton transport
Afu1g03100	hydrogen ion transporting ATP synthase activity, rotational mechanism
Afu1g03110	structural constituent of ribosome
Afu1g03110	cytoplasm
Afu1g03110	cytosolic large ribosomal subunit (sensu Eukaryota)
Afu1g03110	translation
Afu1g03140	alpha-glucosidase activity
Afu1g03140	endoplasmic reticulum
Afu1g03140	fungal-type cell wall biogenesis
Afu1g03150	C-14 sterol reductase activity
Afu1g03150	endoplasmic reticulum
Afu1g03150	ergosterol biosynthetic process
Afu1g03170	lipid catabolic process
Afu1g03170	lipase activity
Afu1g03200	transporter activity
Afu1g03200	integral to plasma membrane
Afu1g03200	transport
Afu1g03230	ATP-binding cassette (ABC) transporter activity
Afu1g03230	mitochondrial inner membrane
Afu1g03230	cellular iron ion homeostasis
Afu1g03250	metabolic process
Afu1g03250	oxidoreductase activity
Afu1g03260	integral to plasma membrane
Afu1g03260	nicotinamide mononucleotide permease activity
Afu1g03260	nicotinamide mononucleotide transport
Afu1g03280	alpha-glucoside transport
Afu1g03280	alpha-glucoside:hydrogen symporter activity
Afu1g03280	maltose:hydrogen symporter activity
Afu1g03280	membrane fraction
Afu1g03280	trehalose transmembrane transporter activity
Afu1g03280	trehalose transport
Afu1g03290	myo-inositol transmembrane transporter activity

Afu1g03290	myo-inositol transport
Afu1g03290	membrane
Afu1g03352	hydrolase activity, hydrolyzing O-glycosyl compounds
Afu1g03352	cellular glucan metabolic process
Afu1g03352	fungal-type cell wall
Afu1g03390	ribosomal large subunit assembly
Afu1g03390	structural constituent of ribosome
Afu1g03390	cytosolic large ribosomal subunit (sensu Eukaryota)
Afu1g03390	translation
Afu1g03400	GTPase activator activity
Afu1g03400	cytoplasm
Afu1g03400	ER to Golgi vesicle-mediated transport
Afu1g03400	autophagy
Afu1g03400	COPII vesicle coat
Afu1g03400	ER-associated protein catabolic process
Afu1g03410	DNA synthesis during DNA repair
Afu1g03410	alpha DNA polymerase activity
Afu1g03410	alpha DNA polymerase:primase complex
Afu1g03410	DNA replication, synthesis of RNA primer
Afu1g03410	DNA replication initiation
Afu1g03410	lagging strand elongation
Afu1g03420	adenylate kinase activity
Afu1g03420	mitochondrial inner membrane
Afu1g03420	nucleobase, nucleoside and nucleotide interconversion
Afu1g03430	biological process unknown
Afu1g03430	nuclease activity
Afu1g03430	molecular function unknown
Afu1g03430	mitochondrion
Afu1g03440	adenine nucleotide transmembrane transporter activity
Afu1g03440	cytoplasm
Afu1g03440	integral to peroxisomal membrane
Afu1g03440	fatty acid beta-oxidation
Afu1g03440	peroxisome organization
Afu1g03440	ATP transport
Afu1g03450	cysteine-type endopeptidase activity
Afu1g03450	cellular component unknown
Afu1g03450	protein processing
Afu1g03500	regulation of mitotic recombination
Afu1g03500	DNA topoisomerase type I activity
Afu1g03500	nucleus
Afu1g03500	DNA topological change
Afu1g03500	DNA strand elongation during DNA replication
Afu1g03500	chromatin assembly or disassembly
Afu1g03500	regulation of transcription from RNA polymerase II promoter
Afu1g03500	RNA elongation from RNA polymerase II promoter
Afu1g03500	mitotic chromosome condensation
Afu1g03500	nuclear migration
Afu1g03510	mitochondrial proton-transporting ATP synthase, central stalk
Afu1g03510	ATP synthesis coupled proton transport
Afu1g03510	hydrogen ion transporting ATP synthase activity, rotational mechanism

Afu1g03530	fructose transmembrane transporter activity
Afu1g03530	glucose transmembrane transporter activity
Afu1g03530	plasma membrane
Afu1g03530	hexose transport
Afu1g03530	mannose transmembrane transporter activity
Afu1g03540	metabolic process
Afu1g03540	hydrolase activity
Afu1g03550	dihydroxy-acid dehydratase activity
Afu1g03550	mitochondrion
Afu1g03550	branched chain family amino acid biosynthetic process
Afu1g03590	nuclear pore
Afu1g03590	cytoplasm
Afu1g03590	protein import into nucleus
Afu1g03590	structural constituent of nuclear pore
Afu1g03600	glucan 1,3-beta-glucosidase activity
Afu1g03600	1,3-beta-glucan metabolic process
Afu1g03600	cell wall organization
Afu1g03600	fungal-type cell wall
Afu1g03620	3-chloroallyl aldehyde dehydrogenase activity
Afu1g03660	acid phosphatase activity
Afu1g03660	cytoplasm
Afu1g03660	response to stress
Afu1g03680	biological process unknown
Afu1g03680	molecular function unknown
Afu1g03680	cytoplasm
Afu1g03680	Golgi apparatus
Afu1g03680	COPI-coated vesicle
Afu1g03690	catechol catabolic process
Afu1g03690	4-carboxymuconolactone decarboxylase activity
Afu1g03710	DNA binding
Afu1g03710	nucleus
Afu1g03710	zinc ion binding
Afu1g03720	biological process unknown
Afu1g03720	molecular function unknown
Afu1g03720	cellular component unknown
Afu1g03730	transporter activity
Afu1g03730	integral to plasma membrane
Afu1g03730	transport
Afu1g03740	proteolysis
Afu1g03740	protein targeting to vacuole
Afu1g03740	metallopeptidase activity
Afu1g03740	cellular component unknown
Afu1g03760	biological process unknown
Afu1g03760	molecular function unknown
Afu1g03760	cellular component unknown
Afu1g03780	DNA binding
Afu1g03790	molecular function unknown
Afu1g03790	protein amino acid N-linked glycosylation
Afu1g03790	protein amino acid O-linked glycosylation
Afu1g03790	response to stress

Afu1g03790	cellular component unknown
Afu1g03800	transcription factor activity
Afu1g03800	nucleus
Afu1g03800	zinc ion binding
Afu1g03800	regulation of transcription
Afu1g03810	dolichyl-diphosphooligosaccharide-protein glycotransferase activity
Afu1g03810	Sec61 translocon complex
Afu1g03810	protein amino acid N-linked glycosylation
Afu1g03810	oligosaccharyltransferase complex
Afu1g03810	programmed cell death
Afu1g03820	formation of catalytic U2-type spliceosome for second transesterification step
Afu1g03820	ATP-dependent RNA helicase activity
Afu1g03820	spliceosomal complex
Afu1g03820	pre-mRNA splicing factor activity
Afu1g03840	regulation of carbohydrate metabolic process
Afu1g03840	transcription
Afu1g03840	transcription activator activity
Afu1g03840	CCAAT-binding factor complex
Afu1g03860	transcription factor activity
Afu1g03860	nucleus
Afu1g03860	zinc ion binding
Afu1g03860	cellular amino acid catabolic process
Afu1g03860	regulation of transcription
Afu1g03870	metabolic process
Afu1g03870	hydrolase activity
Afu1g03890	metabolic process
Afu1g03890	cellular component unknown
Afu1g03890	hydrolase activity
Afu1g03920	chromatin binding
Afu1g03920	ATP-dependent DNA helicase activity
Afu1g03920	nucleus
Afu1g03920	pre-replicative complex
Afu1g03920	cytoplasm
Afu1g03920	pre-replicative complex assembly
Afu1g03920	DNA unwinding during replication
Afu1g03920	DNA replication initiation
Afu1g03930	mitochondrial inner membrane
Afu1g03930	translation
Afu1g03930	aerobic respiration
Afu1g03930	integral to membrane
Afu1g03930	RNA metabolic process
Afu1g03930	translation regulator activity
Afu1g03940	signal sequence binding
Afu1g03940	signal recognition particle, endoplasmic reticulum targeting
Afu1g03940	protein targeting to ER
Afu1g03950	C-22 sterol desaturase activity
Afu1g03950	endoplasmic reticulum
Afu1g03950	ergosterol biosynthetic process
Afu1g03950	metabolic process
Afu1g03950	oxidoreductase activity

Afu1g03960	biological process unknown
Afu1g03960	molecular function unknown
Afu1g03960	mitochondrion
Afu1g03970	translation initiation factor activity
Afu1g03970	GTPase activity
Afu1g03970	cytosolic small ribosomal subunit (sensu Eukaryota)
Afu1g03970	translational initiation
Afu1g04040	structural constituent of ribosome
Afu1g04040	cytosolic large ribosomal subunit (sensu Eukaryota)
Afu1g04040	translation
Afu1g04040	ubiquitin-dependent protein catabolic process
Afu1g04040	protein tagging activity
Afu1g04070	translation initiation factor activity
Afu1g04070	ribosome
Afu1g04070	translational initiation
Afu1g04080	GARP complex
Afu1g04080	protein binding
Afu1g04080	Golgi apparatus
Afu1g04080	Golgi to vacuole transport
Afu1g04080	actin filament-based process
Afu1g04090	metabolic process
Afu1g04090	oxidoreductase activity
Afu1g04090	FAD binding
Afu1g04110	transcription factor activity
Afu1g04110	nucleus
Afu1g04110	regulation of transcription, DNA-dependent
Afu1g04110	zinc ion binding
Afu1g04150	isocitrate dehydrogenase activity
Afu1g04150	cytoplasm
Afu1g04150	mitochondrion
Afu1g04150	tartrate dehydrogenase activity
Afu1g04150	lysine biosynthetic process
Afu1g04150	carboxylic acid catabolic process
Afu1g04160	L-aspartate:2-oxoglutarate aminotransferase activity
Afu1g04160	cytoplasm
Afu1g04160	peroxisome
Afu1g04160	aspartate biosynthetic process
Afu1g04160	aspartate catabolic process
Afu1g04160	glutamate metabolic process
Afu1g04160	nitrogen compound metabolic process
Afu1g04160	asparagine biosynthetic process from oxaloacetate
Afu1g04190	nucleus
Afu1g04190	cytoplasm
Afu1g04190	ribosome
Afu1g04190	regulation of translational initiation
Afu1g04190	poly(A) RNA binding
Afu1g04210	protein polyubiquitination
Afu1g04210	ubiquitin-protein ligase activity
Afu1g04210	nucleus
Afu1g04210	cytoplasm

Afu1g04210	protein monoubiquitination
Afu1g04230	structural constituent of ribosome
Afu1g04230	mitochondrial large ribosomal subunit
Afu1g04230	translation
Afu1g04240	small nucleolar ribonucleoprotein complex
Afu1g04240	maturation of SSU-rRNA
Afu1g04240	snoRNA binding
Afu1g04260	hydrolase activity, hydrolyzing O-glycosyl compounds
Afu1g04260	1,3-beta-glucan metabolic process
Afu1g04260	cytokinesis, completion of separation
Afu1g04260	fungal-type cell wall
Afu1g04260	cell septum
Afu1g04270	fungal-type vacuole
Afu1g04270	vacuolar membrane
Afu1g04270	calcium ion transport
Afu1g04270	cellular calcium ion homeostasis
Afu1g04270	calcium ion transmembrane transporter activity
Afu1g04270	calcium:hydrogen antiporter activity
Afu1g04280	structural constituent of ribosome
Afu1g04280	mitochondrial small ribosomal subunit
Afu1g04280	translation
Afu1g04290	phosphate transport
Afu1g04290	phosphate transmembrane transporter activity
Afu1g04290	membrane
Afu1g04320	structural constituent of ribosome
Afu1g04320	cytosolic small ribosomal subunit (sensu Eukaryota)
Afu1g04320	translation
Afu1g04340	biological process unknown
Afu1g04340	molecular function unknown
Afu1g04340	cytoplasm
Afu1g04360	actin cap (sensu Saccharomyces)
Afu1g04360	exocyst
Afu1g04360	establishment of cell polarity (sensu Saccharomyces)
Afu1g04360	cytokinesis
Afu1g04360	molecular function unknown
Afu1g04360	Golgi to plasma membrane transport
Afu1g04360	vesicle docking during exocytosis
Afu1g04360	vesicle fusion
Afu1g04360	bipolar cellular bud site selection
Afu1g04390	metabolic process
Afu1g04390	oxidoreductase activity
Afu1g04400	structural constituent of ribosome
Afu1g04400	mitochondrial small ribosomal subunit
Afu1g04400	translation
Afu1g04440	biological process unknown
Afu1g04440	molecular function unknown
Afu1g04440	cellular component unknown
Afu1g04460	lysine-tRNA ligase activity
Afu1g04460	cytoplasm
Afu1g04460	lysyl-tRNA aminoacylation

Afu1g04470	chaperone activity
Afu1g04470	mitochondrial intermembrane space
Afu1g04470	mitochondrial translocation
Afu1g04470	protein transporter activity
Afu1g04470	mitochondrial intermembrane space protein transporter complex
Afu1g04480	nucleus
Afu1g04480	transcription repressor activity
Afu1g04480	histone deacetylation
Afu1g04480	Sin3 complex
Afu1g04530	structural constituent of ribosome
Afu1g04530	cytosolic large ribosomal subunit (sensu Eukaryota)
Afu1g04530	translation
Afu1g04540	cytochrome-b5 reductase activity
Afu1g04540	mitochondrial outer membrane
Afu1g04540	mitochondrial intermembrane space
Afu1g04540	electron transport
Afu1g04540	ergosterol biosynthetic process
Afu1g04540	response to oxidative stress
Afu1g04560	urease activity
Afu1g04560	nickel ion binding
Afu1g04560	urea metabolic process
Afu1g04580	molecular function unknown
Afu1g04580	cellular component unknown
Afu1g04580	proline transport
Afu1g04580	urea transport
Afu1g04590	SAGA complex
Afu1g04590	transcription cofactor activity
Afu1g04590	chromatin modification
Afu1g04590	histone acetylation
Afu1g04600	zinc ion binding
Afu1g04620	cellular component unknown
Afu1g04620	oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor
Afu1g04620	hexose metabolic process
Afu1g04640	protein polyubiquitination
Afu1g04640	ubiquitin-protein ligase activity
Afu1g04640	protein monoubiquitination
Afu1g04640	cellular component unknown
Afu1g04660	RNA binding
Afu1g04660	structural constituent of ribosome
Afu1g04660	cytosolic large ribosomal subunit (sensu Eukaryota)
Afu1g04660	translation
Afu1g04670	biological process unknown
Afu1g04670	molecular function unknown
Afu1g04670	cytoplasm
Afu1g04680	molecular function unknown
Afu1g04680	mitochondrial matrix
Afu1g04680	cellular iron ion homeostasis
Afu1g04690	zinc ion binding
Afu1g04700	regulation of progression through cell cycle
Afu1g04700	Ras guanyl-nucleotide exchange factor activity

Afu1g04700	cytoplasm
Afu1g04700	plasma membrane
Afu1g04700	traversing start control point of mitotic cell cycle
Afu1g04700	Ras protein signal transduction
Afu1g04710	biological process unknown
Afu1g04710	ATP binding
Afu1g04720	C-8 sterol isomerase activity
Afu1g04720	endoplasmic reticulum
Afu1g04720	ergosterol biosynthetic process
Afu1g04750	cyclin-dependent protein kinase holoenzyme complex
Afu1g04750	cell cycle
Afu1g04750	cyclin-dependent protein kinase regulator activity
Afu1g04780	ATP-binding cassette (ABC) transporter activity
Afu1g04780	integral to peroxisomal membrane
Afu1g04780	fatty acid transport
Afu1g04790	phosphoprotein phosphatase activity
Afu1g04790	plasma membrane
Afu1g04790	response to stress
Afu1g04800	nucleus
Afu1g04800	cytoplasm
Afu1g04800	protein targeting
Afu1g04800	chromosome segregation
Afu1g04800	protein phosphatase type 1 regulator activity
Afu1g04800	enzyme regulator activity
Afu1g04820	aldo-keto reductase activity
Afu1g04820	cytosol
Afu1g04820	D-xylose metabolic process
Afu1g04840	nucleolus
Afu1g04840	35S primary transcript processing
Afu1g04840	snoRNA binding
Afu1g04840	rRNA primary transcript binding
Afu1g04850	microtubule motor activity
Afu1g04850	cell
Afu1g04850	microtubule-based process
Afu1g04850	actin filament-based process
Afu1g04870	plasma membrane
Afu1g04870	urea transmembrane transporter activity
Afu1g04870	urea transport
Afu1g04890	Sec61 translocon complex
Afu1g04890	cotranslational protein targeting to membrane
Afu1g04890	protein transporter activity
Afu1g04900	replication fork
Afu1g04900	leading strand elongation
Afu1g04900	lagging strand elongation
Afu1g04900	mutagenesis
Afu1g04900	base-excision repair
Afu1g04900	nucleotide-excision repair
Afu1g04900	mismatch repair
Afu1g04900	postreplication repair
Afu1g04900	DNA polymerase processivity factor activity

Afu1g04940	SAR small monomeric GTPase activity
Afu1g04940	ER to Golgi vesicle-mediated transport
Afu1g04940	COPII vesicle coat
Afu1g04950	protein phosphatase type 1 activity
Afu1g04950	protein phosphatase type 1 complex
Afu1g04950	cell morphogenesis during vegetative growth
Afu1g04950	nucleolus
Afu1g04950	mRNA cleavage and polyadenylation specificity factor complex
Afu1g04950	cellular bud neck
Afu1g04950	glycogen metabolic process
Afu1g04950	regulation of carbohydrate metabolic process
Afu1g04950	35S primary transcript processing
Afu1g04950	mitotic cell cycle spindle assembly checkpoint
Afu1g04950	meiosis
Afu1g04950	protein phosphatase type 1\, intrinsic catalyst activity
Afu1g04950	response to heat
Afu1g04950	termination of RNA polymerase II transcription, poly(A)-coupled
Afu1g04950	termination of RNA polymerase II transcription, poly(A)-independent
Afu1g04970	biological process unknown
Afu1g04970	molecular function unknown
Afu1g04970	lipid particle
Afu1g04980	transcription factor TFIIIC complex
Afu1g04980	RNA polymerase III transcription factor activity
Afu1g04980	protein binding
Afu1g04980	transcription initiation from RNA polymerase III promoter
Afu1g04990	RNA binding
Afu1g04990	intracellular transporter activity
Afu1g04990	cytosol
Afu1g04990	protein targeting to vacuole
Afu1g05010	integral to plasma membrane
Afu1g05010	transport
Afu1g05010	signal transduction
Afu1g05010	ascospore formation
Afu1g05020	plasma membrane
Afu1g05020	sulfate transport
Afu1g05020	sulfate transmembrane transporter activity
Afu1g05040	ATPase activator activity
Afu1g05040	cytosol
Afu1g05040	protein targeting to mitochondrion
Afu1g05040	chaperone regulator activity
Afu1g05040	Hsp70/Hsc70 protein regulator activity
Afu1g05050	cytosine deaminase activity
Afu1g05050	nucleus
Afu1g05050	cytoplasm
Afu1g05050	zinc ion binding
Afu1g05050	cytosine metabolic process
Afu1g05060	uroporphyrinogen decarboxylase activity
Afu1g05060	nucleus
Afu1g05060	cytoplasm
Afu1g05060	heme biosynthetic process

Afu1g05070	protein binding
Afu1g05070	nucleus
Afu1g05070	tRNA (guanine-N7-)-methyltransferase activity
Afu1g05070	tRNA methylation
Afu1g05080	ribosomal large subunit assembly
Afu1g05080	structural constituent of ribosome
Afu1g05080	cytosolic large ribosomal subunit (sensu Eukaryota)
Afu1g05080	translation
Afu1g05080	translational elongation
Afu1g05100	GARP complex
Afu1g05100	molecular function unknown
Afu1g05100	cytoplasm
Afu1g05100	Golgi apparatus
Afu1g05100	Golgi to vacuole transport
Afu1g05110	RNA binding
Afu1g05110	protein binding
Afu1g05110	nuclear pore
Afu1g05110	cytoplasm
Afu1g05110	mRNA export from nucleus
Afu1g05110	structural constituent of nuclear pore
Afu1g05120	molecular function unknown
Afu1g05120	ER to Golgi vesicle-mediated transport
Afu1g05120	COPII-coated vesicle
Afu1g05120	integral to Golgi membrane
Afu1g05120	integral to endoplasmic reticulum membrane
Afu1g05130	biological process unknown
Afu1g05130	molecular function unknown
Afu1g05130	cytoplasm
Afu1g05130	cellular bud
Afu1g05130	cellular bud neck
Afu1g05150	RNA polymerase III transcription factor activity
Afu1g05150	transcription factor complex
Afu1g05150	transcription initiation from RNA polymerase III promoter
Afu1g05150	zinc ion binding
Afu1g05160	DNA-directed RNA polymerase activity
Afu1g05160	DNA-directed RNA polymerase II, core complex
Afu1g05160	DNA-directed RNA polymerase III complex
Afu1g05160	DNA-directed RNA polymerase I complex
Afu1g05160	transcription from RNA polymerase I promoter
Afu1g05160	transcription from RNA polymerase II promoter
Afu1g05160	transcription from RNA polymerase III promoter
Afu1g05170	transporter activity
Afu1g05170	transport
Afu1g05170	monocarboxylic acid transmembrane transporter activity
Afu1g05170	membrane
Afu1g05180	peptide alpha-N-acetyltransferase activity
Afu1g05180	cytoplasm
Afu1g05180	N-terminal peptidyl-methionine acetylation
Afu1g05200	translation initiation factor activity
Afu1g05200	eukaryotic translation initiation factor 3 complex

Afu1g05200	translational initiation
Afu1g05210	response to pheromone during conjugation with cellular fusion
Afu1g05210	pheromone-dependent signal transduction involved in conjugation with cellular fusion
Afu1g05210	heterotrimeric G-protein GTPase activity
Afu1g05210	heterotrimeric G-protein complex
Afu1g05210	plasma membrane
Afu1g05230	3',5'-cyclic-AMP phosphodiesterase activity
Afu1g05230	nucleus
Afu1g05230	cytoplasm
Afu1g05230	cAMP-mediated signaling
Afu1g05240	protein binding
Afu1g05240	nucleus
Afu1g05240	zinc ion binding
Afu1g05260	U2-type spliceosome conformational change to release U4 and U1
Afu1g05260	ATP-dependent RNA helicase activity
Afu1g05260	U5 snRNP
Afu1g05260	pre-mRNA splicing factor activity
Afu1g05260	U4/U6 x U5 tri-snRNP complex
Afu1g05280	molecular function unknown
Afu1g05280	membrane fraction
Afu1g05280	late endosome to vacuole transport
Afu1g05290	hydrolase activity, hydrolyzing O-glycosyl compounds
Afu1g05290	1,3-beta-glucan metabolic process
Afu1g05290	fungal-type cell wall
Afu1g05310	biological process unknown
Afu1g05310	molecular function unknown
Afu1g05310	nucleolus
Afu1g05320	fungal-type vacuole
Afu1g05320	protein disulfide isomerase activity
Afu1g05320	protein folding
Afu1g05340	structural constituent of ribosome
Afu1g05340	cytosolic small ribosomal subunit (sensu Eukaryota)
Afu1g05340	translation
Afu1g05390	ATP:ADP antiporter activity
Afu1g05390	mitochondrial inner membrane
Afu1g05390	ATP/ADP exchange
Afu1g05410	molecular function unknown
Afu1g05410	nucleolus
Afu1g05410	ribosome biogenesis
Afu1g05420	transcription cofactor activity
Afu1g05420	nucleus
Afu1g05420	transcription initiation from RNA polymerase II promoter
Afu1g05420	pectin metabolic process
Afu1g05440	UDP-galactose transmembrane transporter activity
Afu1g05440	cellular component unknown
Afu1g05440	UDP-galactose transport
Afu1g05470	molecular function unknown
Afu1g05470	pseudohyphal growth
Afu1g05470	cellular component unknown
Afu1g05490	histone deacetylase complex

Afu1g05490	histone deacetylation
Afu1g05490	NAD-dependent histone deacetylase activity
Afu1g05490	NAD-independent histone deacetylase activity
Afu1g05490	negative regulation of meiosis
Afu1g05500	structural constituent of ribosome
Afu1g05500	cytosolic small ribosomal subunit (sensu Eukaryota)
Afu1g05500	translation
Afu1g05530	nucleus
Afu1g05530	cytoplasm
Afu1g05530	uridine catabolic process
Afu1g05530	pyrimidine salvage
Afu1g05530	hydrolase activity, acting on glycosyl bonds
Afu1g05560	biological process unknown
Afu1g05560	GTP binding
Afu1g05560	cytoplasm
Afu1g05580	glycogen biosynthetic process
Afu1g05580	cellular component unknown
Afu1g05580	glycogenin glucosyltransferase activity
Afu1g05590	metabolic process
Afu1g05590	hydrolase activity
Afu1g05610	protein phosphatase type 2A activity
Afu1g05610	protein phosphatase type 2A complex
Afu1g05610	nucleus
Afu1g05610	cytoplasm
Afu1g05610	spindle pole body
Afu1g05610	cellular bud tip
Afu1g05610	cellular bud neck
Afu1g05610	mating projection
Afu1g05610	translation
Afu1g05610	protein amino acid dephosphorylation
Afu1g05610	actin filament organization
Afu1g05610	mitotic cell cycle spindle assembly checkpoint
Afu1g05610	budding cell bud growth
Afu1g05620	phenylalanine-tRNA ligase activity
Afu1g05620	phenylalanyl-tRNA aminoacylation
Afu1g05620	phenylalanine-tRNA ligase complex
Afu1g05630	structural constituent of ribosome
Afu1g05630	cytosolic small ribosomal subunit (sensu Eukaryota)
Afu1g05630	translation
Afu1g05630	response to DNA damage stimulus
Afu1g05640	biological process unknown
Afu1g05640	cytoplasm
Afu1g05640	phosphatase activity
Afu1g05710	nucleus
Afu1g05710	tRNA modification
Afu1g05710	tRNA-specific adenosine deaminase activity
Afu1g05720	C-14 sterol reductase activity
Afu1g05720	endoplasmic reticulum
Afu1g05720	ergosterol biosynthetic process
Afu1g05730	receptor activity

Afu1g05730	cytoplasm
Afu1g05730	late endosome
Afu1g05730	vacuolar transport
Afu1g05740	transcription factor activity
Afu1g05740	nucleus
Afu1g05740	zinc ion binding
Afu1g05740	regulation of transcription
Afu1g05760	integral to plasma membrane
Afu1g05760	arsenite transmembrane transporter activity
Afu1g05760	arsenite transport
Afu1g05760	response to arsenic
Afu1g05770	hydrolase activity, hydrolyzing O-glycosyl compounds
Afu1g05770	carbohydrate metabolic process
Afu1g05800	MAP kinase kinase activity
Afu1g05800	protein amino acid phosphorylation
Afu1g05800	signal transduction
Afu1g05830	nucleus
Afu1g05830	chromatin remodeling
Afu1g05830	regulation of transcription from RNA polymerase II promoter
Afu1g05830	ATPase activity
Afu1g05870	endoplasmic reticulum
Afu1g05870	phospholipid metabolic process
Afu1g05900	biological process unknown
Afu1g05900	molecular function unknown
Afu1g05900	endoplasmic reticulum
Afu1g05900	endoplasmic reticulum membrane
Afu1g05930	protein amino acid phosphorylation
Afu1g05940	mediator complex
Afu1g05940	transcription from RNA polymerase II promoter
Afu1g05940	RNA polymerase II transcription mediator activity
Afu1g05960	proteolysis
Afu1g05960	metallopeptidase activity
Afu1g05960	cellular component unknown
Afu1g05970	G1/S transition of mitotic cell cycle
Afu1g05970	cellular bud neck contractile ring
Afu1g05970	nuclear ubiquitin ligase complex
Afu1g05970	ubiquitin-protein ligase activity
Afu1g05970	protein binding
Afu1g05970	nucleus
Afu1g05970	cytoplasm
Afu1g05970	ubiquitin-dependent protein catabolic process
Afu1g05980	catalytic activity
Afu1g05980	cytoplasm
Afu1g05980	AMP binding
Afu1g05980	AMP metabolic process
Afu1g05990	RNA binding
Afu1g05990	structural constituent of ribosome
Afu1g05990	cytosolic large ribosomal subunit (sensu Eukaryota)
Afu1g05990	translation
Afu1g06000	phosphate metabolic process

Afu1g06000	phosphoric ester hydrolase activity
Afu1g06030	vesicle-mediated transport
Afu1g06030	AP-1 adaptor complex
Afu1g06030	clathrin binding
Afu1g06040	sterol O-acyltransferase activity
Afu1g06040	endoplasmic reticulum
Afu1g06040	sterol metabolic process
Afu1g06080	protein folding
Afu1g06080	Hsp70 protein binding
Afu1g06100	glutathione transferase activity
Afu1g06100	glutathione peroxidase activity
Afu1g06100	mitochondrion
Afu1g06100	cytosol
Afu1g06100	electron transport
Afu1g06100	response to oxidative stress
Afu1g06100	regulation of cell redox homeostasis
Afu1g06100	thiol-disulfide exchange intermediate activity
Afu1g06110	biological process unknown
Afu1g06110	molecular function unknown
Afu1g06110	mitochondrion
Afu1g06150	biological process unknown
Afu1g06150	molecular function unknown
Afu1g06150	cellular component unknown
Afu1g06170	endopeptidase activity
Afu1g06170	proteasome regulatory particle
Afu1g06170	ubiquitin-dependent protein catabolic process
Afu1g06170	proteasome regulatory particle, base subcomplex
Afu1g06170	ATPase activity
Afu1g06190	nucleus
Afu1g06190	mRNA export from nucleus
Afu1g06190	protein-arginine N-methyltransferase activity
Afu1g06190	peptidyl-arginine modification
Afu1g06200	fungal-type vacuole membrane
Afu1g06200	molecular function unknown
Afu1g06200	response to unfolded protein
Afu1g06200	cellular manganese ion homeostasis
Afu1g06210	phosphoacetylglucosamine mutase activity
Afu1g06210	nucleus
Afu1g06210	cytoplasm
Afu1g06210	N-acetylglucosamine biosynthetic process
Afu1g06220	ATP-dependent RNA helicase activity
Afu1g06220	nucleolus
Afu1g06220	35S primary transcript processing
Afu1g06230	ribosomal large subunit assembly
Afu1g06230	conjugation with cellular fusion
Afu1g06230	nucleolus
Afu1g06230	rRNA binding
Afu1g06240	riboflavin synthase activity
Afu1g06240	soluble fraction
Afu1g06240	riboflavin biosynthetic process

Afu1g06260	DNA binding
Afu1g06260	nucleus
Afu1g06260	chromatin remodeling
Afu1g06260	zinc ion binding
Afu1g06280	biological process unknown
Afu1g06280	molecular function unknown
Afu1g06280	cellular component unknown
Afu1g06290	rRNA modification
Afu1g06290	small nucleolar ribonucleoprotein complex
Afu1g06290	35S primary transcript processing
Afu1g06290	maturation of SSU-rRNA
Afu1g06290	snoRNA binding
Afu1g06290	small nuclear ribonucleoprotein complex
Afu1g06300	endopeptidase activity
Afu1g06300	ubiquitin-dependent protein catabolic process
Afu1g06300	proteasome regulatory particle, lid subcomplex
Afu1g06310	nucleosome remodeling complex
Afu1g06310	chromatin remodeling
Afu1g06310	general RNA polymerase II transcription factor activity
Afu1g06310	SWI/SNF complex
Afu1g06320	biological process unknown
Afu1g06320	molecular function unknown
Afu1g06320	cellular component unknown
Afu1g06330	molecular function unknown
Afu1g06340	structural constituent of ribosome
Afu1g06340	translation
Afu1g06370	biological process unknown
Afu1g06370	molecular function unknown
Afu1g06370	cellular component unknown
Afu1g06380	DNA-directed RNA polymerase activity
Afu1g06380	DNA-directed RNA polymerase III complex
Afu1g06380	transcription from RNA polymerase III promoter
Afu1g06390	translation elongation factor activity
Afu1g06390	ribosome
Afu1g06390	translational elongation
Afu1g06400	protein serine/threonine kinase activity
Afu1g06400	protein amino acid phosphorylation
Afu1g06410	molecular function unknown
Afu1g06410	nucleus
Afu1g06410	protein import into nucleus
Afu1g06420	molecular function unknown
Afu1g06420	cytoplasm
Afu1g06420	endosome
Afu1g06420	late endosome to vacuole transport
Afu1g06440	drug transporter activity
Afu1g06440	drug transport
Afu1g06440	integral to membrane
Afu1g06520	RNA binding
Afu1g06520	translation initiation factor activity
Afu1g06520	GTPase activity

Afu1g06520	mitochondrion
Afu1g06520	translational initiation
Afu1g06530	transporter activity
Afu1g06530	mitochondrial inner membrane
Afu1g06530	transport
Afu1g06540	transcription factor activity
Afu1g06540	regulation of transcription
Afu1g06550	transporter activity
Afu1g06550	transport
Afu1g06550	integral to membrane
Afu1g06560	alpha-glucosidase activity
Afu1g06560	endoplasmic reticulum
Afu1g06560	fungal-type cell wall biogenesis
Afu1g06570	tRNA binding
Afu1g06570	structural constituent of ribosome
Afu1g06570	mitochondrial small ribosomal subunit
Afu1g06570	translation
Afu1g06580	programmed cell death
Afu1g06600	nucleolus
Afu1g06600	ribosomal large subunit biogenesis
Afu1g06620	acyl carrier activity
Afu1g06620	mitochondrion
Afu1g06620	fatty acid biosynthetic process
Afu1g06630	molecular function unknown
Afu1g06630	nucleus
Afu1g06630	cytoplasm
Afu1g06630	protein targeting to vacuole
Afu1g06640	metabolic process
Afu1g06640	zinc ion binding
Afu1g06640	oxidoreductase activity
Afu1g06650	molecular function unknown
Afu1g06650	actin cortical patch (sensu Saccharomyces)
Afu1g06650	actin filament organization
Afu1g06650	actin cytoskeleton
Afu1g06650	actin cytoskeleton organization
Afu1g06660	molecular function unknown
Afu1g06660	cytoplasm
Afu1g06660	DNA metabolic process
Afu1g06660	endocytosis
Afu1g06660	meiosis
Afu1g06680	molecular function unknown
Afu1g06680	trans-Golgi network
Afu1g06680	Golgi to vacuole transport
Afu1g06690	biological process unknown
Afu1g06690	molecular function unknown
Afu1g06690	nucleus
Afu1g06690	cytoplasm
Afu1g06700	cellular component unknown
Afu1g06700	programmed cell death
Afu1g06700	caspase activity

Afu1g06710	chaperone activity
Afu1g06710	cytoplasm
Afu1g06710	cytoskeleton
Afu1g06710	protein folding
Afu1g06710	cytoskeleton organization
Afu1g06720	histone acetyltransferase activity
Afu1g06720	nucleus
Afu1g06720	chromatin remodeling
Afu1g06720	regulation of transcription from RNA polymerase II promoter, global
Afu1g06770	structural constituent of ribosome
Afu1g06770	cytosolic small ribosomal subunit (sensu Eukaryota)
Afu1g06770	translation
Afu1g06790	nucleus
Afu1g06790	cytoplasm
Afu1g06790	mRNA export from nucleus
Afu1g06790	protein transmembrane transporter activity
Afu1g06800	alcohol dehydrogenase activity, iron-dependent
Afu1g06810	biological process unknown
Afu1g06810	aconitate hydratase activity
Afu1g06810	mitochondrion
Afu1g06820	biological process unknown
Afu1g06820	molecular function unknown
Afu1g06820	nucleus
Afu1g06820	cytoplasm
Afu1g06830	structural constituent of ribosome
Afu1g06830	cytosolic large ribosomal subunit (sensu Eukaryota)
Afu1g06830	translation
Afu1g06830	translational elongation
Afu1g06840	biological process unknown
Afu1g06840	fungal-type vacuole membrane
Afu1g06840	molecular function unknown
Afu1g06840	cytoplasm
Afu1g06850	biological process unknown
Afu1g06850	molecular function unknown
Afu1g06850	cytoplasm
Afu1g06860	biological process unknown
Afu1g06860	cellular component unknown
Afu1g06860	protein phosphatase type 2C activity
Afu1g06890	alpha-1,2-mannosyltransferase activity
Afu1g06890	alpha-1,6-mannosyltransferase complex
Afu1g06890	endoplasmic reticulum
Afu1g06890	protein amino acid glycosylation
Afu1g06900	transcription factor activity
Afu1g06900	nucleus
Afu1g06900	cytoplasm
Afu1g06900	regulation of transcription, DNA-dependent
Afu1g06900	response to stress
Afu1g06900	zinc ion binding
Afu1g06900	calcium-mediated signaling
Afu1g06920	protein kinase activity

Afu1g06920	cytoplasm
Afu1g06920	protein amino acid phosphorylation
Afu1g06940	chorismate synthase activity
Afu1g06940	cytoplasm
Afu1g06940	aromatic amino acid family biosynthetic process
Afu1g06950	protein modification process
Afu1g06950	cellular component unknown
Afu1g06950	lipoyltransferase activity
Afu1g06960	pyruvate dehydrogenase (acetyl-transferring) activity
Afu1g06960	mitochondrion
Afu1g06960	pyruvate metabolic process
Afu1g06960	pyruvate dehydrogenase complex
Afu1g06980	structural constituent of ribosome
Afu1g06980	mitochondrial small ribosomal subunit
Afu1g06980	translation
Afu1g07010	phosphatidate cytidylyltransferase activity
Afu1g07010	mitochondrion
Afu1g07010	endoplasmic reticulum
Afu1g07010	phosphatidylglycerol biosynthetic process
Afu1g07010	phosphatidylserine metabolic process
Afu1g07020	nucleus
Afu1g07020	regulation of transcription from RNA polymerase II promoter
Afu1g07020	protein amino acid phosphorylation
Afu1g07020	cyclin-dependent protein kinase regulator activity
Afu1g07070	cyclin-dependent protein kinase holoenzyme complex
Afu1g07070	cyclin-dependent protein kinase regulator activity
Afu1g07070	regulation of phosphate metabolic process
Afu1g07080	zinc ion binding
Afu1g07130	cytoplasm
Afu1g07130	carboxymethylenebutenolidase activity
Afu1g07130	aromatic compound catabolic process
Afu1g07140	delta24(24-1) sterol reductase activity
Afu1g07140	endoplasmic reticulum
Afu1g07140	ergosterol biosynthetic process
Afu1g07150	alkylbase DNA N-glycosylase activity
Afu1g07150	cytoplasm
Afu1g07150	DNA dealkylation
Afu1g07150	zinc ion binding
Afu1g07160	ubiquitin-specific protease activity
Afu1g07160	cytoplasm
Afu1g07160	protein deubiquitination
Afu1g07170	plasma membrane
Afu1g07170	cation:cation antiporter activity
Afu1g07170	cellular monovalent inorganic cation homeostasis
Afu1g07180	ribonuclease H activity
Afu1g07180	ribonuclease H1 activity
Afu1g07180	cell
Afu1g07180	DNA replication
Afu1g07180	RNA catabolic process
Afu1g07180	cell wall organization

Afu1g07200	L-lactate dehydrogenase (cytochrome) activity
Afu1g07200	mitochondrial intermembrane space
Afu1g07200	electron transport
Afu1g07220	6-phosphofructo-2-kinase activity
Afu1g07220	cytoplasm
Afu1g07220	fructose 2,6-bisphosphate metabolic process
Afu1g07220	regulation of glycolysis
Afu1g07250	molecular function unknown
Afu1g07250	vacuolar membrane
Afu1g07250	vacuole fusion, non-autophagic
Afu1g07260	metabolic process
Afu1g07260	hydrolase activity
Afu1g07300	transporter activity
Afu1g07300	transport
Afu1g07320	nuclear chromosome
Afu1g07320	DNA binding
Afu1g07320	nucleus
Afu1g07320	DNA-dependent DNA replication
Afu1g07320	DNA repair
Afu1g07320	sister chromatid cohesion
Afu1g07330	dihydroxy-acid dehydratase activity
Afu1g07330	mitochondrion
Afu1g07330	branched chain family amino acid biosynthetic process
Afu1g07340	metabolic process
Afu1g07340	oxidoreductase activity
Afu1g07350	mitochondrial genome maintenance
Afu1g07350	exonuclease activity
Afu1g07350	mitochondrial inner membrane
Afu1g07350	rRNA processing
Afu1g07380	cell
Afu1g07380	glutamate biosynthetic process
Afu1g07380	glutamate synthase (NADH) activity
Afu1g07420	v-SNARE activity
Afu1g07420	endoplasmic reticulum membrane
Afu1g07420	ER to Golgi vesicle-mediated transport
Afu1g07420	retrograde vesicle-mediated transport, Golgi to ER
Afu1g07420	COPII-coated vesicle
Afu1g07440	fungal-type vacuole membrane
Afu1g07440	heat shock protein activity
Afu1g07440	cytoplasm
Afu1g07440	protein folding
Afu1g07440	SRP-dependent cotranslational protein targeting to membrane, translocation
Afu1g07440	fungal-type cell wall
Afu1g07450	mitochondrial genome maintenance
Afu1g07450	transporter activity
Afu1g07450	mitochondrial inner membrane
Afu1g07450	transport
Afu1g07470	microtubule associated complex
Afu1g07470	protein targeting to vacuole
Afu1g07470	microtubule binding

Afu1g07470	autophagic cell death
Afu1g07480	coproporphyrinogen oxidase activity
Afu1g07480	mitochondrial inner membrane
Afu1g07480	heme biosynthetic process
Afu1g07490	Golgi membrane
Afu1g07490	Golgi organization
Afu1g07490	microtubule binding
Afu1g07510	protein binding
Afu1g07510	mRNA cleavage factor complex
Afu1g07510	termination of RNA polymerase II transcription
Afu1g07510	mRNA polyadenylation
Afu1g07510	mRNA cleavage
Afu1g07510	cleavage and polyadenylylation specificity factor activity
Afu1g07520	metabolic process
Afu1g07520	oxidoreductase activity
Afu1g07530	adenylate kinase activity
Afu1g07530	cytoplasm
Afu1g07530	mitochondrial intermembrane space
Afu1g07530	cell proliferation
Afu1g07540	endopeptidase activity
Afu1g07540	ubiquitin-dependent protein catabolic process
Afu1g07540	proteasome regulatory particle, lid subcomplex
Afu1g07570	biological process unknown
Afu1g07570	molecular function unknown
Afu1g07570	cytoplasm
Afu1g07580	protein binding
Afu1g07580	chaperonin-mediated tubulin folding
Afu1g07580	establishment of cell polarity
Afu1g07600	ribonuclease H activity
Afu1g07600	nucleus
Afu1g07600	DNA replication
Afu1g07630	nucleic acid binding
Afu1g07630	cytoplasm
Afu1g07630	intracellular signaling cascade
Afu1g07630	zinc ion binding
Afu1g07640	biological process unknown
Afu1g07640	molecular function unknown
Afu1g07640	mitochondrion
Afu1g07650	nucleus
Afu1g07650	cytoplasm
Afu1g07650	cellular ketone metabolic process
Afu1g07650	ketoreductase activity
Afu1g07680	GTPase activity
Afu1g07680	Golgi apparatus
Afu1g07680	exocytosis
Afu1g07680	vesicle-mediated transport
Afu1g07690	dolichyl-phosphate-mannose-protein mannosyltransferase activity
Afu1g07690	endoplasmic reticulum
Afu1g07690	protein amino acid O-linked glycosylation
Afu1g07700	transporter activity

Afu1g07700	transport
Afu1g07700	membrane
Afu1g07720	nuclear chromatin
Afu1g07720	transcription elongation regulator activity
Afu1g07720	alpha DNA polymerase:primase complex
Afu1g07720	chromatin remodeling
Afu1g07720	regulation of transcription from RNA polymerase II promoter, global
Afu1g07720	RNA elongation from RNA polymerase II promoter
Afu1g07720	transcription elongation factor complex
Afu1g07720	RNA polymerase II transcription elongation factor activity
Afu1g07740	G1 phase of mitotic cell cycle
Afu1g07740	integral to membrane of membrane fraction
Afu1g07740	late endosome
Afu1g07740	establishment and/or maintenance of cell polarity (sensu Saccharomyces)
Afu1g07740	transcription regulator activity
Afu1g07740	regulation of transcription
Afu1g07750	biological process unknown
Afu1g07750	molecular function unknown
Afu1g07750	cellular component unknown
Afu1g08760	porphobilinogen synthase activity
Afu1g08760	nucleus
Afu1g08760	cytoplasm
Afu1g08760	heme biosynthetic process
Afu1g08765	metabolic process
Afu1g08765	acyltransferase activity
Afu1g08770	zinc ion binding
Afu1g08790	ribosomal large subunit export from nucleus
Afu1g08790	nucleus
Afu1g08790	mRNA export from nucleus
Afu1g08790	protein export from nucleus
Afu1g08790	protein transmembrane transporter activity
Afu1g08800	metabolic process
Afu1g08800	oxidoreductase activity
Afu1g08810	glycerol-3-phosphate dehydrogenase activity
Afu1g08810	mitochondrion
Afu1g08810	glycerol catabolic process
Afu1g08820	biological process unknown
Afu1g08820	molecular function unknown
Afu1g08820	cytoplasm
Afu1g08830	molecular function unknown
Afu1g08830	Golgi apparatus
Afu1g08830	ER to Golgi vesicle-mediated transport
Afu1g08840	guanylate kinase activity
Afu1g08840	nucleus
Afu1g08840	cytoplasm
Afu1g08840	GMP metabolic process
Afu1g08850	cellular bud neck septin ring
Afu1g08850	establishment of cell polarity (sensu Saccharomyces)
Afu1g08850	conjugation with cellular fusion
Afu1g08850	cellular morphogenesis during conjugation with cellular fusion

Afu1g08850	cell morphogenesis
Afu1g08850	cytokinesis
Afu1g08850	structural constituent of cytoskeleton
Afu1g08850	phosphatidylinositol binding
Afu1g08850	cell wall organization
Afu1g08850	axial cellular bud site selection
Afu1g08850	bipolar cellular bud site selection
Afu1g08850	spore wall assembly (sensu Saccharomyces)
Afu1g08860	cytoplasm
Afu1g08860	mRNA catabolic process
Afu1g08860	translation repressor activity
Afu1g08860	meiotic DNA double-strand break formation
Afu1g08880	cytosol
Afu1g08880	copper ion transport
Afu1g08880	high-affinity iron ion transport
Afu1g08880	response to oxidative stress
Afu1g08880	copper chaperone activity
Afu1g08900	zinc ion binding
Afu1g08930	biological process unknown
Afu1g08930	molecular function unknown
Afu1g08930	cytoplasm
Afu1g08940	conjugation with cellular fusion
Afu1g08940	serine-type carboxypeptidase activity
Afu1g08940	carboxypeptidase D activity
Afu1g08940	a-factor processing (proteolytic)
Afu1g08950	biological process unknown
Afu1g08950	molecular function unknown
Afu1g08950	cellular component unknown
Afu1g08960	biological process unknown
Afu1g08960	molecular function unknown
Afu1g08960	nucleus
Afu1g08960	cytoplasm
Afu1g08970	biological process unknown
Afu1g08970	molecular function unknown
Afu1g08970	endoplasmic reticulum
Afu1g08980	biological process unknown
Afu1g08980	molecular function unknown
Afu1g08980	nucleus
Afu1g08980	cytoplasm
Afu1g09010	methionine-tRNA ligase activity
Afu1g09010	cytoplasm
Afu1g09010	tRNA aminoacylation for protein translation
Afu1g09020	structural molecule activity
Afu1g09020	nuclear pore
Afu1g09020	mRNA export from nucleus
Afu1g09020	rRNA export from nucleus
Afu1g09020	snRNA export from nucleus
Afu1g09020	tRNA export from nucleus
Afu1g09020	protein import into nucleus
Afu1g09020	NLS-bearing substrate import into nucleus

Afu1g09020	snRNP protein import into nucleus
Afu1g09020	mRNA-binding (hnRNP) protein import into nucleus
Afu1g09020	ribosomal protein import into nucleus
Afu1g09020	protein export from nucleus
Afu1g09020	nuclear envelope organization
Afu1g09020	nuclear pore organization
Afu1g09040	mitochondrion inheritance
Afu1g09040	structural constituent of cytoskeleton
Afu1g09040	cytoplasm
Afu1g09040	intermediate filament
Afu1g09040	mitochondrion organization
Afu1g09040	nuclear migration
Afu1g09050	phosphatidyl-N-methylethanolamine N-methyltransferase activity
Afu1g09050	endoplasmic reticulum
Afu1g09050	phosphatidylcholine biosynthetic process
Afu1g09090	biological process unknown
Afu1g09090	fungal-type vacuole
Afu1g09090	molecular function unknown
Afu1g09100	structural constituent of ribosome
Afu1g09100	cytosolic large ribosomal subunit (sensu Eukaryota)
Afu1g09100	translation
Afu1g09110	triglyceride lipase activity
Afu1g09110	lipid particle
Afu1g09110	lipid metabolic process
Afu1g09120	plasma membrane
Afu1g09120	choline transmembrane transporter activity
Afu1g09120	choline transport
Afu1g09130	biological process unknown
Afu1g09130	molecular function unknown
Afu1g09130	plasma membrane
Afu1g09170	nucleus
Afu1g09170	cellular bud
Afu1g09170	cellular bud neck
Afu1g09170	mating projection
Afu1g09170	protein amino acid phosphorylation
Afu1g09170	regulation of exit from mitosis
Afu1g09170	protein kinase activator activity
Afu1g09190	nucleus
Afu1g09190	zinc ion binding
Afu1g09200	molecular function unknown
Afu1g09200	nucleus
Afu1g09200	nucleolus
Afu1g09200	rRNA processing
Afu1g09210	helicase activity
Afu1g09210	nucleus
Afu1g09210	nucleolus
Afu1g09210	ATPase activity
Afu1g09210	protein metabolic process
Afu1g09220	molecular function unknown
Afu1g09220	cytoplasm

Afu1g09220	endosome
Afu1g09220	late endosome to vacuole transport
Afu1g09240	U2-dependent spliceosome disassembly
Afu1g09240	ATP-dependent RNA helicase activity
Afu1g09240	spliceosomal complex
Afu1g09240	pre-mRNA splicing factor activity
Afu1g09250	ubiquitin binding
Afu1g09270	cellular bud site selection
Afu1g09270	molecular function unknown
Afu1g09270	integral to plasma membrane
Afu1g09270	cellular bud
Afu1g09270	cellular bud neck
Afu1g09270	septin ring
Afu1g09270	axial cellular bud site selection
Afu1g09280	DNA damage checkpoint
Afu1g09280	regulation of cyclin-dependent protein kinase activity
Afu1g09280	G1/S transition of mitotic cell cycle
Afu1g09280	inactivation of MAPK activity involved in osmosensory signaling pathway
Afu1g09280	nucleus
Afu1g09280	cytoplasm
Afu1g09280	protein amino acid dephosphorylation
Afu1g09280	response to unfolded protein
Afu1g09280	protein phosphatase type 2C activity
Afu1g09290	choline-phosphate cytidylyltransferase activity
Afu1g09290	nucleus
Afu1g09290	nuclear envelope
Afu1g09290	Golgi apparatus
Afu1g09290	phosphatidylcholine biosynthetic process
Afu1g09290	CDP-choline pathway
Afu1g09310	biological process unknown
Afu1g09310	molecular function unknown
Afu1g09310	cytoplasm
Afu1g09310	transport
Afu1g09310	integral to membrane
Afu1g09320	molecular function unknown
Afu1g09320	nucleus
Afu1g09320	nucleolus
Afu1g09330	translation initiation factor activity
Afu1g09330	eukaryotic translation initiation factor 3 complex
Afu1g09330	translational initiation
Afu1g09400	nucleic acid binding
Afu1g09410	mitochondrial genome maintenance
Afu1g09410	structural constituent of ribosome
Afu1g09410	mitochondrial large ribosomal subunit
Afu1g09410	translation
Afu1g09440	structural constituent of ribosome
Afu1g09440	cytosolic small ribosomal subunit (sensu Eukaryota)
Afu1g09440	translation
Afu1g09440	regulation of translational fidelity
Afu1g09450	translation initiation factor activity

Afu1g09450	ribosome
Afu1g09450	eukaryotic translation initiation factor 2B complex
Afu1g09450	translational initiation
Afu1g09460	molecular function unknown
Afu1g09460	nucleus organization
Afu1g09460	nuclear envelope-endoplasmic reticulum network
Afu1g09470	glyoxylate cycle
Afu1g09470	cellular component unknown
Afu1g09470	alanine-glyoxylate transaminase activity
Afu1g09480	molecular function unknown
Afu1g09480	endosome
Afu1g09480	retrograde transport, endosome to Golgi
Afu1g09490	cytoplasm
Afu1g09490	poly(A) RNA binding
Afu1g09490	mRNA metabolic process
Afu1g09500	ubiquitin ligase complex
Afu1g09500	protein polyubiquitination
Afu1g09500	ubiquitin-protein ligase activity
Afu1g09500	chromatin assembly or disassembly
Afu1g09500	protein monoubiquitination
Afu1g09540	vacuolar membrane
Afu1g09540	vacuole fusion, non-autophagic
Afu1g09560	protein binding
Afu1g09560	transport
Afu1g09560	signal transduction
Afu1g09600	peptide alpha-N-acetyltransferase activity
Afu1g09600	cytoplasm
Afu1g09600	protein amino acid acetylation
Afu1g09620	biological process unknown
Afu1g09620	molecular function unknown
Afu1g09620	cytoplasm
Afu1g09660	organic acid transmembrane transporter activity
Afu1g09660	intracellular transporter activity
Afu1g09660	mitochondrial inner membrane
Afu1g09660	mitochondrial transport
Afu1g09670	transcription factor activity
Afu1g09670	nucleus
Afu1g09670	transcription
Afu1g09700	biological process unknown
Afu1g09700	molecular function unknown
Afu1g09700	nucleus
Afu1g09700	cytoplasm
Afu1g09730	fungal-type vacuole membrane
Afu1g09730	diacylglycerol pyrophosphate phosphatase activity
Afu1g09730	phospholipid metabolic process
Afu1g09730	phosphatidate phosphatase activity
Afu1g09750	aldo-keto reductase activity
Afu1g09750	nucleus
Afu1g09750	cytoplasm
Afu1g09750	cellular aldehyde metabolic process

Afu1g09760	biological process unknown
Afu1g09760	molecular function unknown
Afu1g09760	cellular component unknown
Afu1g09830	protein binding
Afu1g09830	Hsc70 protein regulator activity
Afu1g09840	mitochondrial matrix
Afu1g09840	mitochondrial translocation
Afu1g09840	protein transporter activity
Afu1g09850	structural constituent of ribosome
Afu1g09850	mitochondrial small ribosomal subunit
Afu1g09850	translation
Afu1g09870	biological process unknown
Afu1g09870	molecular function unknown
Afu1g09870	cellular component unknown
Afu1g09910	fructose transmembrane transporter activity
Afu1g09910	glucose transmembrane transporter activity
Afu1g09910	plasma membrane
Afu1g09910	hexose transport
Afu1g09910	mannose transmembrane transporter activity
Afu1g09930	nucleus
Afu1g09930	cytoplasm
Afu1g09930	glycerol metabolic process
Afu1g09930	response to salt stress
Afu1g09930	glycerol dehydrogenase (NADP+) activity
Afu1g09950	G1/S transition of mitotic cell cycle
Afu1g09950	G2/M transition of mitotic cell cycle
Afu1g09950	flocculation
Afu1g09950	establishment of cell polarity (sensu Saccharomyces)
Afu1g09950	protein kinase CK2 activity
Afu1g09950	protein kinase CK2 complex
Afu1g09950	regulation of transcription from RNA polymerase I promoter
Afu1g09950	regulation of transcription from RNA polymerase III promoter
Afu1g09950	protein amino acid phosphorylation
Afu1g09950	cellular ion homeostasis
Afu1g09950	response to DNA damage stimulus
Afu1g09970	translation initiation factor activity
Afu1g09970	eukaryotic translation initiation factor 3 complex
Afu1g09970	translational initiation
Afu1g09980	S-adenosylmethionine transmembrane transporter activity
Afu1g09980	mitochondrion
Afu1g09980	mitochondrial inner membrane
Afu1g09980	S-adenosylmethionine transport
Afu1g10050	U2-type nuclear mRNA branch site recognition
Afu1g10050	ATP-dependent RNA helicase activity
Afu1g10050	spliceosomal complex
Afu1g10050	pre-mRNA splicing factor activity
Afu1g10080	specific RNA polymerase II transcription factor activity
Afu1g10080	nucleus
Afu1g10080	regulation of transcription from RNA polymerase II promoter
Afu1g10080	zinc ion binding

Afu1g10130	adenosylhomocysteinase activity
Afu1g10130	cytoplasm
Afu1g10130	methionine metabolic process
Afu1g10130	selenocysteine metabolic process
Afu1g10190	nuclear mRNA splicing, via spliceosome
Afu1g10190	pre-mRNA splicing factor activity
Afu1g10190	small nuclear ribonucleoprotein complex
Afu1g10200	nuclear mRNA splicing, via spliceosome
Afu1g10200	molecular function unknown
Afu1g10200	spliceosomal complex
Afu1g10200	cell cycle
Afu1g10200	RNA splicing
Afu1g10230	transcription factor activity
Afu1g10230	nucleus
Afu1g10230	glucose metabolic process
Afu1g10230	regulation of transcription from RNA polymerase II promoter
Afu1g10230	zinc ion binding
Afu1g10270	nucleus
Afu1g10270	cytoplasm
Afu1g10270	pyridoxine metabolic process
Afu1g10270	pyridoxine 4-dehydrogenase activity
Afu1g10280	DNA binding
Afu1g10280	nucleus
Afu1g10280	zinc ion binding
Afu1g10290	chromatin remodeling
Afu1g10290	RNA elongation from RNA polymerase II promoter
Afu1g10290	transcription elongation factor complex
Afu1g10290	ATPase activity
Afu1g10290	RNA polymerase II transcription elongation factor activity
Afu1g10310	ATP-binding cassette (ABC) transporter activity
Afu1g10310	electron carrier activity
Afu1g10310	ATP-binding cassette (ABC) transporter complex (sensu Eukaryota)
Afu1g10320	commitment complex
Afu1g10320	nuclear mRNA splicing, via spliceosome
Afu1g10320	RNA binding
Afu1g10320	U1 snRNP
Afu1g10340	biological process unknown
Afu1g10340	molecular function unknown
Afu1g10350	phosphoglycerate kinase activity
Afu1g10350	cytoplasm
Afu1g10350	cytosol
Afu1g10350	gluconeogenesis
Afu1g10350	glycolysis
Afu1g10360	molecular function unknown
Afu1g10360	nucleus
Afu1g10360	cytoplasm
Afu1g10370	drug transporter activity
Afu1g10370	drug transport
Afu1g10370	integral to membrane
Afu1g10380	catalytic activity

Afu1g10380	nonribosomal peptide biosynthetic process
Afu1g10380	secondary metabolic process
Afu1g10380	amino acid adenylylation by nonribosomal peptide synthase
Afu1g10390	ATP-binding cassette (ABC) transporter activity
Afu1g10390	integral to plasma membrane
Afu1g10390	transport
Afu1g10390	ATP-binding cassette (ABC) transporter complex (sensu Eukaryota)
Afu1g10410	recombinase activity
Afu1g10410	nuclear chromosome
Afu1g10410	meiotic joint molecule formation
Afu1g10410	telomere maintenance via recombination
Afu1g10410	double-strand break repair via break-induced replication
Afu1g10410	condensed nuclear chromosome
Afu1g10410	chromatin remodeling
Afu1g10410	heteroduplex formation
Afu1g10410	strand invasion
Afu1g10410	double-strand break repair via single-strand annealing
Afu1g10410	double-strand break repair via synthesis-dependent strand annealing
Afu1g10440	biological process unknown
Afu1g10440	molecular function unknown
Afu1g10440	nucleus
Afu1g10440	nucleolus
Afu1g10480	beta DNA polymerase activity
Afu1g10480	nucleus
Afu1g10480	base-excision repair, gap-filling
Afu1g10480	double-strand break repair
Afu1g10490	molecular function unknown
Afu1g10490	mitochondrial envelope
Afu1g10490	protein complex assembly
Afu1g10510	structural constituent of ribosome
Afu1g10510	cytosolic large ribosomal subunit (sensu Eukaryota)
Afu1g10510	translation
Afu1g10540	DNA binding
Afu1g10540	nucleus
Afu1g10540	cytoplasm
Afu1g10540	chromatin silencing at telomere
Afu1g10540	short-chain fatty acid metabolic process
Afu1g10560	GTP binding
Afu1g10560	nucleus
Afu1g10560	nucleolus
Afu1g10560	rRNA processing
Afu1g10570	cytoplasm
Afu1g10570	glycerol metabolic process
Afu1g10570	phosphatase activity
Afu1g10580	transcription factor activity
Afu1g10580	regulation of transcription
Afu1g10590	biological process unknown
Afu1g10590	molecular function unknown
Afu1g10600	molecular function unknown
Afu1g10600	nucleus

Afu1g10600	protein import into nucleus
Afu1g10630	methionine adenosyltransferase activity
Afu1g10630	methionine metabolic process
Afu1g10630	cellular component unknown
Afu1g10640	ATP binding
Afu1g10640	molecular function unknown
Afu1g10640	cellular component unknown
Afu1g10660	zinc ion binding
Afu1g10670	vacuolar proton-transporting V-type ATPase, V1 domain
Afu1g10670	fungal-type vacuole membrane
Afu1g10670	vacuolar acidification
Afu1g10670	proton-transporting ATPase activity, rotational mechanism
Afu1g10690	biological process unknown
Afu1g10690	molecular function unknown
Afu1g10690	Golgi apparatus
Afu1g10690	COPI-coated vesicle
Afu1g10700	molecular function unknown
Afu1g10700	proteasome regulatory particle
Afu1g10700	proteolysis
Afu1g10710	nuclear mRNA splicing, via spliceosome
Afu1g10710	molecular function unknown
Afu1g10710	spliceosomal complex
Afu1g10720	DNA replication origin binding
Afu1g10720	protein binding
Afu1g10720	nuclear origin of replication recognition complex
Afu1g10720	pre-replicative complex assembly
Afu1g10720	DNA replication initiation
Afu1g10720	ATPase activity
Afu1g10740	cytoplasm
Afu1g10740	tubulin complex assembly
Afu1g10740	tubulin binding
Afu1g10750	biological process unknown
Afu1g10750	proline-tRNA ligase activity
Afu1g10750	cellular component unknown
Afu1g10760	ribosomal large subunit assembly
Afu1g10760	molecular function unknown
Afu1g10760	nucleus
Afu1g10760	nucleolus
Afu1g10780	glycine dehydrogenase (decarboxylating) activity
Afu1g10780	mitochondrion
Afu1g10780	glycine metabolic process
Afu1g10780	one-carbon metabolic process
Afu1g10800	mitochondrion
Afu1g10800	fatty acid metabolic process
Afu1g10800	CoA hydrolase activity
Afu1g10810	vacuolar proton-transporting V-type ATPase, V1 domain
Afu1g10810	fungal-type vacuole membrane
Afu1g10810	vacuolar acidification
Afu1g10810	proton-transporting ATPase activity, rotational mechanism
Afu1g10820	sulfate assimilation

Afu1g10820	adenylylsulfate kinase activity
Afu1g10820	cell
Afu1g10820	methionine metabolic process
Afu1g10830	succinate-CoA ligase (ADP-forming) activity
Afu1g10830	mitochondrion
Afu1g10830	tricarboxylic acid cycle
Afu1g10830	succinyl-CoA metabolic process
Afu1g10850	nucleus
Afu1g10850	septin ring
Afu1g10850	protein tagging activity
Afu1g10850	protein sumoylation
Afu1g10870	cellular component unknown
Afu1g10870	hydrolase activity
Afu1g10880	fungal-type vacuole membrane
Afu1g10880	calcium-transporting ATPase activity
Afu1g10880	calcium ion transport
Afu1g10880	cellular calcium ion homeostasis
Afu1g10890	plasma membrane
Afu1g10890	vitamin or cofactor transporter activity
Afu1g10890	vitamin or cofactor transport
Afu1g10910	mitotic sister chromatid segregation
Afu1g10910	nuclear migration during conjugation with cellular fusion
Afu1g10910	structural constituent of cytoskeleton
Afu1g10910	spindle pole body
Afu1g10910	polar microtubule
Afu1g10910	kinetochore microtubule
Afu1g10910	nuclear microtubule
Afu1g10910	cytoplasmic microtubule
Afu1g10910	homologous chromosome segregation
Afu1g10920	nuclear mRNA splicing, via spliceosome
Afu1g10920	RNA binding
Afu1g10920	U2 snRNP
Afu1g10930	plasma membrane
Afu1g10930	pseudohyphal growth
Afu1g10930	ammonium transmembrane transporter activity
Afu1g10930	ammonium transport
Afu1g10940	activation of MAPKK activity
Afu1g10940	MAP kinase kinase kinase activity
Afu1g10950	molecular function unknown
Afu1g10950	cytoplasmic membrane-bounded vesicle
Afu1g10950	vesicle-mediated transport
Afu1g10950	extrinsic to membrane
Afu1g10950	negative regulation of gluconeogenesis
Afu1g10970	molecular function unknown
Afu1g10970	ER to Golgi vesicle-mediated transport
Afu1g10970	COPI vesicle coat
Afu1g10970	coated vesicle
Afu1g10980	membrane fraction
Afu1g10980	soluble fraction
Afu1g10980	endoplasmic reticulum

Afu1g10980	Golgi apparatus
Afu1g10980	sphingolipid metabolic process
Afu1g10980	D-erythro-sphingosine kinase activity
Afu1g10980	calcium-mediated signaling
Afu1g11000	nucleus
Afu1g11000	galactose metabolic process
Afu1g11000	regulation of transcription, DNA-dependent
Afu1g11000	transcription activator activity
Afu1g11010	nucleus
Afu1g11010	cytoplasm
Afu1g11010	oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acc
Afu1g11020	L-iditol 2-dehydrogenase activity
Afu1g11020	fructose metabolic process
Afu1g11020	mannose metabolic process
Afu1g11020	cellular component unknown
Afu1g11030	monosaccharide metabolic process
Afu1g11030	cellular component unknown
Afu1g11030	D-xylulose reductase activity
Afu1g11050	transporter activity
Afu1g11050	transport
Afu1g11050	membrane
Afu1g11060	protein tagging activity
Afu1g11070	RNA binding
Afu1g11080	protein kinase activity
Afu1g11080	membrane fraction
Afu1g11090	nucleus
Afu1g11090	RNA elongation
Afu1g11090	regulation of transcription, DNA-dependent
Afu1g11090	histone methylation
Afu1g11090	histone-lysine N-methyltransferase activity
Afu1g11110	calcium channel activity
Afu1g11110	calcium ion binding
Afu1g11110	plasma membrane
Afu1g11110	voltage-gated calcium channel complex
Afu1g11110	calcium ion transport
Afu1g11130	ribosomal large subunit assembly
Afu1g11130	RNA binding
Afu1g11130	structural constituent of ribosome
Afu1g11130	cytosolic large ribosomal subunit (sensu Eukaryota)
Afu1g11130	translation
Afu1g11150	cytoplasm
Afu1g11150	endoplasmic reticulum
Afu1g11150	3-keto-sphinganine metabolic process
Afu1g11150	oxidoreductase activity, acting on NADH or NADPH
Afu1g11150	sphingolipid biosynthetic process
Afu1g11160	nucleus
Afu1g11160	small nucleolar ribonucleoprotein complex
Afu1g11160	chromatin organization
Afu1g11160	maturation of SSU-rRNA
Afu1g11160	snoRNA binding

Afu1g11170	nucleus
Afu1g11170	reciprocal meiotic recombination
Afu1g11180	mitochondrial genome maintenance
Afu1g11180	chaperone activity
Afu1g11180	heat shock protein activity
Afu1g11180	ATP-dependent peptidase activity
Afu1g11180	mitochondrial matrix
Afu1g11180	protein folding
Afu1g11180	mitochondrial translocation
Afu1g11180	response to stress
Afu1g11190	translation elongation factor activity
Afu1g11190	ribosome
Afu1g11190	translational elongation
Afu1g11230	hydroxymethylglutaryl-CoA reductase (NADPH) activity
Afu1g11230	nuclear envelope
Afu1g11230	mitochondrial matrix
Afu1g11230	endoplasmic reticulum membrane
Afu1g11230	ergosterol biosynthetic process
Afu1g11250	carboxypeptidase activity
Afu1g11250	proteolysis
Afu1g11280	metabolic process
Afu1g11280	oxidoreductase activity
Afu1g11290	DNA binding
Afu1g11290	zinc ion binding
Afu1g11310	acetate-CoA ligase activity
Afu1g11310	cytosol
Afu1g11310	acetyl-CoA biosynthetic process
Afu1g11310	acetate fermentation
Afu1g11350	biological process unknown
Afu1g11350	molecular function unknown
Afu1g11350	cellular component unknown
Afu1g11360	biological process unknown
Afu1g11360	cellular component unknown
Afu1g11360	dihydrokaempferol 4-reductase activity
Afu1g11370	metabolic process
Afu1g11370	oxidoreductase activity
Afu1g11390	metabolic process
Afu1g11390	oxidoreductase activity
Afu1g11410	protein polyubiquitination
Afu1g11410	proteasome complex
Afu1g11410	ubiquitin conjugating enzyme activity
Afu1g11410	protein monoubiquitination
Afu1g11410	endocytosis
Afu1g11420	RNA binding
Afu1g11420	cytoplasm
Afu1g11420	cell wall organization
Afu1g11460	1,3-beta-glucan metabolic process
Afu1g11460	cell wall organization
Afu1g11460	fungal-type cell wall
Afu1g11460	1,3-beta-glucanosyltransferase activity

Afu1g11470	molecular function unknown
Afu1g11470	endoplasmic reticulum
Afu1g11470	ER to Golgi vesicle-mediated transport
Afu1g11470	integral to membrane
Afu1g11470	vesicle organization
Afu1g11470	COPII-coated vesicle
Afu1g11490	endopolyphosphatase activity
Afu1g11490	vacuolar membrane
Afu1g11490	polyphosphate metabolic process
Afu1g11550	cytosol
Afu1g11570	metabolic process
Afu1g11570	oxidoreductase activity
Afu1g11580	transporter activity
Afu1g11580	plasma membrane
Afu1g11580	transport
Afu1g11590	3-dehydroquinate dehydratase activity
Afu1g11590	3-dehydroquinate synthase activity
Afu1g11590	3-phosphoshikimate 1-carboxyvinyltransferase activity
Afu1g11590	shikimate 5-dehydrogenase activity
Afu1g11590	shikimate kinase activity
Afu1g11590	cytoplasm
Afu1g11590	aromatic amino acid family biosynthetic process
Afu1g11600	inositol metabolic process
Afu1g11600	cellular component unknown
Afu1g11600	inositol-1(or 4)-monophosphatase activity
Afu1g11610	3-dehydroquinate dehydratase activity
Afu1g11620	transcription factor activity
Afu1g11620	nucleus
Afu1g11620	zinc ion binding
Afu1g11620	carbon utilization
Afu1g11620	regulation of transcription
Afu1g11630	3-dehydroquinate dehydratase activity
Afu1g11630	3-dehydroquinate synthase activity
Afu1g11630	3-phosphoshikimate 1-carboxyvinyltransferase activity
Afu1g11630	shikimate 5-dehydrogenase activity
Afu1g11630	shikimate kinase activity
Afu1g11630	cytoplasm
Afu1g11630	aromatic amino acid family biosynthetic process
Afu1g11670	nuclear-transcribed mRNA catabolic process, deadenylation-dependent decay
Afu1g11670	deadenylation-dependent decapping of nuclear-transcribed mRNA
Afu1g11670	RNA cap binding
Afu1g11670	cytoplasmic mRNA processing body
Afu1g11670	mRNA cap binding complex
Afu1g11670	rRNA processing
Afu1g11710	structural constituent of ribosome
Afu1g11710	cytosolic large ribosomal subunit (sensu Eukaryota)
Afu1g11710	translation
Afu1g11730	ARF small monomeric GTPase activity
Afu1g11730	Golgi-associated vesicle
Afu1g11730	cytosol

Afu1g11730	ER to Golgi vesicle-mediated transport
Afu1g11730	intra-Golgi vesicle-mediated transport
Afu1g11770	ER to Golgi vesicle-mediated transport
Afu1g11770	COPII-coated vesicle
Afu1g11790	purine ribonucleoside salvage
Afu1g11790	purine nucleosidase activity
Afu1g11790	pyrimidine nucleoside salvage
Afu1g11790	ribosylpyrimidine nucleosidase activity
Afu1g11800	transcription factor activity
Afu1g11800	nucleus
Afu1g11800	transcription
Afu1g11820	transporter activity
Afu1g11820	integral to plasma membrane
Afu1g11820	transport
Afu1g11830	transporter activity
Afu1g11830	plasma membrane
Afu1g11830	transport
Afu1g11860	mitochondrial outer membrane translocase complex
Afu1g11860	mitochondrial translocation
Afu1g11860	protein transporter activity
Afu1g11870	mitochondrial processing peptidase activity
Afu1g11870	mitochondrial protein processing during import
Afu1g11870	mitochondrial processing peptidase complex
Afu1g11880	acetate-CoA ligase activity
Afu1g11880	cytosol
Afu1g11880	acetyl-CoA biosynthetic process
Afu1g11890	serine C-palmitoyltransferase activity
Afu1g11890	membrane fraction
Afu1g11890	microsome
Afu1g11890	serine C-palmitoyltransferase complex
Afu1g11890	sphingolipid biosynthetic process
Afu1g11900	biological process unknown
Afu1g11900	molecular function unknown
Afu1g11900	cellular component unknown
Afu1g11920	protein binding
Afu1g11930	protein kinase activity
Afu1g11930	cytoplasm
Afu1g11930	proteolysis
Afu1g11940	structural constituent of ribosome
Afu1g11940	mitochondrial large ribosomal subunit
Afu1g11940	translation
Afu1g11960	NADH dehydrogenase activity
Afu1g11960	mitochondrion
Afu1g11960	NADH oxidation
Afu1g11960	glucose catabolic process to ethanol
Afu1g11970	mitochondrial genome maintenance
Afu1g11970	mitochondrial intermembrane space
Afu1g11970	mitochondrion organization
Afu1g11970	mitochondrial fusion
Afu1g11970	dynamin GTPase activity

Afu1g11980	cytoplasm
Afu1g12000	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
Afu1g12000	nucleus
Afu1g12000	cytoplasm
Afu1g12000	heterogeneous nuclear ribonucleoprotein complex
Afu1g12020	biological process unknown
Afu1g12020	cytoplasm
Afu1g12020	cyclin binding
Afu1g12040	molecular function unknown
Afu1g12040	cell wall chitin biosynthetic process
Afu1g12040	ER to Golgi vesicle-mediated transport
Afu1g12040	integral to endoplasmic reticulum membrane
Afu1g12050	N-acetyltransferase activity
Afu1g12050	metabolic process
Afu1g12070	glycine dehydrogenase (decarboxylating) activity
Afu1g12070	mitochondrion
Afu1g12070	one-carbon metabolic process
Afu1g12080	intracellular
Afu1g12080	protein transport
Afu1g12080	ligase activity
Afu1g12090	molecular function unknown
Afu1g12090	endoplasmic reticulum
Afu1g12090	zinc ion transport
Afu1g12130	regulation of progression through cell cycle
Afu1g12130	translation initiation factor activity
Afu1g12130	nucleus
Afu1g12130	cytoplasm
Afu1g12130	ribosome
Afu1g12130	translational initiation
Afu1g12150	guanosine-diphosphatase activity
Afu1g12150	Golgi apparatus
Afu1g12150	protein amino acid glycosylation
Afu1g12150	uridine-diphosphatase activity
Afu1g12160	translation initiation factor activity
Afu1g12160	translational initiation
Afu1g12170	translation elongation factor activity
Afu1g12170	mitochondrial matrix
Afu1g12170	mitochondrial ribosome
Afu1g12170	translational elongation
Afu1g12180	molecular function unknown
Afu1g12180	cytoplasm
Afu1g12180	membrane organization
Afu1g12200	biological process unknown
Afu1g12200	molecular function unknown
Afu1g12200	endoplasmic reticulum
Afu1g12210	biological process unknown
Afu1g12210	NADPH dehydrogenase activity
Afu1g12210	nucleus
Afu1g12210	cytoplasm
Afu1g12230	pheromone-dependent signal transduction involved in conjugation with cellular fusion

Afu1g12240	plasma membrane
Afu1g12240	peptide transporter activity
Afu1g12240	peptide transport
Afu1g12250	biological process unknown
Afu1g12250	molecular function unknown
Afu1g12250	mitochondrion
Afu1g12260	RNA elongation from RNA polymerase II promoter
Afu1g12260	transcription elongation factor complex
Afu1g12260	RNA polymerase II transcription elongation factor activity
Afu1g12280	structural molecule activity
Afu1g12280	nuclear pore
Afu1g12280	mRNA export from nucleus
Afu1g12280	rRNA export from nucleus
Afu1g12280	snRNA export from nucleus
Afu1g12280	tRNA export from nucleus
Afu1g12280	protein import into nucleus
Afu1g12280	NLS-bearing substrate import into nucleus
Afu1g12280	snRNP protein import into nucleus
Afu1g12280	mRNA-binding (hnRNP) protein import into nucleus
Afu1g12280	ribosomal protein import into nucleus
Afu1g12280	protein export from nucleus
Afu1g12280	nuclear pore organization
Afu1g12310	biological process unknown
Afu1g12310	molecular function unknown
Afu1g12310	cellular component unknown
Afu1g12332	negative regulation of transcription from RNA polymerase II promoter
Afu1g12332	nucleus
Afu1g12332	DNA repair
Afu1g12332	chromatin remodeling
Afu1g12340	carnitine O-acetyltransferase activity
Afu1g12340	mitochondrion
Afu1g12340	alcohol metabolic process
Afu1g12340	carnitine metabolic process
Afu1g12350	fungal-type vacuole
Afu1g12350	nuclear envelope
Afu1g12350	endoplasmic reticulum
Afu1g12380	protein binding
Afu1g12390	cytoplasm
Afu1g12400	catalytic activity
Afu1g12490	antibiotic biosynthetic process
Afu1g12490	secondary metabolic process
Afu1g12490	sporocarp development
Afu1g12520	meiotic DNA recombinase assembly
Afu1g12520	telomere maintenance via recombination
Afu1g12520	double-strand break repair via break-induced replication
Afu1g12520	DNA recombinase assembly
Afu1g12520	protein binding
Afu1g12520	nucleus
Afu1g12520	double-strand break repair via single-strand annealing
Afu1g12520	double-strand break repair via synthesis-dependent strand annealing

Afu1g12550	endoplasmic reticulum membrane
Afu1g12550	fatty acid metabolic process
Afu1g12550	response to cold
Afu1g12550	transcription activator activity
Afu1g12550	positive regulation of transcription from RNA polymerase II promoter
Afu1g12570	biological process unknown
Afu1g12570	RNA binding
Afu1g12570	cellular component unknown
Afu1g12590	RNA binding
Afu1g12590	nucleus
Afu1g12590	nucleoplasm
Afu1g12590	nucleolus
Afu1g12590	tRNA processing
Afu1g12600	chitin synthase activity
Afu1g12600	plasma membrane
Afu1g12600	chitin biosynthetic process
Afu1g12600	cell wall organization
Afu1g12610	heat shock protein activity
Afu1g12610	cytoplasm
Afu1g12610	protein folding
Afu1g12620	multidrug transport
Afu1g12620	multidrug efflux pump activity
Afu1g12620	response to drug
Afu1g12630	molecular function unknown
Afu1g12630	protein amino acid N-linked glycosylation
Afu1g12630	protein amino acid O-linked glycosylation
Afu1g12630	response to stress
Afu1g12630	cellular component unknown
Afu1g12650	acetyl-CoA C-acyltransferase activity
Afu1g12680	pheromone-dependent signal transduction involved in conjugation with cellular fusion
Afu1g12680	signal transducer activity
Afu1g12680	Rho GTPase activator activity
Afu1g12680	intracellular
Afu1g12680	actin filament organization
Afu1g12680	invasive growth
Afu1g12680	small GTPase mediated signal transduction
Afu1g12690	integral to plasma membrane
Afu1g12690	multidrug transport
Afu1g12690	xenobiotic-transporting ATPase activity
Afu1g12690	ABC-type efflux porter activity
Afu1g12690	multidrug efflux pump activity
Afu1g12690	response to drug
Afu1g12730	structural constituent of ribosome
Afu1g12730	mitochondrial large ribosomal subunit
Afu1g12730	translation
Afu1g12750	metabolic process
Afu1g12750	cellular component unknown
Afu1g12750	kinase activity
Afu1g12750	virus-host interaction
Afu1g12760	actin cortical patch (sensu Saccharomyces)

Afu1g12760	cytoskeleton organization
Afu1g12760	Ras protein signal transduction
Afu1g12760	cytoskeletal protein binding
Afu1g12760	adenylate cyclase binding
Afu1g12790	actin cap (sensu Saccharomyces)
Afu1g12790	exocyst
Afu1g12790	establishment of cell polarity (sensu Saccharomyces)
Afu1g12790	cytokinesis
Afu1g12790	molecular function unknown
Afu1g12790	Golgi to plasma membrane transport
Afu1g12790	vesicle docking during exocytosis
Afu1g12790	vesicle fusion
Afu1g12790	bipolar cellular bud site selection
Afu1g12800	isocitrate dehydrogenase (NAD+) activity
Afu1g12800	mitochondrion
Afu1g12800	mitochondrial matrix
Afu1g12800	tricarboxylic acid cycle
Afu1g12800	isocitrate metabolic process
Afu1g12800	glutamate biosynthetic process
Afu1g12820	gamma-tubulin complex
Afu1g12830	electron transport
Afu1g12830	nitrate assimilation
Afu1g12830	nitrate reductase (NADPH) activity
Afu1g12840	nitrate assimilation
Afu1g12840	nitrite reductase (NO-forming) activity
Afu1g12850	integral to plasma membrane
Afu1g12850	nitrate transmembrane transporter activity
Afu1g12850	nitrate transport
Afu1g12880	metabolic process
Afu1g12880	hydrolase activity
Afu1g12890	ribosomal large subunit assembly
Afu1g12890	RNA binding
Afu1g12890	structural constituent of ribosome
Afu1g12890	cytosolic large ribosomal subunit (sensu Eukaryota)
Afu1g12890	translation
Afu1g12900	structural constituent of cytoskeleton
Afu1g12900	microtubule
Afu1g12900	negative regulation of microtubule depolymerization
Afu1g12900	cell wall organization
Afu1g12910	ATP-binding cassette (ABC) transporter activity
Afu1g12910	ATP binding
Afu1g12910	integral to peroxisomal membrane
Afu1g12910	transport
Afu1g12910	fatty acid transport
Afu1g12920	cytoplasm
Afu1g12920	glycogen catabolic process
Afu1g12920	glycogen phosphorylase activity
Afu1g12930	heterotrimeric G-protein GTPase activity
Afu1g12930	heterotrimeric G-protein complex
Afu1g12930	signal transduction

Afu1g12930	G-protein signaling, coupled to cAMP nucleotide second messenger
Afu1g12930	cell growth and/or maintenance
Afu1g12930	pathogenesis
Afu1g12940	MAP kinase activity
Afu1g12940	protein amino acid phosphorylation
Afu1g12940	response to stress
Afu1g12940	osmosensory signaling pathway
Afu1g12940	positive regulation of transcription from RNA polymerase II promoter
Afu1g12960	G1/S transition of mitotic cell cycle
Afu1g12960	G2/M transition of mitotic cell cycle
Afu1g12960	nuclear ubiquitin ligase complex
Afu1g12960	ubiquitin-protein ligase activity
Afu1g12960	structural molecule activity
Afu1g12960	ubiquitin-dependent protein catabolic process
Afu1g12960	SCF ubiquitin ligase complex
Afu1g12980	biological process unknown
Afu1g12980	molecular function unknown
Afu1g12980	cellular component unknown
Afu1g13010	helicase activity
Afu1g13020	actin cortical patch assembly
Afu1g13020	cytokinesis
Afu1g13020	actin cortical patch (sensu Saccharomyces)
Afu1g13020	endocytosis
Afu1g13020	actin filament organization
Afu1g13020	bipolar cellular bud site selection
Afu1g13020	cytoskeletal adaptor activity
Afu1g13050	transcription factor activity
Afu1g13050	nucleus
Afu1g13050	regulation of transcription, DNA-dependent
Afu1g13050	zinc ion binding
Afu1g13060	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
Afu1g13060	nucleic acid binding
Afu1g13060	cytoplasm
Afu1g13060	polysome
Afu1g13060	mRNA catabolic process
Afu1g13060	regulation of translational termination
Afu1g13060	ATP-dependent helicase activity
Afu1g13060	ATPase activity
Afu1g13070	rRNA modification
Afu1g13070	small nucleolar ribonucleoprotein complex
Afu1g13070	35S primary transcript processing
Afu1g13070	maturation of SSU-rRNA
Afu1g13070	small nuclear ribonucleoprotein complex
Afu1g13070	rRNA primary transcript binding
Afu1g13090	tryptophan biosynthetic process
Afu1g13090	anthranilate synthase activity
Afu1g13090	indole-3-glycerol-phosphate synthase activity
Afu1g13090	cytoplasm
Afu1g13100	structural molecule activity
Afu1g13100	nuclear pore

Afu1g13100	mRNA export from nucleus
Afu1g13100	rRNA export from nucleus
Afu1g13100	snRNA export from nucleus
Afu1g13100	tRNA export from nucleus
Afu1g13100	NLS-bearing substrate import into nucleus
Afu1g13100	snRNP protein import into nucleus
Afu1g13100	mRNA-binding (hnRNP) protein import into nucleus
Afu1g13100	ribosomal protein import into nucleus
Afu1g13100	protein export from nucleus
Afu1g13100	nuclear pore organization
Afu1g13110	long-chain-fatty-acid-CoA ligase activity
Afu1g13110	peroxisome
Afu1g13110	N-terminal protein myristoylation
Afu1g13110	lipid metabolic process
Afu1g13140	response to pheromone during conjugation with cellular fusion
Afu1g13140	pheromone-dependent signal transduction involved in conjugation with cellular fusion
Afu1g13140	heterotrimeric G-protein GTPase activity
Afu1g13140	heterotrimeric G-protein complex
Afu1g13140	response to stress
Afu1g13140	signal transduction
Afu1g13140	pathogenesis
Afu1g13150	biological process unknown
Afu1g13150	molecular function unknown
Afu1g13150	cytoplasm
Afu1g13160	farnesyltranstransferase activity
Afu1g13160	mitochondrion
Afu1g13160	terpenoid biosynthetic process
Afu1g13210	allantoin uptake transmembrane transporter activity
Afu1g13210	allantoin transport
Afu1g13210	membrane
Afu1g13220	oxidoreductase activity
Afu1g13220	xenobiotic catabolic process
Afu1g13250	condensed nuclear chromosome kinetochore
Afu1g13250	phosphoinositide phospholipase C activity
Afu1g13250	nucleus
Afu1g13250	pseudohyphal growth
Afu1g13250	signal transduction
Afu1g13250	cell growth and/or maintenance
Afu1g13280	cell wall mannoprotein biosynthetic process
Afu1g13280	mannose-6-phosphate isomerase activity
Afu1g13280	nucleus
Afu1g13280	cytoplasm
Afu1g13280	protein amino acid glycosylation
Afu1g13280	GDP-mannose biosynthetic process
Afu1g13290	SAGA complex
Afu1g13290	molecular function unknown
Afu1g13290	histone acetylation
Afu1g13300	GTP cyclohydrolase II activity
Afu1g13300	nucleus
Afu1g13300	cytoplasm

Afu1g13300	riboflavin biosynthetic process
Afu1g13300	riboflavin biosynthetic process
Afu1g13330	actin binding
Afu1g13330	structural constituent of cytoskeleton
Afu1g13330	mitochondrion
Afu1g13330	Arp2/3 protein complex
Afu1g13330	actin filament organization
Afu1g13340	biological process unknown
Afu1g13340	molecular function unknown
Afu1g13340	integral to membrane
Afu1g13350	transporter activity
Afu1g13350	transport
Afu1g13350	membrane
Afu1g13360	sulfite transport
Afu1g13360	sulfite transmembrane transporter activity
Afu1g13360	plasma membrane
Afu1g13370	aldo-keto reductase activity
Afu1g13370	cellular aldehyde metabolic process
Afu1g13370	cellular component unknown
Afu1g13380	nitrogen compound metabolic process
Afu1g13380	cellular component unknown
Afu1g13380	racemase and epimerase activity
Afu1g13390	structural constituent of cytoskeleton
Afu1g13390	inner plaque of spindle pole body
Afu1g13390	outer plaque of spindle pole body
Afu1g13390	microtubule nucleation
Afu1g13400	biological process unknown
Afu1g13400	molecular function unknown
Afu1g13400	nucleus
Afu1g13420	cell fraction
Afu1g13420	cytosol
Afu1g13420	response to osmotic stress
Afu1g13420	mitotic spindle organization
Afu1g13420	protein phosphatase type 2A regulator activity
Afu1g13460	biological process unknown
Afu1g13460	molecular function unknown
Afu1g13460	cytoplasm
Afu1g13470	replicative cell aging
Afu1g13470	molecular function unknown
Afu1g13470	mitochondrion
Afu1g13470	mitochondrial inner membrane
Afu1g13470	proteolysis
Afu1g13480	electron transport
Afu1g13480	ubiquinol-cytochrome-c reductase activity
Afu1g13480	ubiquinol-cytochrome-c reductase complex (sensu Eukaryota)
Afu1g13490	spermidine synthase activity
Afu1g13490	nucleus
Afu1g13490	cytoplasm
Afu1g13490	spermidine biosynthetic process
Afu1g13490	pantothenate biosynthetic process

Afu1g13500	transketolase activity
Afu1g13500	cytoplasm
Afu1g13500	pentose-phosphate shunt
Afu1g13510	specific RNA polymerase II transcription factor activity
Afu1g13510	nucleus
Afu1g13510	zinc ion binding
Afu1g13510	acetate catabolic process
Afu1g13510	positive regulation of transcription from RNA polymerase II promoter
Afu1g13540	biological process unknown
Afu1g13540	molecular function unknown
Afu1g13540	cytoplasm
Afu1g13570	rRNA modification
Afu1g13570	RNA binding
Afu1g13570	35S primary transcript processing
Afu1g13570	small nuclear ribonucleoprotein complex
Afu1g13600	regulation of progression through cell cycle
Afu1g13600	G1/S transition of mitotic cell cycle
Afu1g13600	S phase of mitotic cell cycle
Afu1g13600	G2/M transition of mitotic cell cycle
Afu1g13600	cyclin-dependent protein kinase activity
Afu1g13600	nucleus
Afu1g13600	cytoplasm
Afu1g13600	protein amino acid phosphorylation
Afu1g13600	regulation of meiosis
Afu1g13620	biological process unknown
Afu1g13620	molecular function unknown
Afu1g13620	cellular component unknown
Afu1g13660	monooxygenase activity
Afu1g13660	cellular aromatic compound metabolic process
Afu1g13690	vacuolar proton-transporting V-type ATPase, V1 domain
Afu1g13690	molecular function unknown
Afu1g13690	cytoplasm
Afu1g13690	vacuolar acidification
Afu1g13710	isoleucine-tRNA ligase activity
Afu1g13710	cytosol
Afu1g13710	translation
Afu1g13720	molecular function unknown
Afu1g13720	soluble fraction
Afu1g13720	protein complex assembly
Afu1g13720	ER to Golgi vesicle-mediated transport
Afu1g13730	5'-3' exoribonuclease activity
Afu1g13730	nucleus
Afu1g13730	35S primary transcript processing
Afu1g13730	RNA processing
Afu1g13740	3-dehydroquinate dehydratase activity
Afu1g13740	3-dehydroquinate synthase activity
Afu1g13740	3-phosphoshikimate 1-carboxyvinyltransferase activity
Afu1g13740	shikimate 5-dehydrogenase activity
Afu1g13740	shikimate kinase activity
Afu1g13740	cytoplasm

Afu1g13740	aromatic amino acid family biosynthetic process
Afu1g13750	DNA binding
Afu1g13750	zinc ion binding
Afu1g13750	transcription activator activity
Afu1g13760	extrinsic to plasma membrane
Afu1g13780	nuclear nucleosome
Afu1g13780	DNA binding
Afu1g13780	chromatin assembly or disassembly
Afu1g13790	nuclear nucleosome
Afu1g13790	DNA binding
Afu1g13790	nucleus
Afu1g13790	chromatin assembly or disassembly
Afu1g13800	drug transporter activity
Afu1g13800	drug transport
Afu1g13800	integral to membrane
Afu1g13840	biological process unknown
Afu1g13840	molecular function unknown
Afu1g13840	cellular component unknown
Afu1g13870	alpha-1,2-mannosyltransferase activity
Afu1g13870	endoplasmic reticulum membrane
Afu1g13870	protein amino acid glycosylation
Afu1g13870	dolichol-linked oligosaccharide biosynthetic process
Afu1g13880	snoRNA metabolic process
Afu1g13900	DNA-directed RNA polymerase activity
Afu1g13900	DNA-directed RNA polymerase I complex
Afu1g13900	transcription from RNA polymerase I promoter
Afu1g13910	nucleotide-excision repair factor 3 complex
Afu1g13910	nucleotide-excision repair, DNA duplex unwinding
Afu1g13910	DNA helicase activity
Afu1g13910	holo TFIIH complex
Afu1g13910	transcription initiation from RNA polymerase II promoter
Afu1g13910	negative regulation of transcription from RNA polymerase II promoter, mitotic
Afu1g13910	general RNA polymerase II transcription factor activity
Afu1g13940	cell wall organization
Afu1g13940	beta-glucosidase activity
Afu1g13940	fungal-type cell wall
Afu1g13950	metabolic process
Afu1g13950	oxidoreductase activity
Afu1g13970	transporter activity
Afu1g13970	integral to plasma membrane
Afu1g13970	transport
Afu1g14010	molecular function unknown
Afu1g14010	vesicle-mediated transport
Afu1g14010	AP-2 adaptor complex
Afu1g14020	diphthine synthase activity
Afu1g14020	cytoplasm
Afu1g14020	peptidyl-diphthamide biosynthetic process from peptidyl-histidine
Afu1g14030	SAGA complex
Afu1g14030	conjugation with cellular fusion
Afu1g14030	transcription cofactor activity

Afu1g14030	pseudohyphal growth
Afu1g14030	invasive growth
Afu1g14030	chromatin modification
Afu1g14030	histone acetylation
Afu1g14030	ascospore formation
Afu1g14060	DNA binding
Afu1g14060	nucleus
Afu1g14060	zinc ion binding
Afu1g14070	kinetochore
Afu1g14070	nucleus
Afu1g14070	spindle
Afu1g14070	chromosome segregation
Afu1g14090	histidine biosynthetic process
Afu1g14090	histidinol-phosphate transaminase activity
Afu1g14090	cell
Afu1g14100	biological process unknown
Afu1g14100	molecular function unknown
Afu1g14100	mitochondrion
Afu1g14110	DNA-directed RNA polymerase activity
Afu1g14110	DNA-directed RNA polymerase II, core complex
Afu1g14110	DNA-directed RNA polymerase III complex
Afu1g14110	DNA-directed RNA polymerase I complex
Afu1g14110	transcription from RNA polymerase I promoter
Afu1g14110	transcription from RNA polymerase II promoter
Afu1g14110	transcription from RNA polymerase III promoter
Afu1g14120	cytokinesis
Afu1g14120	RNA binding
Afu1g14120	polysome
Afu1g14120	spindle organization
Afu1g14120	regulation of mitosis
Afu1g14120	meiosis
Afu1g14120	nuclear envelope-endoplasmic reticulum network
Afu1g14140	biological process unknown
Afu1g14140	molecular function unknown
Afu1g14140	cellular component unknown
Afu1g14180	nucleus
Afu1g14180	tRNA (cytosine-5-)-methyltransferase activity
Afu1g14180	tRNA methylation
Afu1g14200	mitochondrial processing peptidase activity
Afu1g14200	mitochondrial protein processing during import
Afu1g14200	mitochondrial processing peptidase complex
Afu1g14220	ribosomal large subunit assembly
Afu1g14220	rRNA modification
Afu1g14220	RNA methylation
Afu1g14220	nucleolus
Afu1g14220	small nucleolar ribonucleoprotein complex
Afu1g14220	35S primary transcript processing
Afu1g14220	methyltransferase activity
Afu1g14220	maturation of SSU-rRNA
Afu1g14220	small nuclear ribonucleoprotein complex

Afu1g14240	Golgi membrane
Afu1g14240	molecular function unknown
Afu1g14240	Golgi vesicle transport
Afu1g14250	potassium channel activity
Afu1g14250	plasma membrane
Afu1g14250	cellular potassium ion homeostasis
Afu1g14290	nuclear mRNA splicing, via spliceosome
Afu1g14290	U6 snRNP
Afu1g14290	mRNA catabolic process
Afu1g14290	U6 snRNA binding
Afu1g14310	poly(A)-specific ribonuclease activity
Afu1g14310	cytoplasm
Afu1g14310	DNA repair
Afu1g14310	postreplication repair
Afu1g14320	biological process unknown
Afu1g14320	molecular function unknown
Afu1g14320	cytoplasm
Afu1g14330	ATP-binding cassette (ABC) transporter activity
Afu1g14330	transport
Afu1g14330	integral to membrane
Afu1g14340	ferric-chelate reductase activity
Afu1g14340	plasma membrane
Afu1g14340	iron ion transport
Afu1g14340	copper ion import
Afu1g14350	3-hydroxyacyl-CoA dehydrogenase activity
Afu1g14350	enoyl-CoA hydratase activity
Afu1g14350	peroxisomal matrix
Afu1g14350	fatty acid beta-oxidation
Afu1g14360	transcription factor activity
Afu1g14360	regulation of transcription
Afu1g14380	peroxisomal matrix
Afu1g14380	sporulation (sensu Saccharomyces)
Afu1g14380	metabolic process
Afu1g14380	2,4-dienoyl-CoA reductase (NADPH) activity
Afu1g14380	fatty acid catabolic process
Afu1g14380	oxidoreductase activity
Afu1g14390	L-iditol 2-dehydrogenase activity
Afu1g14390	fructose metabolic process
Afu1g14390	mannose metabolic process
Afu1g14390	zinc ion binding
Afu1g14390	cellular component unknown
Afu1g14400	nucleus
Afu1g14400	cytoplasm
Afu1g14400	metabolic process
Afu1g14400	oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor
Afu1g14400	NAD or NADH binding
Afu1g14410	structural constituent of ribosome
Afu1g14410	cytoplasm
Afu1g14410	cytosolic large ribosomal subunit (sensu Eukaryota)
Afu1g14410	translation

Afu1g14450	hydrolase activity, hydrolyzing O-glycosyl compounds
Afu1g14450	1,3-beta-glucan metabolic process
Afu1g14450	fungal-type cell wall
Afu1g14490	biological process unknown
Afu1g14490	molecular function unknown
Afu1g14490	nucleus
Afu1g14490	cytoplasm
Afu1g14510	molecular function unknown
Afu1g14530	amidase activity
Afu1g14550	mitochondrion
Afu1g14550	mitochondrial matrix
Afu1g14550	oxygen and reactive oxygen species metabolic process
Afu1g14550	manganese superoxide dismutase activity
Afu1g14570	histidine biosynthetic process
Afu1g14570	histidinol dehydrogenase activity
Afu1g14580	maturation of SSU-rRNA
Afu1g14630	tRNA modification
Afu1g14650	biological process unknown
Afu1g14650	molecular function unknown
Afu1g14650	nucleus
Afu1g14660	pathogenesis
Afu1g14660	secondary metabolic process
Afu1g14680	DNA-directed RNA polymerase activity
Afu1g14680	DNA-directed RNA polymerase II, core complex
Afu1g14680	transcription from RNA polymerase II promoter
Afu1g14690	ubiquitin-protein ligase activity
Afu1g14690	endoplasmic reticulum
Afu1g14690	ER-associated protein catabolic process
Afu1g14700	plasma membrane
Afu1g14700	allantoate transmembrane transporter activity
Afu1g14700	allantoate transport
Afu1g14730	mitotic spindle elongation
Afu1g14730	mitotic sister chromatid segregation
Afu1g14730	anaphase-promoting complex
Afu1g14730	ubiquitin-dependent protein catabolic process
Afu1g14730	mitotic metaphase/anaphase transition
Afu1g14730	enzyme activator activity
Afu1g14730	cyclin catabolic process
Afu1g14740	transcription factor TFIIA complex
Afu1g14740	transcription initiation from RNA polymerase II promoter
Afu1g14740	general RNA polymerase II transcription factor activity
Afu1g14750	transcription factor activity
Afu1g14750	nucleus
Afu1g14750	regulation of transcription, DNA-dependent
Afu1g14750	zinc ion binding
Afu1g14750	regulation of cell size
Afu1g14770	nucleus
Afu1g14770	cytoplasm
Afu1g14770	tRNA modification
Afu1g14770	tRNA dihydrouridine synthase activity

Afu1g14780	molecular function unknown
Afu1g14780	endoplasmic reticulum
Afu1g14780	programmed cell death
Afu1g14790	mitochondrion inheritance
Afu1g14790	molecular function unknown
Afu1g14790	mitochondrial outer membrane
Afu1g14790	mitochondrion organization
Afu1g14810	biological process unknown
Afu1g14810	protein kinase activity
Afu1g14810	cytoplasm
Afu1g14860	transcription factor activity
Afu1g14870	GPI anchor biosynthetic process
Afu1g14870	membrane
Afu1g14880	allophanate hydrolase activity
Afu1g14880	amidase activity
Afu1g14880	urea carboxylase activity
Afu1g14880	cytoplasm
Afu1g14880	urea metabolic process
Afu1g14890	3',5'-cyclic-AMP phosphodiesterase activity
Afu1g14890	cellular component unknown
Afu1g14890	cAMP-mediated signaling
Afu1g14910	biological process unknown
Afu1g14910	molecular function unknown
Afu1g14910	endosome
Afu1g14920	cytoplasm
Afu1g14920	proteolysis
Afu1g14920	X-Pro aminopeptidase activity
Afu1g14940	endoplasmic reticulum membrane
Afu1g14940	SRP-dependent cotranslational protein targeting to membrane, translocation
Afu1g14940	protein transporter activity
Afu1g14950	D-arabinono-1,4-lactone oxidase activity
Afu1g14950	mitochondrion
Afu1g14950	response to oxidative stress
Afu1g14950	FAD binding
Afu1g14960	actin binding
Afu1g14960	cytoskeleton organization
Afu1g14960	actin filament organization
Afu1g14960	actin cytoskeleton
Afu1g14970	small monomeric GTPase activity
Afu1g14970	soluble fraction
Afu1g14970	protein targeting to vacuole
Afu1g14970	vesicle-mediated transport
Afu1g14990	ribosomal large subunit assembly
Afu1g14990	ATP-dependent RNA helicase activity
Afu1g14990	nucleolus
Afu1g14990	35S primary transcript processing
Afu1g15000	2-isopropylmalate synthase activity
Afu1g15000	cytoplasm
Afu1g15000	mitochondrion
Afu1g15000	leucine biosynthetic process

Afu1g15010	biological process unknown
Afu1g15010	catalytic activity
Afu1g15010	cellular component unknown
Afu1g15010	AMP binding
Afu1g15020	structural constituent of ribosome
Afu1g15020	cytosolic small ribosomal subunit (sensu Eukaryota)
Afu1g15020	translation
Afu1g15030	molecular function unknown
Afu1g15030	nucleus
Afu1g15030	traversing start control point of mitotic cell cycle
Afu1g15030	actin cytoskeleton organization
Afu1g15050	chaperone activity
Afu1g15050	endoplasmic reticulum lumen
Afu1g15050	response to unfolded protein
Afu1g15050	protein transport
Afu1g15070	mitochondrial genome maintenance
Afu1g15070	plasmid maintenance
Afu1g15070	cellular component unknown
Afu1g15120	DNA binding
Afu1g15120	nucleus
Afu1g15120	mitotic recombination
Afu1g15120	reciprocal meiotic recombination
Afu1g15120	DNA-dependent ATPase activity
Afu1g15130	GPI-anchor transamidase activity
Afu1g15130	attachment of GPI anchor to protein
Afu1g15130	integral to endoplasmic reticulum membrane
Afu1g15170	peroxisome
Afu1g15170	acyl-CoA thioesterase activity
Afu1g15170	fatty acid oxidation
Afu1g15210	S-adenosylmethionine-dependent methyltransferase activity
Afu1g15230	transcription factor activity
Afu1g15230	nucleus
Afu1g15230	regulation of transcription
Afu1g15240	cytoplasm
Afu1g15240	tubulin complex assembly
Afu1g15240	tubulin binding
Afu1g15270	telomere maintenance
Afu1g15270	response to stress
Afu1g15270	ATPase activity
Afu1g15270	protein metabolic process
Afu1g15270	chaperone mediated protein folding requiring cofactor
Afu1g15300	plasma membrane
Afu1g15300	choline transmembrane transporter activity
Afu1g15300	choline transport
Afu1g15340	polynucleotide adenylyltransferase activity
Afu1g15340	nucleoplasm
Afu1g15340	mRNA cleavage and polyadenylation specificity factor complex
Afu1g15340	mRNA polyadenylation
Afu1g15350	metabolic process
Afu1g15350	hydrolase activity

Afu1g15400	peroxisome targeting signal receptor activity
Afu1g15400	peroxisome matrix targeting signal-2 binding
Afu1g15400	peroxisomal matrix
Afu1g15400	cytosol
Afu1g15400	protein targeting to peroxisome
Afu1g15400	peroxisome organization
Afu1g15410	ubiquitin binding
Afu1g15440	cell morphogenesis
Afu1g15440	plasma membrane
Afu1g15440	cellular glucan metabolic process
Afu1g15440	fungal-type cell wall biogenesis
Afu1g15440	pathogenesis
Afu1g15440	alpha-1,3-glucan synthase activity
Afu1g15450	adenylosuccinate synthase activity
Afu1g15450	cytoplasm
Afu1g15450	purine ribonucleotide biosynthetic process
Afu1g15450	adenosine biosynthetic process
Afu1g15470	transcription factor activity
Afu1g15470	nucleus
Afu1g15470	regulation of transcription, DNA-dependent
Afu1g15470	uracil biosynthetic process
Afu1g15490	transporter activity
Afu1g15490	transport
Afu1g15500	biological process unknown
Afu1g15500	molecular function unknown
Afu1g15500	cellular component unknown
Afu1g15510	DNA binding
Afu1g15510	chromatin remodeling
Afu1g15520	allophanate hydrolase activity
Afu1g15520	urea carboxylase activity
Afu1g15520	cytoplasm
Afu1g15520	urea metabolic process
Afu1g15550	DNA binding
Afu1g15550	transcription factor activity
Afu1g15550	nucleus
Afu1g15550	zinc ion binding
Afu1g15550	regulation of transcription
Afu1g15610	cytoplasm
Afu1g15610	metabolic process
Afu1g15610	zinc ion binding
Afu1g15610	oxidoreductase activity
Afu1g15620	RNA helicase activity
Afu1g15620	mitochondrial matrix
Afu1g15620	RNA splicing
Afu1g15670	ferroxidase activity
Afu1g15670	plasma membrane
Afu1g15670	high-affinity iron ion transport
Afu1g15680	zinc ion binding
Afu1g15720	nuclear pore
Afu1g15720	cytoplasm

Afu1g15720	protein import into nucleus
Afu1g15720	protein transmembrane transporter activity
Afu1g15730	structural constituent of ribosome
Afu1g15730	cytosolic small ribosomal subunit (sensu Eukaryota)
Afu1g15730	cytosolic small ribosomal subunit (sensu Eukaryota)
Afu1g15730	translation
Afu1g15740	nucleus
Afu1g15740	cytoplasm
Afu1g15740	metabolic process
Afu1g15760	phosphatidylserine decarboxylase activity
Afu1g15760	mitochondrion
Afu1g15760	mitochondrial inner membrane
Afu1g15760	phosphatidylcholine biosynthetic process
Afu1g15770	mitotic spindle elongation
Afu1g15770	mitotic sister chromatid segregation
Afu1g15770	anaphase-promoting complex
Afu1g15770	ubiquitin-dependent protein catabolic process
Afu1g15770	mitotic metaphase/anaphase transition
Afu1g15770	cyclin catabolic process
Afu1g15770	enzyme regulator activity
Afu1g15780	3-isopropylmalate dehydrogenase activity
Afu1g15780	cytosol
Afu1g15780	leucine biosynthetic process
Afu1g15790	CDP-diacylglycerol-inositol 3-phosphatidyltransferase activity
Afu1g15790	endoplasmic reticulum
Afu1g15790	phosphatidylinositol biosynthetic process
Afu1g15800	biological process unknown
Afu1g15800	phosphoprotein phosphatase activity
Afu1g15800	mitochondrion
Afu1g15810	ribosomal small subunit assembly
Afu1g15810	single-stranded DNA binding
Afu1g15810	RNA binding
Afu1g15810	nucleus
Afu1g15810	nucleolus
Afu1g15810	rRNA processing
Afu1g15820	endoplasmic reticulum
Afu1g15820	fatty acid metabolic process
Afu1g15820	oxidoreductase activity
Afu1g15850	transcription factor activity
Afu1g15850	nucleus
Afu1g15850	regulation of transcription
Afu1g15860	protein binding
Afu1g15860	ER to Golgi vesicle-mediated transport
Afu1g15860	retrograde vesicle-mediated transport, Golgi to ER
Afu1g15860	COPI vesicle coat
Afu1g15890	inositol or phosphatidylinositol phosphatase activity
Afu1g15890	dephosphorylation
Afu1g15890	integral to Golgi membrane
Afu1g15890	integral to endoplasmic reticulum membrane
Afu1g15890	phosphoinositide metabolic process

Afu1g15900	cytosol
Afu1g15900	protein import into nucleus
Afu1g15900	mRNA-binding (hnRNP) protein import into nucleus
Afu1g15900	cell cycle
Afu1g15900	nuclear localization sequence binding
Afu1g15910	RNA polymerase II transcription factor activity
Afu1g15910	nucleus
Afu1g15910	regulation of transcription
Afu1g15930	choline kinase activity
Afu1g15930	cytosol
Afu1g15930	phosphatidylcholine biosynthetic process
Afu1g15940	biological process unknown
Afu1g15940	molecular function unknown
Afu1g15940	endoplasmic reticulum
Afu1g15950	activation of MAPK activity involved in osmosensory signaling pathway
Afu1g15950	MAP kinase kinase activity
Afu1g15950	protein amino acid phosphorylation
Afu1g15950	osmosensory signaling pathway
Afu1g15960	glutathione-disulfide reductase activity
Afu1g15960	nucleus
Afu1g15960	cytoplasm
Afu1g15960	mitochondrion
Afu1g15960	response to oxidative stress
Afu1g15970	aldo-keto reductase activity
Afu1g15970	cytoplasm
Afu1g15970	cellular aldehyde metabolic process
Afu1g16000	protein kinase activity
Afu1g16040	ferric-chelate reductase activity
Afu1g16040	integral to plasma membrane
Afu1g16040	cellular iron ion homeostasis
Afu1g16040	ferrous iron transport
Afu1g16090	cytoplasm
Afu1g16090	arsenite transport
Afu1g16090	arsenate reductase activity
Afu1g16090	response to arsenic
Afu1g16100	integral to plasma membrane
Afu1g16100	arsenite transmembrane transporter activity
Afu1g16100	arsenite transport
Afu1g16100	response to arsenic
Afu1g16110	cytoplasm
Afu1g16110	S-adenosylmethionine-dependent methyltransferase activity
Afu1g16110	response to arsenic
Afu1g16120	electron transport
Afu1g16120	FMN reductase activity
Afu1g16120	response to arsenic
Afu1g16130	copper-exporting ATPase activity
Afu1g16130	copper ion transmembrane transporter activity
Afu1g16130	copper ion transport
Afu1g16130	cellular copper ion homeostasis
Afu1g16130	membrane

Afu1g16160	transcription factor activity
Afu1g16160	nucleus
Afu1g16160	zinc ion binding
Afu1g16160	regulation of transcription
Afu1g16190	hydrolase activity, hydrolyzing O-glycosyl compounds
Afu1g16190	cellular glucan metabolic process
Afu1g16190	fungal-type cell wall
Afu1g16210	threonine-tRNA ligase activity
Afu1g16210	cytoplasm
Afu1g16210	translation
Afu1g16220	transcription factor activity
Afu1g16220	nucleus
Afu1g16220	regulation of transcription, DNA-dependent
Afu1g16230	fructose transmembrane transporter activity
Afu1g16230	galactose transmembrane transporter activity
Afu1g16230	glucose transmembrane transporter activity
Afu1g16230	plasma membrane
Afu1g16230	hexose transport
Afu1g16230	mannose transmembrane transporter activity
Afu1g16250	alpha-glucosidase activity
Afu1g16250	endoplasmic reticulum
Afu1g16250	fungal-type cell wall biogenesis
Afu1g16270	metabolic process
Afu1g16270	zinc ion binding
Afu1g16270	cellular component unknown
Afu1g16270	oxidoreductase activity
Afu1g16280	mitochondrial proton-transporting ATP synthase complex, coupling factor F(o)
Afu1g16280	structural molecule activity
Afu1g16280	ATP synthesis coupled proton transport
Afu1g16290	ATP-dependent RNA helicase activity
Afu1g16290	nucleolus
Afu1g16290	35S primary transcript processing
Afu1g16290	ATPase activity
Afu1g16310	cytoplasm
Afu1g16310	S-adenosylmethionine-dependent methyltransferase activity
Afu1g16320	endosome
Afu1g16320	protein targeting to membrane
Afu1g16320	protein targeting to vacuole
Afu1g16330	ribosomal subunit export from nucleus
Afu1g16330	nucleus
Afu1g16330	ribosome assembly
Afu1g16340	plasma membrane
Afu1g16340	potassium ion transmembrane transporter activity
Afu1g16340	cellular potassium ion homeostasis
Afu1g16390	transporter activity
Afu1g16390	transport
Afu1g16390	membrane
Afu1g16440	ATP-binding cassette (ABC) transporter activity
Afu1g16440	ATP binding
Afu1g16440	cytoplasm

Afu1g16440	transport
Afu1g16440	internal side of plasma membrane
Afu1g16460	transcription factor activity
Afu1g16460	nucleus
Afu1g16460	transcription
Afu1g16470	nucleus
Afu1g16470	cytoplasm
Afu1g16470	purine nucleotide binding
Afu1g16470	tRNA 3'-trailer cleavage
Afu1g16470	3'-tRNA processing endoribonuclease activity
Afu1g16490	metabolic process
Afu1g16490	oxidoreductase activity
Afu1g16500	biological process unknown
Afu1g16500	small monomeric GTPase activity
Afu1g16500	nucleus
Afu1g16500	cytoplasm
Afu1g16550	nucleus
Afu1g16550	tRNA modification
Afu1g16550	tRNA dihydrouridine synthase activity
Afu1g16570	chromosome segregation
Afu1g16590	DNA binding
Afu1g16590	transcription factor activity
Afu1g16590	nucleus
Afu1g16590	cytosol
Afu1g16590	regulation of transcription, DNA-dependent
Afu1g16590	response to stress
Afu1g16590	zinc ion binding
Afu1g16600	cell morphogenesis
Afu1g16600	endoribonuclease activity
Afu1g16600	extracellular region
Afu1g16600	RNA catabolic process
Afu1g16610	nucleus
Afu1g16620	transcription factor activity
Afu1g16620	nucleus
Afu1g16620	regulation of transcription
Afu1g16630	metabolic process
Afu1g16630	oxidoreductase activity
Afu1g16660	translation initiation factor activity
Afu1g16660	ribosome
Afu1g16660	eukaryotic translation initiation factor 2B complex
Afu1g16660	translational initiation
Afu1g16660	acyltransferase activity
Afu1g16690	integral to plasma membrane
Afu1g16690	nicotinamide mononucleotide permease activity
Afu1g16690	nicotinamide mononucleotide transport
Afu1g16710	endoplasmic reticulum
Afu1g16710	endoplasmic reticulum membrane
Afu1g16710	fatty acid biosynthetic process
Afu1g16710	post-Golgi vesicle-mediated transport
Afu1g16710	fatty acid elongase activity

Afu1g16710	sphingolipid biosynthetic process
Afu1g16710	fatty acid elongation
Afu1g16730	pseudouridine synthesis
Afu1g16730	nucleus
Afu1g16730	pseudouridine synthase activity
Afu1g16750	mitochondrion
Afu1g16750	iron ion transport
Afu1g16750	cation transmembrane transporter activity
Afu1g16750	integral to membrane
Afu1g16770	amidase activity
Afu1g16770	mitochondrion
Afu1g16770	aerobic respiration
Afu1g16780	protein kinase activity
Afu1g16780	nucleus
Afu1g16780	cytoplasm
Afu1g16780	protein amino acid phosphorylation
Afu1g16780	cell growth and/or maintenance
Afu1g16800	mRNA cleavage and polyadenylation specificity factor complex
Afu1g16800	mRNA cleavage factor complex
Afu1g16800	mRNA polyadenylation
Afu1g16800	mRNA cleavage
Afu1g16800	cleavage and polyadenylylation specificity factor activity
Afu1g16810	N2-acetyl-L-ornithine:2-oxoglutarate 5-aminotransferase activity
Afu1g16810	mitochondrial matrix
Afu1g16810	arginine biosynthetic process
Afu1g16810	ornithine biosynthetic process
Afu1g16820	molecular function unknown
Afu1g16820	signal recognition particle, endoplasmic reticulum targeting
Afu1g16820	SRP-dependent cotranslational protein targeting to membrane, signal sequence recognition
Afu1g16820	protein targeting to ER
Afu1g16840	biological process unknown
Afu1g16840	molecular function unknown
Afu1g16840	cytoplasm
Afu1g16850	sphingosine hydroxylase activity
Afu1g16850	endoplasmic reticulum
Afu1g16850	sphingolipid metabolic process
Afu1g16850	sphingolipid biosynthetic process
Afu1g16880	fungal-type vacuole
Afu1g16880	ATP-binding cassette (ABC) transporter activity
Afu1g16880	bile acid transmembrane transporter activity
Afu1g16880	bile acid and bile salt transport
Afu1g16910	multidrug transport
Afu1g16910	multidrug efflux pump activity
Afu1g16910	membrane
Afu1g16910	response to drug
Afu1g16920	hydrolase activity, hydrolyzing O-glycosyl compounds
Afu1g16920	carbohydrate metabolic process
Afu1g16930	Golgi membrane
Afu1g16930	fungal-type vacuole membrane
Afu1g16930	phosphatidylserine decarboxylase activity

Afu1g16930	phosphatidylcholine biosynthetic process
Afu1g16940	ribosomal large subunit assembly
Afu1g16940	ATP-dependent RNA helicase activity
Afu1g16940	nucleolus
Afu1g16940	35S primary transcript processing
Afu1g16950	polysaccharide biosynthetic process
Afu1g16950	endoplasmic reticulum
Afu1g16950	GPI anchor biosynthetic process
Afu1g16950	transferase activity, transferring hexosyl groups
Afu1g16970	small monomeric GTPase activity
Afu1g16970	soluble fraction
Afu1g16970	intracellular protein transport
Afu1g16970	nuclear envelope-endoplasmic reticulum network
Afu1g16990	nuclear mRNA splicing, via spliceosome
Afu1g16990	protein binding
Afu1g16990	spliceosomal complex
Afu1g16990	pre-mRNA splicing factor activity
Afu1g17010	glutathione transferase activity
Afu1g17010	endoplasmic reticulum
Afu1g17010	glutathione metabolic process
Afu1g17030	transferase activity, transferring glycosyl groups
Afu1g17040	phosphoglycerate dehydrogenase activity
Afu1g17040	cytoplasm
Afu1g17040	serine family amino acid biosynthetic process
Afu1g17040	NAD or NADH binding
Afu1g17060	DNA binding
Afu1g17060	nucleus
Afu1g17070	zinc ion binding
Afu1g17090	biological process unknown
Afu1g17090	molecular function unknown
Afu1g17090	nucleus
Afu1g17100	biological process unknown
Afu1g17100	molecular function unknown
Afu1g17100	nucleus
Afu1g17100	cytoplasm
Afu1g17120	translation elongation factor activity
Afu1g17120	ribosome
Afu1g17120	translational elongation
Afu1g17140	aldo-keto reductase activity
Afu1g17140	voltage-gated potassium channel activity
Afu1g17140	potassium ion transport
Afu1g17140	voltage-gated potassium channel complex
Afu1g17150	transcription factor activity
Afu1g17150	nucleus
Afu1g17150	carbohydrate metabolic process
Afu1g17150	regulation of transcription, DNA-dependent
Afu1g17160	transporter activity
Afu1g17160	transport
Afu1g17160	membrane
Afu1g17170	sulfonate dioxygenase activity

Afu1g17170	sulfur metabolic process
Afu1g17170	cellular component unknown
Afu1g17170	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecu
Afu1g17180	nucleus
Afu1g17180	mitochondrion
Afu1g17180	DNA fragmentation involved in apoptosis
Afu1g17180	electron carrier activity
Afu1g17190	cytoplasm
Afu1g17190	peroxisomal membrane
Afu1g17190	peroxisomal matrix
Afu1g17190	AMP binding
Afu1g17200	catalytic activity
Afu1g17200	nonribosomal peptide biosynthetic process
Afu1g17200	amino acid adenylylation by nonribosomal peptide synthase
Afu1g17220	polygalacturonase activity
Afu1g17220	extracellular region
Afu1g17220	pseudohyphal growth
Afu1g17220	pectin catabolic process
Afu1g17240	transcription factor activity
Afu1g17240	nucleus
Afu1g17240	regulation of transcription
Afu1g17250	cell wall organization
Afu1g17270	transition metal ion transport
Afu1g17270	transition metal ion transport
Afu1g17270	ferric-chelate reductase activity
Afu1g17270	plasma membrane
Afu1g17310	fructose transmembrane transporter activity
Afu1g17310	glucose transmembrane transporter activity
Afu1g17310	plasma membrane
Afu1g17310	hexose transport
Afu1g17310	mannose transmembrane transporter activity
Afu1g17320	metabolic process
Afu1g17320	hydrolase activity, hydrolyzing N-glycosyl compounds
Afu1g17360	transcription factor activity
Afu1g17360	nucleus
Afu1g17360	transcription
Afu1g17370	heat shock protein activity
Afu1g17370	nucleus
Afu1g17370	cytoplasm
Afu1g17370	hyperosmotic response
Afu1g17370	response to oxidative stress
Afu1g17370	cell adhesion
Afu1g17370	response to desiccation
Afu1g17370	response to heat
Afu1g17410	hydrolase activity, hydrolyzing O-glycosyl compounds
Afu1g17410	carbohydrate metabolic process
Afu1g17440	plasma membrane
Afu1g17440	multidrug transport
Afu1g17440	xenobiotic-transporting ATPase activity
Afu1g17440	ABC-type efflux porter activity

Afu1g17440	response to drug
Afu1g17460	transcription factor activity
Afu1g17460	nucleus
Afu1g17460	regulation of transcription
Afu1g17520	D-lactate dehydrogenase (cytochrome) activity
Afu1g17520	mitochondrial inner membrane
Afu1g17520	carbohydrate metabolic process
Afu1g17520	aerobic respiration
Afu1g17530	plasma membrane
Afu1g17530	allantoate transmembrane transporter activity
Afu1g17530	allantoate transport
Afu1g17570	plasma membrane
Afu1g17570	urea transmembrane transporter activity
Afu1g17570	solute:sodium symporter activity
Afu1g17570	urea transport
Afu1g17620	protein binding
Afu1g17630	FAD binding
Afu1g17640	transcription factor activity
Afu1g17640	nucleus
Afu1g17640	regulation of transcription, DNA-dependent
Afu1g17640	zinc ion binding
Afu1g17640	melanin biosynthetic process
Afu1g17650	cytoplasm
Afu1g17650	metabolic process
Afu1g17650	oxidoreductase activity
Afu1g17660	histidine biosynthetic process
Afu1g17660	histidinol dehydrogenase activity
Afu1g17660	cell
Afu1g17670	monooxygenase activity
Afu1g17670	cellular aromatic compound metabolic process
Afu1g17680	transporter activity
Afu1g17680	plasma membrane
Afu1g17680	transport
Afu1g17690	FAD binding
Afu1g17700	metabolic process
Afu1g17700	oxidoreductase activity
Afu1g17710	DNA binding
Afu1g17720	metabolic process
Afu1g17720	hydrolase activity, acting on ester bonds
Afu1g17723	racemase and epimerase activity
Afu1g17723	hexose metabolic process
Afu1g17725	metabolic process
Afu1g17725	oxidoreductase activity
Afu1g17730	metabolic process
Afu1g17730	zinc ion binding
Afu1g17730	oxidoreductase activity
Afu1g17740	acyltransferase activity
Afu1g17740	polyketide synthase activity
Afu1g17740	secondary metabolic process
Afu1g17740	polyketide biosynthetic process

Afu1g17750	chromatin silencing at rDNA
Afu1g17750	cytoplasm
Afu1g17750	nicotinamide metabolic process
Afu1g17750	nicotinamide N-methyltransferase activity
Afu2g00100	specific RNA polymerase II transcription factor activity
Afu2g00100	nucleus
Afu2g00100	positive regulation of transcription from RNA polymerase II promoter
Afu2g00110	integral to plasma membrane
Afu2g00110	nicotinamide mononucleotide permease activity
Afu2g00110	nicotinamide mononucleotide transport
Afu2g00140	cellular aromatic compound metabolic process
Afu2g00170	monosaccharide metabolic process
Afu2g00170	cellular component unknown
Afu2g00170	D-xylulose reductase activity
Afu2g00200	catalase activity
Afu2g00200	peroxisomal matrix
Afu2g00200	oxygen and reactive oxygen species metabolic process
Afu2g00200	response to oxidative stress
Afu2g00220	fungal-type vacuole
Afu2g00220	aminopeptidase activity
Afu2g00220	vacuolar protein catabolic process
Afu2g00230	nucleus
Afu2g00230	mitochondrion
Afu2g00230	DNA damage response, signal transduction resulting in induction of apoptosis
Afu2g00230	electron carrier activity
Afu2g00230	oxidoreductase activity
Afu2g00230	coenzyme binding
Afu2g00310	vacuole
Afu2g00310	neutral amino acid transmembrane transporter activity
Afu2g00310	neutral amino acid transport
Afu2g00320	C-5 sterol desaturase activity
Afu2g00320	endoplasmic reticulum
Afu2g00320	ergosterol biosynthetic process
Afu2g00350	proteolysis
Afu2g00350	metallopeptidase activity
Afu2g00360	DNA binding
Afu2g00360	transcription factor activity
Afu2g00360	nucleus
Afu2g00360	zinc ion binding
Afu2g00360	regulation of transcription
Afu2g00380	N-acetyltransferase activity
Afu2g00380	metabolic process
Afu2g00420	biological process unknown
Afu2g00420	molecular function unknown
Afu2g00420	integral to membrane
Afu2g00430	hydrolase activity, hydrolyzing O-glycosyl compounds
Afu2g00430	1,3-beta-glucan metabolic process
Afu2g00430	fungal-type cell wall
Afu2g00450	hexokinase activity
Afu2g00450	cytosol

Afu2g00450	fructose metabolic process
Afu2g00470	RNA polymerase II transcription factor activity
Afu2g00470	nucleus
Afu2g00470	regulation of transcription
Afu2g00480	cellular aldehyde metabolic process
Afu2g00480	response to oxidative stress
Afu2g00480	cellular component unknown
Afu2g00480	aryl-alcohol dehydrogenase activity
Afu2g00530	integral to membrane
Afu2g00540	isocitrate lyase activity
Afu2g00540	glyoxylate cycle
Afu2g00540	cellular component unknown
Afu2g00570	N-acetyltransferase activity
Afu2g00570	metabolic process
Afu2g00570	cellular component unknown
Afu2g00630	lipase activity
Afu2g00640	beta-N-acetylhexosaminidase activity
Afu2g00640	cell wall chitin metabolic process
Afu2g00640	fungal-type cell wall
Afu2g00660	two-component sensor activity
Afu2g00660	protein histidine kinase activity
Afu2g00660	protein amino acid phosphorylation
Afu2g00680	molecular function unknown
Afu2g00680	pseudohyphal growth
Afu2g00680	fungal-type cell wall biogenesis
Afu2g00680	anchored to plasma membrane
Afu2g00690	fungal-type vacuole
Afu2g00690	glucan 1,4-alpha-glucosidase activity
Afu2g00690	polysaccharide metabolic process
Afu2g00710	polysaccharide catabolic process
Afu2g00710	alpha-amylase activity
Afu2g00710	extracellular region
Afu2g00720	aldehyde dehydrogenase (NAD) activity
Afu2g00720	mitochondrion
Afu2g00720	fermentation
Afu2g00820	lipase activity
Afu2g00830	metabolic process
Afu2g00830	oxidoreductase activity
Afu2g00840	integral to plasma membrane
Afu2g00840	nicotinamide mononucleotide permease activity
Afu2g00840	nicotinamide mononucleotide transport
Afu2g00910	nucleotide binding
Afu2g00910	protein binding
Afu2g00910	signal transduction
Afu2g00910	cellular component unknown
Afu2g00930	carbohydrate metabolic process
Afu2g00930	hydrolase activity, hydrolyzing N-glycosyl compounds
Afu2g00960	signal transduction
Afu2g00970	metabolic process
Afu2g00970	zinc ion binding

Afu2g00970	oxidoreductase activity
Afu2g00970	oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor
Afu2g00990	cytoplasm
Afu2g00990	endoplasmic reticulum
Afu2g00990	glycerophosphodiester phosphodiesterase activity
Afu2g00990	phospholipid catabolic process
Afu2g01000	biological process unknown
Afu2g01000	molecular function unknown
Afu2g01000	cytoplasm
Afu2g01000	cellular bud
Afu2g01000	cellular bud neck
Afu2g01010	inositol-3-phosphate synthase activity
Afu2g01010	cytoplasm
Afu2g01010	inositol metabolic process
Afu2g01030	1-aminocyclopropane-1-carboxylate deaminase activity
Afu2g01030	1-aminocyclopropane-1-carboxylate catabolic process
Afu2g01040	formaldehyde dehydrogenase (glutathione) activity
Afu2g01040	cytoplasm
Afu2g01040	formaldehyde assimilation
Afu2g01050	chaperone activity
Afu2g01050	mitochondrial intermembrane space
Afu2g01050	mitochondrial translocation
Afu2g01050	protein transporter activity
Afu2g01050	mitochondrial intermembrane space protein transporter complex
Afu2g01060	signal transducer activity
Afu2g01060	Rho GTPase activator activity
Afu2g01060	intracellular
Afu2g01060	small GTPase mediated signal transduction
Afu2g01060	actin filament reorganization during cell cycle
Afu2g01090	DNA helicase activity
Afu2g01090	alpha DNA polymerase:primase complex
Afu2g01090	lagging strand elongation
Afu2g01120	oxidized pyrimidine base lesion DNA N-glycosylase activity
Afu2g01120	DNA-(apurinic or apyrimidinic site) lyase activity
Afu2g01120	nucleus
Afu2g01120	mitochondrion
Afu2g01120	DNA repair
Afu2g01120	base-excision repair
Afu2g01120	base-excision repair, AP site formation
Afu2g01120	oxidized purine base lesion DNA N-glycosylase activity
Afu2g01130	ubiquitin conjugating enzyme activity
Afu2g01130	ubiquitin-protein ligase activity
Afu2g01130	peroxisome
Afu2g01130	peroxisome organization
Afu2g01130	protein import into peroxisome matrix
Afu2g01130	protein ubiquitination
Afu2g01160	C-4 methylsterol oxidase activity
Afu2g01160	endoplasmic reticulum membrane
Afu2g01160	plasma membrane
Afu2g01160	ergosterol biosynthetic process

Afu2g01170	biological process unknown
Afu2g01170	molecular function unknown
Afu2g01170	cell wall organization
Afu2g01170	fungal-type cell wall
Afu2g01170	1,3-beta-glucanosyltransferase activity
Afu2g01180	metabolic process
Afu2g01180	oxidoreductase activity
Afu2g01200	cytoplasm
Afu2g01200	actin cortical patch (sensu Saccharomyces)
Afu2g01200	actin filament organization
Afu2g01200	response to salt stress
Afu2g01210	RNA helicase activity
Afu2g01210	nuclear pore
Afu2g01210	cytoplasm
Afu2g01210	mRNA export from nucleus
Afu2g01220	GTP cyclohydrolase II activity
Afu2g01230	catalytic activity
Afu2g01230	metabolic process
Afu2g01240	beta-fructofuranosidase activity
Afu2g01240	extracellular region
Afu2g01240	cytoplasm
Afu2g01240	sucrose catabolic process
Afu2g01260	transcription factor activity
Afu2g01260	nucleus
Afu2g01270	transition metal ion transport
Afu2g01270	ferric-chelate reductase activity
Afu2g01270	plasma membrane
Afu2g01270	cellular iron ion homeostasis
Afu2g01270	integral to membrane
Afu2g01280	nucleus
Afu2g01280	cytoplasm
Afu2g01280	metabolic process
Afu2g01280	oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor
Afu2g01280	NAD or NADH binding
Afu2g01290	polyketide synthase activity
Afu2g01290	oxidoreductase activity
Afu2g01290	secondary metabolic process
Afu2g01320	plasma membrane
Afu2g01320	sodium ion transport
Afu2g01320	ATPase activity, coupled to transmembrane movement of ions, phosphorylative mechanism
Afu2g01350	NAD+ kinase activity
Afu2g01350	nucleus
Afu2g01350	cytoplasm
Afu2g01350	cellular iron ion homeostasis
Afu2g01350	NAD phosphorylation and dephosphorylation
Afu2g01360	nucleus
Afu2g01360	cytoplasm
Afu2g01370	plasma membrane
Afu2g01380	N-acetyltransferase activity
Afu2g01380	metabolic process

Afu2g01390	biological process unknown
Afu2g01390	cytosol
Afu2g01390	S-adenosylmethionine-dependent methyltransferase activity
Afu2g01400	metabolic process
Afu2g01400	oxidoreductase activity
Afu2g01410	aldo-keto reductase activity
Afu2g01410	cellular aldehyde metabolic process
Afu2g01410	cellular component unknown
Afu2g01440	transporter activity
Afu2g01440	mitochondrial inner membrane
Afu2g01440	transport
Afu2g01450	alpha-1,6-mannosyltransferase activity
Afu2g01450	alpha-1,6-mannosyltransferase complex
Afu2g01450	Golgi membrane
Afu2g01450	cis-Golgi network
Afu2g01450	protein amino acid N-linked glycosylation
Afu2g01460	biological process unknown
Afu2g01460	molecular function unknown
Afu2g01460	cellular component unknown
Afu2g01460	metal ion transport
Afu2g01460	metal ion transmembrane transporter activity
Afu2g01480	molecular function unknown
Afu2g01480	nucleus
Afu2g01480	nucleolus
Afu2g01480	ribosomal large subunit biogenesis
Afu2g01500	fungal-type vacuole
Afu2g01500	ATP-binding cassette (ABC) transporter activity
Afu2g01500	bile acid transmembrane transporter activity
Afu2g01500	bile acid and bile salt transport
Afu2g01510	molecular function unknown
Afu2g01510	peroxisomal membrane
Afu2g01510	peroxisome organization
Afu2g01520	protein kinase activity
Afu2g01520	nucleus
Afu2g01520	cytoplasm
Afu2g01520	protein amino acid phosphorylation
Afu2g01520	cell growth and/or maintenance
Afu2g01530	ER to Golgi vesicle-mediated transport
Afu2g01530	COPII-coated vesicle
Afu2g01530	integral to Golgi membrane
Afu2g01530	integral to endoplasmic reticulum membrane
Afu2g01550	nucleus
Afu2g01550	negative regulation of transcription from RNA polymerase III promoter
Afu2g01570	vesicle-mediated transport
Afu2g01570	AP-1 adaptor complex
Afu2g01570	clathrin binding
Afu2g01580	monooxygenase activity
Afu2g01580	cellular aromatic compound metabolic process
Afu2g01590	molecular function unknown
Afu2g01590	cytoplasm

Afu2g01590	endoplasmic reticulum
Afu2g01590	protein secretion
Afu2g01590	integral to membrane
Afu2g01630	biological process unknown
Afu2g01630	molecular function unknown
Afu2g01630	mitochondrion
Afu2g01640	tryptophan-tRNA ligase activity
Afu2g01640	cytoplasm
Afu2g01640	tryptophanyl-tRNA aminoacylation
Afu2g01650	biological process unknown
Afu2g01650	molecular function unknown
Afu2g01650	cytoplasm
Afu2g01660	protein binding
Afu2g01660	mitochondrial outer membrane
Afu2g01660	mitochondrial outer membrane translocase complex
Afu2g01660	protein targeting to mitochondrion
Afu2g01660	protein transporter activity
Afu2g01700	fungal-type vacuole
Afu2g01700	AMP-activated protein kinase activity
Afu2g01700	nucleus
Afu2g01700	cytoplasm
Afu2g01700	glucose metabolic process
Afu2g01700	regulation of carbohydrate metabolic process
Afu2g01700	protein amino acid phosphorylation
Afu2g01700	cellular response to nitrogen starvation
Afu2g01700	cell adhesion
Afu2g01700	signal transduction
Afu2g01700	filamentous growth
Afu2g01750	methionyl aminopeptidase activity
Afu2g01750	cytoplasm
Afu2g01750	proteolysis
Afu2g01760	cellular component unknown
Afu2g01780	small nucleolar ribonucleoprotein complex
Afu2g01780	maturation of SSU-rRNA
Afu2g01780	snoRNA binding
Afu2g01820	assembly of spliceosomal tri-snRNP
Afu2g01820	spliceosome assembly
Afu2g01820	spliceosomal complex
Afu2g01820	pre-mRNA splicing factor activity
Afu2g01840	biological process unknown
Afu2g01840	molecular function unknown
Afu2g01840	nucleus
Afu2g01840	cytoplasm
Afu2g01870	chitin synthase activity
Afu2g01870	plasma membrane
Afu2g01870	chitin biosynthetic process
Afu2g01870	chitosome
Afu2g01880	protein tyrosine phosphatase activity
Afu2g01880	nucleus
Afu2g01880	cytoplasm

Afu2g01880	protein amino acid dephosphorylation
Afu2g01890	molecular function unknown
Afu2g01890	mitochondrial inner membrane
Afu2g01890	ubiquinone metabolic process
Afu2g01900	transcription from RNA polymerase II promoter
Afu2g01900	RNA elongation from RNA polymerase II promoter
Afu2g01900	transcription elongation factor complex
Afu2g01900	Cdc73/Paf1 complex
Afu2g01900	RNA polymerase II transcription elongation factor activity
Afu2g01920	glutamine-tRNA ligase activity
Afu2g01920	cytoplasm
Afu2g01920	tRNA aminoacylation for protein translation
Afu2g01940	biological process unknown
Afu2g01940	molecular function unknown
Afu2g01940	cellular component unknown
Afu2g01960	prenyltransferase activity
Afu2g01960	coenzyme and prosthetic group biosynthetic process
Afu2g01980	molecular function unknown
Afu2g01980	nucleus
Afu2g01980	osmoregulation
Afu2g02040	transporter activity
Afu2g02040	plasma membrane
Afu2g02040	transport
Afu2g02050	chaperone activity
Afu2g02050	peptidyl-prolyl cis-trans isomerase activity
Afu2g02050	cytoplasm
Afu2g02050	protein folding
Afu2g02060	aminoacyl-tRNA hydrolase activity
Afu2g02060	metabolic process
Afu2g02070	3'-5'-exoribonuclease activity
Afu2g02070	nuclear-transcribed mRNA poly(A) tail shortening
Afu2g02070	cytoplasm
Afu2g02070	regulation of transcription from RNA polymerase II promoter
Afu2g02070	CCR4-NOT core complex
Afu2g02080	DNA binding
Afu2g02080	nucleus
Afu2g02080	zinc ion binding
Afu2g02100	dihydrolipoyl dehydrogenase activity
Afu2g02100	mitochondrial matrix
Afu2g02100	mitochondrial pyruvate dehydrogenase complex
Afu2g02100	acetyl-CoA biosynthetic process from pyruvate
Afu2g02100	glycine catabolic process
Afu2g02100	isoleucine catabolic process
Afu2g02100	leucine catabolic process
Afu2g02100	L-serine biosynthetic process
Afu2g02100	valine catabolic process
Afu2g02110	transporter activity
Afu2g02110	transport
Afu2g02110	membrane
Afu2g02120	biological process unknown

Afu2g02120	molecular function unknown
Afu2g02120	nucleus
Afu2g02120	cytoplasm
Afu2g02130	stearoyl-CoA 9-desaturase activity
Afu2g02130	fatty acid biosynthetic process
Afu2g02140	ubiquitin binding
Afu2g02150	structural constituent of ribosome
Afu2g02150	cytosolic small ribosomal subunit (sensu Eukaryota)
Afu2g02150	translation
Afu2g02170	mitotic sister chromatid segregation
Afu2g02170	nuclear condensin complex
Afu2g02170	mitotic chromosome condensation
Afu2g02170	ATPase activity
Afu2g02190	RNA metabolic process
Afu2g02220	cytoplasm
Afu2g02220	sterol metabolic process
Afu2g02220	sterol 3-beta-glucosyltransferase activity
Afu2g02230	cytoplasm
Afu2g02230	tubulin complex assembly
Afu2g02230	tubulin binding
Afu2g02250	allantoin catabolic process
Afu2g02250	allantoinase activity
Afu2g02250	intracellular
Afu2g02270	structural constituent of ribosome
Afu2g02270	mitochondrial small ribosomal subunit
Afu2g02270	translation
Afu2g02275	ATP synthesis coupled proton transport
Afu2g02290	structural constituent of ribosome
Afu2g02290	mitochondrial small ribosomal subunit
Afu2g02290	translation
Afu2g02310	cell cortex
Afu2g02310	sphingolipid metabolic process
Afu2g02310	sporulation (sensu Saccharomyces)
Afu2g02310	integral to membrane
Afu2g02310	actin cortical patch
Afu2g02320	chaperone activity
Afu2g02320	cytoplasm
Afu2g02320	translation
Afu2g02340	3'-5'-exoribonuclease activity
Afu2g02340	nuclear exosome (RNase complex)
Afu2g02340	cytoplasmic exosome (RNase complex)
Afu2g02340	35S primary transcript processing
Afu2g02340	mRNA catabolic process
Afu2g02350	biological process unknown
Afu2g02350	molecular function unknown
Afu2g02350	nucleolus
Afu2g02360	UDP-glucose:glycoprotein glucosyltransferase activity
Afu2g02360	endoplasmic reticulum
Afu2g02360	1,6-beta-glucan biosynthetic process
Afu2g02360	response to stress

Afu2g02360	glycoprotein metabolic process
Afu2g02420	cell cycle arrest in response to pheromone
Afu2g02420	molecular function unknown
Afu2g02420	cytoplasm
Afu2g02420	endoplasmic reticulum membrane
Afu2g02420	protein targeting to vacuole
Afu2g02430	mitochondrial genome maintenance
Afu2g02430	molecular function unknown
Afu2g02430	cellular component unknown
Afu2g02510	fungal-type vacuole membrane
Afu2g02510	protein binding
Afu2g02520	cytogamy
Afu2g02520	cell morphogenesis
Afu2g02520	molecular function unknown
Afu2g02520	cytoplasm
Afu2g02520	cellular bud tip
Afu2g02520	cellular bud neck
Afu2g02520	mating projection
Afu2g02520	regulation of cell shape
Afu2g02520	plasma membrane fusion
Afu2g02530	nuclear division
Afu2g02530	protein kinase activity
Afu2g02530	casein kinase activity
Afu2g02530	nucleus
Afu2g02530	DNA repair
Afu2g02530	chromosome segregation
Afu2g02530	mitosis
Afu2g02530	meiosis
Afu2g02530	cell growth and/or maintenance
Afu2g02540	transcription factor activity
Afu2g02540	nucleus
Afu2g02540	transcription
Afu2g02540	response to drug
Afu2g02550	GTPase inhibitor activity
Afu2g02550	cytoplasm
Afu2g02550	positive regulation of transcription from RNA polymerase II promoter by pheromones
Afu2g02560	molecular function unknown
Afu2g02560	ER to Golgi vesicle-mediated transport
Afu2g02560	retrograde vesicle-mediated transport, Golgi to ER
Afu2g02560	COPI vesicle coat
Afu2g02570	ubiquitin ligase complex
Afu2g02570	protein binding
Afu2g02570	ubiquitin-dependent protein catabolic process
Afu2g02580	biological process unknown
Afu2g02580	molecular function unknown
Afu2g02580	mitochondrion
Afu2g02590	aspartate-tRNA ligase activity
Afu2g02590	cytoplasm
Afu2g02590	translation
Afu2g02620	telomere maintenance

Afu2g02620	double-strand break repair via homologous recombination
Afu2g02620	nuclear chromatin
Afu2g02620	damaged DNA binding
Afu2g02620	nuclear telomeric heterochromatin
Afu2g02620	double-strand break repair via nonhomologous end joining
Afu2g02620	chromatin assembly or disassembly
Afu2g02620	transcriptional gene silencing
Afu2g02660	regulation of DNA recombination
Afu2g02660	DNA topoisomerase type I activity
Afu2g02660	nucleus
Afu2g02660	telomere maintenance via telomerase
Afu2g02660	reciprocal meiotic recombination
Afu2g02680	cytoplasm
Afu2g02680	mitochondrion
Afu2g02680	mitochondrial inner membrane
Afu2g02680	m-AAA complex
Afu2g02680	protein complex assembly
Afu2g02680	proteolysis
Afu2g02680	metallopeptidase activity
Afu2g02680	ATPase activity
Afu2g02680	protein import into mitochondrial intermembrane space
Afu2g02690	transcription factor activity
Afu2g02690	nucleus
Afu2g02690	regulation of transcription
Afu2g02700	molecular function unknown
Afu2g02700	mitochondrial inner membrane
Afu2g02700	protein folding
Afu2g02710	structural constituent of ribosome
Afu2g02710	nucleolus
Afu2g02710	ribosomal large subunit biogenesis
Afu2g02750	biological process unknown
Afu2g02750	cytoplasm
Afu2g02750	S-adenosylmethionine-dependent methyltransferase activity
Afu2g02760	MAPKKK cascade during cell wall biogenesis
Afu2g02760	nucleus
Afu2g02760	cytoplasm
Afu2g02760	MAP kinase tyrosine/serine/threonine phosphatase activity
Afu2g02780	nuclear chromosome, telomeric region
Afu2g02780	mRNA binding
Afu2g02780	cytoplasm
Afu2g02780	telomere maintenance via telomerase
Afu2g02780	intracellular mRNA localization
Afu2g02810	metabolic process
Afu2g02810	zinc ion binding
Afu2g02810	cellular component unknown
Afu2g02810	oxidoreductase activity
Afu2g02810	oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor
Afu2g02820	biological process unknown
Afu2g02820	molecular function unknown
Afu2g02820	cellular component unknown

Afu2g02850	protein serine/threonine kinase activity
Afu2g02850	cytoplasm
Afu2g02850	protein amino acid phosphorylation
Afu2g02850	hexose metabolic process
Afu2g02870	molecular function unknown
Afu2g02870	nucleus
Afu2g02870	cytoplasm
Afu2g02870	maturation of SSU-rRNA
Afu2g02880	biological process unknown
Afu2g02880	molecular function unknown
Afu2g02880	cytoplasm
Afu2g02890	tRNA 2'-phosphotransferase activity
Afu2g02890	nucleus
Afu2g02890	tRNA splicing, via endonucleolytic cleavage and ligation
Afu2g02950	aldo-keto reductase activity
Afu2g02950	cellular aldehyde metabolic process
Afu2g02950	cellular component unknown
Afu2g02960	molecular function unknown
Afu2g02960	cytoplasm
Afu2g02960	translation
Afu2g02960	meiosis
Afu2g02980	protein retention in ER lumen
Afu2g02980	integral to endoplasmic reticulum membrane
Afu2g02980	HDEL sequence binding
Afu2g02990	DNA binding
Afu2g03000	plasma membrane
Afu2g03000	vitamin or cofactor transporter activity
Afu2g03000	vitamin or cofactor transport
Afu2g03010	cytochrome-c oxidase activity
Afu2g03010	mitochondrial respiratory chain complex IV
Afu2g03010	aerobic respiration
Afu2g03020	DNA binding
Afu2g03030	nuclear mRNA splicing, via spliceosome
Afu2g03030	U5 snRNP
Afu2g03030	pre-mRNA splicing factor activity
Afu2g03030	small nuclear ribonucleoprotein complex
Afu2g03040	structural constituent of ribosome
Afu2g03040	cytosolic large ribosomal subunit (sensu Eukaryota)
Afu2g03040	translation
Afu2g03040	ribosome biogenesis
Afu2g03080	biological process unknown
Afu2g03080	fungal-type vacuole
Afu2g03080	molecular function unknown
Afu2g03090	ATP-binding cassette (ABC) transporter activity
Afu2g03090	transport
Afu2g03110	fungal-type vacuole membrane
Afu2g03110	alkaline phosphatase activity
Afu2g03110	protein amino acid dephosphorylation
Afu2g03110	histone dephosphorylation
Afu2g03120	hydrolase activity, hydrolyzing O-glycosyl compounds

Afu2g03120	cellular glucan metabolic process
Afu2g03120	cell wall organization
Afu2g03120	chitin binding
Afu2g03120	fungal-type cell wall
Afu2g03140	nucleus
Afu2g03140	cytoplasm
Afu2g03140	response to oxidative stress
Afu2g03140	peptide-methionine-(S)-S-oxide reductase activity
Afu2g03150	establishment of mitotic spindle orientation
Afu2g03150	microtubule motor activity
Afu2g03150	kinesin complex
Afu2g03150	nuclear microtubule
Afu2g03150	cytoplasmic microtubule
Afu2g03150	microtubule depolymerization
Afu2g03220	programmed cell death
Afu2g03290	activation of MAPK (pseudohyphal growth)
Afu2g03290	DNA binding
Afu2g03290	protein binding
Afu2g03290	nucleus
Afu2g03290	glycogen metabolic process
Afu2g03290	sporulation (sensu Saccharomyces)
Afu2g03290	Ras protein signal transduction
Afu2g03310	ribosomal large subunit export from nucleus
Afu2g03310	structural molecule activity
Afu2g03310	nuclear pore
Afu2g03310	RNA export from nucleus
Afu2g03310	mRNA export from nucleus
Afu2g03310	rRNA export from nucleus
Afu2g03310	snRNA export from nucleus
Afu2g03310	tRNA export from nucleus
Afu2g03310	protein import into nucleus
Afu2g03310	NLS-bearing substrate import into nucleus
Afu2g03310	snRNP protein import into nucleus
Afu2g03310	mRNA-binding (hnRNP) protein import into nucleus
Afu2g03310	ribosomal protein import into nucleus
Afu2g03310	protein export from nucleus
Afu2g03310	nuclear pore organization
Afu2g03340	biological process unknown
Afu2g03340	molecular function unknown
Afu2g03340	cellular component unknown
Afu2g03360	cell morphogenesis
Afu2g03360	phospholipid binding
Afu2g03360	Rho protein signal transduction
Afu2g03370	biological process unknown
Afu2g03370	molecular function unknown
Afu2g03370	endoplasmic reticulum
Afu2g03380	structural constituent of ribosome
Afu2g03380	cytosolic large ribosomal subunit (sensu Eukaryota)
Afu2g03380	translation
Afu2g03390	histone deacetylase complex

Afu2g03390	chromatin silencing at rDNA
Afu2g03390	loss of chromatin silencing during replicative cell aging
Afu2g03390	histone deacetylase activity
Afu2g03390	mitotic recombination
Afu2g03390	chromatin organization
Afu2g03390	chromatin silencing
Afu2g03390	chromatin silencing at HML and HMR (sensu Saccharomyces)
Afu2g03390	chromatin silencing at telomere
Afu2g03390	regulation of transcription, DNA-dependent
Afu2g03390	protein amino acid deacetylation
Afu2g03400	endopeptidase activity
Afu2g03400	ubiquitin-dependent protein catabolic process
Afu2g03400	proteasome regulatory particle, lid subcomplex
Afu2g03420	molecular function unknown
Afu2g03420	mitochondrial inner membrane presequence translocase complex
Afu2g03420	protein import into mitochondrial matrix
Afu2g03430	specific RNA polymerase II transcription factor activity
Afu2g03430	nucleus
Afu2g03430	regulation of transcription from RNA polymerase II promoter
Afu2g03460	specific RNA polymerase II transcription factor activity
Afu2g03460	nucleus
Afu2g03460	regulation of transcription from RNA polymerase II promoter
Afu2g03460	leucine biosynthetic process
Afu2g03490	protein serine/threonine kinase activity
Afu2g03490	regulation of meiosis
Afu2g03510	pheromone-dependent signal transduction involved in conjugation with cellular fusion
Afu2g03510	carboxypeptidase D activity
Afu2g03510	trans-Golgi network
Afu2g03510	protein processing
Afu2g03520	transporter activity
Afu2g03520	transport
Afu2g03520	monocarboxylic acid transmembrane transporter activity
Afu2g03520	membrane
Afu2g03560	two-component sensor activity
Afu2g03560	protein histidine kinase activity
Afu2g03560	protein amino acid phosphorylation
Afu2g03580	phenylalanine-tRNA ligase activity
Afu2g03580	cytoplasm
Afu2g03580	phenylalanyl-tRNA aminoacylation
Afu2g03580	phenylalanine-tRNA ligase complex
Afu2g03590	structural constituent of ribosome
Afu2g03590	cytosolic small ribosomal subunit (sensu Eukaryota)
Afu2g03590	translation
Afu2g03600	metabolic process
Afu2g03600	hydrolase activity
Afu2g03610	IMP dehydrogenase activity
Afu2g03610	cytoplasm
Afu2g03610	purine ribonucleotide biosynthetic process
Afu2g03620	nucleus
Afu2g03620	cytoplasm

Afu2g03620	L-serine metabolic process
Afu2g03620	oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acc
Afu2g03640	cytokinesis
Afu2g03640	response to osmotic stress
Afu2g03640	actin filament organization
Afu2g03640	cytoskeletal protein binding
Afu2g03650	actin cortical patch assembly
Afu2g03650	actin cortical patch (sensu Saccharomyces)
Afu2g03650	Golgi to endosome transport
Afu2g03650	endocytosis
Afu2g03650	actin filament organization
Afu2g03650	cytoskeletal adaptor activity
Afu2g03650	clathrin vesicle coat
Afu2g03680	biological process unknown
Afu2g03680	molecular function unknown
Afu2g03680	cellular component unknown
Afu2g03700	hydroxymethylglutaryl-CoA reductase (NADPH) activity
Afu2g03700	nuclear envelope
Afu2g03700	mitochondrial matrix
Afu2g03700	endoplasmic reticulum membrane
Afu2g03700	ergosterol biosynthetic process
Afu2g03710	incipient cellular bud site
Afu2g03710	polarisome
Afu2g03710	cytoskeletal regulatory protein binding
Afu2g03710	cellular bud tip
Afu2g03710	cellular bud neck
Afu2g03710	mating projection
Afu2g03710	actin filament organization
Afu2g03710	bipolar cellular bud site selection
Afu2g03710	pseudohyphal growth
Afu2g03710	Rho protein signal transduction
Afu2g03720	histone deacetylase complex
Afu2g03720	peptidyl-prolyl cis-trans isomerase activity
Afu2g03720	protein metabolic process
Afu2g03730	integral to plasma membrane
Afu2g03730	copper uptake transmembrane transporter activity
Afu2g03730	copper ion import
Afu2g03740	3'-5'-exoribonuclease activity
Afu2g03740	nuclear exosome (RNase complex)
Afu2g03740	cytoplasmic exosome (RNase complex)
Afu2g03740	35S primary transcript processing
Afu2g03740	mRNA catabolic process
Afu2g03750	helicase activity
Afu2g03750	nucleus
Afu2g03750	transcription-coupled nucleotide-excision repair
Afu2g03750	nucleotide-excision repair
Afu2g03750	DNA-dependent ATPase activity
Afu2g03760	phosphoprotein phosphatase activity
Afu2g03760	protein tyrosine phosphatase activity
Afu2g03760	nucleus

Afu2g03760	mRNA cleavage and polyadenylation specificity factor complex
Afu2g03760	35S primary transcript processing
Afu2g03760	transcription initiation from RNA polymerase II promoter
Afu2g03760	termination of RNA polymerase II transcription
Afu2g03760	snoRNA transcription
Afu2g03760	termination of RNA polymerase II transcription, poly(A)-coupled
Afu2g03760	termination of RNA polymerase II transcription, poly(A)-independent
Afu2g03760	phosphoric ester hydrolase activity
Afu2g03770	chromatin silencing at rDNA
Afu2g03770	nucleus
Afu2g03770	cytoplasm
Afu2g03770	peroxisome
Afu2g03770	chromatin silencing at telomere
Afu2g03770	cell aging
Afu2g03770	nicotinamidase activity
Afu2g03770	nicotinate nucleotide salvage
Afu2g03780	biological process unknown
Afu2g03780	molecular function unknown
Afu2g03780	cytoplasm
Afu2g03790	steroid biosynthetic process
Afu2g03790	oxysterol binding
Afu2g03790	cellular component unknown
Afu2g03810	histone deacetylase complex
Afu2g03810	chromatin organization
Afu2g03810	regulation of transcription, DNA-dependent
Afu2g03810	histone deacetylation
Afu2g03810	NAD-dependent histone deacetylase activity
Afu2g03810	NAD-independent histone deacetylase activity
Afu2g03810	negative regulation of meiosis
Afu2g03820	isocitrate lyase activity
Afu2g03820	glyoxylate cycle
Afu2g03820	cellular component unknown
Afu2g03830	pathogenesis
Afu2g03860	low-affinity zinc ion transmembrane transporter activity
Afu2g03860	plasma membrane
Afu2g03860	low-affinity zinc ion transport
Afu2g03870	peptidyl-prolyl cis-trans isomerase activity
Afu2g03870	endoplasmic reticulum membrane
Afu2g03870	protein folding
Afu2g03880	cytoplasm
Afu2g03890	DNA damage checkpoint
Afu2g03890	regulation of cyclin-dependent protein kinase activity
Afu2g03890	G1/S transition of mitotic cell cycle
Afu2g03890	inactivation of MAPK activity involved in osmosensory signaling pathway
Afu2g03890	nucleus
Afu2g03890	cytoplasm
Afu2g03890	protein amino acid dephosphorylation
Afu2g03890	response to unfolded protein
Afu2g03890	protein phosphatase type 2C activity
Afu2g03900	hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in linear amides

Afu2g03910	DNA helicase activity
Afu2g03910	nucleus
Afu2g03910	DNA repair
Afu2g03910	double-strand break repair via nonhomologous end joining
Afu2g03920	regulation of cyclin-dependent protein kinase activity
Afu2g03920	G1/S transition of mitotic cell cycle
Afu2g03920	G2/M transition of mitotic cell cycle
Afu2g03920	nucleus
Afu2g03920	spindle pole body
Afu2g03920	cyclin-dependent protein kinase regulator activity
Afu2g03930	small nucleolar ribonucleoprotein complex
Afu2g03930	maturation of SSU-rRNA
Afu2g03930	snoRNA binding
Afu2g03950	protein serine/threonine phosphatase activity
Afu2g03950	cellular sodium ion homeostasis
Afu2g03950	cellular component unknown
Afu2g03970	biological process unknown
Afu2g03970	molecular function unknown
Afu2g03970	nucleus
Afu2g03970	cytoplasm
Afu2g03980	hydrolase activity, hydrolyzing O-glycosyl compounds
Afu2g03980	cellular glucan metabolic process
Afu2g03980	fungal-type cell wall
Afu2g03980	carbohydrate binding
Afu2g03980	sporocarp development
Afu2g04000	peptide-N4-(N-acetyl-beta-glucosaminyl)asparagine amidase activity
Afu2g04000	nucleus
Afu2g04000	cytosol
Afu2g04000	misfolded or incompletely synthesized protein catabolic process
Afu2g04000	protein deglycosylation
Afu2g04010	alpha,alpha-trehalose-phosphate synthase (UDP-forming) activity
Afu2g04010	cytoplasm
Afu2g04010	alpha,alpha-trehalose-phosphate synthase complex (UDP-forming)
Afu2g04010	carbohydrate metabolic process
Afu2g04010	trehalose biosynthetic process
Afu2g04010	response to stress
Afu2g04020	alpha,alpha-trehalose-phosphate synthase complex (UDP-forming)
Afu2g04020	trehalose biosynthetic process
Afu2g04020	response to stress
Afu2g04020	enzyme regulator activity
Afu2g04030	chromosome, centromeric region
Afu2g04030	molecular function unknown
Afu2g04030	chromatin assembly complex
Afu2g04030	DNA repair
Afu2g04030	nucleosome assembly
Afu2g04030	chromatin silencing
Afu2g04060	NADPH dehydrogenase activity
Afu2g04060	metabolic process
Afu2g04060	oxidoreductase activity
Afu2g04060	coenzyme binding

Afu2g04070	transporter activity
Afu2g04070	transport
Afu2g04070	integral to membrane
Afu2g04080	transporter activity
Afu2g04080	DNA metabolic process
Afu2g04080	transport
Afu2g04080	meiosis
Afu2g04080	membrane
Afu2g04080	nitrogen utilization
Afu2g04130	ribosomal small subunit assembly
Afu2g04130	structural constituent of ribosome
Afu2g04130	cytosolic small ribosomal subunit (sensu Eukaryota)
Afu2g04130	translation
Afu2g04130	regulation of translational fidelity
Afu2g04140	structural constituent of cytoskeleton
Afu2g04140	spindle pole body
Afu2g04140	microtubule nucleation
Afu2g04150	biological process unknown
Afu2g04150	molecular function unknown
Afu2g04150	nucleus
Afu2g04200	4-hydroxyphenylpyruvate dioxygenase activity
Afu2g04200	L-phenylalanine catabolic process
Afu2g04200	tyrosine catabolic process
Afu2g04200	pathogenesis
Afu2g04220	homogentisate 1,2-dioxygenase activity
Afu2g04220	L-phenylalanine catabolic process
Afu2g04220	tyrosine catabolic process
Afu2g04230	fumarylacetoacetase activity
Afu2g04230	L-phenylalanine catabolic process
Afu2g04230	tyrosine catabolic process
Afu2g04240	L-phenylalanine catabolic process
Afu2g04240	tyrosine catabolic process
Afu2g04240	maleylacetoacetate isomerase activity
Afu2g04262	specific RNA polymerase II transcription factor activity
Afu2g04262	nucleus
Afu2g04262	positive regulation of transcription from RNA polymerase II promoter
Afu2g04270	mitochondrial inner membrane presequence translocase complex
Afu2g04270	mitochondrial translocation
Afu2g04270	protein transporter activity
Afu2g04290	metabolic process
Afu2g04290	oxidoreductase activity
Afu2g04310	citrulline metabolic process
Afu2g04310	argininosuccinate metabolic process
Afu2g04310	argininosuccinate synthase activity
Afu2g04310	cytosol
Afu2g04310	arginine biosynthetic process
Afu2g04320	biological process unknown
Afu2g04320	NADPH dehydrogenase activity
Afu2g04320	nucleus
Afu2g04320	cytoplasm

Afu2g04360	biological process unknown
Afu2g04360	molecular function unknown
Afu2g04360	nucleus
Afu2g04360	cytoplasm
Afu2g04390	biological process unknown
Afu2g04390	molecular function unknown
Afu2g04390	cellular component unknown
Afu2g04430	fungal-type vacuole membrane
Afu2g04430	molecular function unknown
Afu2g04430	mitochondrion organization
Afu2g04440	biological process unknown
Afu2g04440	DNA binding
Afu2g04440	nucleus
Afu2g04440	zinc ion binding
Afu2g04450	protein polyubiquitination
Afu2g04450	ubiquitin-protein ligase activity
Afu2g04450	protein monoubiquitination
Afu2g04450	cellular component unknown
Afu2g04480	metabolic process
Afu2g04480	hydrolase activity, hydrolyzing N-glycosyl compounds
Afu2g04490	phosphoglycerate dehydrogenase activity
Afu2g04490	cytoplasm
Afu2g04490	serine family amino acid biosynthetic process
Afu2g04520	alcohol dehydrogenase activity, zinc-dependent
Afu2g04520	mitochondrion
Afu2g04520	fermentation
Afu2g04550	sugar:hydrogen symporter activity
Afu2g04550	plasma membrane
Afu2g04550	transport
Afu2g04560	biological process unknown
Afu2g04560	lipid particle
Afu2g04560	oxidoreductase activity
Afu2g04590	alcohol dehydrogenase (NAD) activity
Afu2g04590	cytoplasm
Afu2g04590	ethanol metabolic process
Afu2g04590	fermentation
Afu2g04590	zinc ion binding
Afu2g04600	transcription factor activity
Afu2g04600	nucleus
Afu2g04600	carbohydrate metabolic process
Afu2g04600	regulation of transcription, DNA-dependent
Afu2g04610	biological process unknown
Afu2g04610	molecular function unknown
Afu2g04610	cytoplasm
Afu2g04620	karyogamy during conjugation with cellular fusion
Afu2g04620	chaperone activity
Afu2g04620	heat shock protein activity
Afu2g04620	endoplasmic reticulum lumen
Afu2g04620	protein folding
Afu2g04620	SRP-dependent cotranslational protein targeting to membrane, translocation

Afu2g04620	response to stress
Afu2g04620	response to unfolded protein
Afu2g04620	ATPase activity
Afu2g04620	unfolded protein binding
Afu2g04630	translation elongation factor activity
Afu2g04630	ribosome
Afu2g04630	translational elongation
Afu2g04650	poly(A)-specific ribonuclease activity
Afu2g04650	cytoplasm
Afu2g04650	postreplication repair
Afu2g04650	mRNA processing
Afu2g04670	protein binding
Afu2g04670	endosome
Afu2g04670	protein targeting to vacuole
Afu2g04680	pheromone-dependent signal transduction involved in conjugation with cellular fusion
Afu2g04680	response to pheromone during conjugation without cellular fusion
Afu2g04680	protein serine/threonine kinase activity
Afu2g04680	protein amino acid phosphorylation
Afu2g04680	hyphal growth
Afu2g04690	plasma membrane
Afu2g04690	vitamin or cofactor transporter activity
Afu2g04690	vitamin or cofactor transport
Afu2g04700	RNA binding
Afu2g04700	endoplasmic reticulum membrane
Afu2g04700	polysome
Afu2g04700	chromosome segregation
Afu2g04700	intracellular mRNA localization
Afu2g04700	nuclear envelope-endoplasmic reticulum network
Afu2g04710	electron transporter activity
Afu2g04710	endoplasmic reticulum membrane
Afu2g04710	microsome
Afu2g04710	sterol biosynthetic process
Afu2g04720	ubiquitin-specific protease activity
Afu2g04720	cytoplasm
Afu2g04720	protein deubiquitination
Afu2g04740	protein binding
Afu2g04740	endosome
Afu2g04740	zinc ion binding
Afu2g04740	protein retention in Golgi apparatus
Afu2g04780	biological process unknown
Afu2g04780	cellular component unknown
Afu2g04800	molecular function unknown
Afu2g04800	nucleus
Afu2g04800	cytoplasm
Afu2g04800	maturation of SSU-rRNA
Afu2g04820	translation release factor activity
Afu2g04820	cytosol
Afu2g04820	translational termination
Afu2g04830	biological process unknown
Afu2g04830	protein binding

Afu2g04830	nucleus
Afu2g04830	cytoplasm
Afu2g04830	enzyme regulator activity
Afu2g04860	repairosome
Afu2g04860	nucleotide-excision repair factor 2 complex
Afu2g04860	nucleotide-excision repair, DNA damage recognition
Afu2g04860	damaged DNA binding
Afu2g04870	mitochondrion
Afu2g04880	molecular function unknown
Afu2g04880	nucleus
Afu2g04880	cytoplasm
Afu2g04880	cell wall organization
Afu2g04910	endopeptidase activity
Afu2g04910	proteasome core complex
Afu2g04910	ubiquitin-dependent protein catabolic process
Afu2g04910	proteasome core complex, beta-subunit complex
Afu2g04920	ribosomal subunit export from nucleus
Afu2g04920	structural molecule activity
Afu2g04920	nuclear pore
Afu2g04920	mRNA export from nucleus
Afu2g04920	rRNA export from nucleus
Afu2g04920	nuclear pore organization
Afu2g04940	biological process unknown
Afu2g04940	molecular function unknown
Afu2g04940	cytoplasm
Afu2g04960	mitotic sister chromatid segregation
Afu2g04960	ATP-dependent DNA helicase activity
Afu2g04960	nucleolus
Afu2g04960	DNA unwinding during replication
Afu2g04960	chromosome organization and biogenesis (sensu Eukaryota)
Afu2g04970	biological process unknown
Afu2g04970	molecular function unknown
Afu2g04970	cytoplasm
Afu2g05010	fungal-type vacuole membrane
Afu2g05010	molecular function unknown
Afu2g05010	cytosol
Afu2g05010	protein targeting to vacuole
Afu2g05010	autophagy
Afu2g05020	cell morphogenesis
Afu2g05020	cytoplasm
Afu2g05030	zinc ion binding
Afu2g05040	plasma membrane
Afu2g05040	glycerol transmembrane transporter activity
Afu2g05040	glycerol transport
Afu2g05040	glycerol catabolic process
Afu2g05085	N-acetyltransferase activity
Afu2g05085	metabolic process
Afu2g05090	molecular function unknown
Afu2g05090	mitochondrial intermembrane space
Afu2g05090	gluconeogenesis

Afu2g05090	carbon utilization by utilization of organic compounds
Afu2g05100	biological process unknown
Afu2g05100	nucleus
Afu2g05100	cytoplasm
Afu2g05100	S-adenosylmethionine-dependent methyltransferase activity
Afu2g05180	DNA binding
Afu2g05180	DNA helicase activity
Afu2g05180	RNA helicase activity
Afu2g05180	nucleus
Afu2g05180	zinc ion binding
Afu2g05190	fructose transmembrane transporter activity
Afu2g05190	galactose transmembrane transporter activity
Afu2g05190	glucose transmembrane transporter activity
Afu2g05190	plasma membrane
Afu2g05190	hexose transport
Afu2g05190	mannose transmembrane transporter activity
Afu2g05200	biological process unknown
Afu2g05200	molecular function unknown
Afu2g05200	endoplasmic reticulum
Afu2g05210	mitotic spindle elongation
Afu2g05210	mitotic sister chromatid segregation
Afu2g05210	ubiquitin-protein ligase activity
Afu2g05210	protein binding
Afu2g05210	anaphase-promoting complex
Afu2g05210	ubiquitin-dependent protein catabolic process
Afu2g05210	mitotic metaphase/anaphase transition
Afu2g05210	cyclin catabolic process
Afu2g05230	biological process unknown
Afu2g05230	molecular function unknown
Afu2g05230	cytoplasm
Afu2g05310	transcription factor activity
Afu2g05310	nucleus
Afu2g05310	regulation of transcription
Afu2g05320	fungal-type vacuole
Afu2g05320	vacuolar membrane
Afu2g05320	calcium ion transport
Afu2g05320	cellular calcium ion homeostasis
Afu2g05320	calcium ion transmembrane transporter activity
Afu2g05320	calcium:hydrogen antiporter activity
Afu2g05330	fungal-type vacuole
Afu2g05330	vacuolar membrane
Afu2g05330	calcium ion transport
Afu2g05330	cellular calcium ion homeostasis
Afu2g05330	calcium ion transmembrane transporter activity
Afu2g05330	calcium:hydrogen antiporter activity
Afu2g05340	plasma membrane
Afu2g05340	cell wall organization
Afu2g05340	1,3-beta-glucanosyltransferase activity
Afu2g05350	transporter activity
Afu2g05350	transport

Afu2g05360	transcription factor activity
Afu2g05360	regulation of transcription
Afu2g05380	transcription factor activity
Afu2g05380	nucleus
Afu2g05380	regulation of transcription
Afu2g05390	biological process unknown
Afu2g05390	fungal-type vacuole membrane
Afu2g05390	molecular function unknown
Afu2g05400	alpha-glucosidase activity
Afu2g05400	endoplasmic reticulum
Afu2g05400	fungal-type cell wall biogenesis
Afu2g05420	molecular function unknown
Afu2g05420	nucleus
Afu2g05420	nucleolus
Afu2g05420	rRNA processing
Afu2g05430	uridine kinase activity
Afu2g05430	nucleus
Afu2g05430	cytoplasm
Afu2g05430	pyrimidine salvage
Afu2g05450	NADH dehydrogenase activity
Afu2g05450	mitochondrion
Afu2g05450	NADH oxidation
Afu2g05450	glucose catabolic process to ethanol
Afu2g05480	DNA-directed RNA polymerase activity
Afu2g05480	DNA-directed RNA polymerase I complex
Afu2g05480	transcription from RNA polymerase I promoter
Afu2g05490	biological process unknown
Afu2g05490	molecular function unknown
Afu2g05490	nucleus
Afu2g05490	cytoplasm
Afu2g05510	mitochondrial proton-transporting ATP synthase complex, coupling factor F(o)
Afu2g05510	ATP synthesis coupled proton transport
Afu2g05510	hydrogen ion transporting ATP synthase activity, rotational mechanism
Afu2g05530	regulation of progression through cell cycle
Afu2g05530	histone acetyltransferase complex
Afu2g05530	histone acetyltransferase activity
Afu2g05530	regulation of transcription from RNA polymerase II promoter
Afu2g05530	histone acetylation
Afu2g05540	nuclear mRNA splicing, via spliceosome
Afu2g05540	spliceosomal complex
Afu2g05540	pre-mRNA splicing factor activity
Afu2g05550	biological process unknown
Afu2g05550	molecular function unknown
Afu2g05550	nucleus
Afu2g05550	nucleolus
Afu2g05560	nucleus
Afu2g05560	nucleolus
Afu2g05560	rRNA processing
Afu2g05560	3'-5' exonuclease activity
Afu2g05560	ribosome assembly

Afu2g05580	deadenylation-dependent decapping of nuclear-transcribed mRNA
Afu2g05580	nucleus
Afu2g05580	cytoplasm
Afu2g05580	hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides
Afu2g05590	ubiquitin-specific protease activity
Afu2g05590	cytoplasm
Afu2g05590	protein deubiquitination
Afu2g05610	nuclear-transcribed mRNA catabolic process, deadenylation-dependent decay
Afu2g05610	mRNA binding
Afu2g05610	cellular component unknown
Afu2g05620	signal transducer activity
Afu2g05620	plasma membrane
Afu2g05620	pseudohyphal growth
Afu2g05620	invasive growth
Afu2g05620	cell-cell adhesion
Afu2g05620	filamentous growth
Afu2g05650	asparagine-tRNA ligase activity
Afu2g05650	ATP binding
Afu2g05650	cytoplasm
Afu2g05650	asparaginyl-tRNA aminoacylation
Afu2g05670	cytoplasm
Afu2g05730	plasma membrane
Afu2g05730	cellular iron ion homeostasis
Afu2g05730	siderophore-iron transmembrane transporter activity
Afu2g05730	siderophore-iron transport
Afu2g05730	integral to membrane
Afu2g05740	pheromone-dependent signal transduction involved in conjugation with cellular fusion
Afu2g05740	Rho small monomeric GTPase activity
Afu2g05740	signal transducer activity
Afu2g05740	soluble fraction
Afu2g05740	plasma membrane
Afu2g05740	exocytosis
Afu2g05740	Rho protein signal transduction
Afu2g05750	spermidine biosynthetic process
Afu2g05750	agmatinase activity
Afu2g05760	fatty-acid synthase activity
Afu2g05760	lipid biosynthetic process
Afu2g05770	SAGA complex
Afu2g05770	molecular function unknown
Afu2g05770	histone acetylation
Afu2g05780	mRNA guanylyltransferase activity
Afu2g05780	nucleus
Afu2g05780	mRNA capping
Afu2g05790	dolichyl-diphosphooligosaccharide-protein glycotransferase activity
Afu2g05790	endoplasmic reticulum lumen
Afu2g05790	protein amino acid N-linked glycosylation
Afu2g05790	oligosaccharyltransferase complex
Afu2g05790	protein amino acid N-linked glycosylation via asparagine
Afu2g05820	FMN adenylyltransferase activity
Afu2g05820	mitochondrial inner membrane

Afu2g05820	microsome
Afu2g05820	riboflavin kinase activity
Afu2g05820	FMN biosynthetic process
Afu2g05830	biological process unknown
Afu2g05830	DNA binding
Afu2g05830	nucleus
Afu2g05830	zinc ion binding
Afu2g05840	drug transporter activity
Afu2g05840	drug transport
Afu2g05840	integral to membrane
Afu2g05850	nuclear cohesin complex
Afu2g05850	molecular function unknown
Afu2g05850	mitotic sister chromatid cohesion
Afu2g05850	mitotic chromosome condensation
Afu2g05860	calcium-transporting ATPase activity
Afu2g05860	Golgi apparatus
Afu2g05860	calcium ion transport
Afu2g05860	manganese ion transport
Afu2g05860	manganese-transporting ATPase activity
Afu2g05880	plasma membrane
Afu2g05880	ammonium transmembrane transporter activity
Afu2g05880	ammonium transport
Afu2g05900	cytoplasm
Afu2g05900	chromatin silencing at telomere
Afu2g05900	NAD-dependent histone deacetylase activity
Afu2g05910	hexokinase activity
Afu2g05910	nucleus
Afu2g05910	cytosol
Afu2g05910	fructose metabolic process
Afu2g05930	nucleolus
Afu2g05930	maturation of SSU-rRNA
Afu2g05930	snoRNA binding
Afu2g05940	biological process unknown
Afu2g05940	fungal-type vacuole membrane
Afu2g05940	molecular function unknown
Afu2g05950	nuclear mRNA splicing, via spliceosome
Afu2g05950	nucleolus
Afu2g05950	small nucleolar ribonucleoprotein complex
Afu2g05950	pre-mRNA splicing factor activity
Afu2g05950	maturation of SSU-rRNA
Afu2g05950	small nuclear ribonucleoprotein complex
Afu2g05970	DNA binding
Afu2g05970	nucleus
Afu2g05970	chromatin remodeling
Afu2g05970	zinc ion binding
Afu2g05980	biological process unknown
Afu2g05980	molecular function unknown
Afu2g05980	cellular component unknown
Afu2g06000	glutamate dehydrogenase activity
Afu2g06000	soluble fraction

Afu2g06000	nitrogen compound metabolic process
Afu2g06040	actin filament severing activity
Afu2g06040	nucleus
Afu2g06040	cytoplasm
Afu2g06040	actin cortical patch (sensu Saccharomyces)
Afu2g06040	response to osmotic stress
Afu2g06040	actin filament depolymerization
Afu2g06070	nuclear mRNA splicing, via spliceosome
Afu2g06070	protein binding
Afu2g06070	pre-mRNA splicing factor activity
Afu2g06070	small nuclear ribonucleoprotein complex
Afu2g06090	nucleus
Afu2g06090	mRNA cleavage factor complex
Afu2g06090	mRNA polyadenylation
Afu2g06090	mRNA cleavage
Afu2g06090	cleavage and polyadenylylation specificity factor activity
Afu2g06100	biological process unknown
Afu2g06100	molecular function unknown
Afu2g06100	cytoplasm
Afu2g06110	histone acetyltransferase complex
Afu2g06110	nuclear chromatin
Afu2g06110	chromatin binding
Afu2g06110	histone acetyltransferase activity
Afu2g06110	nucleus
Afu2g06110	chromatin organization
Afu2g06110	regulation of transcription, DNA-dependent
Afu2g06110	regulation of transcription from RNA polymerase II promoter
Afu2g06110	histone acetylation
Afu2g06110	chromatin remodeling complex
Afu2g06130	transcription factor activity
Afu2g06130	nucleus
Afu2g06130	regulation of transcription
Afu2g06140	uracil DNA N-glycosylase activity
Afu2g06140	nucleus
Afu2g06140	mitochondrion
Afu2g06140	DNA repair
Afu2g06140	base-excision repair
Afu2g06150	protein disulfide isomerase activity
Afu2g06150	endoplasmic reticulum lumen
Afu2g06150	protein folding
Afu2g06170	molecular function unknown
Afu2g06170	protein targeting to vacuole
Afu2g06170	autophagy
Afu2g06170	cellular component unknown
Afu2g06180	mediator complex
Afu2g06180	transcription from RNA polymerase II promoter
Afu2g06180	RNA polymerase II transcription mediator activity
Afu2g06190	epsilon DNA polymerase activity
Afu2g06190	replication fork
Afu2g06190	leading strand elongation

Afu2g06190	lagging strand elongation
Afu2g06190	nucleotide-excision repair
Afu2g06190	mismatch repair
Afu2g06220	molecular function unknown
Afu2g06220	mRNA cleavage and polyadenylation specificity factor complex
Afu2g06220	mRNA polyadenylation
Afu2g06220	mRNA cleavage
Afu2g06230	histidine biosynthetic process
Afu2g06230	imidazoleglycerol-phosphate synthase activity
Afu2g06230	intracellular
Afu2g06230	purine nucleoside monophosphate biosynthetic process
Afu2g06240	dCMP deaminase activity
Afu2g06240	cytoplasm
Afu2g06240	pyrimidine nucleotide metabolic process
Afu2g06240	zinc ion binding
Afu2g06250	protein binding
Afu2g06250	cytoplasm
Afu2g06250	protein targeting to vacuole
Afu2g06250	autophagy
Afu2g06250	APG12 activating enzyme activity
Afu2g06280	dolichyl-diphosphooligosaccharide-protein glycotransferase activity
Afu2g06280	protein complex assembly
Afu2g06280	protein amino acid glycosylation
Afu2g06280	protein amino acid N-linked glycosylation
Afu2g06280	oligosaccharyltransferase complex
Afu2g06280	integral to membrane
Afu2g06290	endoplasmic reticulum membrane
Afu2g06290	protein amino acid N-linked glycosylation
Afu2g06290	oligosaccharide transmembrane transporter activity
Afu2g06290	oligosaccharide transport
Afu2g06300	endoplasmic reticulum membrane
Afu2g06300	protein amino acid N-linked glycosylation
Afu2g06300	oligosaccharide transmembrane transporter activity
Afu2g06300	oligosaccharide transport
Afu2g06310	ribosomal large subunit assembly
Afu2g06310	ATP-dependent RNA helicase activity
Afu2g06310	nucleolus
Afu2g06310	35S primary transcript processing
Afu2g06320	damaged DNA binding
Afu2g06320	single-stranded DNA binding
Afu2g06320	DNA replication factor A complex
Afu2g06320	DNA unwinding during replication
Afu2g06320	DNA replication, synthesis of RNA primer
Afu2g06320	DNA strand elongation during DNA replication
Afu2g06320	nucleotide-excision repair
Afu2g06320	postreplication repair
Afu2g06320	double-strand break repair
Afu2g06320	DNA recombination
Afu2g06330	ubiquitin-specific protease activity
Afu2g06330	cytoplasm

Afu2g06330	protein deubiquitination
Afu2g06330	negative regulation of gluconeogenesis
Afu2g07350	glutamate-5-semialdehyde dehydrogenase activity
Afu2g07350	nucleus
Afu2g07350	cytoplasm
Afu2g07350	proline biosynthetic process
Afu2g07380	structural constituent of ribosome
Afu2g07380	cytosolic large ribosomal subunit (sensu Eukaryota)
Afu2g07380	translation
Afu2g07400	transporter activity
Afu2g07400	mitochondrial inner membrane
Afu2g07400	transport
Afu2g07420	actin cable (sensu Saccharomyces)
Afu2g07420	actin cross-linking activity
Afu2g07420	actin cortical patch (sensu Saccharomyces)
Afu2g07420	endocytosis
Afu2g07420	response to osmotic stress
Afu2g07420	actin filament organization
Afu2g07420	bipolar cellular bud site selection
Afu2g07430	biological process unknown
Afu2g07430	phospholipase activity
Afu2g07430	mitochondrion
Afu2g07440	fatty acid metabolic process
Afu2g07440	CoA hydrolase activity
Afu2g07480	DNA binding
Afu2g07500	biological process unknown
Afu2g07500	cytoplasm
Afu2g07500	X-Pro aminopeptidase activity
Afu2g07520	aminopeptidase activity
Afu2g07520	epoxide hydrolase activity
Afu2g07520	leukotriene-A4 hydrolase activity
Afu2g07520	nucleus
Afu2g07520	cytoplasm
Afu2g07520	lipid metabolic process
Afu2g07520	protein catabolic process
Afu2g07540	molecular function unknown
Afu2g07540	nucleus
Afu2g07540	cytoplasm
Afu2g07540	signal transduction
Afu2g07550	protein kinase activity
Afu2g07550	kinetochore microtubule
Afu2g07550	spindle microtubule
Afu2g07550	chromosome segregation
Afu2g07570	glutamate 5-kinase activity
Afu2g07570	cytoplasm
Afu2g07570	proline biosynthetic process
Afu2g07590	cell wall biogenesis
Afu2g07600	signal recognition particle binding
Afu2g07600	integral to endoplasmic reticulum membrane
Afu2g07600	protein targeting to ER

Afu2g07610	metabolic process
Afu2g07610	oxidoreductase activity
Afu2g07620	cystathionine beta-synthase activity
Afu2g07620	cytoplasm
Afu2g07620	cysteine biosynthetic process
Afu2g07630	fungal-type vacuole
Afu2g07630	vacuolar membrane
Afu2g07630	calcium ion transport
Afu2g07630	cellular calcium ion homeostasis
Afu2g07630	calcium ion transmembrane transporter activity
Afu2g07630	calcium:hydrogen antiporter activity
Afu2g07660	cyclin-dependent protein kinase holoenzyme complex
Afu2g07660	regulation of glycogen biosynthetic process
Afu2g07660	regulation of glycogen catabolic process
Afu2g07660	cyclin-dependent protein kinase regulator activity
Afu2g07670	endocytosis
Afu2g07670	membrane
Afu2g07670	palmitoyltransferase activity
Afu2g07670	protein amino acid palmitoylation
Afu2g07680	pathogenesis
Afu2g07680	pathogenesis
Afu2g07690	protein tyrosine kinase activity
Afu2g07710	U2-dependent spliceosome disassembly
Afu2g07710	ATP-dependent RNA helicase activity
Afu2g07710	spliceosomal complex
Afu2g07710	pre-mRNA splicing factor activity
Afu2g07720	L-lactate dehydrogenase (cytochrome) activity
Afu2g07720	mitochondrial intermembrane space
Afu2g07720	electron transport
Afu2g07770	RAS small monomeric GTPase activity
Afu2g07770	plasma membrane
Afu2g07770	activation of adenylate cyclase activity
Afu2g07770	Ras protein signal transduction
Afu2g07780	acetate-CoA ligase activity
Afu2g07780	cytosol
Afu2g07780	acetyl-CoA biosynthetic process
Afu2g07780	acetate fermentation
Afu2g07810	glycine hydroxymethyltransferase activity
Afu2g07810	mitochondrion
Afu2g07810	one-carbon metabolic process
Afu2g07880	integral to membrane
Afu2g07900	specific RNA polymerase II transcription factor activity
Afu2g07900	nucleus
Afu2g07900	anatomical structure morphogenesis
Afu2g07910	myo-inositol transmembrane transporter activity
Afu2g07910	myo-inositol transport
Afu2g07910	membrane
Afu2g07920	metabolic process
Afu2g07920	oxidoreductase activity
Afu2g07940	electron transporter activity

Afu2g07940	microsome
Afu2g07940	ergosterol biosynthetic process
Afu2g07950	U2-dependent spliceosome disassembly
Afu2g07950	ATP-dependent RNA helicase activity
Afu2g07950	spliceosomal complex
Afu2g07950	pre-mRNA splicing factor activity
Afu2g07960	molecular function unknown
Afu2g07960	cytosol
Afu2g07960	cytosolic ribosome (sensu Eukaryota)
Afu2g07960	regulation of translational elongation
Afu2g07970	structural constituent of ribosome
Afu2g07970	cytosolic large ribosomal subunit (sensu Eukaryota)
Afu2g07970	translation
Afu2g08040	DNA binding
Afu2g08040	nucleus
Afu2g08040	zinc ion binding
Afu2g08050	metabolic process
Afu2g08050	cellular component unknown
Afu2g08050	oxidoreductase activity
Afu2g08070	magnesium ion transmembrane transporter activity
Afu2g08070	magnesium ion transport
Afu2g08070	membrane
Afu2g08080	vacuole inheritance
Afu2g08080	fungal-type vacuole
Afu2g08080	cytoplasm
Afu2g08080	phospholipid metabolic process
Afu2g08080	integral to membrane
Afu2g08080	enzyme regulator activity
Afu2g08110	biological process unknown
Afu2g08110	molecular function unknown
Afu2g08110	cytoplasm
Afu2g08120	fructose transmembrane transporter activity
Afu2g08120	glucose transmembrane transporter activity
Afu2g08120	plasma membrane
Afu2g08120	hexose transport
Afu2g08120	mannose transmembrane transporter activity
Afu2g08130	structural constituent of ribosome
Afu2g08130	cytosolic large ribosomal subunit (sensu Eukaryota)
Afu2g08130	translation
Afu2g08150	regulation of progression through cell cycle
Afu2g08150	protein binding
Afu2g08150	regulation of transcription from RNA polymerase II promoter
Afu2g08150	protein modification process
Afu2g08150	protein localization
Afu2g08150	protein tagging activity
Afu2g08150	SCF ubiquitin ligase complex
Afu2g08150	NEDD8 class-dependent protein catabolic process
Afu2g08150	protein neddylation during NEDD8 class-dependent protein catabolic process
Afu2g08150	regulation of developmental process
Afu2g08180	membrane

Afu2g08230	biological process unknown
Afu2g08230	molecular function unknown
Afu2g08230	cellular component unknown
Afu2g08240	transcription factor activity
Afu2g08240	nucleus
Afu2g08240	regulation of transcription, DNA-dependent
Afu2g08240	zinc ion binding
Afu2g08250	glycerol-3-phosphate dehydrogenase (NAD+) activity
Afu2g08250	cytosol
Afu2g08250	glycerol metabolic process
Afu2g08250	response to osmotic stress
Afu2g08260	metabolic process
Afu2g08260	oxidoreductase activity
Afu2g08260	coenzyme binding
Afu2g08280	mitochondrion
Afu2g08280	pyruvate metabolic process
Afu2g08280	cellular amino acid metabolic process
Afu2g08280	malate dehydrogenase (oxaloacetate-decarboxylating) activity
Afu2g08300	co-chaperone activity
Afu2g08300	endoplasmic reticulum lumen
Afu2g08300	protein folding
Afu2g08320	rRNA modification
Afu2g08320	small nucleolar ribonucleoprotein complex
Afu2g08320	35S primary transcript processing
Afu2g08320	ribosome biogenesis
Afu2g08320	maturation of SSU-rRNA
Afu2g08320	snoRNA binding
Afu2g08320	small nuclear ribonucleoprotein complex
Afu2g08350	plasma membrane
Afu2g08350	allantoate transmembrane transporter activity
Afu2g08350	allantoate transport
Afu2g08360	orotidine-5'-phosphate decarboxylase activity
Afu2g08360	cellular component unknown
Afu2g08360	pathogenesis
Afu2g08360	pyrimidine base biosynthetic process
Afu2g08380	diacylglycerol O-acyltransferase activity
Afu2g08380	response to external stimulus
Afu2g08380	membrane
Afu2g08380	triglyceride biosynthetic process
Afu2g08380	heme binding
Afu2g08390	mRNA cleavage and polyadenylation specificity factor complex
Afu2g08390	mRNA polyadenylation
Afu2g08390	mRNA cleavage
Afu2g08390	cleavage and polyadenylylation specificity factor activity
Afu2g08420	conjugation with cellular fusion
Afu2g08420	protein-S-isoprenylcysteine O-methyltransferase activity
Afu2g08420	endoplasmic reticulum membrane
Afu2g08420	peptide pheromone maturation
Afu2g08430	biological process unknown
Afu2g08430	cellular component unknown

Afu2g08430	acetyltransferase activity
Afu2g08440	ubiquitin-specific protease activity
Afu2g08440	cellular component unknown
Afu2g08440	protein deubiquitination
Afu2g08450	transcription factor TFIIE complex
Afu2g08450	transcription initiation from RNA polymerase II promoter
Afu2g08450	general RNA polymerase II transcription factor activity
Afu2g08460	pseudouridylate synthase activity
Afu2g08460	nucleus
Afu2g08460	tRNA modification
Afu2g08470	cellular bud site selection
Afu2g08470	GTP binding
Afu2g08470	axial cellular bud site selection
Afu2g08480	RNA helicase activity
Afu2g08480	mitochondrion
Afu2g08480	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process
Afu2g08480	ribosome biogenesis
Afu2g08480	ATP-dependent helicase activity
Afu2g08520	structural constituent of ribosome
Afu2g08520	mitochondrial large ribosomal subunit
Afu2g08520	translation
Afu2g08550	peptidyl-prolyl cis-trans isomerase activity
Afu2g08550	nucleus
Afu2g08550	mRNA processing
Afu2g08550	negative regulation of phosphorylation
Afu2g08570	commitment complex
Afu2g08570	nuclear mRNA splicing, via spliceosome
Afu2g08570	nuclear cap binding complex
Afu2g08570	pre-mRNA splicing factor activity
Afu2g08580	imidazoleglycerol-phosphate synthase activity
Afu2g08580	protein binding
Afu2g08580	cytoplasm
Afu2g08580	pyridoxine metabolic process
Afu2g08580	thiamin biosynthetic process
Afu2g08590	secondary metabolic process
Afu2g08600	1-acylglycerol-3-phosphate O-acyltransferase activity
Afu2g08600	lipid particle
Afu2g08600	sphingolipid biosynthetic process
Afu2g08620	mitotic spindle elongation
Afu2g08620	mitotic sister chromatid segregation
Afu2g08620	regulation of progression through cell cycle
Afu2g08620	ubiquitin-protein ligase activity
Afu2g08620	protein binding
Afu2g08620	anaphase-promoting complex
Afu2g08620	spindle pole body
Afu2g08620	ubiquitin-dependent protein catabolic process
Afu2g08620	mitotic metaphase/anaphase transition
Afu2g08620	regulation of exit from mitosis
Afu2g08620	cyclin catabolic process
Afu2g08650	ubiquitin-protein ligase activity

Afu2g08650	nuclear envelope
Afu2g08650	mRNA polyadenylation
Afu2g08670	biological process unknown
Afu2g08670	acetyl-CoA carboxylase activity
Afu2g08670	mitochondrion
Afu2g08700	metabolic process
Afu2g08700	hydrolase activity
Afu2g08720	molecular function unknown
Afu2g08720	ER to Golgi vesicle-mediated transport
Afu2g08720	TRAPP complex
Afu2g08740	zinc ion transmembrane transporter activity
Afu2g08740	vacuolar membrane
Afu2g08740	zinc ion transport
Afu2g08740	cellular zinc ion homeostasis
Afu2g08750	endodeoxyribonuclease activity
Afu2g08750	exodeoxyribonuclease activity
Afu2g08750	ribonuclease activity
Afu2g08750	mitochondrial inner membrane
Afu2g08750	DNA catabolic process
Afu2g08750	DNA recombination
Afu2g08750	RNA catabolic process
Afu2g08780	ARF guanyl-nucleotide exchange factor activity
Afu2g08780	cellular component unknown
Afu2g08780	secretory pathway
Afu2g08790	fungal-type vacuole
Afu2g08790	molecular function unknown
Afu2g08790	cell wall organization
Afu2g08800	plasma membrane
Afu2g08800	amino acid transport
Afu2g08800	amino acid transmembrane transporter activity
Afu2g08800	amino acid permease activity
Afu2g08830	nickel ion transmembrane transporter activity
Afu2g08830	nickel ion transport
Afu2g08840	nucleotidyltransferase activity
Afu2g08850	Golgi membrane
Afu2g08850	phospholipid-translocating ATPase activity
Afu2g08850	intracellular protein transport
Afu2g08850	post-Golgi vesicle-mediated transport
Afu2g08850	trans-Golgi network transport vesicle
Afu2g08860	3'-5'-exoribonuclease activity
Afu2g08860	nuclear exosome (RNase complex)
Afu2g08860	cytoplasmic exosome (RNase complex)
Afu2g08860	35S primary transcript processing
Afu2g08860	mRNA catabolic process
Afu2g08890	dihydrofolate reductase activity
Afu2g08890	cytosol
Afu2g08890	folic acid and derivative metabolic process
Afu2g08900	voltage-gated chloride channel activity
Afu2g08900	transport
Afu2g08900	cellular cation homeostasis

Afu2g08910	transporter activity
Afu2g08910	transport
Afu2g08910	cellular component unknown
Afu2g08920	acetate metabolic process
Afu2g08920	cellular component unknown
Afu2g08920	hydrolase activity, acting on ester bonds
Afu2g08970	hydroxyethylthiazole kinase activity
Afu2g08970	thiamin-phosphate diphosphorylase activity
Afu2g08970	cytoplasm
Afu2g08970	thiamin biosynthetic process
Afu2g08990	translation initiation factor activity
Afu2g08990	GTPase activator activity
Afu2g08990	cytosolic small ribosomal subunit (sensu Eukaryota)
Afu2g08990	regulation of translational initiation
Afu2g08990	mature ribosome assembly
Afu2g09000	biological process unknown
Afu2g09000	molecular function unknown
Afu2g09000	cytoplasm
Afu2g09010	DNA ligase (ATP) activity
Afu2g09010	replication fork
Afu2g09010	DNA ligation
Afu2g09010	lagging strand elongation
Afu2g09010	base-excision repair
Afu2g09010	nucleotide-excision repair
Afu2g09010	DNA recombination
Afu2g09030	proteolysis
Afu2g09030	serine-type peptidase activity
Afu2g09040	molecular function unknown
Afu2g09040	vacuolar membrane
Afu2g09040	vacuole fusion, non-autophagic
Afu2g09060	chromatin binding
Afu2g09060	ATP-dependent DNA helicase activity
Afu2g09060	nucleus
Afu2g09060	pre-replicative complex
Afu2g09060	cytoplasm
Afu2g09060	pre-replicative complex assembly
Afu2g09060	DNA unwinding during replication
Afu2g09060	DNA replication initiation
Afu2g09070	biological process unknown
Afu2g09070	molecular function unknown
Afu2g09070	cellular component unknown
Afu2g09080	nucleus
Afu2g09080	cytoplasm
Afu2g09080	protein-arginine N-methyltransferase activity
Afu2g09080	peptidyl-arginine methylation
Afu2g09090	replicative cell aging
Afu2g09090	molecular function unknown
Afu2g09090	mitochondrion
Afu2g09090	mitochondrial inner membrane
Afu2g09090	proteolysis

Afu2g09100	mRNA cleavage factor complex
Afu2g09100	mRNA polyadenylation
Afu2g09100	mRNA cleavage
Afu2g09100	cleavage and polyadenylylation specificity factor activity
Afu2g09120	nucleus
Afu2g09120	chromatin assembly or disassembly
Afu2g09120	DNA-dependent ATPase activity
Afu2g09150	adenine deaminase activity
Afu2g09150	nucleus
Afu2g09150	cytoplasm
Afu2g09150	adenine catabolic process
Afu2g09160	molecular function unknown
Afu2g09160	cytoplasm
Afu2g09160	cell growth and/or maintenance
Afu2g09170	biological process unknown
Afu2g09170	molecular function unknown
Afu2g09170	cytoplasm
Afu2g09180	protein binding
Afu2g09180	retrograde vesicle-mediated transport, Golgi to ER
Afu2g09180	COPI vesicle coat
Afu2g09200	structural constituent of ribosome
Afu2g09200	cytoplasm
Afu2g09200	cytosolic large ribosomal subunit (sensu Eukaryota)
Afu2g09200	rRNA processing
Afu2g09200	translation
Afu2g09200	negative regulation of translation
Afu2g09200	negative regulation of nuclear mRNA splicing, via spliceosome
Afu2g09210	ribosomal large subunit assembly
Afu2g09210	structural constituent of ribosome
Afu2g09210	cytosolic large ribosomal subunit (sensu Eukaryota)
Afu2g09210	translation
Afu2g09230	U2-dependent spliceosome disassembly
Afu2g09230	ATP-dependent RNA helicase activity
Afu2g09230	spliceosomal complex
Afu2g09230	pre-mRNA splicing factor activity
Afu2g09240	nuclear ubiquitin ligase complex
Afu2g09240	ubiquitin-protein ligase activity
Afu2g09240	ubiquitin-dependent protein catabolic process
Afu2g09250	transporter activity
Afu2g09250	mitochondrion
Afu2g09250	mitochondrial inner membrane
Afu2g09250	transport
Afu2g09250	manganese ion transport
Afu2g09250	metallochaperone activity
Afu2g09290	heat shock protein activity
Afu2g09290	mitochondrion
Afu2g09290	protein folding
Afu2g09290	mitochondrial translocation
Afu2g09320	acetyl-CoA:L-glutamate N-acetyltransferase activity
Afu2g09320	cytoplasm

Afu2g09320	N-terminal protein amino acid acetylation
Afu2g09320	virus-host interaction
Afu2g09350	1,6-beta-glucan metabolic process
Afu2g09350	fungal-type cell wall
Afu2g09350	glucan endo-1,6-beta-glucosidase activity
Afu2g09355	metabolic process
Afu2g09355	hydrolase activity
Afu2g09450	plasma membrane
Afu2g09450	lactate transmembrane transporter activity
Afu2g09450	lactate transport
Afu2g09470	molecular function unknown
Afu2g09470	membrane
Afu2g09470	membrane organization
Afu2g09490	translation initiation factor activity
Afu2g09490	ribosome
Afu2g09490	translational initiation
Afu2g09520	polysaccharide catabolic process
Afu2g09520	hydrolase activity, hydrolyzing O-glycosyl compounds
Afu2g09550	biotin-[acetyl-CoA-carboxylase] ligase activity
Afu2g09550	biotin-[methylcrotonoyl-CoA-carboxylase] ligase activity
Afu2g09550	biotin-[methylmalonyl-CoA-carboxytransferase] ligase activity
Afu2g09550	biotin-[propionyl-CoA-carboxylase (ATP-hydrolyzing)] ligase activity
Afu2g09550	intracellular
Afu2g09550	cytoplasm
Afu2g09550	protein modification process
Afu2g09560	mitochondrial genome maintenance
Afu2g09560	mitochondrial chromosome
Afu2g09560	DNA binding
Afu2g09560	DNA repair
Afu2g09580	UDP-N-acetylmuramate dehydrogenase activity
Afu2g09580	peptidoglycan biosynthetic process
Afu2g09640	zinc ion binding
Afu2g09650	L-aspartate:2-oxoglutarate aminotransferase activity
Afu2g09650	cytoplasm
Afu2g09650	peroxisome
Afu2g09650	aspartate biosynthetic process
Afu2g09650	aspartate catabolic process
Afu2g09650	glutamate metabolic process
Afu2g09650	nitrogen compound metabolic process
Afu2g09650	asparagine biosynthetic process from oxaloacetate
Afu2g09680	protein binding
Afu2g09700	cytosol
Afu2g09700	superoxide metabolic process
Afu2g09700	intracellular copper ion transport
Afu2g09700	superoxide dismutase copper chaperone activity
Afu2g09700	removal of superoxide radicals
Afu2g09710	regulation of progression through cell cycle
Afu2g09710	G1/S transition of mitotic cell cycle
Afu2g09710	S phase of mitotic cell cycle
Afu2g09710	G2/M transition of mitotic cell cycle

Afu2g09710	protein kinase activity
Afu2g09710	cyclin-dependent protein kinase activity
Afu2g09710	nucleus
Afu2g09710	cytoplasm
Afu2g09710	protein amino acid phosphorylation
Afu2g09710	regulation of meiosis
Afu2g09790	glucose-6-phosphate isomerase activity
Afu2g09790	cytosol
Afu2g09790	gluconeogenesis
Afu2g09790	glycolysis
Afu2g09790	pentose-phosphate shunt
Afu2g09820	biological process unknown
Afu2g09820	molecular function unknown
Afu2g09820	mitochondrion
Afu2g09830	ER-Golgi intermediate compartment
Afu2g09830	ER to Golgi vesicle-mediated transport
Afu2g09830	retrograde vesicle-mediated transport, Golgi to ER
Afu2g09830	ARF GTPase activator activity
Afu2g09840	2-amino-4-hydroxy-6-hydroxymethyldihydropteridine diphosphokinase activity
Afu2g09840	dihydroneopterin aldolase activity
Afu2g09840	dihydropteroate synthase activity
Afu2g09840	cytoplasm
Afu2g09840	folic acid and derivative biosynthetic process
Afu2g09850	metabolic process
Afu2g09850	oxidoreductase activity
Afu2g09860	plasma membrane
Afu2g09860	purine transport
Afu2g09860	cytosine-purine permease activity
Afu2g09860	cytosine transport
Afu2g09870	translation initiation factor activity
Afu2g09870	eukaryotic translation initiation factor 3 complex
Afu2g09870	translational initiation
Afu2g09910	long-chain-fatty-acid-CoA ligase activity
Afu2g09910	lipid particle
Afu2g09910	N-terminal protein myristoylation
Afu2g09910	lipid metabolic process
Afu2g09910	lipid transport
Afu2g09960	heat shock protein activity
Afu2g09960	mitochondrion
Afu2g09960	mitochondrial inner membrane
Afu2g09960	protein folding
Afu2g09960	mitochondrial translocation
Afu2g09960	protein transporter activity
Afu2g09960	ATPase activity
Afu2g09960	enzyme regulator activity
Afu2g10000	RNA helicase activity
Afu2g10000	cytoplasm
Afu2g10000	mRNA catabolic process
Afu2g10000	regulation of translation
Afu2g10000	translation repressor activity

Afu2g10010	nucleus
Afu2g10010	cytoplasm
Afu2g10010	protein import into nucleus
Afu2g10010	protein transmembrane transporter activity
Afu2g10070	carbamoyl-phosphate synthase (glutamine-hydrolyzing) activity
Afu2g10070	cytosol
Afu2g10070	arginine biosynthetic process
Afu2g10080	nucleus
Afu2g10080	regulation of transcription, DNA-dependent
Afu2g10080	zinc ion binding
Afu2g10080	chromatin modification
Afu2g10090	structural constituent of ribosome
Afu2g10090	cytosolic small ribosomal subunit (sensu Eukaryota)
Afu2g10090	translation
Afu2g10100	structural constituent of ribosome
Afu2g10100	cytosolic large ribosomal subunit (sensu Eukaryota)
Afu2g10100	translation
Afu2g10100	translational elongation
Afu2g10120	biological process unknown
Afu2g10120	molecular function unknown
Afu2g10120	cytoplasm
Afu2g10140	chromatin binding
Afu2g10140	ATP-dependent DNA helicase activity
Afu2g10140	ATP binding
Afu2g10140	nucleus
Afu2g10140	pre-replicative complex
Afu2g10140	cytoplasm
Afu2g10140	pre-replicative complex assembly
Afu2g10140	DNA unwinding during replication
Afu2g10140	DNA replication initiation
Afu2g10150	peroxisome
Afu2g10150	peroxisome organization
Afu2g10150	ATPase activity
Afu2g10160	cytoplasm
Afu2g10160	AMP binding
Afu2g10160	CoA-ligase activity
Afu2g10160	secondary metabolic process
Afu2g10220	nucleus
Afu2g10220	cytoplasm
Afu2g10220	glycerol metabolic process
Afu2g10220	response to salt stress
Afu2g10220	glycerol dehydrogenase (NADP+) activity
Afu2g10240	metabolic process
Afu2g10240	oxidoreductase activity
Afu2g10270	regulation of progression through cell cycle
Afu2g10270	G1 phase of mitotic cell cycle
Afu2g10270	protein binding
Afu2g10270	vacuolar membrane
Afu2g10270	plasma membrane
Afu2g10270	cytoskeleton organization

Afu2g10270	ribosome biogenesis
Afu2g10270	signal transduction
Afu2g10270	Rho protein signal transduction
Afu2g10270	1-phosphatidylinositol-3-kinase activity
Afu2g10270	actin filament reorganization during cell cycle
Afu2g10280	biological process unknown
Afu2g10280	molecular function unknown
Afu2g10280	nucleus
Afu2g10280	cytoplasm
Afu2g10280	dihydrokaempferol 4-reductase activity
Afu2g10300	ribosomal small subunit assembly
Afu2g10300	structural constituent of ribosome
Afu2g10300	cytosolic small ribosomal subunit (sensu Eukaryota)
Afu2g10300	translation
Afu2g10320	actin cortical patch (sensu Saccharomyces)
Afu2g10320	myosin I binding
Afu2g10320	actin cytoskeleton organization
Afu2g10340	molecular function unknown
Afu2g10340	vesicle-mediated transport
Afu2g10340	AP-2 adaptor complex
Afu2g10350	biological process unknown
Afu2g10350	molecular function unknown
Afu2g10350	endoplasmic reticulum
Afu2g10360	nucleus
Afu2g10360	cytoplasm
Afu2g10360	NAD biosynthetic process
Afu2g10360	kynureninase activity
Afu2g10370	molecular function unknown
Afu2g10370	mitochondrial intermembrane space
Afu2g10370	iron ion transport
Afu2g10380	translation initiation factor activity
Afu2g10380	eukaryotic translation initiation factor 3 complex
Afu2g10380	translational initiation
Afu2g10400	transcription factor activity
Afu2g10400	nucleus
Afu2g10400	regulation of transcription
Afu2g10420	branched-chain-amino-acid transaminase activity
Afu2g10420	nucleus
Afu2g10420	cytoplasm
Afu2g10420	cellular amino acid catabolic process
Afu2g10420	branched chain family amino acid biosynthetic process
Afu2g10440	ribosomal small subunit assembly
Afu2g10440	RNA binding
Afu2g10440	structural constituent of ribosome
Afu2g10440	cytosolic small ribosomal subunit (sensu Eukaryota)
Afu2g10440	translation
Afu2g10450	cytoplasm
Afu2g10450	tyrosine metabolic process
Afu2g10450	prephenate dehydrogenase activity
Afu2g10460	protein binding

Afu2g10460	cellular component unknown
Afu2g10460	sphingolipid biosynthetic process
Afu2g10480	cytoplasm
Afu2g10500	structural constituent of ribosome
Afu2g10500	cytosolic small ribosomal subunit (sensu Eukaryota)
Afu2g10500	translation
Afu2g10520	urate oxidase activity
Afu2g10520	purine base metabolic process
Afu2g10530	transporter activity
Afu2g10530	transport
Afu2g10550	transcription factor activity
Afu2g10550	nucleus
Afu2g10550	regulation of transcription, DNA-dependent
Afu2g10550	zinc ion binding
Afu2g10560	gamma-aminobutyric acid transporter activity
Afu2g10560	transport
Afu2g10560	membrane
Afu2g10590	protein disulfide isomerase activity
Afu2g10590	endoplasmic reticulum membrane
Afu2g10590	protein retention in ER lumen
Afu2g10610	molecular function unknown
Afu2g10610	ER to Golgi vesicle-mediated transport
Afu2g10610	retrograde vesicle-mediated transport, Golgi to ER
Afu2g10610	COPI vesicle coat
Afu2g10620	protein serine/threonine kinase activity
Afu2g10620	cytosol
Afu2g10620	plasma membrane
Afu2g10620	protein amino acid phosphorylation
Afu2g10640	SAGA complex
Afu2g10640	transcription coactivator activity
Afu2g10640	chromatin modification
Afu2g10640	histone acetylation
Afu2g10690	inorganic phosphate transmembrane transporter activity
Afu2g10690	integral to plasma membrane
Afu2g10690	phosphate transport
Afu2g10700	microtubule-based process
Afu2g10730	DNA synthesis during DNA repair
Afu2g10730	alpha DNA polymerase activity
Afu2g10730	alpha DNA polymerase:primase complex
Afu2g10730	DNA replication, synthesis of RNA primer
Afu2g10730	DNA replication initiation
Afu2g10730	lagging strand elongation
Afu2g10740	cellular component unknown
Afu2g10740	phosphomethylpyrimidine kinase activity
Afu2g10740	thiamin biosynthetic process
Afu2g10750	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
Afu2g10750	RNA helicase activity
Afu2g10750	nucleus
Afu2g10750	cytoplasm
Afu2g10770	transcription factor activity

Afu2g10770	nucleus
Afu2g10770	regulation of transcription, DNA-dependent
Afu2g10770	zinc ion binding
Afu2g10810	structural molecule activity
Afu2g10810	nuclear pore
Afu2g10810	mRNA export from nucleus
Afu2g10810	rRNA export from nucleus
Afu2g10810	snRNA export from nucleus
Afu2g10810	tRNA export from nucleus
Afu2g10810	NLS-bearing substrate import into nucleus
Afu2g10810	snRNP protein import into nucleus
Afu2g10810	mRNA-binding (hnRNP) protein import into nucleus
Afu2g10810	ribosomal protein import into nucleus
Afu2g10810	protein export from nucleus
Afu2g10810	nuclear pore organization
Afu2g10820	biological process unknown
Afu2g10820	helicase activity
Afu2g10820	nucleus
Afu2g10840	biological process unknown
Afu2g10840	molecular function unknown
Afu2g10840	integral to membrane
Afu2g10850	zinc ion binding
Afu2g10900	vacuolar lumen
Afu2g10900	vacuolar protein processing
Afu2g10900	autophagy
Afu2g10900	integral to membrane
Afu2g10900	lipase activity
Afu2g10900	membrane disassembly
Afu2g10910	alpha-glucoside transport
Afu2g10910	alpha-glucoside:hydrogen symporter activity
Afu2g10910	maltose:hydrogen symporter activity
Afu2g10910	membrane fraction
Afu2g10910	trehalose transmembrane transporter activity
Afu2g10910	trehalose transport
Afu2g10920	3-hydroxyisobutyryl-CoA hydrolase activity
Afu2g10920	mitochondrion
Afu2g10920	fatty acid beta-oxidation
Afu2g10920	endocytosis
Afu2g10930	molecular function unknown
Afu2g10930	ER to Golgi vesicle-mediated transport
Afu2g10930	COPII-coated vesicle
Afu2g10960	alcohol dehydrogenase (NAD) activity
Afu2g10960	cytoplasm
Afu2g10960	alcohol metabolic process
Afu2g10960	zinc ion binding
Afu2g10980	small monomeric GTPase activity
Afu2g10980	soluble fraction
Afu2g10980	protein targeting to vacuole
Afu2g10980	vesicle-mediated transport
Afu2g10990	chromatin remodeling complex

Afu2g11010	dihydroorotate oxidase activity
Afu2g11010	pyrimidine ribonucleotide biosynthetic process
Afu2g11020	triose-phosphate isomerase activity
Afu2g11020	cytoplasm
Afu2g11020	cytosol
Afu2g11020	gluconeogenesis
Afu2g11020	glycolysis
Afu2g11080	dolichyl-phosphate-glucose-glycolipid alpha-glucosyltransferase activity
Afu2g11080	endoplasmic reticulum membrane
Afu2g11080	protein amino acid N-linked glycosylation
Afu2g11080	dolichol-linked oligosaccharide biosynthetic process
Afu2g11090	GINS complex
Afu2g11090	DNA binding
Afu2g11090	DNA-dependent DNA replication
Afu2g11100	receptor activity
Afu2g11100	cellular component movement
Afu2g11100	signal transduction
Afu2g11100	integral to membrane
Afu2g11100	ubiquitin binding
Afu2g11110	mitotic sister chromatid segregation
Afu2g11110	DNA secondary structure binding
Afu2g11110	nuclear condensin complex
Afu2g11110	AT DNA binding
Afu2g11110	double-stranded DNA binding
Afu2g11110	mitotic chromosome condensation
Afu2g11110	ATPase activity
Afu2g11130	regulation of progression through cell cycle
Afu2g11130	negative regulation of transcription from RNA polymerase II promoter
Afu2g11130	3'-5'-exoribonuclease activity
Afu2g11130	nuclear-transcribed mRNA catabolic process, deadenylation-dependent decay
Afu2g11130	nuclear-transcribed mRNA poly(A) tail shortening
Afu2g11130	response to pheromone during conjugation with cellular fusion
Afu2g11130	nucleus
Afu2g11130	cytoplasm
Afu2g11130	regulation of transcription from RNA polymerase II promoter
Afu2g11130	CCR4-NOT core complex
Afu2g11150	Rab GDP-dissociation inhibitor activity
Afu2g11150	membrane fraction
Afu2g11150	soluble fraction
Afu2g11150	vesicle-mediated transport
Afu2g11170	DNA replication origin binding
Afu2g11170	nuclear origin of replication recognition complex
Afu2g11170	pre-replicative complex assembly
Afu2g11170	DNA replication initiation
Afu2g11180	response to pheromone during conjugation with cellular fusion
Afu2g11180	pheromone-dependent signal transduction involved in conjugation with cellular fusion
Afu2g11180	response to stress
Afu2g11180	regulation of sporulation resulting in formation of a cellular spore
Afu2g11190	RNA elongation from RNA polymerase II promoter
Afu2g11190	transcription elongation factor complex

Afu2g11190	RNA polymerase II transcription elongation factor activity
Afu2g11210	histone deacetylase complex
Afu2g11210	zinc ion binding
Afu2g11210	histone deacetylation
Afu2g11210	NAD-dependent histone deacetylase activity
Afu2g11210	NAD-independent histone deacetylase activity
Afu2g11210	negative regulation of meiosis
Afu2g11220	plasma membrane
Afu2g11220	neutral amino acid transmembrane transporter activity
Afu2g11220	amino acid permease activity
Afu2g11220	neutral amino acid transport
Afu2g11230	structural molecule activity
Afu2g11230	nuclear pore
Afu2g11230	mRNA export from nucleus
Afu2g11230	rRNA export from nucleus
Afu2g11230	snRNA export from nucleus
Afu2g11230	tRNA export from nucleus
Afu2g11230	NLS-bearing substrate import into nucleus
Afu2g11230	snRNP protein import into nucleus
Afu2g11230	mRNA-binding (hnRNP) protein import into nucleus
Afu2g11230	ribosomal protein import into nucleus
Afu2g11230	protein export from nucleus
Afu2g11230	nuclear pore organization
Afu2g11240	UDP-N-acetylglucosamine-dolichyl-phosphate N-acetylglucosaminephosphotransferase acti
Afu2g11240	endoplasmic reticulum
Afu2g11240	protein amino acid N-linked glycosylation
Afu2g11250	cellular aldehyde metabolic process
Afu2g11250	cellular component unknown
Afu2g11250	aryl-alcohol dehydrogenase activity
Afu2g11260	3-isopropylmalate dehydratase activity
Afu2g11260	cytosol
Afu2g11260	leucine biosynthetic process
Afu2g11260	3-isopropylmalate dehydratase complex
Afu2g11270	cell morphogenesis
Afu2g11270	plasma membrane
Afu2g11270	cellular glucan metabolic process
Afu2g11270	fungal-type cell wall biogenesis
Afu2g11270	alpha-1,3-glucan synthase activity
Afu2g11290	orotate phosphoribosyltransferase activity
Afu2g11290	nucleus
Afu2g11290	cytoplasm
Afu2g11290	pyrimidine base biosynthetic process
Afu2g11300	sulfur amino acid biosynthetic process
Afu2g11300	structural constituent of ribosome
Afu2g11300	methylenetetrahydrofolate reductase (NADPH) activity
Afu2g11300	cell
Afu2g11300	mitochondrial large ribosomal subunit
Afu2g11300	translation
Afu2g11300	methionine metabolic process
Afu2g11310	nucleotide binding

Afu2g11330	ATP biosynthetic process
Afu2g11330	hydrogen-exporting ATPase activity, phosphorylative mechanism
Afu2g11330	vacuolar proton-transporting V-type ATPase complex
Afu2g11340	biological process unknown
Afu2g11340	fungal-type vacuole
Afu2g11340	molecular function unknown
Afu2g11350	acetyl-CoA C-acyltransferase activity
Afu2g11350	fatty acid metabolic process
Afu2g11360	very-long-chain fatty acid metabolic process
Afu2g11360	long-chain-fatty-acid-CoA ligase activity
Afu2g11360	long-chain fatty acid transporter activity
Afu2g11360	peroxisome
Afu2g11360	microsome
Afu2g11360	lipid particle
Afu2g11360	plasma membrane
Afu2g11360	lipid transport
Afu2g11370	molecular function unknown
Afu2g11370	protein targeting to vacuole
Afu2g11370	autophagy
Afu2g11370	cellular component unknown
Afu2g11380	molecular function unknown
Afu2g11380	nucleolus
Afu2g11380	rRNA processing
Afu2g11380	ribosome biogenesis
Afu2g11420	drug transporter activity
Afu2g11420	drug transport
Afu2g11420	integral to membrane
Afu2g11430	gamma-tubulin complex
Afu2g11430	structural constituent of cytoskeleton
Afu2g11430	inner plaque of spindle pole body
Afu2g11430	outer plaque of spindle pole body
Afu2g11430	microtubule nucleation
Afu2g11440	endopeptidase activity
Afu2g11440	proteasome core complex
Afu2g11440	ubiquitin-dependent protein catabolic process
Afu2g11440	response to stress
Afu2g11440	sporulation (sensu Saccharomyces)
Afu2g11440	proteasome core complex, alpha-subunit complex
Afu2g11450	nucleolus
Afu2g11450	rRNA processing
Afu2g11450	methyltransferase activity
Afu2g11460	DNA binding
Afu2g11460	zinc ion binding
Afu2g11470	biological process unknown
Afu2g11470	molecular function unknown
Afu2g11490	acetyl-CoA:L-glutamate N-acetyltransferase activity
Afu2g11490	mitochondrial matrix
Afu2g11490	arginine biosynthetic process
Afu2g11490	ornithine biosynthetic process
Afu2g11500	biological process unknown

Afu2g11500	molecular function unknown
Afu2g11500	cytoplasm
Afu2g11520	fructose transmembrane transporter activity
Afu2g11520	glucose transmembrane transporter activity
Afu2g11520	plasma membrane
Afu2g11520	hexose transport
Afu2g11520	mannose transmembrane transporter activity
Afu2g11540	endoplasmic reticulum
Afu2g11540	integral to membrane
Afu2g11540	fatty acid elongation
Afu2g11540	ketoreductase activity
Afu2g11550	molecular function unknown
Afu2g11550	endoplasmic reticulum membrane
Afu2g11550	ergosterol biosynthetic process
Afu2g11560	UTP:hexose-1-phosphate uridylyltransferase activity
Afu2g11560	cytoplasm
Afu2g11560	galactose metabolic process
Afu2g11580	drug transporter activity
Afu2g11580	drug transport
Afu2g11580	integral to membrane
Afu2g11600	NAD or NADH binding
Afu2g11610	cellular component unknown
Afu2g11620	biological process unknown
Afu2g11620	molecular function unknown
Afu2g11620	cellular component unknown
Afu2g11660	repairosome
Afu2g11660	nucleotide-excision repair factor 2 complex
Afu2g11660	nucleotide-excision repair, DNA damage recognition
Afu2g11660	damaged DNA binding
Afu2g11680	biological process unknown
Afu2g11680	molecular function unknown
Afu2g11680	nucleus
Afu2g11680	cytoplasm
Afu2g11720	biological process unknown
Afu2g11720	molecular function unknown
Afu2g11720	cytoplasm
Afu2g11730	protein kinase activity
Afu2g11740	ATP-dependent peptidase activity
Afu2g11740	mitochondrial matrix
Afu2g11740	proteolysis
Afu2g11740	response to heat
Afu2g11750	co-chaperone activity
Afu2g11750	mitochondrial inner membrane
Afu2g11750	protein folding
Afu2g11750	proteolysis
Afu2g11760	intracellular transporter activity
Afu2g11760	cytoplasm
Afu2g11760	endosome
Afu2g11760	ubiquitin-dependent protein catabolic process
Afu2g11760	vacuolar transport

Afu2g11760	signal transduction
Afu2g11780	specific RNA polymerase II transcription factor activity
Afu2g11780	nucleus
Afu2g11780	cytoplasm
Afu2g11780	glucose metabolic process
Afu2g11780	regulation of transcription from RNA polymerase II promoter
Afu2g11780	zinc ion binding
Afu2g11800	nuclear-transcribed mRNA catabolic process, deadenylation-dependent decay
Afu2g11800	deadenylation-dependent decapping of nuclear-transcribed mRNA
Afu2g11800	RNA cap binding
Afu2g11800	cytoplasmic mRNA processing body
Afu2g11800	mRNA cap binding complex
Afu2g11800	rRNA processing
Afu2g11810	molecular function unknown
Afu2g11810	ribosome
Afu2g11810	ribosome biogenesis
Afu2g11810	maturation of SSU-rRNA
Afu2g11840	transcription coactivator activity
Afu2g11840	transcription coactivator activity
Afu2g11840	protein binding
Afu2g11840	nucleus
Afu2g11840	regulation of transcription, mating-type specific
Afu2g11840	negative regulation of transcription
Afu2g11840	general transcriptional repressor activity
Afu2g11840	negative regulation of transcription by glucose
Afu2g11850	ribosomal large subunit assembly
Afu2g11850	structural constituent of ribosome
Afu2g11850	cytosolic large ribosomal subunit (sensu Eukaryota)
Afu2g11850	translation
Afu2g11870	Golgi cis cisterna
Afu2g11870	1,6-beta-glucan biosynthetic process
Afu2g11870	cell wall organization
Afu2g11870	glucosidase activity
Afu2g11870	integral to membrane
Afu2g11900	biological process unknown
Afu2g11900	mitochondrion
Afu2g11900	kinase activity
Afu2g11940	N6-(1,2-dicarboxyethyl)AMP AMP-lyase (fumarate-forming) activity
Afu2g11940	purine base metabolic process
Afu2g11940	purine nucleotide biosynthetic process
Afu2g11970	lysophospholipase activity
Afu2g11970	glycerophospholipid metabolic process
Afu2g11970	fungal-type cell wall
Afu2g11990	inositol or phosphatidylinositol phosphatase activity
Afu2g11990	cellular component unknown
Afu2g12030	H3/H4 histone acetyltransferase activity
Afu2g12030	nucleus
Afu2g12030	cytoplasm
Afu2g12030	chromatin silencing at telomere
Afu2g12030	histone acetylation

Afu2g12050	Golgi membrane
Afu2g12050	manganese ion transmembrane transporter activity
Afu2g12050	cellular manganese ion homeostasis
Afu2g12060	nuclear ubiquitin ligase complex
Afu2g12060	protein binding
Afu2g12060	ubiquitin-dependent protein catabolic process
Afu2g12060	cell cycle
Afu2g12060	protein ubiquitination
Afu2g12060	SCF ubiquitin ligase complex
Afu2g12080	biological process unknown
Afu2g12080	fungal-type vacuole
Afu2g12080	inorganic phosphate transmembrane transporter activity
Afu2g12080	mitochondrion
Afu2g12110	biological process unknown
Afu2g12110	molecular function unknown
Afu2g12110	cytoplasm
Afu2g12140	voltage-gated chloride channel activity
Afu2g12140	Golgi-associated vesicle
Afu2g12140	cellular cation homeostasis
Afu2g12150	ribosomal large subunit assembly
Afu2g12150	nucleus
Afu2g12150	rRNA processing
Afu2g12190	mitochondrial intermembrane space
Afu2g12190	mitochondrial translocation
Afu2g12190	protein transporter activity
Afu2g12190	mitochondrial intermembrane space protein transporter complex
Afu2g12200	cAMP-dependent protein kinase activity
Afu2g12200	signal transduction
Afu2g12200	pathogenesis
Afu2g12210	regulation of cell growth
Afu2g12210	molecular function unknown
Afu2g12210	cytoplasm
Afu2g12220	DNA replication factor C complex
Afu2g12220	leading strand elongation
Afu2g12220	DNA repair
Afu2g12220	mismatch repair
Afu2g12220	purine nucleotide binding
Afu2g12230	peptidyltransferase activity
Afu2g12230	structural constituent of ribosome
Afu2g12230	mitochondrial large ribosomal subunit
Afu2g12230	translation
Afu2g12250	DNA clamp loader activity
Afu2g12250	DNA replication factor C complex
Afu2g12250	leading strand elongation
Afu2g12250	mismatch repair
Afu2g12250	sister chromatid cohesion
Afu2g12260	molecular function unknown
Afu2g12260	mitochondrial inner membrane
Afu2g12260	aerobic respiration
Afu2g12310	transcription factor activity

Afu2g12310	nucleus
Afu2g12310	transcription
Afu2g12330	transcription factor activity
Afu2g12330	nucleus
Afu2g12330	cytoplasm
Afu2g12330	response to xenobiotic stimulus
Afu2g12370	molecular function unknown
Afu2g12370	mitochondrion
Afu2g12370	mitochondrion organization
Afu2g12380	guanyl-nucleotide exchange factor activity
Afu2g12380	Golgi apparatus
Afu2g12380	intracellular protein transport
Afu2g12390	cellular bud neck
Afu2g12390	protein amino acid phosphorylation
Afu2g12390	regulation of exit from mitosis
Afu2g12390	kinase regulator activity
Afu2g12400	mitochondrial proton-transporting ATP synthase, stator stalk
Afu2g12400	structural molecule activity
Afu2g12400	ATP synthesis coupled proton transport
Afu2g12400	hydrogen ion transporting ATP synthase activity, rotational mechanism
Afu2g12410	biological process unknown
Afu2g12410	molecular function unknown
Afu2g12410	cytoplasm
Afu2g12440	cytoplasm
Afu2g12470	N2-acetyl-L-ornithine:2-oxoglutarate 5-aminotransferase activity
Afu2g12470	mitochondrial matrix
Afu2g12470	arginine biosynthetic process
Afu2g12470	ornithine biosynthetic process
Afu2g12480	fungal-type vacuole
Afu2g12480	molecular function unknown
Afu2g12480	regulation of pH
Afu2g12480	intracellular protein transport
Afu2g12500	drug transporter activity
Afu2g12500	drug transport
Afu2g12500	integral to membrane
Afu2g12530	carnitine O-acetyltransferase activity
Afu2g12530	mitochondrion
Afu2g12530	peroxisome
Afu2g12530	peroxisomal matrix
Afu2g12530	carnitine metabolic process
Afu2g12550	integral to plasma membrane
Afu2g12550	response to toxin
Afu2g12550	multidrug transporter activity
Afu2g12580	protein binding
Afu2g12580	endoplasmic reticulum membrane
Afu2g12580	SRP-dependent cotranslational protein targeting to membrane, translocation
Afu2g12580	protein transporter activity
Afu2g12590	biological process unknown
Afu2g12590	molecular function unknown
Afu2g12590	cellular component unknown

Afu2g12610	mitochondrial inner membrane
Afu2g12610	heme a biosynthetic process
Afu2g12610	cellular iron ion homeostasis
Afu2g12610	NADPH-adrenodoxin reductase activity
Afu2g12640	sexual reproduction
Afu2g12700	zinc ion binding
Afu2g12700	programmed cell death
Afu2g12710	fungal-type vacuole membrane
Afu2g12710	transporter activity
Afu2g12710	transport
Afu2g12710	monocarboxylic acid transmembrane transporter activity
Afu2g12790	transporter activity
Afu2g12790	transport
Afu2g12790	monocarboxylic acid transmembrane transporter activity
Afu2g12790	membrane
Afu2g12820	metabolic process
Afu2g12820	oxidoreductase activity
Afu2g12850	cell wall organization
Afu2g12850	fungal-type cell wall
Afu2g12850	1,3-beta-glucanosyltransferase activity
Afu2g12860	biological process unknown
Afu2g12860	molecular function unknown
Afu2g12860	cellular component unknown
Afu2g12870	peripheral to membrane of membrane fraction
Afu2g12870	soluble NSF attachment protein activity
Afu2g12870	ER to Golgi vesicle-mediated transport
Afu2g12880	molecular function unknown
Afu2g12880	nucleolus
Afu2g12880	rRNA processing
Afu2g12880	ribosome biogenesis
Afu2g12890	small nucleolar ribonucleoprotein complex
Afu2g12890	maturation of SSU-rRNA
Afu2g12890	snoRNA binding
Afu2g12900	metallochaperone activity
Afu2g12900	urea metabolic process
Afu2g12900	metal ion binding
Afu2g12920	mitochondrial outer membrane
Afu2g12920	mitochondrial translocation
Afu2g12920	ATPase activity
Afu2g12980	structural molecule activity
Afu2g12980	ER to Golgi vesicle-mediated transport
Afu2g12980	COPII vesicle coat
Afu2g13010	cytochrome-c oxidase activity
Afu2g13010	mitochondrial respiratory chain complex IV
Afu2g13010	respiratory chain complex IV assembly
Afu2g13020	dicarboxylic acid transmembrane transporter activity
Afu2g13020	mitochondrial envelope
Afu2g13020	dicarboxylic acid transport
Afu2g13030	phenylalanine-tRNA ligase activity
Afu2g13030	mitochondrion

Afu2g13030	translation
Afu2g13040	chaperone activity
Afu2g13040	mitochondrion
Afu2g13040	mitochondrial matrix
Afu2g13040	mitochondrial translocation
Afu2g13080	nucleus
Afu2g13080	cytoplasm
Afu2g13080	diphosphoinositol-polyphosphate diphosphatase activity
Afu2g13080	diadenosine polyphosphate metabolic process
Afu2g13090	DNA-directed RNA polymerase activity
Afu2g13090	DNA-directed RNA polymerase II, core complex
Afu2g13090	transcription from RNA polymerase II promoter
Afu2g13110	mitochondrial intermembrane space
Afu2g13110	electron transport
Afu2g13110	electron carrier activity
Afu2g13130	3'-5'-exoribonuclease activity
Afu2g13130	nuclear exosome (RNase complex)
Afu2g13130	cytoplasmic exosome (RNase complex)
Afu2g13130	35S primary transcript processing
Afu2g13130	mRNA catabolic process
Afu2g13140	protein kinase activity
Afu2g13140	nucleus
Afu2g13140	protein amino acid phosphorylation
Afu2g13140	regulation of meiosis
Afu2g13200	pseudouridylate synthase activity
Afu2g13200	cytoplasm
Afu2g13200	riboflavin biosynthetic process
Afu2g13200	DRAP deaminase activity
Afu2g13210	biological process unknown
Afu2g13210	nucleus
Afu2g13210	mitochondrion
Afu2g13210	chaperone regulator activity
Afu2g13230	response to stress
Afu2g13240	vacuolar proton-transporting V-type ATPase, V1 domain
Afu2g13240	cytoplasm
Afu2g13240	vacuolar acidification
Afu2g13240	proton-transporting ATPase activity, rotational mechanism
Afu2g13250	tryptophan biosynthetic process
Afu2g13250	tryptophan synthase activity
Afu2g13250	nucleus
Afu2g13250	cytoplasm
Afu2g13270	alcohol dehydrogenase (NAD) activity
Afu2g13270	cytoplasm
Afu2g13270	alcohol metabolic process
Afu2g13270	zinc ion binding
Afu2g13310	zinc ion binding
Afu2g13350	mediator complex
Afu2g13350	transcription from RNA polymerase II promoter
Afu2g13350	RNA polymerase II transcription mediator activity
Afu2g13360	repairosome

Afu2g13360	nucleotide-excision repair factor 4 complex
Afu2g13360	nucleotide-excision repair, DNA damage recognition
Afu2g13360	DNA-dependent ATPase activity
Afu2g13370	1-phosphatidylinositol 4-kinase activity
Afu2g13370	membrane fraction
Afu2g13370	cytoplasm
Afu2g13370	vacuolar membrane
Afu2g13370	plasma membrane
Afu2g13370	actin filament organization
Afu2g13380	negative regulation of transcription from RNA polymerase II promoter
Afu2g13380	specific RNA polymerase II transcription factor activity
Afu2g13380	nucleus
Afu2g13380	nitrogen compound metabolic process
Afu2g13380	regulation of nitrogen utilization
Afu2g13380	zinc ion binding
Afu2g13390	transporter activity
Afu2g13390	integral to plasma membrane
Afu2g13390	transport
Afu2g13400	biological process unknown
Afu2g13400	molecular function unknown
Afu2g13400	membrane
Afu2g13410	nuclear chromosome
Afu2g13410	nuclear chromosome
Afu2g13410	DNA binding
Afu2g13410	DNA binding
Afu2g13410	ATP binding
Afu2g13410	ATP binding
Afu2g13410	mismatch repair
Afu2g13410	mismatch repair
Afu2g13410	ATPase activity
Afu2g13410	ATPase activity
Afu2g13430	chitin synthase activity
Afu2g13430	chitin biosynthetic process
Afu2g13440	chitin synthase activity
Afu2g13440	plasma membrane
Afu2g13440	chitin biosynthetic process
Afu2g13440	response to osmotic stress
Afu2g13440	pathogenesis
Afu2g13450	molecular function unknown
Afu2g13450	soluble fraction
Afu2g13450	protein complex assembly
Afu2g13450	ER to Golgi vesicle-mediated transport
Afu2g13460	alpha-amylase activity
Afu2g13460	carbohydrate utilization
Afu2g13470	pyrimidine base metabolic process
Afu2g13470	nucleotidase activity
Afu2g13470	cellular component unknown
Afu2g13512	biological process unknown
Afu2g13512	molecular function unknown
Afu2g13512	cellular component unknown

Afu2g13520	molecular function unknown
Afu2g13520	fermentation
Afu2g13520	cellular component unknown
Afu2g13530	translation elongation factor activity
Afu2g13530	ribosome
Afu2g13530	translational elongation
Afu2g13550	lactoylglutathione lyase activity
Afu2g13550	carbohydrate metabolic process
Afu2g13570	GTP binding
Afu2g13570	nucleus
Afu2g13570	nucleolus
Afu2g13570	cytoplasm
Afu2g13570	rRNA processing
Afu2g13570	35S primary transcript processing
Afu2g13570	ribosome assembly
Afu2g13600	biological process unknown
Afu2g13600	mitochondrion
Afu2g13600	kinase activity
Afu2g13610	cytoplasm
Afu2g13610	mitochondrion
Afu2g13610	propionate metabolic process
Afu2g13610	propionate catabolic process, 2-methylcitrate cycle
Afu2g13610	2-methylcitrate dehydratase activity
Afu2g13630	cytoplasm
Afu2g13630	aromatic-amino-acid:2-oxoglutarate aminotransferase activity
Afu2g13630	aromatic amino acid family metabolic process
Afu2g13640	cell morphogenesis
Afu2g13640	protein kinase activity
Afu2g13640	cytoplasm
Afu2g13640	cell wall organization
Afu2g13680	calcium- and calmodulin-dependent protein kinase activity
Afu2g13690	proteasome complex
Afu2g13690	ubiquitin conjugating enzyme activity
Afu2g13690	nucleus
Afu2g13690	cytoplasm
Afu2g13690	DNA repair
Afu2g13690	ubiquitin-dependent protein catabolic process
Afu2g13690	protein monoubiquitination
Afu2g13690	histone ubiquitination
Afu2g13720	DNA-directed RNA polymerase activity
Afu2g13720	DNA-directed RNA polymerase III complex
Afu2g13720	DNA-directed RNA polymerase I complex
Afu2g13720	transcription from RNA polymerase I promoter
Afu2g13720	transcription from RNA polymerase III promoter
Afu2g13730	cytoplasm
Afu2g13730	NEDD8 activating enzyme activity
Afu2g13730	NEDD8 class-dependent protein catabolic process
Afu2g13730	protein neddylation during NEDD8 class-dependent protein catabolic process
Afu2g13750	fungal-type vacuole membrane
Afu2g13750	ATP binding

Afu2g13750	cytosol
Afu2g13750	Golgi to endosome transport
Afu2g13750	homotypic vacuole fusion, non-autophagic
Afu2g13750	late endosome to vacuole transport
Afu2g13760	v-SNARE activity
Afu2g13760	Golgi to plasma membrane transport
Afu2g13760	vesicle fusion
Afu2g13760	membrane
Afu2g13770	DNA binding
Afu2g13770	nucleus
Afu2g13770	zinc ion binding
Afu2g13770	sporulation resulting in formation of a cellular spore
Afu2g13780	spliceosome assembly
Afu2g13780	mRNA binding
Afu2g13780	U2 snRNP
Afu2g13820	DNA binding
Afu2g13860	nuclear nucleosome
Afu2g13860	DNA binding
Afu2g13860	chromatin assembly or disassembly
Afu2g13870	adenine nucleotide transmembrane transporter activity
Afu2g13870	cytoplasm
Afu2g13870	integral to peroxisomal membrane
Afu2g13870	fatty acid beta-oxidation
Afu2g13870	peroxisome organization
Afu2g13870	ATP transport
Afu2g13960	mitochondrion
Afu2g13960	acyltransferase activity
Afu2g13960	phospholipid biosynthetic process
Afu2g13980	ribosomal large subunit assembly
Afu2g13980	ATP-dependent RNA helicase activity
Afu2g13980	nucleolus
Afu2g13980	35S primary transcript processing
Afu2g14020	ATP-binding cassette (ABC) transporter activity
Afu2g14020	cytoplasm
Afu2g14020	endoplasmic reticulum
Afu2g14020	transport
Afu2g14020	integral to membrane
Afu2g14030	arginine-tRNA ligase activity
Afu2g14030	cytoplasm
Afu2g14030	translation
Afu2g14060	cytochrome-b5 reductase activity
Afu2g14060	microsome
Afu2g14060	electron transport
Afu2g14080	nuclear cohesin complex
Afu2g14080	mitotic sister chromatid cohesion
Afu2g14080	synaptonemal complex assembly
Afu2g14080	ATPase activity
Afu2g14090	S phase of mitotic cell cycle
Afu2g14090	protein kinase activity
Afu2g14090	cytoplasm

Afu2g14090	regulation of exit from mitosis
Afu2g14090	maturation of SSU-rRNA
Afu2g14110	nuclear ubiquitin ligase complex
Afu2g14110	protein binding
Afu2g14110	ubiquitin-dependent protein catabolic process
Afu2g14110	sulfur metabolic process
Afu2g14110	cell cycle
Afu2g14110	protein ubiquitination
Afu2g14110	SCF ubiquitin ligase complex
Afu2g14130	ubiquitin-specific protease activity
Afu2g14130	protein deubiquitination
Afu2g14150	metabolic process
Afu2g14150	hydrolase activity, hydrolyzing N-glycosyl compounds
Afu2g14160	endosome
Afu2g14160	protein transporter activity
Afu2g14160	protein transport
Afu2g14180	biological process unknown
Afu2g14180	molecular function unknown
Afu2g14180	cytoplasm
Afu2g14190	mitochondrion
Afu2g14190	mitochondrial inner membrane presequence translocase complex
Afu2g14190	mitochondrial translocation
Afu2g14190	protein transporter activity
Afu2g14200	protein kinase activity
Afu2g14200	cytoplasm
Afu2g14230	transporter activity
Afu2g14230	transport
Afu2g14230	integral to membrane
Afu2g14250	negative regulation of transcription from RNA polymerase II promoter
Afu2g14250	transcription corepressor activity
Afu2g14250	nucleus
Afu2g14270	actin cross-linking activity
Afu2g14270	actin cortical patch (sensu Saccharomyces)
Afu2g14270	actin filament organization
Afu2g14270	microtubule-based process
Afu2g14270	microtubule binding
Afu2g14280	karyogamy during conjugation with cellular fusion
Afu2g14280	motor activity
Afu2g14280	microtubule motor activity
Afu2g14280	spindle pole body
Afu2g14280	microtubule
Afu2g14280	mitosis
Afu2g14280	meiosis
Afu2g14290	metabolic process
Afu2g14290	hydrolase activity
Afu2g14310	biological process unknown
Afu2g14310	molecular function unknown
Afu2g14310	cellular component unknown
Afu2g14350	AT DNA binding
Afu2g14350	nucleus

Afu2g14400	biological process unknown
Afu2g14400	molecular function unknown
Afu2g14400	cellular component unknown
Afu2g14430	metabolic process
Afu2g14430	oxidoreductase activity
Afu2g14460	acylglycerone-phosphate reductase activity
Afu2g14460	cytoplasm
Afu2g14460	endoplasmic reticulum
Afu2g14460	lipid particle
Afu2g14460	phosphatidic acid biosynthetic process
Afu2g14560	catalytic activity
Afu2g14560	metabolic process
Afu2g14570	fungal-type vacuole
Afu2g14570	zinc ion transmembrane transporter activity
Afu2g14570	glutathione metabolic process
Afu2g14570	cobalt ion transport
Afu2g14570	zinc ion transport
Afu2g14570	cellular zinc ion homeostasis
Afu2g14570	di-, tri-valent inorganic cation transmembrane transporter activity
Afu2g14580	conjugation with cellular fusion
Afu2g14580	molecular function unknown
Afu2g14580	DNA repair
Afu2g14580	integral to membrane
Afu2g14580	cellular manganese ion homeostasis
Afu2g14580	actin cytoskeleton organization
Afu2g14590	receptor activity
Afu2g14590	glucose transmembrane transporter activity
Afu2g14590	glucose binding
Afu2g14590	plasma membrane
Afu2g14590	signal transduction
Afu2g14590	response to glucose stimulus
Afu2g14600	biological process unknown
Afu2g14600	molecular function unknown
Afu2g14600	lipid particle
Afu2g14650	protein kinase activity
Afu2g14670	RNA binding
Afu2g14670	translation initiation factor activity
Afu2g14670	eukaryotic translation initiation factor 3 complex
Afu2g14670	translational initiation
Afu2g14720	nucleus
Afu2g14720	regulation of carbohydrate metabolic process
Afu2g14720	transcription
Afu2g14720	transcription activator activity
Afu2g14720	CCAAT-binding factor complex
Afu2g14730	establishment of mitotic spindle orientation
Afu2g14730	microtubule motor activity
Afu2g14730	kinesin complex
Afu2g14730	nuclear microtubule
Afu2g14730	cytoplasmic microtubule
Afu2g14730	microtubule depolymerization

Afu2g14760	mitochondrial inner membrane
Afu2g14760	aerobic respiration
Afu2g14760	ATPase activity
Afu2g14770	biological process unknown
Afu2g14770	molecular function unknown
Afu2g14770	cellular component unknown
Afu2g14800	transcription factor activity
Afu2g14800	nucleus
Afu2g14800	transcription
Afu2g14810	nucleus
Afu2g14810	metabolic process
Afu2g14810	oxidoreductase activity
Afu2g14840	metabolic process
Afu2g14840	oxidoreductase activity
Afu2g14860	metabolic process
Afu2g14860	hydrolase activity
Afu2g14880	regulation of transcription involved in G1 phase of mitotic cell cycle
Afu2g14880	nucleus
Afu2g14880	transcription factor TFIID complex
Afu2g14880	transcription initiation from RNA polymerase II promoter
Afu2g14880	general RNA polymerase II transcription factor activity
Afu2g14910	alpha-1,6-mannosyltransferase activity
Afu2g14910	cell wall mannoprotein biosynthetic process
Afu2g14910	alpha-1,6-mannosyltransferase complex
Afu2g14910	substituted mannan metabolic process
Afu2g14910	N-glycan processing
Afu2g14920	protein kinase activity
Afu2g14920	nucleus
Afu2g14920	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process
Afu2g14920	DNA repair
Afu2g14930	threonine aldolase activity
Afu2g14930	cytosol
Afu2g14930	glycine biosynthetic process
Afu2g14930	threonine catabolic process
Afu2g14950	ribonuclease H activity
Afu2g14950	nucleus
Afu2g14950	DNA replication
Afu2g14950	RNA processing
Afu2g14950	3'-5' exonuclease activity
Afu2g14960	intracellular
Afu2g14960	response to oxidative stress
Afu2g14960	thiol-disulfide exchange intermediate activity
Afu2g14970	biological process unknown
Afu2g14970	molecular function unknown
Afu2g14970	mitochondrion
Afu2g14980	transporter activity
Afu2g14980	mitochondrial envelope
Afu2g14980	mitochondrial inner membrane
Afu2g14980	transport
Afu2g14990	nuclear migration (sensu Saccharomyces)

Afu2g14990	mitotic sister chromatid segregation
Afu2g14990	nuclear migration during conjugation with cellular fusion
Afu2g14990	structural constituent of cytoskeleton
Afu2g14990	spindle pole body
Afu2g14990	polar microtubule
Afu2g14990	kinetochore microtubule
Afu2g14990	nuclear microtubule
Afu2g14990	cytoplasmic microtubule
Afu2g14990	homologous chromosome segregation
Afu2g15010	protein kinase activity
Afu2g15010	cytoplasm
Afu2g15010	protein amino acid phosphorylation
Afu2g15010	response to stress
Afu2g15010	regulation of meiosis
Afu2g15030	C-3 sterol dehydrogenase (C-4 sterol decarboxylase) activity
Afu2g15030	endoplasmic reticulum
Afu2g15030	endoplasmic reticulum membrane
Afu2g15030	ergosterol biosynthetic process
Afu2g15050	Rho GTPase activator activity
Afu2g15050	cytoplasm
Afu2g15050	cellular bud neck
Afu2g15050	small GTPase mediated signal transduction
Afu2g15050	fungal-type cell wall biogenesis
Afu2g15070	endopeptidase activity
Afu2g15070	proteasome regulatory particle
Afu2g15070	ubiquitin-dependent protein catabolic process
Afu2g15130	plasma membrane
Afu2g15130	xenobiotic-transporting ATPase activity
Afu2g15130	drug transport
Afu2g15130	response to drug
Afu2g15140	transporter activity
Afu2g15140	integral to plasma membrane
Afu2g15140	transport
Afu2g15150	plasma membrane
Afu2g15150	choline transmembrane transporter activity
Afu2g15150	choline transport
Afu2g15180	biological process unknown
Afu2g15180	molecular function unknown
Afu2g15180	cytoplasm
Afu2g15180	cellular bud
Afu2g15190	ribulose-phosphate 3-epimerase activity
Afu2g15190	cytosol
Afu2g15190	pentose-phosphate shunt
Afu2g15210	nuclear mRNA splicing, via spliceosome
Afu2g15210	rRNA processing
Afu2g15210	pre-mRNA splicing factor activity
Afu2g15210	small nuclear ribonucleoprotein complex
Afu2g15220	damaged DNA binding
Afu2g15220	nucleus
Afu2g15220	DNA repair

Afu2g15220	double-strand break repair
Afu2g15230	metabolic process
Afu2g15230	oxidoreductase activity
Afu2g15240	endoplasmic reticulum
Afu2g15240	integral to plasma membrane
Afu2g15240	sulfur metabolic process
Afu2g15240	oligopeptide transporter activity
Afu2g15260	specific RNA polymerase II transcription factor activity
Afu2g15260	nucleus
Afu2g15260	regulation of transcription from RNA polymerase II promoter
Afu2g15260	leucine biosynthetic process
Afu2g15312	citrate (Si)-synthase activity
Afu2g15312	tricarboxylic acid cycle
Afu2g15320	plasma membrane
Afu2g15320	integral to plasma membrane
Afu2g15320	multidrug transport
Afu2g15320	multidrug transporter activity
Afu2g15340	DNA binding
Afu2g15340	nucleus
Afu2g15340	transcription
Afu2g15340	zinc ion binding
Afu2g15370	molecular function unknown
Afu2g15370	protein targeting to vacuole
Afu2g15370	autophagy
Afu2g15370	cellular component unknown
Afu2g15390	glutamate-ammonia ligase activity
Afu2g15390	glutamine biosynthetic process
Afu2g15410	transporter activity
Afu2g15410	transport
Afu2g15410	membrane
Afu2g15430	peroxisomal matrix
Afu2g15430	sporulation (sensu Saccharomyces)
Afu2g15430	2,4-dienoyl-CoA reductase (NADPH) activity
Afu2g15430	fatty acid catabolic process
Afu2g15500	nuclear mRNA splicing, via spliceosome
Afu2g15500	pre-mRNA splicing factor activity
Afu2g15500	small nuclear ribonucleoprotein complex
Afu2g15520	monooxygenase activity
Afu2g15520	cellular aromatic compound metabolic process
Afu2g15540	biological process unknown
Afu2g15540	phospholipase activity
Afu2g15540	mitochondrion
Afu2g15550	catalytic activity
Afu2g15550	Mo-molybdopterin cofactor biosynthetic process
Afu2g15560	vacuolar proton-transporting V-type ATPase, V0 domain
Afu2g15560	vacuolar acidification
Afu2g15560	programmed cell death
Afu2g15560	proton-transporting ATPase activity, rotational mechanism
Afu2g15570	GTPase activity
Afu2g15570	Golgi apparatus

Afu2g15570	intracellular protein transport
Afu2g15570	retrograde transport, endosome to Golgi
Afu2g15590	sulfate assimilation
Afu2g15590	sulfite reductase (NADPH) activity
Afu2g15590	electron transporter activity
Afu2g15590	cytoplasm
Afu2g15590	electron transport
Afu2g15590	cell wall organization
Afu2g15610	mitochondrial genome maintenance
Afu2g15610	DNA-directed RNA polymerase activity
Afu2g15610	mitochondrial matrix
Afu2g15610	transcription from mitochondrial promoter
Afu2g15620	transcription factor activity
Afu2g15620	nucleus
Afu2g15620	zinc ion binding
Afu2g15620	regulation of transcription
Afu2g15660	3-chloroallyl aldehyde dehydrogenase activity
Afu2g15660	cytoplasm
Afu2g15680	transcription factor TFIIA complex
Afu2g15680	transcription initiation from RNA polymerase II promoter
Afu2g15680	general RNA polymerase II transcription factor activity
Afu2g15700	glucokinase activity
Afu2g15700	cytosol
Afu2g15700	carbohydrate metabolic process
Afu2g15730	transporter activity
Afu2g15730	integral to plasma membrane
Afu2g15730	transport
Afu2g15740	peroxisomal matrix
Afu2g15740	sporulation (sensu Saccharomyces)
Afu2g15740	2,4-dienoyl-CoA reductase (NADPH) activity
Afu2g15740	fatty acid catabolic process
Afu2g15750	gamma-tubulin complex
Afu2g15750	structural constituent of cytoskeleton
Afu2g15750	microtubule-based process
Afu2g15760	ubiquitin activating enzyme activity
Afu2g15760	ubiquitin cycle
Afu2g15760	sensory perception of chemical stimulus
Afu2g15760	amino acid binding
Afu2g15760	extrinsic to plasma membrane
Afu2g15770	molecular function unknown
Afu2g15770	cytoplasm
Afu2g15770	cell wall organization
Afu2g15780	transporter activity
Afu2g15780	calcium ion binding
Afu2g15780	mitochondrial inner membrane
Afu2g15780	transport
Afu2g15780	ascospore formation
Afu2g15790	negative regulation of transcription from RNA polymerase II promoter
Afu2g15790	transcription factor complex
Afu2g15790	meiosis

Afu2g15790	general RNA polymerase II transcription factor activity
Afu2g15790	cyclin-dependent protein kinase regulator activity
Afu2g15830	signal transducer activity
Afu2g15830	signal transduction
Afu2g15830	zinc ion binding
Afu2g15840	signal transduction
Afu2g15840	programmed cell death
Afu2g15870	nucleus
Afu2g15870	cytoplasm
Afu2g15870	protein import into nucleus
Afu2g15870	protein transmembrane transporter activity
Afu2g15900	biological process unknown
Afu2g15900	molecular function unknown
Afu2g15900	nucleus
Afu2g15900	cytoplasm
Afu2g15910	mannosyltransferase activity
Afu2g15910	alpha-1,6-mannosyltransferase complex
Afu2g15910	Golgi cis cisterna
Afu2g15910	protein amino acid N-linked glycosylation
Afu2g15930	biological process unknown
Afu2g15930	nucleus
Afu2g15930	cytoplasm
Afu2g15930	oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor
Afu2g15940	tRNA binding
Afu2g15940	cytoplasm
Afu2g15940	tRNA export from nucleus
Afu2g15940	tRNA aminoacylation for protein translation
Afu2g15940	methionyl glutamyl tRNA synthetase complex
Afu2g15950	aspartic-type endopeptidase activity
Afu2g15950	extracellular region
Afu2g15950	protein catabolic process
Afu2g15960	biological process unknown
Afu2g15960	nucleus
Afu2g15960	ATPase activity
Afu2g15970	phosphatidylethanolamine N-methyltransferase activity
Afu2g15970	endoplasmic reticulum
Afu2g15970	phosphatidylcholine biosynthetic process
Afu2g16010	biological process unknown
Afu2g16010	proline-tRNA ligase activity
Afu2g16010	cellular component unknown
Afu2g16020	chaperone activity
Afu2g16020	cytoplasm
Afu2g16020	cytoskeleton
Afu2g16020	protein folding
Afu2g16020	cytoskeleton organization
Afu2g16040	RNA binding
Afu2g16040	nucleolus
Afu2g16040	nucleolus organizer region
Afu2g16040	rRNA processing
Afu2g16040	maturation of SSU-rRNA

Afu2g16040	snoRNA binding
Afu2g16060	biological process unknown
Afu2g16060	molecular function unknown
Afu2g16060	cellular component unknown
Afu2g16080	cytogamy
Afu2g16080	nuclear cohesin complex
Afu2g16080	protein binding
Afu2g16080	mitotic sister chromatid cohesion
Afu2g16080	colony morphology
Afu2g16090	nucleus
Afu2g16090	cytoplasm
Afu2g16090	nucleocytoplasmic transport
Afu2g16090	protein transmembrane transporter activity
Afu2g16130	biological process unknown
Afu2g16130	molecular function unknown
Afu2g16130	nucleus
Afu2g16130	cytoplasm
Afu2g16140	biological process unknown
Afu2g16140	helicase activity
Afu2g16140	cytoplasm
Afu2g16150	regulation of cyclin-dependent protein kinase activity
Afu2g16150	G1/S transition of mitotic cell cycle
Afu2g16150	G2/M transition of mitotic cell cycle
Afu2g16150	nucleus
Afu2g16150	spindle pole body
Afu2g16150	cyclin-dependent protein kinase regulator activity
Afu2g16210	biological process unknown
Afu2g16210	molecular function unknown
Afu2g16210	cellular component unknown
Afu2g16230	biological process unknown
Afu2g16230	DNA binding
Afu2g16230	nucleus
Afu2g16230	zinc ion binding
Afu2g16240	regulation of progression through cell cycle
Afu2g16240	Ras guanyl-nucleotide exchange factor activity
Afu2g16240	cytoplasm
Afu2g16240	plasma membrane
Afu2g16240	traversing start control point of mitotic cell cycle
Afu2g16240	Ras protein signal transduction
Afu2g16250	protein deneddylation
Afu2g16250	adaptation to pheromone during conjugation with cellular fusion
Afu2g16250	metalloendopeptidase activity
Afu2g16250	signalosome
Afu2g16250	sporocarp development
Afu2g16260	mitotic anaphase B
Afu2g16260	spindle microtubule
Afu2g16260	nuclear microtubule
Afu2g16260	mitotic spindle organization
Afu2g16260	microtubule binding
Afu2g16280	glutamate-tRNA ligase activity

Afu2g16280	mitochondrion
Afu2g16280	translation
Afu2g16280	glutamyl-tRNA aminoacylation
Afu2g16290	ATPase activator activity
Afu2g16290	cytosol
Afu2g16290	protein targeting to mitochondrion
Afu2g16290	chaperone regulator activity
Afu2g16290	Hsp70/Hsc70 protein regulator activity
Afu2g16300	dihydroxy-acid dehydratase activity
Afu2g16300	mitochondrion
Afu2g16300	branched chain family amino acid biosynthetic process
Afu2g16310	transcription factor activity
Afu2g16310	regulation of transcription
Afu2g16320	integral to plasma membrane
Afu2g16320	response to toxin
Afu2g16320	multidrug transporter activity
Afu2g16330	biological process unknown
Afu2g16330	molecular function unknown
Afu2g16330	cytoplasm
Afu2g16350	fatty acid metabolic process
Afu2g16350	CoA hydrolase activity
Afu2g16360	pseudouridylate synthase activity
Afu2g16360	cytoplasm
Afu2g16360	riboflavin biosynthetic process
Afu2g16360	DRAP deaminase activity
Afu2g16370	structural constituent of ribosome
Afu2g16370	cytosolic large ribosomal subunit (sensu Eukaryota)
Afu2g16370	translation
Afu2g16380	biological process unknown
Afu2g16380	molecular function unknown
Afu2g16380	nucleus
Afu2g16380	cytoplasm
Afu2g16420	biological process unknown
Afu2g16420	molecular function unknown
Afu2g16420	cellular component unknown
Afu2g16470	protein polyubiquitination
Afu2g16470	ubiquitin conjugating enzyme activity
Afu2g16470	nuclear envelope
Afu2g16470	endoplasmic reticulum membrane
Afu2g16470	ubiquitin cycle
Afu2g16470	protein monoubiquitination
Afu2g16470	ER-associated protein catabolic process
Afu2g16520	phospholipase D activity
Afu2g16520	phospholipid metabolic process
Afu2g16520	regulation of lipid biosynthetic process
Afu2g16530	cyanate hydratase activity
Afu2g16530	response to toxin
Afu2g16540	DNA binding
Afu2g16540	nucleus
Afu2g16540	zinc ion binding

Afu2g16570	metabolic process
Afu2g16570	oxidoreductase activity
Afu2g16600	delta DNA polymerase activity
Afu2g16600	delta DNA polymerase complex
Afu2g16600	leading strand elongation
Afu2g16600	lagging strand elongation
Afu2g16600	mutagenesis
Afu2g16600	base-excision repair
Afu2g16600	nucleotide-excision repair
Afu2g16600	mismatch repair
Afu2g16600	postreplication repair
Afu2g16620	protein kinase activity
Afu2g16620	protein amino acid phosphorylation
Afu2g16640	cellular morphogenesis during conjugation with cellular fusion
Afu2g16640	polyphosphoinositide phosphatase activity
Afu2g16640	extrinsic to membrane
Afu2g16660	tRNA adenylyltransferase activity
Afu2g16660	nucleus
Afu2g16660	cytoplasm
Afu2g16660	mitochondrial matrix
Afu2g16660	tRNA modification
Afu2g16700	nuclear chromatin
Afu2g16700	single-stranded DNA binding
Afu2g16700	ubiquitin conjugating enzyme activity
Afu2g16700	DNA repair
Afu2g16700	DNA-dependent ATPase activity
Afu2g16730	protein binding
Afu2g16730	peroxisomal membrane
Afu2g16730	peroxisome organization
Afu2g16750	ribosomal large subunit assembly
Afu2g16750	RNA binding
Afu2g16750	protein binding
Afu2g16750	cytosol
Afu2g16750	cytosolic large ribosomal subunit (sensu Eukaryota)
Afu2g16760	biological process unknown
Afu2g16760	nucleolus
Afu2g16760	cytoplasm
Afu2g16760	transcription regulator activity
Afu2g16770	mitochondrial inner membrane
Afu2g16770	coenzyme A transmembrane transporter activity
Afu2g16770	coenzyme A transport
Afu2g16780	molecular function unknown
Afu2g16780	nucleus
Afu2g16780	chromatin remodeling
Afu2g16780	negative regulation of transcription from RNA polymerase II promoter by pheromones
Afu2g16790	oligosaccharyl transferase activity
Afu2g16790	endoplasmic reticulum membrane
Afu2g16790	dolichol-linked oligosaccharide biosynthetic process
Afu2g16790	oligosaccharide-lipid intermediate assembly
Afu2g16810	DNA binding

Afu2g16810	nucleus
Afu2g16810	zinc ion binding
Afu2g16840	nucleosome remodeling complex
Afu2g16840	chromatin remodeling
Afu2g16840	regulation of transcription from RNA polymerase II promoter
Afu2g16840	general RNA polymerase II transcription factor activity
Afu2g16840	SWI/SNF complex
Afu2g16850	condensed nuclear chromosome
Afu2g16850	structural molecule activity
Afu2g16850	mitotic sister chromatid cohesion
Afu2g16850	mitotic chromosome condensation
Afu2g16860	drug transporter activity
Afu2g16860	drug transport
Afu2g16860	integral to membrane
Afu2g16870	DNA binding
Afu2g16870	nucleus
Afu2g16870	zinc ion binding
Afu2g16880	structural constituent of ribosome
Afu2g16880	cytosolic large ribosomal subunit (sensu Eukaryota)
Afu2g16880	translation
Afu2g16920	actin monomer binding
Afu2g16920	bipolar cellular bud site selection
Afu2g16920	actin polymerization or depolymerization
Afu2g16920	sequestering of actin monomers
Afu2g16930	succinate:fumarate antiporter activity
Afu2g16930	mitochondrial inner membrane
Afu2g16930	fumarate transport
Afu2g16930	succinate transport
Afu2g16940	biological process unknown
Afu2g16940	cellular component unknown
Afu2g16940	sterol transporter activity
Afu2g16970	structural constituent of ribosome
Afu2g16970	mitochondrial large ribosomal subunit
Afu2g16970	translation
Afu2g17050	chromatin binding
Afu2g17050	protein binding
Afu2g17050	nucleus
Afu2g17050	nucleolus
Afu2g17050	DNA replication initiation
Afu2g17050	rRNA processing
Afu2g17060	ribosomal large subunit assembly
Afu2g17060	molecular function unknown
Afu2g17060	nucleolus
Afu2g17060	cytosolic large ribosomal subunit (sensu Eukaryota)
Afu2g17060	rRNA processing
Afu2g17070	biological process unknown
Afu2g17070	molecular function unknown
Afu2g17070	cellular component unknown
Afu2g17110	nucleus
Afu2g17110	endoplasmic reticulum

Afu2g17110	microsome
Afu2g17110	cytosol
Afu2g17110	ubiquitin-dependent protein catabolic process
Afu2g17110	vesicle fusion
Afu2g17110	cell cycle
Afu2g17110	programmed cell death
Afu2g17110	protein transport
Afu2g17110	ATPase activity
Afu2g17110	ER-associated protein catabolic process
Afu2g17130	MAPKKK cascade involved in osmosensory signaling pathway
Afu2g17130	MAPKKK cascade (pseudohyphal growth)
Afu2g17130	response to pheromone during conjugation with cellular fusion
Afu2g17130	pheromone-dependent signal transduction involved in conjugation with cellular fusion
Afu2g17130	cytoplasm
Afu2g17130	osmosensory signaling pathway
Afu2g17130	protein kinase regulator activity
Afu2g17170	plasma membrane
Afu2g17170	cation:cation antiporter activity
Afu2g17170	cellular monovalent inorganic cation homeostasis
Afu2g17180	molecular function unknown
Afu2g17180	cytoplasm
Afu2g17180	protein targeting to vacuole
Afu2g17220	transcription factor activity
Afu2g17220	nucleus
Afu2g17220	regulation of transcription, DNA-dependent
Afu2g17220	zinc ion binding
Afu2g17230	GTP binding
Afu2g17230	programmed cell death
Afu2g17250	lipase activity
Afu2g17260	phosphate metabolic process
Afu2g17260	phosphoric ester hydrolase activity
Afu2g17270	transporter activity
Afu2g17270	transport
Afu2g17270	clathrin-coated vesicle
Afu2g17270	COPI-coated vesicle
Afu2g17300	glutathione transferase activity
Afu2g17300	endoplasmic reticulum
Afu2g17300	glutathione metabolic process
Afu2g17360	fungal-type vacuole membrane
Afu2g17360	transporter activity
Afu2g17360	transport
Afu2g17360	monocarboxylic acid transmembrane transporter activity
Afu2g17400	C-3 sterol dehydrogenase (C-4 sterol decarboxylase) activity
Afu2g17400	endoplasmic reticulum
Afu2g17400	endoplasmic reticulum membrane
Afu2g17400	ergosterol biosynthetic process
Afu2g17420	nucleotide binding
Afu2g17420	purine-nucleoside phosphorylase activity
Afu2g17420	signal transduction
Afu2g17420	cellular component unknown

Afu2g17430	metabolic process
Afu2g17430	oxidoreductase activity
Afu2g17440	hydrolase activity
Afu2g17440	quinolinate metabolic process
Afu2g17450	3-hydroxyanthranilate 3,4-dioxygenase activity
Afu2g17450	cytoplasm
Afu2g17450	NAD biosynthetic process
Afu2g17460	3-chloroallyl aldehyde dehydrogenase activity
Afu2g17460	aldehyde dehydrogenase (NAD) activity
Afu2g17460	fermentation
Afu2g17470	endoribonuclease activity
Afu2g17470	mRNA catabolic process
Afu2g17500	cellular component unknown
Afu2g17520	N-acetyltransferase activity
Afu2g17520	metabolic process
Afu2g17520	secondary metabolic process
Afu2g17530	ferroxidase activity
Afu2g17530	membrane fraction
Afu2g17530	iron ion transport
Afu2g17540	ferroxidase activity
Afu2g17540	plasma membrane
Afu2g17540	high-affinity iron ion transport
Afu2g17540	pigment biosynthetic process
Afu2g17550	pigment biosynthetic process
Afu2g17560	pathogenesis
Afu2g17560	pigment biosynthetic process
Afu2g17560	tetrahydroxynaphthalene reductase activity
Afu2g17580	scytalone dehydratase activity
Afu2g17580	pigment biosynthetic process
Afu2g17600	pathogenesis
Afu2g17600	polyketide synthase activity
Afu2g17600	pigment biosynthetic process
Afu2g17610	metabolic process
Afu2g17610	sulfuric ester hydrolase activity
Afu2g17650	biological process unknown
Afu2g17650	molecular function unknown
Afu2g17650	cytoplasm
Afu2g17730	integral to plasma membrane
Afu2g17730	response to toxin
Afu2g17730	multidrug transporter activity
Afu2g17840	transporter activity
Afu2g17840	plasma membrane
Afu2g17840	transport
Afu2g17850	biological process unknown
Afu2g17850	molecular function unknown
Afu2g17850	nucleus
Afu2g17850	cytoplasm
Afu2g17850	dihydrokaempferol 4-reductase activity
Afu2g17870	cytoplasm
Afu2g17870	L-serine metabolic process

Afu2g17870	oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acc
Afu2g17880	DNA binding
Afu2g17890	endoplasmic reticulum
Afu2g17890	plasma membrane
Afu2g17890	fatty acid transport
Afu2g17890	integral to membrane
Afu2g17895	transcription factor activity
Afu2g17895	regulation of transcription
Afu2g17960	NADPH dehydrogenase activity
Afu2g17960	metabolic process
Afu2g17960	coenzyme binding
Afu2g17980	metabolic process
Afu2g17980	oxidoreductase activity
Afu2g17980	oxidoreductase activity
Afu2g18000	cytoplasm
Afu2g18000	oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acc
Afu2g18000	secondary metabolic process
Afu2g18010	metabolic process
Afu2g18010	oxidoreductase activity
Afu2g18030	catalase activity
Afu2g18030	peroxisomal matrix
Afu2g18030	oxygen and reactive oxygen species metabolic process
Afu2g18040	alkaloid biosynthetic process
Afu2g18040	tryptophan dimethylallyltransferase activity
Afu2g18050	FAD binding
Afu2g18060	secondary metabolic process
Afu2g18100	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process
Afu2g18100	ATP-dependent helicase activity
Afu3g00100	amine oxidase (flavin-containing) activity
Afu3g00100	cytoplasm
Afu3g00100	polyamine catabolic process
Afu3g00100	amine oxidase activity
Afu3g00100	pantothenate biosynthetic process
Afu3g00110	glutamate catabolic process
Afu3g00110	response to oxidative stress
Afu3g00110	succinate-semialdehyde dehydrogenase [NAD(P)+] activity
Afu3g00120	integral to plasma membrane
Afu3g00120	amino acid transmembrane transporter activity
Afu3g00120	amino acid import
Afu3g00130	biological process unknown
Afu3g00150	cytoplasm
Afu3g00150	metabolic process
Afu3g00150	oxidoreductase activity
Afu3g00180	cytoplasm
Afu3g00180	metabolic process
Afu3g00180	oxidoreductase activity
Afu3g00200	fructose transmembrane transporter activity
Afu3g00200	glucose transmembrane transporter activity
Afu3g00200	plasma membrane
Afu3g00200	hexose transport

Afu3g00200	mannose transmembrane transporter activity
Afu3g00210	zinc ion binding
Afu3g00220	fructose transmembrane transporter activity
Afu3g00220	glucose transmembrane transporter activity
Afu3g00220	plasma membrane
Afu3g00220	hexose transport
Afu3g00220	mannose transmembrane transporter activity
Afu3g00230	hydrolase activity, hydrolyzing O-glycosyl compounds
Afu3g00230	carbohydrate metabolic process
Afu3g00250	metabolic process
Afu3g00250	oxidoreductase activity
Afu3g00250	FAD binding
Afu3g00270	hydrolase activity, hydrolyzing O-glycosyl compounds
Afu3g00270	cellular glucan metabolic process
Afu3g00270	cell wall organization
Afu3g00270	fungal-type cell wall
Afu3g00280	catalytic activity
Afu3g00280	metabolic process
Afu3g00310	acid phosphatase activity
Afu3g00310	extracellular region
Afu3g00310	phosphate metabolic process
Afu3g00320	xylan metabolic process
Afu3g00330	nucleotide-sugar metabolic process
Afu3g00330	NAD or NADH binding
Afu3g00340	molecular function unknown
Afu3g00340	membrane fraction
Afu3g00340	fungal-type cell wall biogenesis
Afu3g00340	anchored to plasma membrane
Afu3g00360	cellular component unknown
Afu3g00360	diaminohydroxyphosphoribosylaminopyrimidine deaminase activity
Afu3g00360	riboflavin biosynthetic process
Afu3g00370	carbohydrate metabolic process
Afu3g00370	aldehyde-lyase activity
Afu3g00420	cellulose binding
Afu3g00420	xylan metabolic process
Afu3g00420	acetylxylan esterase activity
Afu3g00430	fructose transmembrane transporter activity
Afu3g00430	glucose transmembrane transporter activity
Afu3g00430	plasma membrane
Afu3g00430	hexose transport
Afu3g00430	mannose transmembrane transporter activity
Afu3g00470	xylan metabolic process
Afu3g00520	cytoplasm
Afu3g00520	chromatin silencing at telomere
Afu3g00520	NAD-dependent histone deacetylase activity
Afu3g00540	plasma membrane
Afu3g00540	peptide transporter activity
Afu3g00540	peptide transport
Afu3g00570	biological process unknown
Afu3g00570	molecular function unknown

Afu3g00570	endoplasmic reticulum
Afu3g00590	pathogenesis
Afu3g00590	hemolysis by symbiont of host erythrocytes
Afu3g00590	low-density lipoprotein binding
Afu3g00610	fungal-type vacuole
Afu3g00610	glucan 1,4-alpha-glucosidase activity
Afu3g00610	polysaccharide metabolic process
Afu3g00610	sporulation (sensu Saccharomyces)
Afu3g00620	metabolic process
Afu3g00620	zinc ion binding
Afu3g00620	cellular component unknown
Afu3g00620	oxidoreductase activity
Afu3g00650	aminopeptidase activity
Afu3g00650	proteolysis
Afu3g00670	integral to membrane
Afu3g00690	transcription factor activity
Afu3g00690	regulation of transcription
Afu3g00700	molecular function unknown
Afu3g00700	membrane fraction
Afu3g00700	fungal-type cell wall biogenesis
Afu3g00700	anchored to plasma membrane
Afu3g00720	biological process unknown
Afu3g00720	molecular function unknown
Afu3g00720	cellular component unknown
Afu3g00740	nucleus
Afu3g00740	cytoplasm
Afu3g00740	2-dehydropantoate 2-reductase activity
Afu3g00740	FAD binding
Afu3g00750	metabolic process
Afu3g00750	oxidoreductase activity
Afu3g00760	N-acetyltransferase activity
Afu3g00760	metabolic process
Afu3g00765	N-acetyltransferase activity
Afu3g00765	metabolic process
Afu3g00790	anaerobic glutamate catabolic process
Afu3g00790	methylaspartate ammonia-lyase activity
Afu3g00800	metabolic process
Afu3g00800	oxidoreductase activity
Afu3g00840	FAD binding
Afu3g00910	cell morphogenesis
Afu3g00910	plasma membrane
Afu3g00910	cellular glucan metabolic process
Afu3g00910	fungal-type cell wall biogenesis
Afu3g00910	alpha-1,3-glucan synthase activity
Afu3g00920	biological process unknown
Afu3g00920	molecular function unknown
Afu3g00920	integral to membrane
Afu3g00930	RNA polymerase II transcription factor activity
Afu3g00930	nucleus
Afu3g00930	regulation of transcription

Afu3g00980	transporter activity
Afu3g00980	transport
Afu3g00980	membrane
Afu3g01002	electron transport
Afu3g01002	metabolic process
Afu3g01002	oxidoreductase activity
Afu3g01002	FAD binding
Afu3g01002	coenzyme binding
Afu3g01010	sulfonate dioxygenase activity
Afu3g01010	sulfur metabolic process
Afu3g01010	cellular component unknown
Afu3g01030	biological process unknown
Afu3g01030	molecular function unknown
Afu3g01030	integral to membrane
Afu3g01100	DNA binding
Afu3g01100	nucleus
Afu3g01100	zinc ion binding
Afu3g01110	GMP synthase (glutamine-hydrolyzing) activity
Afu3g01110	cellular component unknown
Afu3g01110	GMP metabolic process
Afu3g01120	integral to plasma membrane
Afu3g01120	response to toxin
Afu3g01120	multidrug transporter activity
Afu3g01170	cystathionine beta-lyase activity
Afu3g01170	cytoplasm
Afu3g01170	sulfur metabolic process
Afu3g01220	aspartic-type endopeptidase activity
Afu3g01220	extracellular region
Afu3g01220	protein catabolic process
Afu3g01220	cell wall-bounded periplasmic space
Afu3g01230	transporter activity
Afu3g01230	transport
Afu3g01230	membrane
Afu3g01290	electron transport
Afu3g01290	oxidoreductase activity
Afu3g01290	coenzyme binding
Afu3g01360	siderophore-iron transmembrane transporter activity
Afu3g01360	siderophore-iron transport
Afu3g01360	integral to membrane
Afu3g01370	transporter activity
Afu3g01370	plasma membrane
Afu3g01370	pantothenate transport
Afu3g01400	plasma membrane
Afu3g01400	xenobiotic-transporting ATPase activity
Afu3g01400	response to drug
Afu3g01410	3-oxoacyl-[acyl-carrier-protein] synthase activity
Afu3g01410	polyketide synthase activity
Afu3g01420	catalytic activity
Afu3g01420	metabolic process
Afu3g01440	molecular function unknown

Afu3g01440	integral to membrane
Afu3g01450	binding
Afu3g01460	monooxygenase activity
Afu3g01460	cellular aromatic compound metabolic process
Afu3g01490	metabolic process
Afu3g01490	zinc ion binding
Afu3g01490	cellular component unknown
Afu3g01490	oxidoreductase activity
Afu3g01510	transcription factor activity
Afu3g01510	nucleus
Afu3g01510	regulation of transcription
Afu3g01520	integral to plasma membrane
Afu3g01520	multidrug transport
Afu3g01520	multidrug efflux pump activity
Afu3g01520	response to drug
Afu3g01540	fungal-type vacuole membrane
Afu3g01540	transporter activity
Afu3g01540	transport
Afu3g01540	monocarboxylic acid transmembrane transporter activity
Afu3g01560	arginine permease activity
Afu3g01560	lysine permease activity
Afu3g01560	plasma membrane
Afu3g01560	basic amino acid transmembrane transporter activity
Afu3g01560	basic amino acid transport
Afu3g01580	metabolic process
Afu3g01580	oxidoreductase activity
Afu3g01600	monooxygenase activity
Afu3g01600	cellular aromatic compound metabolic process
Afu3g01620	programmed cell death
Afu3g01630	biological process unknown
Afu3g01630	molecular function unknown
Afu3g01630	integral to membrane
Afu3g01640	zinc ion binding
Afu3g01640	regulation of transcription
Afu3g01650	carbohydrate binding
Afu3g01660	carbohydrate metabolic process
Afu3g01660	hydrolase activity, hydrolyzing N-glycosyl compounds
Afu3g01670	fructose transmembrane transporter activity
Afu3g01670	galactose transmembrane transporter activity
Afu3g01670	glucose transmembrane transporter activity
Afu3g01670	plasma membrane
Afu3g01670	hexose transport
Afu3g01670	mannose transmembrane transporter activity
Afu3g01700	alpha-glucoside transport
Afu3g01700	alpha-glucoside:hydrogen symporter activity
Afu3g01700	maltose:hydrogen symporter activity
Afu3g01700	membrane fraction
Afu3g01700	trehalose transmembrane transporter activity
Afu3g01700	trehalose transport
Afu3g01780	cytoplasm

Afu3g01780	zinc ion binding
Afu3g01780	oxidoreductase activity
Afu3g01780	formaldehyde assimilation
Afu3g01840	transporter activity
Afu3g01840	transport
Afu3g01840	integral to membrane
Afu3g01880	transcription factor activity
Afu3g01880	regulation of transcription
Afu3g01890	drug transporter activity
Afu3g01890	drug transport
Afu3g01890	integral to membrane
Afu3g01920	acyl-CoA dehydrogenase activity
Afu3g01920	fatty acid catabolic process
Afu3g01920	phospholipid catabolic process
Afu3g01940	transporter activity
Afu3g01940	transport
Afu3g01950	cellular component unknown
Afu3g01950	oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor
Afu3g01950	hexose metabolic process
Afu3g01980	DNA binding
Afu3g01980	zinc ion binding
Afu3g02000	transcription factor activity
Afu3g02000	regulation of transcription
Afu3g02040	molecular function unknown
Afu3g02040	membrane fraction
Afu3g02040	fungal-type cell wall biogenesis
Afu3g02040	anchored to plasma membrane
Afu3g02060	drug transporter activity
Afu3g02060	drug transport
Afu3g02060	integral to membrane
Afu3g02070	transcription factor activity
Afu3g02070	nucleus
Afu3g02070	regulation of transcription, DNA-dependent
Afu3g02070	zinc ion binding
Afu3g02080	plasma membrane
Afu3g02080	allantoate transmembrane transporter activity
Afu3g02080	allantoate transport
Afu3g02090	hydrolase activity, hydrolyzing O-glycosyl compounds
Afu3g02090	carbohydrate metabolic process
Afu3g02100	lipid particle
Afu3g02100	metabolic process
Afu3g02100	oxidoreductase activity
Afu3g02110	transporter activity
Afu3g02110	transport
Afu3g02110	membrane
Afu3g02130	alcohol dehydrogenase (NAD) activity
Afu3g02130	cytoplasm
Afu3g02130	ethanol metabolic process
Afu3g02130	fermentation
Afu3g02140	ion channel activity

Afu3g02140	transport
Afu3g02140	nonselective channel activity
Afu3g02150	transporter activity
Afu3g02150	transport
Afu3g02150	monocarboxylic acid transmembrane transporter activity
Afu3g02150	membrane
Afu3g02160	transcription factor activity
Afu3g02160	nucleus
Afu3g02160	regulation of transcription
Afu3g02210	transcription factor activity
Afu3g02210	nucleus
Afu3g02210	zinc ion binding
Afu3g02210	regulation of transcription
Afu3g02250	nucleus
Afu3g02250	cytoplasm
Afu3g02250	response to stress
Afu3g02250	oxidoreductase activity
Afu3g02250	methylglyoxal reductase (NADH-dependent) activity
Afu3g02270	catalase activity
Afu3g02270	peroxisomal matrix
Afu3g02270	oxygen and reactive oxygen species metabolic process
Afu3g02270	response to oxidative stress
Afu3g02270	pathogenesis
Afu3g02280	fungal-type vacuole
Afu3g02280	alpha,alpha-trehalase activity
Afu3g02280	trehalose catabolic process
Afu3g02280	response to stress
Afu3g02290	metabolic process
Afu3g02290	sulfuric ester hydrolase activity
Afu3g02300	proline dehydrogenase activity
Afu3g02300	mitochondrion
Afu3g02300	glutamate biosynthetic process
Afu3g02300	proline catabolic process
Afu3g02310	pyrroline-5-carboxylate reductase activity
Afu3g02310	cytoplasm
Afu3g02310	proline biosynthetic process
Afu3g02320	biological process unknown
Afu3g02320	DNA binding
Afu3g02320	molecular function unknown
Afu3g02320	nucleus
Afu3g02320	zinc ion binding
Afu3g02330	nucleosome remodeling complex
Afu3g02330	chromatin remodeling
Afu3g02330	SWI/SNF complex
Afu3g02330	RSC complex
Afu3g02330	regulation of transcription
Afu3g02340	negative regulation of transcription from RNA polymerase II promoter
Afu3g02340	transcription corepressor activity
Afu3g02340	nucleus
Afu3g02360	biological process unknown

Afu3g02360	molecular function unknown
Afu3g02360	cytoplasm
Afu3g02370	cytoplasm
Afu3g02370	metabolic process
Afu3g02370	oxidoreductase activity
Afu3g02470	allophanate hydrolase activity
Afu3g02470	urea carboxylase activity
Afu3g02470	cytoplasm
Afu3g02470	urea metabolic process
Afu3g02480	regulation of transcription
Afu3g02500	protein kinase activity
Afu3g02500	cytoplasm
Afu3g02520	transporter activity
Afu3g02520	transport
Afu3g02530	catalytic activity
Afu3g02530	polyketide synthase activity
Afu3g02530	antibiotic biosynthetic process
Afu3g02530	secondary metabolic process
Afu3g02530	polyketide biosynthetic process
Afu3g02570	3-oxoacyl-[acyl-carrier-protein] synthase activity
Afu3g02570	polyketide synthase activity
Afu3g02580	metabolic process
Afu3g02580	integral to membrane
Afu3g02580	oxidoreductase activity
Afu3g02610	transporter activity
Afu3g02610	transport
Afu3g02620	monooxygenase activity
Afu3g02620	cellular aromatic compound metabolic process
Afu3g02710	metabolic process
Afu3g02710	zinc ion binding
Afu3g02710	oxidoreductase activity
Afu3g02720	transporter activity
Afu3g02720	integral to plasma membrane
Afu3g02720	transport
Afu3g02750	DNA binding
Afu3g02760	ATP-binding cassette (ABC) transporter activity
Afu3g02760	ATP-binding cassette (ABC) transporter activity
Afu3g02760	ATP binding
Afu3g02760	transport
Afu3g02760	transport
Afu3g02780	integral to plasma membrane
Afu3g02780	response to toxin
Afu3g02780	multidrug transporter activity
Afu3g02830	molecular function unknown
Afu3g02890	transporter activity
Afu3g02890	transport
Afu3g02890	membrane
Afu3g02910	transketolase activity
Afu3g02910	cytoplasm
Afu3g02910	pentose-phosphate shunt

Afu3g02920	transcription factor activity
Afu3g02920	nucleus
Afu3g02920	regulation of transcription
Afu3g02930	metabolic process
Afu3g02930	transferase activity, transferring glycosyl groups
Afu3g02950	metabolic process
Afu3g02950	oxidoreductase activity
Afu3g02980	transition metal ion transport
Afu3g02980	plasma membrane
Afu3g02980	oxidoreductase activity, oxidizing metal ions
Afu3g03010	plasma membrane
Afu3g03010	phosphate transport
Afu3g03010	sodium:inorganic phosphate symporter activity
Afu3g03070	regulation of transcription, DNA-dependent
Afu3g03070	zinc ion binding
Afu3g03070	chromatin modification
Afu3g03080	hydrolase activity, hydrolyzing O-glycosyl compounds
Afu3g03080	1,3-beta-glucan metabolic process
Afu3g03080	fungal-type cell wall
Afu3g03160	nucleus
Afu3g03160	cytoplasm
Afu3g03160	glycerol metabolic process
Afu3g03160	response to salt stress
Afu3g03160	glycerol dehydrogenase (NADP+) activity
Afu3g03180	metabolic process
Afu3g03180	oxidoreductase activity
Afu3g03190	plasma membrane
Afu3g03190	integral to plasma membrane
Afu3g03190	multidrug transport
Afu3g03190	multidrug transporter activity
Afu3g03240	transporter activity
Afu3g03240	transport
Afu3g03240	monocarboxylic acid transmembrane transporter activity
Afu3g03240	membrane
Afu3g03250	aldehyde dehydrogenase (NAD) activity
Afu3g03250	mitochondrion
Afu3g03270	metabolic process
Afu3g03270	hydrolase activity
Afu3g03300	FAD binding
Afu3g03310	biological process unknown
Afu3g03310	molecular function unknown
Afu3g03310	integral to membrane
Afu3g03320	fungal-type vacuole membrane
Afu3g03320	transporter activity
Afu3g03320	transport
Afu3g03320	monocarboxylic acid transmembrane transporter activity
Afu3g03330	mitochondrion
Afu3g03330	fatty acid biosynthetic process
Afu3g03330	aerobic respiration
Afu3g03330	enoyl-[acyl-carrier-protein] reductase activity

Afu3g03380	metabolic process
Afu3g03380	acetyltransferase activity
Afu3g03430	ATP-binding cassette (ABC) transporter activity
Afu3g03430	ATP binding
Afu3g03430	transport
Afu3g03440	cellular iron ion homeostasis
Afu3g03440	siderophore-iron (ferrioxamine) uptake transmembrane transporter activity
Afu3g03440	siderophore-iron transport
Afu3g03440	integral to membrane
Afu3g03450	metabolic process
Afu3g03450	oxidoreductase activity
Afu3g03460	metabolic process
Afu3g03460	hydrolase activity
Afu3g03480	metabolic process
Afu3g03480	oxidoreductase activity
Afu3g03490	O-methyltransferase activity
Afu3g03500	transporter activity
Afu3g03500	transport
Afu3g03620	carbohydrate metabolic process
Afu3g03620	transferase activity, transferring glycosyl groups
Afu3g03640	cellular iron ion homeostasis
Afu3g03640	siderophore-iron (ferrioxamine) uptake transmembrane transporter activity
Afu3g03640	siderophore-iron transport
Afu3g03640	integral to membrane
Afu3g03650	N-acetyltransferase activity
Afu3g03650	metabolic process
Afu3g03660	hydrolase activity, acting on ester bonds
Afu3g03670	ATP-binding cassette (ABC) transporter activity
Afu3g03670	ATP-binding cassette (ABC) transporter activity
Afu3g03670	ATP binding
Afu3g03670	transport
Afu3g03670	transport
Afu3g03700	fructose transmembrane transporter activity
Afu3g03700	glucose transmembrane transporter activity
Afu3g03700	plasma membrane
Afu3g03700	hexose transport
Afu3g03700	mannose transmembrane transporter activity
Afu3g03820	integral to plasma membrane
Afu3g03820	nicotinamide mononucleotide permease activity
Afu3g03820	nicotinamide mononucleotide transport
Afu3g03920	transcription factor activity
Afu3g03920	nucleus
Afu3g03920	zinc ion binding
Afu3g03920	regulation of transcription
Afu3g03930	metabolic process
Afu3g03930	oxidoreductase activity
Afu3g03940	biological process unknown
Afu3g03940	molecular function unknown
Afu3g03940	nucleus
Afu3g03940	cytoplasm

Afu3g03970	cytochrome-b5 reductase activity
Afu3g03970	microsome
Afu3g03970	electron transport
Afu3g03980	metabolic process
Afu3g03980	oxidoreductase activity
Afu3g04000	transporter activity
Afu3g04000	transport
Afu3g04010	integral to plasma membrane
Afu3g04010	nicotinamide mononucleotide permease activity
Afu3g04010	nicotinamide mononucleotide transport
Afu3g04060	late endosome to vacuole transport
Afu3g04070	transcription factor activity
Afu3g04070	nucleus
Afu3g04070	transcription
Afu3g04070	positive regulation of gene-specific transcription involved in unfolded protein response
Afu3g04110	nucleus
Afu3g04110	nucleolus
Afu3g04110	rRNA processing
Afu3g04110	cell growth and/or maintenance
Afu3g04110	maturation of SSU-rRNA
Afu3g04110	snoRNA binding
Afu3g04120	nuclear chromatin
Afu3g04120	chromatin binding
Afu3g04120	chromatin silencing at telomere
Afu3g04120	transcription
Afu3g04120	histone methylation
Afu3g04120	histone-lysine N-methyltransferase activity
Afu3g04120	transcription regulator activity
Afu3g04130	amidase activity
Afu3g04130	mitochondrion
Afu3g04130	aerobic respiration
Afu3g04150	mitochondrion
Afu3g04150	fatty acid biosynthetic process
Afu3g04150	aerobic respiration
Afu3g04150	enoyl-[acyl-carrier-protein] reductase activity
Afu3g04160	biological process unknown
Afu3g04160	fungal-type vacuole
Afu3g04160	molecular function unknown
Afu3g04170	pyruvate dehydrogenase (acetyl-transferring) activity
Afu3g04170	binding
Afu3g04170	mitochondrion
Afu3g04170	pyruvate metabolic process
Afu3g04170	pyruvate dehydrogenase complex
Afu3g04180	DNA binding
Afu3g04180	nucleus
Afu3g04180	zinc ion binding
Afu3g04200	tRNA (guanine-N2-)-methyltransferase activity
Afu3g04200	nuclear outer membrane
Afu3g04200	mitochondrion
Afu3g04200	tRNA methylation

Afu3g04210	fatty-acid synthase activity
Afu3g04210	fatty acid biosynthetic process
Afu3g04220	fatty-acid synthase activity
Afu3g04220	[acyl-carrier-protein] S-acetyltransferase activity
Afu3g04220	[acyl-carrier-protein] S-malonyltransferase activity
Afu3g04220	3-hydroxypalmitoyl-[acyl-carrier-protein] dehydratase activity
Afu3g04220	enoyl-[acyl-carrier-protein] reductase (NADH) activity
Afu3g04220	cytosol
Afu3g04220	fatty acid synthase complex
Afu3g04220	fatty acid biosynthetic process
Afu3g04230	transcription factor TFIIF complex
Afu3g04230	transcription initiation from RNA polymerase II promoter
Afu3g04230	general RNA polymerase II transcription factor activity
Afu3g04240	lipid metabolic process
Afu3g04240	cellular component unknown
Afu3g04240	lipase activity
Afu3g04250	inositol metabolic process
Afu3g04250	cellular component unknown
Afu3g04250	inositol-1(or 4)-monophosphatase activity
Afu3g04260	biological process unknown
Afu3g04260	molecular function unknown
Afu3g04260	cytoplasm
Afu3g04300	molecular function unknown
Afu3g04300	cytoplasm
Afu3g04300	actin cytoskeleton organization
Afu3g04310	nucleus
Afu3g04310	maturation of SSU-rRNA
Afu3g04310	snoRNA binding
Afu3g05320	DNA binding
Afu3g05320	nucleus
Afu3g05320	zinc ion binding
Afu3g05330	nucleic acid binding
Afu3g05340	microtubule associated complex
Afu3g05340	protein targeting to vacuole
Afu3g05340	autophagy
Afu3g05340	microtubule binding
Afu3g05350	nuclear nucleosome
Afu3g05350	DNA binding
Afu3g05350	chromatin assembly or disassembly
Afu3g05360	nuclear nucleosome
Afu3g05360	DNA binding
Afu3g05360	chromatin assembly or disassembly
Afu3g05370	molecular function unknown
Afu3g05370	mitochondrial matrix
Afu3g05370	tricarboxylic acid cycle
Afu3g05370	2-oxoglutarate metabolic process
Afu3g05400	peripheral to membrane of membrane fraction
Afu3g05400	karyogamy during conjugation with cellular fusion
Afu3g05400	co-chaperone activity
Afu3g05400	endoplasmic reticulum

Afu3g05400	protein folding
Afu3g05410	translation release factor activity
Afu3g05410	mitochondrion
Afu3g05410	translation
Afu3g05410	translational termination
Afu3g05420	tricarboxylate secondary active transmembrane transporter activity
Afu3g05420	mitochondrial inner membrane
Afu3g05420	mitochondrial citrate transport
Afu3g05430	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
Afu3g05430	deadenylation-dependent decapping of nuclear-transcribed mRNA
Afu3g05430	cytoplasmic mRNA processing body
Afu3g05430	protein binding
Afu3g05430	cytoplasm
Afu3g05440	molecular function unknown
Afu3g05440	nucleus
Afu3g05440	DNA repair
Afu3g05440	cell proliferation
Afu3g05450	cytoplasm
Afu3g05450	mitochondrion
Afu3g05450	proteolysis
Afu3g05450	metallopeptidase activity
Afu3g05460	mitochondrial genome maintenance
Afu3g05460	structural constituent of ribosome
Afu3g05460	mitochondrial large ribosomal subunit
Afu3g05460	translation
Afu3g05480	nucleus
Afu3g05480	cytoplasm
Afu3g05480	sulfur metabolic process
Afu3g05480	carbon-sulfur lyase activity
Afu3g05490	nucleus
Afu3g05490	nucleolus
Afu3g05490	maturation of SSU-rRNA
Afu3g05490	snoRNA binding
Afu3g05500	structural molecule activity
Afu3g05500	nuclear pore
Afu3g05500	mRNA export from nucleus
Afu3g05500	rRNA export from nucleus
Afu3g05500	snRNA export from nucleus
Afu3g05500	tRNA export from nucleus
Afu3g05500	NLS-bearing substrate import into nucleus
Afu3g05500	snRNP protein import into nucleus
Afu3g05500	mRNA-binding (hnRNP) protein import into nucleus
Afu3g05500	ribosomal protein import into nucleus
Afu3g05500	protein export from nucleus
Afu3g05500	nuclear pore organization
Afu3g05520	steroid biosynthetic process
Afu3g05520	oxysterol binding
Afu3g05520	cellular component unknown
Afu3g05530	nuclear condensin complex
Afu3g05530	molecular function unknown

Afu3g05530	mitotic chromosome condensation
Afu3g05540	protein serine/threonine kinase activity
Afu3g05540	nucleoplasm
Afu3g05540	DNA replication initiation
Afu3g05540	regulation of DNA replication
Afu3g05540	protein amino acid phosphorylation
Afu3g05550	nucleus
Afu3g05550	cytoplasm
Afu3g05550	cysteine-type peptidase activity
Afu3g05550	protein catabolic process
Afu3g05560	RNA polymerase II transcription factor activity
Afu3g05560	protein binding
Afu3g05560	chromatin remodeling
Afu3g05560	RSC complex
Afu3g05560	ascospore formation
Afu3g05560	regulation of transcription
Afu3g05580	cytokinesis
Afu3g05580	cell wall chitin biosynthetic process
Afu3g05580	response to osmotic stress
Afu3g05580	enzyme activator activity
Afu3g05590	DNA helicase activity
Afu3g05590	nucleus
Afu3g05590	chromosome segregation
Afu3g05600	RNA binding
Afu3g05600	structural constituent of ribosome
Afu3g05600	nucleus
Afu3g05600	cytosolic large ribosomal subunit (sensu Eukaryota)
Afu3g05600	translation
Afu3g05630	phospholipase D activity
Afu3g05630	prospore membrane
Afu3g05630	endosome
Afu3g05630	phospholipid metabolic process
Afu3g05630	exocytosis
Afu3g05630	meiosis
Afu3g05630	ascospore formation
Afu3g05630	secretory pathway
Afu3g05630	regulation of lipid biosynthetic process
Afu3g05650	trehalose-phosphatase activity
Afu3g05650	alpha,alpha-trehalose-phosphate synthase complex (UDP-forming)
Afu3g05650	carbohydrate metabolic process
Afu3g05650	trehalose biosynthetic process
Afu3g05650	trehalose biosynthetic process
Afu3g05650	response to stress
Afu3g05660	transporter activity
Afu3g05660	transport
Afu3g05660	monocarboxylic acid transmembrane transporter activity
Afu3g05660	membrane
Afu3g05720	molecular function unknown
Afu3g05720	cytoplasm
Afu3g05720	nuclear migration

Afu3g05730	nicotinate-nucleotide diphosphorylase (carboxylating) activity
Afu3g05730	nucleus
Afu3g05730	cytoplasm
Afu3g05730	NAD biosynthetic process
Afu3g05740	galactose metabolic process
Afu3g05740	cellular component unknown
Afu3g05760	transcription factor activity
Afu3g05760	nucleus
Afu3g05760	zinc ion binding
Afu3g05760	regulation of transcription
Afu3g05770	replicative cell aging
Afu3g05770	RAS small monomeric GTPase activity
Afu3g05770	plasma membrane
Afu3g05770	activation of adenylate cyclase activity
Afu3g05770	Ras protein signal transduction
Afu3g05780	transcription factor activity
Afu3g05780	signal transducer activity
Afu3g05780	nucleus
Afu3g05780	zinc ion binding
Afu3g05780	response to light stimulus
Afu3g05780	blue light signaling pathway
Afu3g05780	regulation of transcription
Afu3g05840	biological process unknown
Afu3g05840	RNA binding
Afu3g05840	nucleoplasm
Afu3g05840	nucleolus
Afu3g05860	3'-5'-exoribonuclease activity
Afu3g05860	nuclear exosome (RNase complex)
Afu3g05860	cytoplasmic exosome (RNase complex)
Afu3g05860	35S primary transcript processing
Afu3g05860	mRNA catabolic process
Afu3g05880	cytoplasm
Afu3g05880	steroid biosynthetic process
Afu3g05880	oxysterol binding
Afu3g05890	nucleus
Afu3g05890	chromatin organization
Afu3g05890	nucleosome assembly
Afu3g05890	regulation of transcription, DNA-dependent
Afu3g05890	RNA elongation from RNA polymerase II promoter
Afu3g05890	transcription elongation factor complex
Afu3g05890	RNA polymerase II transcription elongation factor activity
Afu3g05900	MAP kinase kinase activity
Afu3g05900	cytoplasm
Afu3g05900	protein amino acid phosphorylation
Afu3g05940	molecular function unknown
Afu3g05940	cytoplasm
Afu3g05940	transcription from RNA polymerase II promoter
Afu3g05950	mitotic spindle elongation
Afu3g05950	mitotic sister chromatid segregation
Afu3g05950	ubiquitin-protein ligase activity

Afu3g05950	protein binding
Afu3g05950	anaphase-promoting complex
Afu3g05950	ubiquitin-dependent protein catabolic process
Afu3g05950	mitotic metaphase/anaphase transition
Afu3g05950	cyclin catabolic process
Afu3g05970	translation initiation factor activity
Afu3g05970	cytosolic ribosome (sensu Eukaryota)
Afu3g05970	cytosolic small ribosomal subunit (sensu Eukaryota)
Afu3g05970	translational initiation
Afu3g06030	protein polyubiquitination
Afu3g06030	proteasome complex
Afu3g06030	ubiquitin conjugating enzyme activity
Afu3g06030	protein monoubiquitination
Afu3g06030	response to stress
Afu3g06030	ascospore formation
Afu3g06040	glutaryl-CoA dehydrogenase activity
Afu3g06060	DNA synthesis during DNA repair
Afu3g06060	nucleus
Afu3g06060	DNA replication
Afu3g06060	DNA repair
Afu3g06060	5'-flap endonuclease activity
Afu3g06070	nuclear nucleosome
Afu3g06070	DNA binding
Afu3g06070	nucleus
Afu3g06070	regulation of transcription, DNA-dependent
Afu3g06070	negative regulation of DNA recombination
Afu3g06080	plasma membrane
Afu3g06080	1-phosphatidylinositol-4-phosphate 5-kinase activity
Afu3g06080	actin cytoskeleton organization
Afu3g06080	actin cable formation
Afu3g06090	regulation of transcription involved in G1 phase of mitotic cell cycle
Afu3g06090	SAGA complex
Afu3g06090	transcription factor TFIID complex
Afu3g06090	chromatin organization
Afu3g06090	transcription initiation from RNA polymerase II promoter
Afu3g06090	protein amino acid acetylation
Afu3g06090	general RNA polymerase II transcription factor activity
Afu3g06090	chromatin modification
Afu3g06090	histone acetylation
Afu3g06110	endopeptidase activity
Afu3g06110	ubiquitin-dependent protein catabolic process
Afu3g06110	proteasome regulatory particle, lid subcomplex
Afu3g06120	trans-hexaprenyltranstransferase activity
Afu3g06120	mitochondrion
Afu3g06120	ubiquinone metabolic process
Afu3g06130	biological process unknown
Afu3g06130	molecular function unknown
Afu3g06130	endoplasmic reticulum
Afu3g06140	incipient cellular bud site
Afu3g06140	structural constituent of cytoskeleton

Afu3g06140	exocytosis
Afu3g06140	endocytosis
Afu3g06140	actin filament organization
Afu3g06140	cell wall organization
Afu3g06140	bipolar cellular bud site selection
Afu3g06180	phosphodiesterase I activity
Afu3g06180	nucleus
Afu3g06180	DNA repair
Afu3g06180	double-stranded DNA specific 3'-5' exodeoxyribonuclease activity
Afu3g06190	cytochrome-c oxidase activity
Afu3g06190	mitochondrial respiratory chain complex IV
Afu3g06190	aerobic respiration
Afu3g06190	enzyme regulator activity
Afu3g06210	phosphoribosylaminoimidazolesuccinocarboxamide synthase activity
Afu3g06210	phosphoribosylaminoimidazolesuccinocarboxamide synthase activity
Afu3g06210	nucleus
Afu3g06210	cytoplasm
Afu3g06210	purine base metabolic process
Afu3g06210	purine ribonucleotide biosynthetic process
Afu3g06250	negative regulation of transcription from RNA polymerase II promoter
Afu3g06250	transcription factor complex
Afu3g06250	RNA polymerase II transcription mediator activity
Afu3g06260	translation initiation factor activity
Afu3g06260	ribosome
Afu3g06260	translational initiation
Afu3g06280	Rho GTPase activator activity
Afu3g06280	osmosensory signaling pathway
Afu3g06300	pheromone-dependent signal transduction involved in conjugation with cellular fusion
Afu3g06300	Rho small monomeric GTPase activity
Afu3g06300	signal transducer activity
Afu3g06300	soluble fraction
Afu3g06300	plasma membrane
Afu3g06300	exocytosis
Afu3g06300	invasive growth
Afu3g06300	Rho protein signal transduction
Afu3g06310	molecular function unknown
Afu3g06310	nucleolus
Afu3g06310	rRNA processing
Afu3g06310	response to desiccation
Afu3g06340	chaperone activity
Afu3g06340	mitochondrial inner membrane
Afu3g06340	aerobic respiration
Afu3g06370	biological process unknown
Afu3g06370	molecular function unknown
Afu3g06370	nucleus
Afu3g06370	cytoplasm
Afu3g06390	cytoplasm
Afu3g06390	2-dehydropantoate 2-reductase activity
Afu3g06390	pantothenate biosynthetic process
Afu3g06410	molecular function unknown

Afu3g06410	mitochondrial inner membrane
Afu3g06410	ubiquinone metabolic process
Afu3g06430	guanyl-nucleotide exchange factor activity
Afu3g06430	cytosol
Afu3g06430	exocytosis
Afu3g06430	cytoplasmic membrane-bounded vesicle
Afu3g06450	dolichyl-phosphate-mannose-protein mannosyltransferase activity
Afu3g06450	endoplasmic reticulum membrane
Afu3g06450	protein amino acid O-linked glycosylation
Afu3g06470	protein targeting to membrane
Afu3g06470	palmitoyltransferase activity
Afu3g06470	protein amino acid palmitoylation
Afu3g06470	integral to endoplasmic reticulum membrane
Afu3g06480	nucleus
Afu3g06480	RNA elongation
Afu3g06480	regulation of transcription, DNA-dependent
Afu3g06480	histone methylation
Afu3g06480	histone-lysine N-methyltransferase activity
Afu3g06492	cofactor metabolic process
Afu3g06530	sulfate assimilation
Afu3g06530	sulfate adenylyltransferase (ATP) activity
Afu3g06530	cytoplasm
Afu3g06530	methionine metabolic process
Afu3g06540	sulfate assimilation
Afu3g06540	phosphoadenylyl-sulfate reductase (thioredoxin) activity
Afu3g06540	intracellular
Afu3g06540	methionine metabolic process
Afu3g06550	phosphoserine phosphatase activity
Afu3g06550	nucleus
Afu3g06550	cytoplasm
Afu3g06550	serine family amino acid biosynthetic process
Afu3g06560	catalytic activity
Afu3g06560	mitochondrion
Afu3g06560	fatty acid metabolic process
Afu3g06590	deoxyribose-phosphate aldolase activity
Afu3g06590	deoxyribonucleotide catabolic process
Afu3g06600	sulfate assimilation
Afu3g06600	uroporphyrin-III C-methyltransferase activity
Afu3g06600	methionine metabolic process
Afu3g06600	uroporphyrinogen III biosynthetic process
Afu3g06600	cellular component unknown
Afu3g06600	siroheme biosynthetic process
Afu3g06610	endopeptidase activity
Afu3g06610	ubiquitin-dependent protein catabolic process
Afu3g06610	proteasome regulatory particle, lid subcomplex
Afu3g06620	biological process unknown
Afu3g06620	molecular function unknown
Afu3g06620	cytoplasm
Afu3g06640	structural constituent of ribosome
Afu3g06640	cytosolic small ribosomal subunit (sensu Eukaryota)

Afu3g06640	translation
Afu3g06640	ribosome biogenesis
Afu3g06650	ethanolaminephosphotransferase activity
Afu3g06650	endoplasmic reticulum
Afu3g06650	phosphatidylethanolamine biosynthetic process
Afu3g06680	mitochondrion
Afu3g06680	protein lipoylation
Afu3g06680	ligase activity
Afu3g06690	Rho small monomeric GTPase activity
Afu3g06690	signal transducer activity
Afu3g06690	intracellular
Afu3g06690	exocytosis
Afu3g06690	actin filament organization
Afu3g06690	small GTPase mediated signal transduction
Afu3g06700	protein deneddylation
Afu3g06700	signalosome
Afu3g06700	regulation of developmental process
Afu3g06730	fructose transmembrane transporter activity
Afu3g06730	galactose transmembrane transporter activity
Afu3g06730	glucose transmembrane transporter activity
Afu3g06730	plasma membrane
Afu3g06730	hexose transport
Afu3g06730	mannose transmembrane transporter activity
Afu3g06740	nucleus
Afu3g06740	galactose metabolic process
Afu3g06740	regulation of transcription, DNA-dependent
Afu3g06740	zinc ion binding
Afu3g06740	transcription activator activity
Afu3g06760	structural constituent of ribosome
Afu3g06760	cytosolic large ribosomal subunit (sensu Eukaryota)
Afu3g06760	translation
Afu3g06770	nuclear mRNA splicing, via spliceosome
Afu3g06770	protein binding
Afu3g06770	spliceosomal complex
Afu3g06770	pre-mRNA splicing factor activity
Afu3g06780	zeta DNA polymerase activity
Afu3g06780	nucleus
Afu3g06780	mutagenesis
Afu3g06780	DNA repair
Afu3g06790	RNA-directed RNA polymerase activity
Afu3g06790	cytoplasm
Afu3g06790	posttranscriptional gene silencing
Afu3g06820	D-lactate dehydrogenase (cytochrome) activity
Afu3g06820	mitochondrial inner membrane
Afu3g06820	carbohydrate metabolic process
Afu3g06820	aerobic respiration
Afu3g06830	aspartate-semialdehyde dehydrogenase activity
Afu3g06830	nucleus
Afu3g06830	cytoplasm
Afu3g06830	methionine metabolic process

Afu3g06830	threonine metabolic process
Afu3g06830	homoserine biosynthetic process
Afu3g06840	structural constituent of ribosome
Afu3g06840	cytosolic small ribosomal subunit (sensu Eukaryota)
Afu3g06840	translation
Afu3g06870	DNA binding
Afu3g06880	protein binding
Afu3g06880	cytosol
Afu3g06880	protein localization
Afu3g06910	nucleus
Afu3g06910	negative regulation of transcription
Afu3g06910	general transcriptional repressor activity
Afu3g06922	RNA helicase activity
Afu3g06922	cytoplasm
Afu3g06922	mRNA catabolic process
Afu3g06922	regulation of translation
Afu3g06922	translation repressor activity
Afu3g06940	DNA binding
Afu3g06940	nucleus
Afu3g06940	zinc ion binding
Afu3g06950	mitochondrial genome maintenance
Afu3g06950	transporter activity
Afu3g06950	mitochondrion
Afu3g06960	structural constituent of ribosome
Afu3g06960	cytosolic large ribosomal subunit (sensu Eukaryota)
Afu3g06960	translation
Afu3g06970	structural constituent of ribosome
Afu3g06970	cytosolic small ribosomal subunit (sensu Eukaryota)
Afu3g06970	translation
Afu3g06970	regulation of translational fidelity
Afu3g07020	conjugation with cellular fusion
Afu3g07020	cell morphogenesis
Afu3g07020	cytokinesis
Afu3g07020	structural constituent of cytoskeleton
Afu3g07020	phosphatidylinositol binding
Afu3g07020	ascospore wall
Afu3g07020	prospore membrane
Afu3g07020	cell wall organization
Afu3g07020	axial cellular bud site selection
Afu3g07040	fungal-type vacuole
Afu3g07040	Gly-X carboxypeptidase activity
Afu3g07040	proteolysis
Afu3g07040	nitrogen compound metabolic process
Afu3g07080	biological process unknown
Afu3g07080	fungal-type vacuole
Afu3g07080	molecular function unknown
Afu3g07110	chitinase activity
Afu3g07110	cell wall chitin catabolic process
Afu3g07110	fungal-type cell wall
Afu3g07120	transporter activity

Afu3g07120	plasma membrane
Afu3g07120	transport
Afu3g07130	two-component sensor activity
Afu3g07130	protein histidine kinase activity
Afu3g07130	protein amino acid phosphorylation
Afu3g07150	cytoplasm
Afu3g07150	glutamate catabolic process
Afu3g07150	response to oxidative stress
Afu3g07150	succinate-semialdehyde dehydrogenase [NAD(P)+] activity
Afu3g07160	chitinase activity
Afu3g07160	chitin catabolic process
Afu3g07160	chitin binding
Afu3g07160	fungal-type cell wall
Afu3g07170	molecular function unknown
Afu3g07170	endoplasmic reticulum
Afu3g07170	GPI anchor biosynthetic process
Afu3g07180	pantothenate kinase activity
Afu3g07180	intracellular
Afu3g07180	coenzyme A biosynthetic process
Afu3g07200	RNA helicase activity
Afu3g07200	cytoplasm
Afu3g07200	translational initiation
Afu3g07210	polysaccharide metabolic process
Afu3g07210	deacetylase activity
Afu3g07230	phosphopantothenate--cysteine ligase activity
Afu3g07230	intracellular
Afu3g07230	coenzyme A biosynthetic process
Afu3g07290	biological process unknown
Afu3g07290	molecular function unknown
Afu3g07290	cellular component unknown
Afu3g07300	plasma membrane
Afu3g07300	xenobiotic-transporting ATPase activity
Afu3g07300	drug transport
Afu3g07300	response to drug
Afu3g07330	biological process unknown
Afu3g07330	molecular function unknown
Afu3g07330	nucleus
Afu3g07330	cytoplasm
Afu3g07360	molecular function unknown
Afu3g07360	mitochondrial inner membrane
Afu3g07360	generation of precursor metabolites and energy
Afu3g07360	protein complex assembly
Afu3g07360	copper ion transport
Afu3g07380	biological process unknown
Afu3g07380	hydrolase activity, hydrolyzing O-glycosyl compounds
Afu3g07380	cellular component unknown
Afu3g07430	histone deacetylase complex
Afu3g07430	peptidyl-prolyl cis-trans isomerase activity
Afu3g07430	protein metabolic process
Afu3g07440	pseudouridylate synthase activity

Afu3g07440	cytoplasm
Afu3g07440	riboflavin biosynthetic process
Afu3g07440	DRAP deaminase activity
Afu3g07480	RNA binding
Afu3g07520	hydrolase activity, hydrolyzing O-glycosyl compounds
Afu3g07520	1,3-beta-glucan metabolic process
Afu3g07520	fungal-type cell wall
Afu3g07550	integral to membrane
Afu3g07590	t-SNARE activity
Afu3g07590	cis-Golgi network
Afu3g07590	ER to Golgi vesicle-mediated transport
Afu3g07590	retrograde vesicle-mediated transport, Golgi to ER
Afu3g07590	intra-Golgi vesicle-mediated transport
Afu3g07590	vesicle fusion
Afu3g07620	biological process unknown
Afu3g07620	molecular function unknown
Afu3g07620	mitochondrion
Afu3g07640	plasma membrane
Afu3g07640	regulation of pH
Afu3g07640	hydrogen-exporting ATPase activity, phosphorylative mechanism
Afu3g07640	proton transport
Afu3g07670	nucleoplasm
Afu3g07670	RNA elongation from RNA polymerase II promoter
Afu3g07670	reciprocal meiotic recombination
Afu3g07670	positive transcription elongation factor activity
Afu3g07680	ribosomal subunit export from nucleus
Afu3g07680	Ran GTPase activator activity
Afu3g07680	nucleus
Afu3g07680	cytosol
Afu3g07680	rRNA export from nucleus
Afu3g07680	protein import into nucleus
Afu3g07680	rRNA metabolic process
Afu3g07700	endoplasmic reticulum
Afu3g07700	protein amino acid glycosylation
Afu3g07700	dolichol-linked oligosaccharide biosynthetic process
Afu3g07700	transferase activity, transferring hexosyl groups
Afu3g07710	ribosomal small subunit assembly
Afu3g07710	single-stranded DNA binding
Afu3g07710	RNA binding
Afu3g07710	nucleus
Afu3g07710	nucleolus
Afu3g07710	rRNA processing
Afu3g07710	programmed cell death
Afu3g07790	argininosuccinate lyase activity
Afu3g07790	cytosol
Afu3g07790	arginine biosynthetic process
Afu3g07810	mitochondrial respiratory chain complex II
Afu3g07810	tricarboxylic acid cycle
Afu3g07810	mitochondrial electron transport, succinate to ubiquinone
Afu3g07810	succinate dehydrogenase (ubiquinone) activity

Afu3g07820	endopeptidase activity
Afu3g07820	proteasome regulatory particle
Afu3g07820	ubiquitin-dependent protein catabolic process
Afu3g07820	ATPase activity
Afu3g07830	chaperone activity
Afu3g07830	cytoplasm
Afu3g07830	chaperonin-containing T-complex
Afu3g07830	cytoskeleton
Afu3g07830	protein folding
Afu3g07830	cytoskeleton organization
Afu3g07850	fungal-type vacuole membrane
Afu3g07850	conjugation with cellular fusion
Afu3g07850	peptide pheromone maturation
Afu3g07850	protein processing
Afu3g07850	dipeptidyl-peptidase and tripeptidyl-peptidase activity
Afu3g07860	transferase activity, transferring glycosyl groups
Afu3g07910	UDP-glucose 4-epimerase activity
Afu3g07910	galactose metabolic process
Afu3g07910	cellular component unknown
Afu3g07940	condensed nuclear chromosome kinetochore
Afu3g07940	phosphoinositide phospholipase C activity
Afu3g07940	nucleus
Afu3g07940	pseudohyphal growth
Afu3g07940	signal transduction
Afu3g07940	cell growth and/or maintenance
Afu3g07950	transporter activity
Afu3g07950	transport
Afu3g07950	membrane
Afu3g07960	sulfonate dioxygenase activity
Afu3g07960	sulfur metabolic process
Afu3g07960	cellular component unknown
Afu3g07970	molecular function unknown
Afu3g07970	cellular component unknown
Afu3g07990	gamma-aminobutyric acid transporter activity
Afu3g07990	plasma membrane
Afu3g07990	transport
Afu3g08000	peroxisome
Afu3g08000	peroxisome organization
Afu3g08000	ATPase activity
Afu3g08010	transcription factor activity
Afu3g08010	nucleus
Afu3g08010	regulation of transcription, DNA-dependent
Afu3g08010	zinc ion binding
Afu3g08010	glucan catabolic process
Afu3g08020	biological process unknown
Afu3g08020	molecular function unknown
Afu3g08020	cellular component unknown
Afu3g08030	nucleus
Afu3g08030	cytoplasm
Afu3g08030	tRNA (guanine) methyltransferase activity

Afu3g08030	tRNA methylation
Afu3g08040	DNA-directed RNA polymerase activity
Afu3g08040	DNA-directed RNA polymerase II, core complex
Afu3g08040	transcription from RNA polymerase II promoter
Afu3g08050	specific RNA polymerase II transcription factor activity
Afu3g08050	nucleus
Afu3g08050	regulation of transcription from RNA polymerase II promoter
Afu3g08050	nitrogen utilization
Afu3g08080	structural constituent of ribosome
Afu3g08080	mitochondrial large ribosomal subunit
Afu3g08080	translation
Afu3g08090	nucleus
Afu3g08090	translation
Afu3g08090	ribosomal large subunit biogenesis
Afu3g08100	condensed nuclear chromosome kinetochore
Afu3g08100	protein serine/threonine/tyrosine kinase activity
Afu3g08100	spindle pole body
Afu3g08100	mitotic cell cycle spindle assembly checkpoint
Afu3g08100	spindle pole body duplication in nuclear envelope
Afu3g08120	RNA metabolic process
Afu3g08140	catalytic activity
Afu3g08140	mitochondrion
Afu3g08140	metabolic process
Afu3g08160	RNA helicase activity
Afu3g08160	translation initiation factor activity
Afu3g08160	cytoplasm
Afu3g08160	ribosome
Afu3g08160	translational initiation
Afu3g08160	regulation of translational initiation
Afu3g08170	chromatin remodeling
Afu3g08170	protein ubiquitination during ubiquitin-dependent protein catabolic process
Afu3g08180	fungal-type vacuole membrane
Afu3g08180	copper ion transmembrane transporter activity
Afu3g08180	copper uptake transmembrane transporter activity
Afu3g08180	copper ion import
Afu3g08180	intracellular copper ion transport
Afu3g08200	alpha-mannosidase activity
Afu3g08200	vacuolar membrane
Afu3g08200	carbohydrate metabolic process
Afu3g08220	biological process unknown
Afu3g08220	peroxisome
Afu3g08220	pyrophosphatase activity
Afu3g08230	mitochondrion
Afu3g08240	biological process unknown
Afu3g08240	molecular function unknown
Afu3g08240	integral to membrane
Afu3g08260	mitotic sister chromatid segregation
Afu3g08260	DNA secondary structure binding
Afu3g08260	nuclear cohesin complex
Afu3g08260	AT DNA binding

Afu3g08260	double-stranded DNA binding
Afu3g08260	ATPase activity
Afu3g08270	protein binding
Afu3g08270	mitochondrion
Afu3g08270	mitochondrial pyruvate dehydrogenase complex
Afu3g08270	acetyl-CoA biosynthetic process from pyruvate
Afu3g08280	mitotic spindle elongation
Afu3g08280	mitotic sister chromatid segregation
Afu3g08280	nucleus
Afu3g08280	anaphase-promoting complex
Afu3g08280	cytoplasm
Afu3g08280	ubiquitin-dependent protein catabolic process
Afu3g08280	mitotic metaphase/anaphase transition
Afu3g08280	enzyme activator activity
Afu3g08280	cyclin catabolic process
Afu3g08280	regulation of cell size
Afu3g08290	biological process unknown
Afu3g08290	molecular function unknown
Afu3g08290	cytoplasm
Afu3g08300	cell cycle checkpoint
Afu3g08300	DNA clamp loader activity
Afu3g08300	DNA replication factor C complex
Afu3g08300	leading strand elongation
Afu3g08300	mismatch repair
Afu3g08300	sister chromatid cohesion
Afu3g08300	purine nucleotide binding
Afu3g08310	4-nitrophenylphosphatase activity
Afu3g08310	alkaline phosphatase activity
Afu3g08310	nucleus
Afu3g08310	cytoplasm
Afu3g08310	protein amino acid dephosphorylation
Afu3g08310	histone dephosphorylation
Afu3g08380	inorganic diphosphatase activity
Afu3g08380	cytosol
Afu3g08380	phosphate metabolic process
Afu3g08390	nucleus
Afu3g08390	cytoplasm
Afu3g08390	tRNA modification
Afu3g08390	tRNA processing
Afu3g08390	tRNA dihydrouridine synthase activity
Afu3g08400	molecular function unknown
Afu3g08400	nucleus
Afu3g08400	chromosome organization and biogenesis (sensu Eukaryota)
Afu3g08430	biological process unknown
Afu3g08430	fungal-type vacuole
Afu3g08430	inorganic phosphate transmembrane transporter activity
Afu3g08430	molecular function unknown
Afu3g08430	mitochondrion
Afu3g08460	structural constituent of ribosome
Afu3g08460	cytosolic large ribosomal subunit (sensu Eukaryota)

Afu3g08460	translation
Afu3g08470	glucose-6-phosphate dehydrogenase activity
Afu3g08470	cytoplasm
Afu3g08470	pentose-phosphate shunt
Afu3g08520	DNA binding
Afu3g08520	nucleus
Afu3g08520	cell wall organization
Afu3g08520	signal transduction
Afu3g08520	DNA bending activity
Afu3g08520	transcription activator activity
Afu3g08520	positive regulation of transcription from RNA polymerase II promoter
Afu3g08530	multidrug transport
Afu3g08530	multidrug efflux pump activity
Afu3g08530	response to drug
Afu3g08540	calcium ion binding
Afu3g08540	nucleus
Afu3g08540	cytoplasm
Afu3g08540	signal transduction
Afu3g08540	cell proliferation
Afu3g08540	cell differentiation
Afu3g08560	biological process unknown
Afu3g08560	molecular function unknown
Afu3g08560	nucleus
Afu3g08560	cytoplasm
Afu3g08580	ribosomal small subunit assembly
Afu3g08580	single-stranded DNA binding
Afu3g08580	RNA binding
Afu3g08580	nucleus
Afu3g08580	nucleolus
Afu3g08580	rRNA processing
Afu3g08600	translation initiation factor activity
Afu3g08600	ribosome
Afu3g08600	translational initiation
Afu3g08620	biological process unknown
Afu3g08620	molecular function unknown
Afu3g08620	nucleus
Afu3g08620	cytoplasm
Afu3g08630	DNA binding
Afu3g08640	translation initiation factor activity
Afu3g08640	eukaryotic translation initiation factor 3 complex
Afu3g08640	translational initiation
Afu3g08650	formate-tetrahydrofolate ligase activity
Afu3g08650	nucleus
Afu3g08650	cytoplasm
Afu3g08650	purine base biosynthetic process
Afu3g08660	isocitrate dehydrogenase (NADP+) activity
Afu3g08660	mitochondrion
Afu3g08660	isocitrate metabolic process
Afu3g08660	glutamate biosynthetic process
Afu3g08680	polygalacturonase activity

Afu3g08680	extracellular region
Afu3g08680	pseudohyphal growth
Afu3g08680	pectin catabolic process
Afu3g08710	protein kinase activity
Afu3g08740	molecular function unknown
Afu3g08740	response to oxidative stress
Afu3g08740	cellular component unknown
Afu3g08750	biological process unknown
Afu3g08750	molecular function unknown
Afu3g08750	cytoplasm
Afu3g08760	nucleus
Afu3g08760	cytoplasm
Afu3g08760	tRNA (guanine) methyltransferase activity
Afu3g08760	tRNA methylation
Afu3g08780	protein binding
Afu3g08780	nucleus
Afu3g08780	protein export from nucleus
Afu3g08780	importin-alpha export receptor activity
Afu3g08810	nuclear-transcribed mRNA catabolic process, exonucleolytic
Afu3g08810	protein binding
Afu3g08810	cytoplasm
Afu3g08810	response to virus
Afu3g08810	negative regulation of translation
Afu3g08810	translation repressor activity
Afu3g08810	defense response to pathogen
Afu3g08820	biological process unknown
Afu3g08820	molecular function unknown
Afu3g08820	cytoplasm
Afu3g08840	molecular function unknown
Afu3g08840	ER to Golgi vesicle-mediated transport
Afu3g08840	retrograde vesicle-mediated transport, Golgi to ER
Afu3g08840	COPI vesicle coat
Afu3g08850	mitochondrion
Afu3g08850	mitochondrial intermembrane space
Afu3g08850	cellular iron ion homeostasis
Afu3g08850	mitochondrion organization
Afu3g08850	thiol oxidase activity
Afu3g08930	tripeptidyl-peptidase activity
Afu3g08930	protein catabolic process
Afu3g08940	endopeptidase activity
Afu3g08940	ubiquitin-dependent protein catabolic process
Afu3g08940	proteasome regulatory particle, lid subcomplex
Afu3g08970	vesicle-mediated transport
Afu3g08970	AP-1 adaptor complex
Afu3g08970	clathrin binding
Afu3g08980	threonine synthase activity
Afu3g08980	nucleus
Afu3g08980	cytoplasm
Afu3g08980	threonine metabolic process
Afu3g09020	alpha DNA polymerase activity

Afu3g09020	alpha DNA polymerase:primase complex
Afu3g09020	DNA replication, synthesis of RNA primer
Afu3g09020	DNA replication initiation
Afu3g09020	lagging strand elongation
Afu3g09030	mitochondrial matrix
Afu3g09040	biological process unknown
Afu3g09040	molecular function unknown
Afu3g09040	nucleus
Afu3g09050	exonuclease activity
Afu3g09050	nucleus
Afu3g09050	mismatch repair
Afu3g09050	5'-3' exonuclease activity
Afu3g09050	5'-flap endonuclease activity
Afu3g09110	nucleus
Afu3g09110	cytoplasm
Afu3g09130	transcription factor activity
Afu3g09130	nucleus
Afu3g09130	zinc ion binding
Afu3g09130	regulation of transcription
Afu3g09150	fatty acid catabolic process
Afu3g09170	integral to plasma membrane
Afu3g09170	nicotinamide mononucleotide permease activity
Afu3g09170	nicotinamide mononucleotide transport
Afu3g09190	aldo-keto reductase activity
Afu3g09190	cytoplasm
Afu3g09190	cellular aldehyde metabolic process
Afu3g09220	electron transporter activity
Afu3g09220	microsome
Afu3g09220	ergosterol biosynthetic process
Afu3g09250	hydrolase activity, hydrolyzing O-glycosyl compounds
Afu3g09250	cellular glucan metabolic process
Afu3g09250	fungal-type cell wall
Afu3g09250	extrinsic to plasma membrane
Afu3g09280	translation initiation factor activity
Afu3g09280	eukaryotic translation initiation factor 3 complex
Afu3g09280	translational initiation
Afu3g09320	glycine hydroxymethyltransferase activity
Afu3g09320	glycine metabolic process
Afu3g09320	lysine metabolic process
Afu3g09320	threonine metabolic process
Afu3g09320	folic acid and derivative metabolic process
Afu3g09340	biological process unknown
Afu3g09340	molecular function unknown
Afu3g09340	cytoplasm
Afu3g09350	cytoplasm
Afu3g09350	protein folding
Afu3g09350	tubulin complex assembly
Afu3g09350	tubulin binding
Afu3g09360	cytoplasm
Afu3g09360	endoplasmic reticulum

Afu3g09360	ATPase activity
Afu3g09360	protein retention in Golgi apparatus
Afu3g09360	late endosome to vacuole transport
Afu3g09370	molecular function unknown
Afu3g09370	spindle pole body
Afu3g09390	biological process unknown
Afu3g09390	molecular function unknown
Afu3g09390	nucleus
Afu3g09390	cytoplasm
Afu3g09450	metabolic process
Afu3g09450	hydrolase activity
Afu3g09540	monooxygenase activity
Afu3g09540	cellular aromatic compound metabolic process
Afu3g09550	nuclear division
Afu3g09550	calcium- and calmodulin-dependent protein kinase activity
Afu3g09560	telomere maintenance
Afu3g09560	DNA synthesis during DNA repair
Afu3g09560	epsilon DNA polymerase activity
Afu3g09560	replication fork
Afu3g09560	leading strand elongation
Afu3g09560	lagging strand elongation
Afu3g09560	DNA repair
Afu3g09560	nucleotide-excision repair
Afu3g09560	mismatch repair
Afu3g09560	sister chromatid cohesion
Afu3g09560	aging
Afu3g09590	chaperone activity
Afu3g09590	cytoplasm
Afu3g09590	cytoskeleton
Afu3g09590	protein folding
Afu3g09590	cytoskeleton organization
Afu3g09600	rRNA modification
Afu3g09600	nucleus
Afu3g09600	nucleolus
Afu3g09600	small nucleolar ribonucleoprotein complex
Afu3g09600	35S primary transcript processing
Afu3g09600	maturation of SSU-rRNA
Afu3g09600	small nuclear ribonucleoprotein complex
Afu3g09610	nuclear nucleosome
Afu3g09610	chromatin silencing at telomere
Afu3g09610	acetyltransferase activity
Afu3g09610	chromatin modification
Afu3g09620	single-stranded DNA binding
Afu3g09620	RNA binding
Afu3g09630	asparagine-tRNA ligase activity
Afu3g09630	mitochondrion
Afu3g09630	translation
Afu3g09640	biological process unknown
Afu3g09640	molecular function unknown
Afu3g09640	nucleus

Afu3g09640	cytoplasm
Afu3g09670	transcription factor activity
Afu3g09670	nucleus
Afu3g09670	zinc ion binding
Afu3g09670	regulation of transcription
Afu3g09680	transport
Afu3g09680	regulation of pH
Afu3g09680	endocytosis
Afu3g09680	endosome membrane
Afu3g09680	ABC-type efflux porter activity
Afu3g09680	integral to membrane
Afu3g09700	peripheral to membrane of membrane fraction
Afu3g09700	molecular function unknown
Afu3g09700	endoplasmic reticulum
Afu3g09700	ER to Golgi vesicle-mediated transport
Afu3g09700	COPII vesicle coat
Afu3g09710	gamma-aminobutyric acid transporter activity
Afu3g09710	transport
Afu3g09710	membrane
Afu3g09720	mRNA cleavage and polyadenylation specificity factor complex
Afu3g09720	mRNA cleavage factor complex
Afu3g09720	mRNA polyadenylation
Afu3g09720	mRNA cleavage
Afu3g09720	cleavage and polyadenylylation specificity factor activity
Afu3g09740	molecular function unknown
Afu3g09740	integral to plasma membrane
Afu3g09740	cellular bud tip
Afu3g09740	cellular bud neck
Afu3g09740	cell wall organization
Afu3g09740	signal transduction
Afu3g09750	small nucleolar ribonucleoprotein complex
Afu3g09750	maturation of SSU-rRNA
Afu3g09750	snoRNA binding
Afu3g09760	biological process unknown
Afu3g09760	molecular function unknown
Afu3g09760	cellular component unknown
Afu3g09770	nucleoplasm
Afu3g09770	poly(A) RNA binding
Afu3g09810	molecular function unknown
Afu3g09810	intra-Golgi vesicle-mediated transport
Afu3g09810	Golgi transport complex
Afu3g09820	negative regulation of transcription from RNA polymerase II promoter
Afu3g09820	RNA polymerase II transcription factor activity
Afu3g09820	nucleus
Afu3g09820	zinc ion binding
Afu3g09850	nuclear chromosome
Afu3g09850	catalytic activity
Afu3g09850	DNA repair
Afu3g09850	mismatch repair
Afu3g09860	GPI anchor biosynthetic process

Afu3g09860	membrane
Afu3g09880	3'-5'-exoribonuclease activity
Afu3g09880	nuclear exosome (RNase complex)
Afu3g09880	35S primary transcript processing
Afu3g09910	cytosol
Afu3g09910	Golgi to plasma membrane transport
Afu3g09910	phosphatidylinositol transporter activity
Afu3g09910	phospholipid transport
Afu3g09940	peptide alpha-N-acetyltransferase activity
Afu3g09940	cytoplasm
Afu3g09940	N-terminal protein amino acid acetylation
Afu3g09940	virus-host interaction
Afu3g09950	endoplasmic reticulum
Afu3g09950	triglyceride biosynthetic process
Afu3g09950	lipid storage
Afu3g09950	phospholipid:diacylglycerol acyltransferase activity
Afu3g09960	Golgi apparatus
Afu3g09960	sphingolipid metabolic process
Afu3g09960	inositol phosphoceramide synthase activity
Afu3g09970	membrane fraction
Afu3g09970	Golgi apparatus
Afu3g09970	cellular calcium ion homeostasis
Afu3g09970	cellular iron ion homeostasis
Afu3g09970	cellular manganese ion homeostasis
Afu3g10000	cAMP-dependent protein kinase inhibitor activity
Afu3g10000	nucleus
Afu3g10000	cytoplasm
Afu3g10000	response to stress
Afu3g10000	signal transduction
Afu3g10000	pathogenesis
Afu3g10030	transcription factor activity
Afu3g10030	nucleus
Afu3g10030	rRNA processing
Afu3g10030	transcription from RNA polymerase III promoter
Afu3g10040	cyclin-dependent protein kinase holoenzyme complex
Afu3g10040	cell cycle
Afu3g10040	cyclin-dependent protein kinase regulator activity
Afu3g10050	biological process unknown
Afu3g10050	molecular function unknown
Afu3g10050	nucleus
Afu3g10050	cytoplasm
Afu3g10080	biological process unknown
Afu3g10080	protein kinase activity
Afu3g10080	cytoplasm
Afu3g10100	mRNA binding
Afu3g10100	nucleus
Afu3g10100	cytoplasm
Afu3g10100	mRNA export from nucleus
Afu3g10110	mitochondrion
Afu3g10110	NADH catabolism

Afu3g10110	oxidoreductase activity, acting on the CH-NH group of donors, quinone or similar compound
Afu3g10120	RNA polymerase I transcription factor complex
Afu3g10120	transcription factor TFIIIB complex
Afu3g10120	DNA binding
Afu3g10120	RNA polymerase I transcription factor activity
Afu3g10120	RNA polymerase III transcription factor activity
Afu3g10120	nucleus
Afu3g10120	transcription factor TFIID complex
Afu3g10120	transcription from RNA polymerase I promoter
Afu3g10120	transcription initiation from RNA polymerase II promoter
Afu3g10120	transcription initiation from RNA polymerase III promoter
Afu3g10120	general RNA polymerase II transcription factor activity
Afu3g10140	biological process unknown
Afu3g10140	mitochondrion
Afu3g10140	S-adenosylmethionine-dependent methyltransferase activity
Afu3g10180	condensed nuclear chromosome kinetochore
Afu3g10180	condensed nuclear chromosome, centromeric region
Afu3g10180	structural constituent of cytoskeleton
Afu3g10180	microtubule nucleation
Afu3g10180	chromosome segregation
Afu3g10190	protein binding
Afu3g10190	peroxisomal membrane
Afu3g10190	protein targeting to peroxisome
Afu3g10220	acid phosphatase activity
Afu3g10220	cytoplasm
Afu3g10220	response to stress
Afu3g10240	regulation of progression through cell cycle
Afu3g10240	3'-5'-exoribonuclease activity
Afu3g10240	nuclear-transcribed mRNA catabolic process, deadenylation-dependent decay
Afu3g10240	nuclear-transcribed mRNA poly(A) tail shortening
Afu3g10240	regulation of transcription from RNA polymerase II promoter
Afu3g10240	signal transduction
Afu3g10240	response to extracellular stimulus
Afu3g10240	CCR4-NOT core complex
Afu3g10250	cellular bud neck contractile ring
Afu3g10250	cytokinesis
Afu3g10250	cytoskeletal protein binding
Afu3g10280	chromatin binding
Afu3g10280	nucleus
Afu3g10280	DNA replication initiation
Afu3g10280	DNA strand elongation during DNA replication
Afu3g10300	galactokinase activity
Afu3g10300	galactose metabolic process
Afu3g10300	cellular component unknown
Afu3g10310	acetolactate synthase activity
Afu3g10310	mitochondrion
Afu3g10310	acetolactate synthase complex
Afu3g10310	branched chain family amino acid biosynthetic process
Afu3g10310	isoleucine biosynthetic process
Afu3g10310	valine biosynthetic process

Afu3g10340	1,3-beta-glucan synthase complex
Afu3g10340	Rho small monomeric GTPase activity
Afu3g10340	signal transducer activity
Afu3g10340	actin filament organization
Afu3g10340	cell wall organization
Afu3g10340	small GTPase mediated signal transduction
Afu3g10350	molecular function unknown
Afu3g10350	cytoplasm
Afu3g10350	response to salt stress
Afu3g10360	molecular function unknown
Afu3g10360	endosome
Afu3g10360	retrograde transport, endosome to Golgi
Afu3g10360	protein retention in Golgi apparatus
Afu3g10380	transcription factor TFIIIC complex
Afu3g10380	RNA polymerase III transcription factor activity
Afu3g10380	transcription initiation from RNA polymerase III promoter
Afu3g10400	dolichyl-phosphate beta-D-mannosyltransferase activity
Afu3g10400	endoplasmic reticulum
Afu3g10400	protein amino acid N-linked glycosylation
Afu3g10400	protein amino acid O-linked glycosylation
Afu3g10400	transferase activity, transferring glycosyl groups
Afu3g10460	nuclear envelope
Afu3g10460	protein import into nucleus
Afu3g10460	nucleocytoplasmic transport
Afu3g10460	Ran GTPase binding
Afu3g10490	molecular function unknown
Afu3g10490	membrane
Afu3g10490	sterol metabolic process
Afu3g10520	protein kinase activity
Afu3g10520	nucleus
Afu3g10520	cytoplasm
Afu3g10520	protein amino acid phosphorylation
Afu3g10520	cell growth and/or maintenance
Afu3g10530	G1/S transition of mitotic cell cycle
Afu3g10530	protein kinase activity
Afu3g10530	protein serine/threonine kinase activity
Afu3g10530	cytoplasm
Afu3g10530	protein amino acid phosphorylation
Afu3g10540	3-hydroxyacyl-CoA dehydrogenase activity
Afu3g10540	enoyl-CoA hydratase activity
Afu3g10540	peroxisomal matrix
Afu3g10540	fatty acid beta-oxidation
Afu3g10560	nucleus
Afu3g10560	zinc ion binding
Afu3g10560	regulation of transcription
Afu3g10570	nonselective channel activity
Afu3g10570	integral to membrane
Afu3g10600	biological process unknown
Afu3g10600	molecular function unknown
Afu3g10600	clathrin-coated vesicle

Afu3g10620	nucleoplasm
Afu3g10620	transcription initiation from RNA polymerase II promoter
Afu3g10620	general RNA polymerase II transcription factor activity
Afu3g10650	proteolysis
Afu3g10650	protein targeting to vacuole
Afu3g10650	metallopeptidase activity
Afu3g10660	hydroxymethylglutaryl-CoA synthase activity
Afu3g10660	mitochondrion
Afu3g10660	endoplasmic reticulum
Afu3g10660	ergosterol biosynthetic process
Afu3g10690	calcium-transporting ATPase activity
Afu3g10690	calcium ion transport
Afu3g10690	cellular calcium ion homeostasis
Afu3g10700	actin cortical patch assembly
Afu3g10700	actin binding
Afu3g10700	structural molecule activity
Afu3g10700	mitochondrial envelope
Afu3g10700	Arp2/3 protein complex
Afu3g10730	structural constituent of ribosome
Afu3g10730	cytosolic small ribosomal subunit (sensu Eukaryota)
Afu3g10730	translation
Afu3g10740	GTPase activity
Afu3g10740	RAB small monomeric GTPase activity
Afu3g10740	late endosome
Afu3g10740	protein targeting to vacuole
Afu3g10740	endocytosis
Afu3g10760	carbohydrate metabolic process
Afu3g10760	aldehyde-lyase activity
Afu3g10770	phospholipid-translocating ATPase activity
Afu3g10770	endoplasmic reticulum
Afu3g10770	plasma membrane
Afu3g10770	fatty acid transport
Afu3g10770	integral to membrane
Afu3g10800	translation initiation factor activity
Afu3g10800	cytoplasm
Afu3g10800	eukaryotic translation initiation factor 3 complex
Afu3g10800	translational initiation
Afu3g10800	mitochondrion organization
Afu3g10820	ferric-chelate reductase activity
Afu3g10820	plasma membrane
Afu3g10820	iron ion transport
Afu3g10820	copper ion import
Afu3g10830	transcription corepressor activity
Afu3g10830	soluble fraction
Afu3g10830	regulation of nitrogen utilization
Afu3g10840	commitment complex
Afu3g10840	nuclear mRNA splicing, via spliceosome
Afu3g10840	RNA binding
Afu3g10880	membrane fraction
Afu3g10880	plasma membrane

Afu3g10880	transport
Afu3g10880	anion transmembrane transporter activity
Afu3g10890	ATP-dependent RNA helicase activity
Afu3g10890	nucleolus
Afu3g10890	35S primary transcript processing
Afu3g10920	telomere maintenance
Afu3g10920	nuclear telomere cap complex
Afu3g10920	cytoplasm
Afu3g10920	programmed cell death
Afu3g10920	telomeric DNA binding
Afu3g10930	transcription factor activity
Afu3g10930	transcription
Afu3g10940	molecular function unknown
Afu3g10940	cytosol
Afu3g10940	protein targeting to peroxisome
Afu3g10940	peroxisome organization
Afu3g10970	protein tyrosine phosphatase activity
Afu3g10970	cytoplasm
Afu3g10970	protein amino acid dephosphorylation
Afu3g10980	integral to membrane
Afu3g11000	SAGA complex
Afu3g11000	conjugation with cellular fusion
Afu3g11000	structural molecule activity
Afu3g11000	protein complex assembly
Afu3g11000	chromatin modification
Afu3g11000	histone acetylation
Afu3g11020	nucleus
Afu3g11020	mitochondrion
Afu3g11020	mRNA cleavage factor complex
Afu3g11020	mRNA polyadenylation
Afu3g11020	mRNA cleavage
Afu3g11020	cleavage and polyadenylylation specificity factor activity
Afu3g11030	chromatin assembly complex
Afu3g11030	nucleosome assembly
Afu3g11030	programmed cell death
Afu3g11030	histone binding
Afu3g11040	molecular function unknown
Afu3g11040	plasma membrane
Afu3g11040	exocytosis
Afu3g11040	Golgi to plasma membrane transport
Afu3g11040	programmed cell death
Afu3g11070	pyruvate decarboxylase activity
Afu3g11070	cytoplasm
Afu3g11070	ethanol metabolic process
Afu3g11080	MAP kinase kinase kinase activity
Afu3g11090	peripheral to membrane of membrane fraction
Afu3g11090	retrograde transport, vesicle recycling within Golgi
Afu3g11090	soluble fraction
Afu3g11090	ER to Golgi vesicle-mediated transport
Afu3g11090	intra-Golgi vesicle-mediated transport

Afu3g11090	protein transporter activity
Afu3g11090	Golgi transport complex
Afu3g11100	biological process unknown
Afu3g11100	molecular function unknown
Afu3g11100	cellular component unknown
Afu3g11110	nucleus
Afu3g11110	nucleolus
Afu3g11140	DNA ligase (ATP) activity
Afu3g11140	replication fork
Afu3g11140	DNA ligation
Afu3g11140	lagging strand elongation
Afu3g11140	base-excision repair
Afu3g11140	nucleotide-excision repair
Afu3g11140	DNA recombination
Afu3g11160	biological process unknown
Afu3g11160	molecular function unknown
Afu3g11160	cytoplasm
Afu3g11200	fungal-type vacuole
Afu3g11200	endosome
Afu3g11200	vacuolar membrane
Afu3g11200	high-affinity iron ion transport
Afu3g11200	vacuole organization
Afu3g11200	protein transport
Afu3g11200	Rab guanyl-nucleotide exchange factor activity
Afu3g11200	homotypic vacuole fusion, non-autophagic
Afu3g11210	biological process unknown
Afu3g11210	molecular function unknown
Afu3g11210	cellular component unknown
Afu3g11220	cell morphogenesis
Afu3g11220	endoribonuclease activity
Afu3g11220	extracellular region
Afu3g11220	RNA catabolic process
Afu3g11250	regulation of transcription involved in G1 phase of mitotic cell cycle
Afu3g11250	nucleus
Afu3g11250	cytoplasm
Afu3g11250	zinc ion binding
Afu3g11250	pathogenesis
Afu3g11250	transcription activator activity
Afu3g11260	structural constituent of ribosome
Afu3g11260	cytosolic large ribosomal subunit (sensu Eukaryota)
Afu3g11260	translation
Afu3g11260	ubiquitin-dependent protein catabolic process
Afu3g11260	protein tagging activity
Afu3g11280	chitinase activity
Afu3g11280	cell wall chitin catabolic process
Afu3g11280	fungal-type cell wall
Afu3g11300	endopeptidase activity
Afu3g11300	ubiquitin-dependent protein catabolic process
Afu3g11300	proteasome core complex, alpha-subunit complex
Afu3g11320	structural constituent of cytoskeleton

Afu3g11320	inner plaque of spindle pole body
Afu3g11320	outer plaque of spindle pole body
Afu3g11320	microtubule nucleation
Afu3g11330	negative regulation of transcription from RNA polymerase II promoter
Afu3g11330	RNA polymerase II transcription factor activity
Afu3g11330	nucleus
Afu3g11330	cytosol
Afu3g11350	transporter activity
Afu3g11350	soluble fraction
Afu3g11350	nucleolus
Afu3g11350	cytoplasm
Afu3g11350	transport
Afu3g11350	arsenite transmembrane transporter activity
Afu3g11360	translation initiation factor activity
Afu3g11360	eukaryotic translation initiation factor 3 complex
Afu3g11360	translational initiation
Afu3g11370	structural constituent of ribosome
Afu3g11370	mitochondrial large ribosomal subunit
Afu3g11370	translation
Afu3g11380	nucleosome remodeling complex
Afu3g11380	chromatin remodeling
Afu3g11380	general RNA polymerase II transcription factor activity
Afu3g11390	endopeptidase activity
Afu3g11390	proteasome regulatory particle
Afu3g11390	ubiquitin-dependent protein catabolic process
Afu3g11390	proteasome regulatory particle, base subcomplex
Afu3g11390	ATPase activity
Afu3g11400	aspartic-type endopeptidase activity
Afu3g11400	extracellular region
Afu3g11400	fungal-type cell wall
Afu3g11400	protein catabolic process
Afu3g11410	phosphoprotein phosphatase activity
Afu3g11410	nucleus
Afu3g11410	transcription
Afu3g11410	protein amino acid dephosphorylation
Afu3g11410	phosphatase activity
Afu3g11430	arginase activity
Afu3g11430	cytosol
Afu3g11430	arginine catabolic process to ornithine
Afu3g11440	molecular function unknown
Afu3g11440	mitochondrion
Afu3g11440	translation
Afu3g11440	mitochondrion organization
Afu3g11440	aerobic respiration
Afu3g11480	3-hydroxyisobutyryl-CoA hydrolase activity
Afu3g11480	mitochondrion
Afu3g11480	fatty acid beta-oxidation
Afu3g11480	endocytosis
Afu3g11490	plasma membrane
Afu3g11490	choline transmembrane transporter activity

Afu3g11490	choline transport
Afu3g11500	nucleotide binding
Afu3g11500	cellular component unknown
Afu3g11510	biological process unknown
Afu3g11510	cellular component unknown
Afu3g11510	acetyltransferase activity
Afu3g11530	protein binding
Afu3g11530	mitochondrion
Afu3g11530	protein folding
Afu3g11590	regulation of progression through cell cycle
Afu3g11590	protein binding
Afu3g11590	cellular response to nitrogen starvation
Afu3g11590	multicellular organismal development
Afu3g11610	nuclear chromatin
Afu3g11610	chromatin binding
Afu3g11610	chromatin organization
Afu3g11610	regulation of transcription from RNA polymerase II promoter
Afu3g11610	regulation of transcription from RNA polymerase III promoter
Afu3g11640	homoserine dehydrogenase activity
Afu3g11640	nucleus
Afu3g11640	cytoplasm
Afu3g11640	methionine metabolic process
Afu3g11640	threonine metabolic process
Afu3g11640	homoserine biosynthetic process
Afu3g11660	biological process unknown
Afu3g11660	molecular function unknown
Afu3g11660	cellular component unknown
Afu3g11690	fructose-bisphosphate aldolase activity
Afu3g11690	cytoplasm
Afu3g11690	cytosol
Afu3g11690	gluconeogenesis
Afu3g11690	glycolysis
Afu3g11700	ubiquitin-specific protease activity
Afu3g11700	cytoplasm
Afu3g11700	protein deubiquitination
Afu3g11710	saccharopine dehydrogenase (NAD+, L-lysine-forming) activity
Afu3g11710	cytoplasm
Afu3g11710	peroxisome
Afu3g11710	lysine biosynthetic process via aminoadipic acid
Afu3g11750	steroid biosynthetic process
Afu3g11750	oxysterol binding
Afu3g11750	cellular component unknown
Afu3g11760	transporter activity
Afu3g11760	transport
Afu3g11760	integral to membrane
Afu3g11790	myo-inositol transmembrane transporter activity
Afu3g11790	myo-inositol transport
Afu3g11790	membrane
Afu3g11820	mitochondrion
Afu3g11820	RNA processing

Afu3g11820	3'-5' exonuclease activity
Afu3g11830	phosphoglucomutase activity
Afu3g11830	cytosol
Afu3g11830	glucose 1-phosphate utilization
Afu3g11830	glucose 6-phosphate utilization
Afu3g11840	metabolic process
Afu3g11840	oxidoreductase activity
Afu3g11860	structural constituent of cytoskeleton
Afu3g11860	spindle pole body
Afu3g11860	cytoplasmic microtubule
Afu3g11860	microtubule depolymerization
Afu3g11860	microtubule nucleation
Afu3g11860	negative regulation of microtubule depolymerization
Afu3g11860	mitotic cell cycle spindle assembly checkpoint
Afu3g11870	protein binding
Afu3g11870	ubiquitin-dependent protein catabolic process
Afu3g11870	cell cycle
Afu3g11870	protein ubiquitination
Afu3g11890	asparaginase activity
Afu3g11890	cellular amino acid metabolic process
Afu3g11900	soluble fraction
Afu3g11900	alcohol metabolic process
Afu3g11900	cellular aldehyde metabolic process
Afu3g11900	alcohol dehydrogenase (NADP+) activity
Afu3g11920	catalytic activity
Afu3g11920	metabolic process
Afu3g11940	nuclear nucleosome
Afu3g11940	DNA binding
Afu3g11940	chromatin remodeling
Afu3g11940	regulation of transcription, DNA-dependent
Afu3g11940	zinc ion binding
Afu3g11960	regulation of progression through cell cycle
Afu3g11960	regulation of transcription involved in G2-phase of mitotic cell cycle
Afu3g11960	transcription factor activity
Afu3g11960	nucleus
Afu3g11960	pseudohyphal growth
Afu3g11970	negative regulation of transcription from RNA polymerase II promoter
Afu3g11970	nucleus
Afu3g11970	cytoplasm
Afu3g11970	response to pH
Afu3g11970	specific transcriptional repressor activity
Afu3g11990	transcription factor activity
Afu3g11990	nucleus
Afu3g11990	zinc ion binding
Afu3g11990	regulation of transcription
Afu3g12010	fructose transmembrane transporter activity
Afu3g12010	glucose transmembrane transporter activity
Afu3g12010	plasma membrane
Afu3g12010	hexose transport
Afu3g12010	mannose transmembrane transporter activity

Afu3g12020	transcription initiation
Afu3g12020	sigma factor activity
Afu3g12030	nuclear chromatin
Afu3g12030	chromatin binding
Afu3g12030	regulation of transcription, DNA-dependent
Afu3g12030	zinc ion binding
Afu3g12030	transcription activator activity
Afu3g12080	ARF small monomeric GTPase activity
Afu3g12080	intracellular protein transport
Afu3g12080	cellular component unknown
Afu3g12100	polysaccharide biosynthetic process
Afu3g12100	trehalose biosynthetic process
Afu3g12100	response to stress
Afu3g12100	transferase activity, transferring glycosyl groups
Afu3g12100	transferase activity, transferring glycosyl groups
Afu3g12130	biological process unknown
Afu3g12130	molecular function unknown
Afu3g12130	cellular component unknown
Afu3g12160	DNA binding
Afu3g12160	nucleus
Afu3g12160	negative regulation of transcription from RNA polymerase II promoter, mitotic
Afu3g12160	regulation of mitotic cell cycle
Afu3g12160	specific transcriptional repressor activity
Afu3g12170	transporter activity
Afu3g12170	transport
Afu3g12170	membrane
Afu3g12190	zinc ion binding
Afu3g12200	endoplasmic reticulum
Afu3g12200	integral to plasma membrane
Afu3g12200	sulfur metabolic process
Afu3g12200	oligopeptide transporter activity
Afu3g12210	biological process unknown
Afu3g12210	fungal-type vacuole
Afu3g12210	carboxypeptidase C activity
Afu3g12220	ATP-binding cassette (ABC) transporter activity
Afu3g12220	integral to plasma membrane
Afu3g12220	transport
Afu3g12250	phosphoprotein phosphatase activity
Afu3g12250	nucleus
Afu3g12250	nucleolus
Afu3g12250	spindle pole body
Afu3g12250	protein amino acid dephosphorylation
Afu3g12250	regulation of exit from mitosis
Afu3g12270	glutathione peroxidase activity
Afu3g12270	intracellular
Afu3g12270	response to oxidative stress
Afu3g12270	thiol peroxidase activity
Afu3g12290	nuclear mRNA splicing, via spliceosome
Afu3g12290	pre-mRNA splicing factor activity
Afu3g12290	small nuclear ribonucleoprotein complex

Afu3g12300	structural constituent of ribosome
Afu3g12300	cytosolic large ribosomal subunit (sensu Eukaryota)
Afu3g12300	translation
Afu3g12310	nucleus
Afu3g12310	cytoplasm
Afu3g12310	RNA processing
Afu3g12310	3'-5' exonuclease activity
Afu3g12320	biological process unknown
Afu3g12320	molecular function unknown
Afu3g12320	lipid particle
Afu3g12330	biological process unknown
Afu3g12330	molecular function unknown
Afu3g12330	mitochondrion
Afu3g12350	response to stress
Afu3g12370	vacuolar proton-transporting V-type ATPase, V0 domain
Afu3g12370	protein targeting to vacuole
Afu3g12370	cellular copper ion homeostasis
Afu3g12370	cellular iron ion homeostasis
Afu3g12370	endocytosis
Afu3g12370	vacuole organization
Afu3g12370	vacuolar acidification
Afu3g12370	hydrogen ion transmembrane transporter activity
Afu3g12370	proton transport
Afu3g12400	pheromone-dependent signal transduction involved in conjugation with cellular fusion
Afu3g12400	heterotrimeric G-protein GTPase activity
Afu3g12400	heterotrimeric G-protein complex
Afu3g12400	plasma membrane
Afu3g12430	guanyl-nucleotide exchange factor activity
Afu3g12430	cellular bud
Afu3g12430	regulation of exit from mitosis
Afu3g12450	biological process unknown
Afu3g12450	molecular function unknown
Afu3g12450	cellular component unknown
Afu3g12480	cell morphogenesis
Afu3g12480	intracellular
Afu3g12480	mating projection
Afu3g12480	cytokinesis, completion of separation
Afu3g12480	regulation of cell shape
Afu3g12480	transcription repressor activity
Afu3g12480	regulation of transcription
Afu3g12490	nucleus
Afu3g12490	mRNA export from nucleus
Afu3g12490	histone-arginine N-methyltransferase activity
Afu3g12490	protein-arginine N-methyltransferase activity
Afu3g12490	chromatin modification
Afu3g12490	peptidyl-arginine modification
Afu3g12510	vacuole inheritance
Afu3g12510	cytoplasm
Afu3g12510	ER to Golgi vesicle-mediated transport
Afu3g12510	ATPase activity

Afu3g12510	extrinsic to plasma membrane
Afu3g12530	two-component sensor activity
Afu3g12530	protein histidine kinase activity
Afu3g12530	plasma membrane
Afu3g12530	protein amino acid phosphorylation
Afu3g12550	two-component sensor activity
Afu3g12550	protein histidine kinase activity
Afu3g12550	protein amino acid phosphorylation
Afu3g12550	signal transduction
Afu3g12560	allantoin catabolic process
Afu3g12560	allantoicase activity
Afu3g12560	cellular component unknown
Afu3g12580	myo-inositol transmembrane transporter activity
Afu3g12580	myo-inositol transport
Afu3g12580	membrane
Afu3g12620	secondary metabolic process
Afu3g12630	integral to membrane
Afu3g12640	serine-tRNA ligase activity
Afu3g12640	cytoplasm
Afu3g12640	pseudohyphal growth
Afu3g12640	invasive growth
Afu3g12640	aerobic respiration
Afu3g12660	DNA binding
Afu3g12660	zinc ion binding
Afu3g12670	protein kinase activity
Afu3g12670	nucleus
Afu3g12670	protein amino acid phosphorylation
Afu3g12720	fructose transmembrane transporter activity
Afu3g12720	galactose transmembrane transporter activity
Afu3g12720	glucose transmembrane transporter activity
Afu3g12720	plasma membrane
Afu3g12720	hexose transport
Afu3g12720	mannose transmembrane transporter activity
Afu3g12730	transcription factor TFIIIB complex
Afu3g12730	RNA polymerase III transcription factor activity
Afu3g12730	transcription initiation from RNA polymerase III promoter
Afu3g12740	copper-exporting ATPase activity
Afu3g12740	trans-Golgi network
Afu3g12740	copper ion transport
Afu3g12740	intracellular copper ion transport
Afu3g12750	endonuclease activity
Afu3g12750	nucleus
Afu3g12750	DNA repair
Afu3g12750	reciprocal meiotic recombination
Afu3g12800	cellular bud site selection
Afu3g12800	molecular function unknown
Afu3g12800	clathrin-coated vesicle
Afu3g12810	nucleosome
Afu3g12810	transcription corepressor activity
Afu3g12810	nucleosome assembly

Afu3g12810	gene silencing
Afu3g12820	establishment of mitotic spindle orientation
Afu3g12820	microtubule motor activity
Afu3g12820	kinesin complex
Afu3g12820	nuclear microtubule
Afu3g12820	cytoplasmic microtubule
Afu3g12820	microtubule depolymerization
Afu3g12840	endoplasmic reticulum
Afu3g12840	signal peptidase complex
Afu3g12840	signal peptide processing
Afu3g12840	signal peptidase activity
Afu3g12850	protein polyubiquitination
Afu3g12850	proteasome complex
Afu3g12850	ubiquitin conjugating enzyme activity
Afu3g12850	protein monoubiquitination
Afu3g12850	endocytosis
Afu3g12850	response to stress
Afu3g12850	response to unfolded protein
Afu3g12850	sporulation (sensu Saccharomyces)
Afu3g12870	Rab GTPase activator activity
Afu3g12870	exocytosis
Afu3g12870	actin filament organization
Afu3g12890	transcription factor activity
Afu3g12890	nucleus
Afu3g12890	regulation of transcription
Afu3g12900	fungal-type vacuole membrane
Afu3g12900	transporter activity
Afu3g12900	transport
Afu3g12900	monocarboxylic acid transmembrane transporter activity
Afu3g12910	O-methyltransferase activity
Afu3g12910	S-adenosylmethionine-dependent methyltransferase activity
Afu3g12920	catalytic activity
Afu3g12920	nonribosomal peptide biosynthetic process
Afu3g12920	peptide antibiotic biosynthetic process
Afu3g12920	amino acid adenylylation by nonribosomal peptide synthase
Afu3g12930	alkaloid biosynthetic process
Afu3g12930	secondary metabolic process
Afu3g12930	tryptophan dimethylallyltransferase activity
Afu3g12940	transcription factor activity
Afu3g12940	nucleus
Afu3g12940	regulation of transcription
Afu3g12960	metabolic process
Afu3g12960	pathogenesis
Afu3g12960	oxidoreductase activity
Afu3g13000	mitochondrial inner membrane
Afu3g13000	aerobic respiration
Afu3g13000	ATPase activity
Afu3g13000	protein metabolic process
Afu3g13030	chaperone activity
Afu3g13030	cytoplasm

Afu3g13030	cytoskeleton
Afu3g13030	protein folding
Afu3g13030	cytoskeleton organization
Afu3g13060	ubiquitin conjugating enzyme activity
Afu3g13060	ubiquitin-protein ligase activity
Afu3g13060	endoplasmic reticulum
Afu3g13060	ER-associated protein catabolic process
Afu3g13120	hydroxymethylbilane synthase activity
Afu3g13120	nucleus
Afu3g13120	cytoplasm
Afu3g13120	heme biosynthetic process
Afu3g13200	cellular glucan metabolic process
Afu3g13200	cell wall organization
Afu3g13200	1,3-beta-glucanosyltransferase activity
Afu3g13200	anchored to plasma membrane
Afu3g13210	protein kinase activity
Afu3g13230	AT DNA binding
Afu3g13230	nucleus
Afu3g13240	racemase and epimerase activity
Afu3g13240	hexose metabolic process
Afu3g13270	biological process unknown
Afu3g13270	molecular function unknown
Afu3g13270	integral to membrane
Afu3g13270	integral to endoplasmic reticulum membrane
Afu3g13280	ribosomal large subunit assembly
Afu3g13280	ATP-dependent RNA helicase activity
Afu3g13280	nucleolus
Afu3g13280	35S primary transcript processing
Afu3g13320	ribosomal small subunit assembly
Afu3g13320	structural constituent of ribosome
Afu3g13320	cytosolic small ribosomal subunit (sensu Eukaryota)
Afu3g13320	translation
Afu3g13350	pseudouridylate synthase activity
Afu3g13350	nucleus
Afu3g13350	cytoplasm
Afu3g13350	RNA processing
Afu3g13370	protein binding
Afu3g13370	ubiquitin-dependent protein catabolic process
Afu3g13370	protein tagging activity
Afu3g13380	histidine biosynthetic process
Afu3g13380	tryptophan biosynthetic process
Afu3g13380	ribose phosphate diphosphokinase activity
Afu3g13380	cytoplasm
Afu3g13380	purine ribonucleoside salvage
Afu3g13380	'de novo' IMP biosynthetic process
Afu3g13380	'de novo' pyrimidine base biosynthetic process
Afu3g13390	vacuolar proton-transporting V-type ATPase, V0 domain
Afu3g13390	vacuolar membrane
Afu3g13390	vacuolar transport
Afu3g13390	vacuolar acidification

Afu3g13390	proton-transporting ATPase activity, rotational mechanism
Afu3g13400	rRNA modification
Afu3g13400	molecular function unknown
Afu3g13400	small nucleolar ribonucleoprotein complex
Afu3g13400	35S primary transcript processing
Afu3g13400	maturation of SSU-rRNA
Afu3g13400	small nuclear ribonucleoprotein complex
Afu3g13450	biological process unknown
Afu3g13450	molecular function unknown
Afu3g13450	cytoplasm
Afu3g13470	endoplasmic reticulum
Afu3g13480	RNA binding
Afu3g13480	translation initiation factor activity
Afu3g13480	cytoplasm
Afu3g13480	ribosome
Afu3g13480	translational initiation
Afu3g13490	cation channel activity
Afu3g13490	cation transport
Afu3g13490	membrane
Afu3g13520	transporter activity
Afu3g13520	transport
Afu3g13550	cytoplasm
Afu3g13550	2-dehydropantoate 2-reductase activity
Afu3g13550	pantothenate biosynthetic process
Afu3g13580	GTPase activity
Afu3g13580	membrane fraction
Afu3g13580	protein targeting to vacuole
Afu3g13580	peroxisome organization
Afu3g13580	vacuolar transport
Afu3g13580	protein retention in Golgi apparatus
Afu3g13600	transcription factor activity
Afu3g13600	nucleus
Afu3g13600	zinc ion binding
Afu3g13600	regulation of transcription
Afu3g13670	cellular iron ion homeostasis
Afu3g13670	siderophore-iron (ferrioxamine) uptake transmembrane transporter activity
Afu3g13670	siderophore-iron transport
Afu3g13670	integral to membrane
Afu3g13690	catalytic activity
Afu3g13710	GTP cyclohydrolase I activity
Afu3g13710	secondary metabolic process
Afu3g13720	metabolic process
Afu3g13720	oxidoreductase activity
Afu3g13730	nonribosomal peptide biosynthetic process
Afu3g13770	cytoplasm
Afu3g13770	Golgi to vacuole transport
Afu3g13770	vesicle docking during exocytosis
Afu3g13770	vesicle fusion
Afu3g13770	zinc ion binding
Afu3g13770	external side of endosome membrane

Afu3g13770	extrinsic to plasma membrane
Afu3g13790	endoplasmic reticulum membrane
Afu3g13790	protein amino acid glycosylation
Afu3g13790	cellular calcium ion homeostasis
Afu3g13790	ATPase activity, coupled to transmembrane movement of ions, phosphorylative mechanism
Afu3g13830	molecular function unknown
Afu3g13830	ascospore wall
Afu3g13830	spore wall assembly (sensu Saccharomyces)
Afu3g13840	mitochondrial protein processing during import
Afu3g13840	peptidase activity
Afu3g13840	mitochondrial inner membrane peptidase complex
Afu3g13870	transcription factor activity
Afu3g13870	nucleus
Afu3g13870	zinc ion binding
Afu3g13870	sporocarp development
Afu3g13870	regulation of transcription
Afu3g13870	regulation of developmental process
Afu3g13900	glutamate-cysteine ligase activity
Afu3g13900	intracellular
Afu3g13900	glutathione biosynthetic process
Afu3g13900	response to cadmium ion
Afu3g13920	regulation of progression through cell cycle
Afu3g13920	DNA binding
Afu3g13920	transcription factor activity
Afu3g13920	nucleus
Afu3g13920	DNA replication
Afu3g13940	conjugation with cellular fusion
Afu3g13940	molecular function unknown
Afu3g13940	integral to membrane
Afu3g13970	Golgi membrane
Afu3g13970	fungal-type vacuole membrane
Afu3g13970	phosphatidylserine decarboxylase activity
Afu3g13970	phosphatidylcholine biosynthetic process
Afu3g13980	biological process unknown
Afu3g13980	fungal-type vacuole membrane
Afu3g13980	molecular function unknown
Afu3g13990	negative regulation of transcription from RNA polymerase II promoter
Afu3g13990	cyclin-dependent protein kinase activity
Afu3g13990	transcription factor complex
Afu3g13990	protein amino acid phosphorylation
Afu3g13990	meiosis
Afu3g13990	general RNA polymerase II transcription factor activity
Afu3g13990	regulation of transcription
Afu3g14010	chromatin binding
Afu3g14010	ATP-dependent DNA helicase activity
Afu3g14010	nucleus
Afu3g14010	pre-replicative complex
Afu3g14010	cytoplasm
Afu3g14010	pre-replicative complex assembly
Afu3g14010	DNA unwinding during replication

Afu3g14010	DNA replication initiation
Afu3g14020	biological process unknown
Afu3g14020	molecular function unknown
Afu3g14020	cellular bud neck
Afu3g14090	DNA binding
Afu3g14090	nucleus
Afu3g14090	zinc ion binding
Afu3g14100	cell growth and/or maintenance
Afu3g14100	carbon utilization
Afu3g14100	DNA-directed RNA polymerase II, holoenzyme
Afu3g14100	enzyme regulator activity
Afu3g14110	chromatin silencing at rDNA
Afu3g14110	cytoplasm
Afu3g14110	nicotinamide metabolic process
Afu3g14110	nicotinamide N-methyltransferase activity
Afu3g14140	nucleus
Afu3g14140	programmed cell death
Afu3g14140	caspase activity
Afu3g14170	receptor activity
Afu3g14170	glucose transmembrane transporter activity
Afu3g14170	glucose binding
Afu3g14170	plasma membrane
Afu3g14170	signal transduction
Afu3g14170	response to glucose stimulus
Afu3g14230	endocytosis
Afu3g14230	response to osmotic stress
Afu3g14230	bipolar cellular bud site selection
Afu3g14230	cytoskeletal protein binding
Afu3g14240	mitochondrion
Afu3g14240	cellular iron ion homeostasis
Afu3g14240	cysteine desulfhydrase activity
Afu3g14240	iron-sulfur cluster assembly
Afu3g14250	tryptophan 2,3-dioxygenase activity
Afu3g14250	cytoplasm
Afu3g14250	NAD biosynthetic process
Afu3g14270	nucleus
Afu3g14270	cytoplasm
Afu3g14270	cellular aldehyde metabolic process
Afu3g14270	oxidoreductase activity
Afu3g14290	cellular bud site selection
Afu3g14290	protein serine/threonine kinase activity
Afu3g14290	nucleus
Afu3g14290	cytoplasm
Afu3g14290	protein amino acid phosphorylation
Afu3g14320	SNARE binding
Afu3g14320	endoplasmic reticulum
Afu3g14320	Golgi apparatus
Afu3g14320	ER to Golgi vesicle-mediated transport
Afu3g14320	ER to Golgi transport vesicle
Afu3g14330	response to pheromone during conjugation with cellular fusion

Afu3g14330	mating-type alpha-factor pheromone receptor activity
Afu3g14330	integral to plasma membrane
Afu3g14330	cell projection assembly
Afu3g14340	condensed nuclear chromosome kinetochore
Afu3g14340	molecular function unknown
Afu3g14340	nuclear pore
Afu3g14340	mitotic cell cycle spindle assembly checkpoint
Afu3g14350	biological process unknown
Afu3g14350	GTPase activity
Afu3g14350	mitochondrion
Afu3g14370	DNA-directed RNA polymerase activity
Afu3g14370	DNA-directed RNA polymerase III complex
Afu3g14370	transcription from RNA polymerase III promoter
Afu3g14420	chitin synthase activity
Afu3g14420	plasma membrane
Afu3g14420	chitin biosynthetic process
Afu3g14420	pathogenesis
Afu3g14430	cytoplasm
Afu3g14430	NEDD8 conjugating enzyme activity
Afu3g14430	NEDD8 class-dependent protein catabolic process
Afu3g14430	protein neddylation during NEDD8 class-dependent protein catabolic process
Afu3g14470	biological process unknown
Afu3g14470	molecular function unknown
Afu3g14470	cellular component unknown
Afu3g14490	mitochondrial genome maintenance
Afu3g14490	ketol-acid reductoisomerase activity
Afu3g14490	mitochondrion
Afu3g14490	branched chain family amino acid biosynthetic process
Afu3g14510	lipase activity
Afu3g14540	protein binding
Afu3g14540	response to heat
Afu3g14540	protein stabilization
Afu3g14560	transporter activity
Afu3g14560	transport
Afu3g14580	dUTP diphosphatase activity
Afu3g14580	2'-deoxyribonucleotide metabolic process
Afu3g14610	metabolic process
Afu3g14610	oxidoreductase activity
Afu3g14620	metabolic process
Afu3g14620	hydrolase activity, hydrolyzing N-glycosyl compounds
Afu3g14670	integral to plasma membrane
Afu3g14670	nicotinamide mononucleotide permease activity
Afu3g14670	nicotinamide mononucleotide transport
Afu3g14680	lysophospholipase activity
Afu3g14680	extracellular region
Afu3g14680	plasma membrane
Afu3g14680	phosphatidylserine catabolic process
Afu3g14680	phosphoinositide metabolic process
Afu3g14690	5-aminolevulinate synthase activity
Afu3g14690	mitochondrial matrix

Afu3g14690	heme biosynthetic process
Afu3g14700	polyketide synthase activity
Afu3g14700	polyketide biosynthetic process
Afu3g14710	secondary metabolic process
Afu3g14720	transporter activity
Afu3g14720	transport
Afu3g14750	transcription factor activity
Afu3g14750	regulation of transcription
Afu3g14760	metabolic process
Afu3g14760	oxidoreductase activity
Afu3g14770	catalytic activity
Afu3g14770	cellular metabolic process
Afu3g14770	coenzyme binding
Afu3g14770	NAD or NADH binding
Afu3g14790	3-dehydroquinate dehydratase activity
Afu3g14790	3-dehydroquinate synthase activity
Afu3g14790	3-phosphoshikimate 1-carboxyvinyltransferase activity
Afu3g14790	shikimate 5-dehydrogenase activity
Afu3g14790	shikimate kinase activity
Afu3g14790	cytoplasm
Afu3g14790	aromatic amino acid family biosynthetic process
Afu3g14790	chorismate biosynthetic process
Afu3g14800	3-dehydroquinate dehydratase activity
Afu3g14800	3-dehydroquinate synthase activity
Afu3g14800	3-phosphoshikimate 1-carboxyvinyltransferase activity
Afu3g14800	shikimate 5-dehydrogenase activity
Afu3g14800	shikimate kinase activity
Afu3g14800	cytoplasm
Afu3g14800	aromatic amino acid family biosynthetic process
Afu3g14830	3-dehydroquinate dehydratase activity
Afu3g14830	3-dehydroquinate synthase activity
Afu3g14830	3-phosphoshikimate 1-carboxyvinyltransferase activity
Afu3g14830	shikimate 5-dehydrogenase activity
Afu3g14830	shikimate kinase activity
Afu3g14830	cytoplasm
Afu3g14830	aromatic amino acid family biosynthetic process
Afu3g14840	transcription factor activity
Afu3g14840	nucleus
Afu3g14840	regulation of transcription
Afu3g14970	vacuole inheritance
Afu3g14970	fungal-type vacuole
Afu3g14970	cytoplasm
Afu3g14970	electron transport
Afu3g14970	DNA-dependent DNA replication
Afu3g14970	response to oxidative stress
Afu3g14970	regulation of cell redox homeostasis
Afu3g14970	thiol-disulfide exchange intermediate activity
Afu3g14970	vacuole fusion, non-autophagic
Afu3g14980	cell wall organization
Afu3g14990	biological process unknown

Afu3g14990	molecular function unknown
Afu3g14990	cytoplasm
Afu3g14990	lipid particle
Afu3g15020	amino acid transport
Afu3g15020	L-methionine transmembrane transporter activity
Afu3g15020	membrane
Afu3g15030	metabolic process
Afu3g15030	zinc ion binding
Afu3g15030	oxidoreductase activity
Afu3g15140	isocitrate dehydrogenase activity
Afu3g15140	cytoplasm
Afu3g15140	mitochondrion
Afu3g15140	lysine biosynthetic process
Afu3g15170	catalytic activity
Afu3g15170	Mo-molybdopterin cofactor biosynthetic process
Afu3g15210	polysaccharide catabolic process
Afu3g15210	hydrolase activity, acting on glycosyl bonds
Afu3g15230	amidase activity
Afu3g15230	cellular component unknown
Afu3g15250	transporter activity
Afu3g15250	integral to plasma membrane
Afu3g15250	transport
Afu3g15270	catalytic activity
Afu3g15270	nonribosomal peptide biosynthetic process
Afu3g15270	peptide antibiotic biosynthetic process
Afu3g15270	amino acid adenylylation by nonribosomal peptide synthase
Afu3g15290	regulation of transcription
Afu3g15350	nucleus
Afu3g15350	cytoplasm
Afu3g15350	L-serine metabolic process
Afu3g15350	metabolic process
Afu3g15350	oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acc
Afu3g15380	plasma membrane
Afu3g15380	monocarboxylic acid transmembrane transporter activity
Afu3g15380	drug transporter activity
Afu3g15380	monocarboxylic acid transport
Afu3g15380	drug transport
Afu3g15390	plasma membrane
Afu3g15390	allantoate transmembrane transporter activity
Afu3g15390	allantoate transport
Afu3g15395	helicase activity
Afu3g15395	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process
Afu3g15395	ATP-dependent helicase activity
Afu4g00100	polygalacturonase activity
Afu4g00100	extracellular region
Afu4g00100	pectin catabolic process
Afu4g00110	sulfonate dioxygenase activity
Afu4g00110	sulfur metabolic process
Afu4g00110	cellular component unknown
Afu4g00120	transporter activity

Afu4g00120	transport
Afu4g00120	membrane
Afu4g00150	plasma membrane
Afu4g00150	carbohydrate transport
Afu4g00150	carbohydrate transmembrane transporter activity
Afu4g00150	maltose porter activity
Afu4g00160	metabolic process
Afu4g00160	oxidoreductase activity
Afu4g00210	3-oxoacyl-[acyl-carrier-protein] synthase activity
Afu4g00210	polyketide synthase activity
Afu4g00210	secondary metabolic process
Afu4g00220	catalytic activity
Afu4g00220	metabolic process
Afu4g00230	metabolic process
Afu4g00230	oxidoreductase activity
Afu4g00240	plasma membrane
Afu4g00240	amino acid transport
Afu4g00240	amino acid transmembrane transporter activity
Afu4g00240	amino acid permease activity
Afu4g00260	transporter activity
Afu4g00260	integral to plasma membrane
Afu4g00260	transport
Afu4g00290	succinate-CoA ligase (ADP-forming) activity
Afu4g00290	mitochondrion
Afu4g00290	tricarboxylic acid cycle
Afu4g00290	succinyl-CoA metabolic process
Afu4g00320	two-component sensor activity
Afu4g00320	protein histidine kinase activity
Afu4g00320	protein amino acid phosphorylation
Afu4g00370	biological process unknown
Afu4g00370	amidase activity
Afu4g00370	cellular component unknown
Afu4g00430	FAD binding
Afu4g00440	metabolic process
Afu4g00440	oxidoreductase activity
Afu4g00470	drug transporter activity
Afu4g00470	drug transport
Afu4g00470	integral to membrane
Afu4g00540	GTPase activity
Afu4g00540	membrane fraction
Afu4g00540	protein targeting to vacuole
Afu4g00540	peroxisome organization
Afu4g00540	vacuolar transport
Afu4g00540	protein retention in Golgi apparatus
Afu4g00550	transporter activity
Afu4g00550	transport
Afu4g00550	integral to membrane
Afu4g00560	metabolic process
Afu4g00560	oxidoreductase activity
Afu4g00570	integral to plasma membrane

Afu4g00570	response to toxin
Afu4g00570	multidrug transporter activity
Afu4g00590	monooxygenase activity
Afu4g00590	cellular aromatic compound metabolic process
Afu4g00610	aryl-alcohol oxidase activity
Afu4g00620	membrane fraction
Afu4g00620	fungal-type cell wall biogenesis
Afu4g00620	anchored to plasma membrane
Afu4g00630	arylformamidase activity
Afu4g00630	cytoplasm
Afu4g00630	mitochondrion
Afu4g00630	transaminase activity
Afu4g00630	NAD biosynthetic process
Afu4g00650	biological process unknown
Afu4g00650	molecular function unknown
Afu4g00650	mitochondrion
Afu4g00660	two-component sensor activity
Afu4g00660	protein histidine kinase activity
Afu4g00660	protein amino acid phosphorylation
Afu4g00680	water transport
Afu4g00680	response to osmotic stress
Afu4g00680	water channel activity
Afu4g00680	glycerol channel activity
Afu4g00680	glycerol transport
Afu4g00680	integral to membrane
Afu4g00700	nucleus
Afu4g00700	cytoplasm
Afu4g00700	alcohol dehydrogenase (NADP+) activity
Afu4g00720	dephosphorylation
Afu4g00720	phosphatase activity
Afu4g00800	receptor activity
Afu4g00800	glucose transmembrane transporter activity
Afu4g00800	glucose binding
Afu4g00800	plasma membrane
Afu4g00800	signal transduction
Afu4g00800	response to glucose stimulus
Afu4g00830	plasma membrane
Afu4g00830	peptide transporter activity
Afu4g00830	peptide transport
Afu4g00920	transporter activity
Afu4g00920	plasma membrane
Afu4g00920	transport
Afu4g00920	pantothenate transporter activity
Afu4g00920	pantothenate transport
Afu4g00930	plasma membrane
Afu4g00930	di-, tri-valent inorganic cation transmembrane transporter activity
Afu4g00930	di-, tri-valent inorganic cation transport
Afu4g00930	magnesium ion transport
Afu4g00940	metabolic process
Afu4g00940	oxidoreductase activity

Afu4g00950	mediator complex
Afu4g00950	transcription from RNA polymerase II promoter
Afu4g00950	RNA polymerase II transcription mediator activity
Afu4g00960	6-phosphofructokinase activity
Afu4g00960	cytoplasm
Afu4g00960	6-phosphofructokinase complex
Afu4g00960	glycolysis
Afu4g00970	cellular component unknown
Afu4g00990	fructose transmembrane transporter activity
Afu4g00990	glucose transmembrane transporter activity
Afu4g00990	plasma membrane
Afu4g00990	hexose transport
Afu4g00990	mannose transmembrane transporter activity
Afu4g01000	integral to plasma membrane
Afu4g01000	nicotinamide mononucleotide permease activity
Afu4g01000	nicotinamide mononucleotide transport
Afu4g01010	DNA binding
Afu4g01010	nucleus
Afu4g01010	zinc ion binding
Afu4g01010	transcription activator activity
Afu4g01010	regulation of transcription
Afu4g01020	two-component sensor activity
Afu4g01020	protein histidine kinase activity
Afu4g01020	protein amino acid phosphorylation
Afu4g01040	acylglycerone-phosphate reductase activity
Afu4g01040	cytoplasm
Afu4g01040	endoplasmic reticulum
Afu4g01040	lipid particle
Afu4g01040	phosphatidic acid biosynthetic process
Afu4g01050	plasma membrane
Afu4g01050	xenobiotic-transporting ATPase activity
Afu4g01050	ABC-type efflux porter activity
Afu4g01050	drug transport
Afu4g01050	response to drug
Afu4g01070	acid phosphatase activity
Afu4g01070	response to stress
Afu4g01080	integral to plasma membrane
Afu4g01080	response to toxin
Afu4g01080	multidrug transporter activity
Afu4g01130	molecular function unknown
Afu4g01130	cytoplasm
Afu4g01130	aromatic compound catabolic process
Afu4g01140	drug transporter activity
Afu4g01140	drug transport
Afu4g01140	integral to membrane
Afu4g01200	endoribonuclease activity
Afu4g01200	RNA catabolic process
Afu4g01230	plasma membrane
Afu4g01230	choline transmembrane transporter activity
Afu4g01230	choline transport

Afu4g01260	mitochondrial inner membrane
Afu4g01260	aerobic respiration
Afu4g01260	ATPase activity
Afu4g01310	biological process unknown
Afu4g01310	molecular function unknown
Afu4g01310	nucleus
Afu4g01310	cytoplasm
Afu4g01340	transporter activity
Afu4g01340	transport
Afu4g01340	membrane
Afu4g01360	biological process unknown
Afu4g01360	molecular function unknown
Afu4g01360	cellular component unknown
Afu4g01380	4-nitrophenylphosphatase activity
Afu4g01380	alkaline phosphatase activity
Afu4g01380	nucleus
Afu4g01380	cytoplasm
Afu4g01380	protein amino acid dephosphorylation
Afu4g01380	histone dephosphorylation
Afu4g01392	transcription factor activity
Afu4g01392	regulation of transcription
Afu4g01420	catalytic activity
Afu4g01420	spore wall assembly (sensu Saccharomyces)
Afu4g01420	cellular component unknown
Afu4g01440	transcription corepressor activity
Afu4g01440	soluble fraction
Afu4g01440	regulation of nitrogen utilization
Afu4g01450	3-deoxy-7-phosphoheptulonate synthase activity
Afu4g01450	nucleus
Afu4g01450	cytoplasm
Afu4g01450	aromatic amino acid family biosynthetic process
Afu4g01470	DNA binding
Afu4g01480	transporter activity
Afu4g01480	plasma membrane
Afu4g01480	transport
Afu4g01490	catalytic activity
Afu4g01490	mitochondrion
Afu4g01490	metabolic process
Afu4g01510	transcription factor activity
Afu4g01510	nucleus
Afu4g01510	regulation of transcription
Afu4g01530	monooxygenase activity
Afu4g01530	cellular aromatic compound metabolic process
Afu4g01550	3-chloroallyl aldehyde dehydrogenase activity
Afu4g01550	cytoplasm
Afu4g01550	polyamine catabolic process
Afu4g01550	response to stress
Afu4g01550	beta-alanine biosynthetic process
Afu4g01560	myo-inositol transmembrane transporter activity
Afu4g01560	myo-inositol transport

Afu4g01560	membrane
Afu4g02650	alpha-glucoside transport
Afu4g02650	alpha-glucoside:hydrogen symporter activity
Afu4g02650	maltose:hydrogen symporter activity
Afu4g02650	membrane fraction
Afu4g02650	trehalose transmembrane transporter activity
Afu4g02650	trehalose transport
Afu4g02720	molecular function unknown
Afu4g02720	membrane fraction
Afu4g02720	fungal-type cell wall biogenesis
Afu4g02720	anchored to plasma membrane
Afu4g02730	metabolic process
Afu4g02730	oxidoreductase activity
Afu4g02750	transport
Afu4g02750	monocarboxylic acid transmembrane transporter activity
Afu4g02750	membrane
Afu4g02800	biological process unknown
Afu4g02800	molecular function unknown
Afu4g02800	integral to membrane
Afu4g02830	oxidoreductase activity
Afu4g02870	plasma membrane
Afu4g02870	allantoate transmembrane transporter activity
Afu4g02870	allantoate transport
Afu4g02900	two-component sensor activity
Afu4g02900	protein histidine kinase activity
Afu4g02900	protein amino acid phosphorylation
Afu4g02930	helicase activity
Afu4g02930	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process
Afu4g02940	transcription factor activity
Afu4g02940	nucleus
Afu4g02940	transcription
Afu4g02970	molecular function unknown
Afu4g02970	plasma membrane
Afu4g02970	response to osmotic stress
Afu4g02990	molecular function unknown
Afu4g02990	cytosol
Afu4g02990	vesicle-mediated transport
Afu4g03000	endoplasmic reticulum
Afu4g03000	membrane lipid metabolic process
Afu4g03000	hydrolase activity
Afu4g03020	molecular function unknown
Afu4g03020	nucleus
Afu4g03020	chromatin remodeling complex
Afu4g03030	biological process unknown
Afu4g03030	molecular function unknown
Afu4g03030	nucleus
Afu4g03050	cellular bud neck contractile ring
Afu4g03050	actin cap (sensu Saccharomyces)
Afu4g03050	actin monomer binding
Afu4g03050	response to osmotic stress

Afu4g03050	axial cellular bud site selection
Afu4g03050	bipolar cellular bud site selection
Afu4g03050	actin polymerization or depolymerization
Afu4g03070	RNA helicase activity
Afu4g03070	cytoplasm
Afu4g03070	regulation of translation
Afu4g03080	DNA binding
Afu4g03080	nucleus
Afu4g03080	zinc ion binding
Afu4g03100	RAB small monomeric GTPase activity
Afu4g03100	late endosome
Afu4g03100	protein targeting to vacuole
Afu4g03100	endocytosis
Afu4g03110	transporter activity
Afu4g03110	transport
Afu4g03110	membrane
Afu4g03120	L-lactate dehydrogenase (cytochrome) activity
Afu4g03120	mitochondrial intermembrane space
Afu4g03120	electron transport
Afu4g03130	phosphate metabolic process
Afu4g03130	phosphoric ester hydrolase activity
Afu4g03140	protein kinase activity
Afu4g03140	cytoplasm
Afu4g03160	molecular function unknown
Afu4g03160	nucleus
Afu4g03180	molecular function unknown
Afu4g03180	nuclear envelope
Afu4g03180	mRNA export from nucleus
Afu4g03180	protein export from nucleus
Afu4g03180	nuclear envelope organization
Afu4g03190	alpha,alpha-trehalose-phosphate synthase (UDP-forming) activity
Afu4g03190	cytoplasm
Afu4g03190	alpha,alpha-trehalose-phosphate synthase complex (UDP-forming)
Afu4g03190	carbohydrate metabolic process
Afu4g03190	trehalose biosynthetic process
Afu4g03190	response to stress
Afu4g03220	plasma membrane
Afu4g03220	amino acid transport
Afu4g03220	amino acid transmembrane transporter activity
Afu4g03230	endoribonuclease activity
Afu4g03230	RNA catabolic process
Afu4g03290	biological process unknown
Afu4g03290	lipid particle
Afu4g03290	oxidoreductase activity
Afu4g03320	fungal-type vacuole
Afu4g03320	vacuolar membrane
Afu4g03320	calcium ion transport
Afu4g03320	cellular calcium ion homeostasis
Afu4g03320	calcium ion transmembrane transporter activity
Afu4g03320	calcium:hydrogen antiporter activity

Afu4g03321	metabolic process
Afu4g03321	methyltransferase activity
Afu4g03330	plasma membrane
Afu4g03330	response to osmotic stress
Afu4g03340	conjugation with cellular fusion
Afu4g03340	molecular function unknown
Afu4g03340	integral to membrane
Afu4g03350	hydrolase activity, hydrolyzing O-glycosyl compounds
Afu4g03350	1,3-beta-glucan metabolic process
Afu4g03350	fungal-type cell wall
Afu4g03370	gamma-aminobutyric acid transporter activity
Afu4g03370	transport
Afu4g03370	membrane
Afu4g03390	plasma membrane
Afu4g03390	water transport
Afu4g03390	water channel activity
Afu4g03410	molecular function unknown
Afu4g03410	cytoplasm
Afu4g03410	response to stress
Afu4g03420	endoribonuclease activity
Afu4g03420	mRNA catabolic process
Afu4g03430	transcription factor activity
Afu4g03430	regulation of transcription
Afu4g03435	anion transport
Afu4g03435	anion transmembrane transporter activity
Afu4g03460	DNA binding
Afu4g03460	nucleus
Afu4g03490	tripeptidyl-peptidase activity
Afu4g03490	protein catabolic process
Afu4g03510	plasma membrane
Afu4g03510	choline transmembrane transporter activity
Afu4g03510	choline transport
Afu4g03590	biological process unknown
Afu4g03590	molecular function unknown
Afu4g03590	clathrin-coated vesicle
Afu4g03590	COPI-coated vesicle
Afu4g03610	inorganic phosphate transmembrane transporter activity
Afu4g03610	integral to plasma membrane
Afu4g03610	phosphate transport
Afu4g03620	biological process unknown
Afu4g03620	molecular function unknown
Afu4g03620	cytoplasm
Afu4g03620	endoplasmic reticulum
Afu4g03630	sterol 24-C-methyltransferase activity
Afu4g03630	endoplasmic reticulum
Afu4g03630	lipid particle
Afu4g03630	ergosterol biosynthetic process
Afu4g03650	chaperone activity
Afu4g03650	cytoplasm
Afu4g03650	cytosol

Afu4g03650	ribosome
Afu4g03650	protein folding
Afu4g03670	transcription factor activity
Afu4g03670	nucleus
Afu4g03670	regulation of transcription
Afu4g03690	aldehyde dehydrogenase (NAD) activity
Afu4g03700	biological process unknown
Afu4g03700	molecular function unknown
Afu4g03700	cytoplasm
Afu4g03710	glutamate-ammonia ligase activity
Afu4g03710	glutamine biosynthetic process
Afu4g03722	biological process unknown
Afu4g03722	molecular function unknown
Afu4g03722	cellular component unknown
Afu4g03740	fungal-type vacuole
Afu4g03740	transporter activity
Afu4g03740	transport
Afu4g03750	integral to plasma membrane
Afu4g03750	nicotinamide mononucleotide permease activity
Afu4g03750	nicotinamide mononucleotide transport
Afu4g03760	glycine dehydrogenase (decarboxylating) activity
Afu4g03760	mitochondrion
Afu4g03760	one-carbon metabolic process
Afu4g03770	cytoplasm
Afu4g03770	hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in linear amides
Afu4g03770	guanine metabolic process
Afu4g03800	metabolic process
Afu4g03800	oxidoreductase activity
Afu4g03840	nucleus
Afu4g03840	transcription-coupled nucleotide-excision repair
Afu4g03840	nucleotide-excision repair
Afu4g03840	DNA-dependent ATPase activity
Afu4g03850	protein kinase activity
Afu4g03850	nucleus
Afu4g03850	cytoplasm
Afu4g03850	protein amino acid phosphorylation
Afu4g03850	cell growth and/or maintenance
Afu4g03860	translation initiation factor activity
Afu4g03860	eukaryotic translation initiation factor 3 complex
Afu4g03860	translational initiation
Afu4g03870	molecular function unknown
Afu4g03870	endosome
Afu4g03870	protein targeting to vacuole
Afu4g03870	negative regulation of transcription by glucose
Afu4g03880	structural constituent of ribosome
Afu4g03880	cytosolic large ribosomal subunit (sensu Eukaryota)
Afu4g03880	translation
Afu4g03890	biological process unknown
Afu4g03890	molecular function unknown
Afu4g03890	nucleus

Afu4g03890	cytoplasm
Afu4g03900	3-hydroxyacyl-CoA dehydrogenase activity
Afu4g03900	enoyl-CoA hydratase activity
Afu4g03900	peroxisomal matrix
Afu4g03900	fatty acid beta-oxidation
Afu4g03910	zinc ion binding
Afu4g03920	transporter activity
Afu4g03920	integral to plasma membrane
Afu4g03920	transport
Afu4g03940	ferric-chelate reductase activity
Afu4g03950	cystathionine beta-lyase activity
Afu4g03950	cystathionine beta-lyase activity
Afu4g03950	peroxisome
Afu4g03950	methionine biosynthetic process
Afu4g03950	methionine biosynthetic process
Afu4g03950	cysteine biosynthetic process
Afu4g03960	transcription factor activity
Afu4g03960	nucleus
Afu4g03960	pathogenesis
Afu4g03960	regulation of transcription
Afu4g03970	fungal-type vacuole
Afu4g03970	molecular function unknown
Afu4g03970	GPI anchor biosynthetic process
Afu4g03970	fungal-type cell wall
Afu4g03970	ATP transport
Afu4g03980	centromere and kinetochore complex maturation
Afu4g03980	kinetochore
Afu4g03980	DNA binding
Afu4g03980	nucleus
Afu4g03980	homologous chromosome segregation
Afu4g03990	mitochondrial outer membrane
Afu4g03990	mitochondrial translocation
Afu4g03990	ATPase activity
Afu4g04000	chitin binding
Afu4g04020	peptidyl-prolyl cis-trans isomerase activity
Afu4g04020	FK506 binding
Afu4g04020	nucleus
Afu4g04020	cytoplasm
Afu4g04020	ribosome assembly
Afu4g04030	histidine biosynthetic process
Afu4g04030	histidinol-phosphatase activity
Afu4g04030	cell
Afu4g04070	integral to plasma membrane
Afu4g04100	endosome
Afu4g04100	protein targeting to vacuole
Afu4g04100	regulator of G-protein signaling activity
Afu4g04100	negative regulation of transcription by glucose
Afu4g04100	protein retention in Golgi apparatus
Afu4g04110	biological process unknown
Afu4g04110	molecular function unknown

Afu4g04110	nucleus
Afu4g04120	response to pheromone during conjugation with cellular fusion
Afu4g04120	cellular morphogenesis during conjugation with cellular fusion
Afu4g04120	protein binding
Afu4g04120	actin cytoskeleton
Afu4g04120	protein kinase activator activity
Afu4g04130	biological process unknown
Afu4g04130	mitochondrion
Afu4g04130	ATPase activity
Afu4g04150	fungal-type vacuole
Afu4g04150	zinc ion transmembrane transporter activity
Afu4g04150	cobalt ion transport
Afu4g04150	zinc ion transport
Afu4g04150	cellular zinc ion homeostasis
Afu4g04150	di-, tri-valent inorganic cation transmembrane transporter activity
Afu4g04150	cobalt ion transmembrane transporter activity
Afu4g04160	biological process unknown
Afu4g04160	amidase activity
Afu4g04160	cellular component unknown
Afu4g04180	chitin synthase activity
Afu4g04180	plasma membrane
Afu4g04180	chitin biosynthetic process
Afu4g04180	chitosome
Afu4g04200	sulfate assimilation
Afu4g04200	cytoplasm
Afu4g04200	3'(2'),5'-bisphosphate nucleotidase activity
Afu4g04200	methionine biosynthetic process
Afu4g04200	hyperosmotic salinity response
Afu4g04210	biological process unknown
Afu4g04210	molecular function unknown
Afu4g04210	cellular component unknown
Afu4g04250	transporter activity
Afu4g04250	integral to plasma membrane
Afu4g04250	transport
Afu4g04270	thymidylate synthase activity
Afu4g04270	nucleus
Afu4g04270	dTMP biosynthetic process
Afu4g04270	DNA-dependent DNA replication
Afu4g04280	biological process unknown
Afu4g04280	molecular function unknown
Afu4g04280	nucleus
Afu4g04280	cytoplasm
Afu4g04290	histone deacetylase activity
Afu4g04290	nucleus
Afu4g04290	cytoplasm
Afu4g04290	cellular bud neck
Afu4g04290	histone deacetylation
Afu4g04300	intracellular
Afu4g04300	cellular amino acid metabolic process
Afu4g04300	alanine racemase activity

Afu4g04300	pyridoxal phosphate binding
Afu4g04310	intracellular protein transport
Afu4g04310	endocytosis
Afu4g04310	vesicle-mediated transport
Afu4g04310	AP-2 adaptor complex
Afu4g04320	transcription factor activity
Afu4g04320	regulation of transcription
Afu4g04350	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
Afu4g04350	nucleic acid binding
Afu4g04350	cytoplasm
Afu4g04350	polysome
Afu4g04350	mRNA catabolic process
Afu4g04350	regulation of translational termination
Afu4g04350	ATP-dependent helicase activity
Afu4g04350	ATPase activity
Afu4g04360	nucleotide-excision repair factor 3 complex
Afu4g04360	nucleotide-excision repair, DNA duplex unwinding
Afu4g04360	holo TFIIH complex
Afu4g04360	nucleotide-excision repair
Afu4g04360	transcription initiation from RNA polymerase II promoter
Afu4g04360	negative regulation of transcription from RNA polymerase II promoter, mitotic
Afu4g04360	general RNA polymerase II transcription factor activity
Afu4g04380	biological process unknown
Afu4g04380	molecular function unknown
Afu4g04380	cellular component unknown
Afu4g04390	molecular function unknown
Afu4g04390	cell
Afu4g04390	DNA topological change
Afu4g04420	molecular function unknown
Afu4g04420	cytoplasm
Afu4g04420	protein targeting to vacuole
Afu4g04460	structural constituent of ribosome
Afu4g04460	cytosolic large ribosomal subunit (sensu Eukaryota)
Afu4g04460	translation
Afu4g04470	biological process unknown
Afu4g04470	molecular function unknown
Afu4g04470	mitochondrion
Afu4g04520	succinate-CoA ligase (ADP-forming) activity
Afu4g04520	mitochondrion
Afu4g04520	tricarboxylic acid cycle
Afu4g04520	succinyl-CoA metabolic process
Afu4g04530	metabolic process
Afu4g04530	oxidoreductase activity
Afu4g04550	cytoplasm
Afu4g04550	purine nucleotide biosynthetic process
Afu4g04550	transferase activity, transferring pentosyl groups
Afu4g04590	biological process unknown
Afu4g04590	molecular function unknown
Afu4g04590	mitochondrion
Afu4g04600	holocytochrome-c synthase activity

Afu4g04600	mitochondrial intermembrane space
Afu4g04600	cytochrome c-heme linkage
Afu4g04612	protein catabolic process
Afu4g04630	molecular function unknown
Afu4g04630	Golgi apparatus
Afu4g04630	membrane
Afu4g04630	vesicle-mediated transport
Afu4g04640	protein binding
Afu4g04640	endoplasmic reticulum
Afu4g04640	ubiquitin-dependent protein catabolic process
Afu4g04660	endopeptidase activity
Afu4g04660	nucleus
Afu4g04660	proteasome regulatory particle
Afu4g04660	ubiquitin-dependent protein catabolic process
Afu4g04660	proteasome regulatory particle, base subcomplex
Afu4g04660	ATPase activity
Afu4g04670	biological process unknown
Afu4g04670	molecular function unknown
Afu4g04670	cellular component unknown
Afu4g04680	cellular component unknown
Afu4g04680	kinase activity
Afu4g04710	inactivation of MAPK activity involved in osmosensory signaling pathway
Afu4g04710	pheromone-dependent signal transduction involved in conjugation with cellular fusion
Afu4g04710	protein tyrosine phosphatase activity
Afu4g04710	cytoplasm
Afu4g04710	protein amino acid dephosphorylation
Afu4g04720	structural molecule activity
Afu4g04720	nuclear pore
Afu4g04720	mRNA export from nucleus
Afu4g04720	rRNA export from nucleus
Afu4g04720	snRNA export from nucleus
Afu4g04720	tRNA export from nucleus
Afu4g04720	protein import into nucleus
Afu4g04720	NLS-bearing substrate import into nucleus
Afu4g04720	snRNP protein import into nucleus
Afu4g04720	mRNA-binding (hnRNP) protein import into nucleus
Afu4g04720	ribosomal protein import into nucleus
Afu4g04720	protein export from nucleus
Afu4g04720	nuclear pore organization
Afu4g04730	cellular component unknown
Afu4g04730	diaminohydroxyphosphoribosylaminopyrimidine deaminase activity
Afu4g04730	riboflavin biosynthetic process
Afu4g04740	ribosomal subunit export from nucleus
Afu4g04740	signal transducer activity
Afu4g04740	nucleus
Afu4g04740	rRNA export from nucleus
Afu4g04760	DNA replication checkpoint
Afu4g04760	DNA damage checkpoint
Afu4g04760	inositol or phosphatidylinositol kinase activity
Afu4g04760	nucleus

Afu4g04760	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process
Afu4g04760	DNA recombination
Afu4g04760	reciprocal meiotic recombination
Afu4g04800	intracellular
Afu4g04800	ATPase activity
Afu4g04800	response to drug
Afu4g04810	cytokinesis
Afu4g04810	RAB small monomeric GTPase activity
Afu4g04810	exocytosis
Afu4g04810	Golgi to plasma membrane transport
Afu4g04810	vesicle fusion
Afu4g04810	small GTPase mediated signal transduction
Afu4g04810	protein secretion
Afu4g04810	transport vesicle
Afu4g04820	C-4 methylsterol oxidase activity
Afu4g04820	endoplasmic reticulum membrane
Afu4g04820	plasma membrane
Afu4g04820	ergosterol biosynthetic process
Afu4g05830	translation initiation factor activity
Afu4g05830	nucleus
Afu4g05830	translational initiation
Afu4g05840	structural molecule activity
Afu4g05840	nuclear pore
Afu4g05840	mRNA export from nucleus
Afu4g05840	rRNA export from nucleus
Afu4g05840	snRNA export from nucleus
Afu4g05840	tRNA export from nucleus
Afu4g05840	NLS-bearing substrate import into nucleus
Afu4g05840	snRNP protein import into nucleus
Afu4g05840	mRNA-binding (hnRNP) protein import into nucleus
Afu4g05840	ribosomal protein import into nucleus
Afu4g05840	protein export from nucleus
Afu4g05840	nuclear pore organization
Afu4g05870	biological process unknown
Afu4g05870	molecular function unknown
Afu4g05870	cytoplasm
Afu4g05880	rRNA modification
Afu4g05880	molecular function unknown
Afu4g05880	nucleus
Afu4g05880	nucleolus
Afu4g05880	small nucleolar ribonucleoprotein complex
Afu4g05880	35S primary transcript processing
Afu4g05880	maturation of SSU-rRNA
Afu4g05880	small nuclear ribonucleoprotein complex
Afu4g05890	biological process unknown
Afu4g05890	cytoplasm
Afu4g05890	S-adenosylmethionine-dependent methyltransferase activity
Afu4g05910	nucleus
Afu4g05910	thioredoxin peroxidase activity
Afu4g05910	regulation of cell redox homeostasis

Afu4g05915	response to oxidative stress
Afu4g05915	antioxidant activity
Afu4g05920	biological process unknown
Afu4g05920	molecular function unknown
Afu4g05920	mitochondrion
Afu4g05940	ethanolamine-phosphate cytidylyltransferase activity
Afu4g05940	nucleus
Afu4g05940	cytoplasm
Afu4g05940	phosphatidylethanolamine biosynthetic process
Afu4g05950	mitochondrial matrix
Afu4g05950	electron transport
Afu4g05950	response to osmotic stress
Afu4g05950	response to oxidative stress
Afu4g05950	thiol-disulfide exchange intermediate activity
Afu4g05960	G1/S transition of mitotic cell cycle
Afu4g05960	phosphopantothenoylcysteine decarboxylase activity
Afu4g05960	cellular component unknown
Afu4g05960	coenzyme A biosynthetic process
Afu4g05970	prenyltransferase activity
Afu4g05970	carrier activity
Afu4g05970	mitochondrial inner membrane
Afu4g05970	ubiquinone metabolic process
Afu4g05970	isoprenoid binding
Afu4g05980	DNA binding
Afu4g05980	nucleus
Afu4g05980	chromatin remodeling
Afu4g05990	biological process unknown
Afu4g05990	molecular function unknown
Afu4g05990	mitochondrion
Afu4g06000	ribosomal large subunit assembly
Afu4g06000	peptidyltransferase activity
Afu4g06000	structural constituent of ribosome
Afu4g06000	mitochondrial large ribosomal subunit
Afu4g06000	translation
Afu4g06010	peptide alpha-N-acetyltransferase activity
Afu4g06010	cytoplasm
Afu4g06010	N-terminal peptidyl-methionine acetylation
Afu4g06020	cyclin-dependent protein kinase inhibitor activity
Afu4g06020	nucleus
Afu4g06020	cytoplasm
Afu4g06020	phosphate metabolic process
Afu4g06050	drug transporter activity
Afu4g06050	drug transport
Afu4g06050	integral to membrane
Afu4g06070	ATP binding
Afu4g06070	cytosol
Afu4g06070	cytosolic ribosome (sensu Eukaryota)
Afu4g06070	regulation of translational initiation
Afu4g06070	regulation of translational elongation
Afu4g06080	transporter activity

Afu4g06080	integral to plasma membrane
Afu4g06080	transport
Afu4g06090	molecular function unknown
Afu4g06090	nuclear pore
Afu4g06090	cytoplasm
Afu4g06090	ER to Golgi vesicle-mediated transport
Afu4g06090	nonselective vesicle assembly
Afu4g06090	extrinsic to plasma membrane
Afu4g06090	COPII vesicle coat
Afu4g06090	ER-associated protein catabolic process
Afu4g06120	DNA binding
Afu4g06120	protein binding
Afu4g06120	nucleus
Afu4g06120	chromatin remodeling
Afu4g06120	chromosome segregation
Afu4g06120	RSC complex
Afu4g06130	response to stress
Afu4g06130	cellular component unknown
Afu4g06130	phosphatase activator activity
Afu4g06130	regulation of growth
Afu4g06140	nucleus
Afu4g06140	cytoplasm
Afu4g06140	proteolysis
Afu4g06140	dipeptidyl-peptidase III activity
Afu4g06150	biological process unknown
Afu4g06150	protein kinase activity
Afu4g06160	branched-chain-amino-acid transaminase activity
Afu4g06160	nucleus
Afu4g06160	cytoplasm
Afu4g06160	cellular amino acid catabolic process
Afu4g06160	branched chain family amino acid biosynthetic process
Afu4g06180	G1/S transition of mitotic cell cycle
Afu4g06180	G2/M transition of mitotic cell cycle
Afu4g06180	flocculation
Afu4g06180	establishment of cell polarity (sensu Saccharomyces)
Afu4g06180	protein kinase CK2 activity
Afu4g06180	protein kinase CK2 complex
Afu4g06180	regulation of transcription from RNA polymerase I promoter
Afu4g06180	regulation of transcription from RNA polymerase III promoter
Afu4g06180	protein amino acid phosphorylation
Afu4g06180	cellular ion homeostasis
Afu4g06180	response to DNA damage stimulus
Afu4g06210	DNA binding
Afu4g06230	hydrogen:amino acid symporter activity
Afu4g06230	vacuolar membrane
Afu4g06230	endoplasmic reticulum membrane
Afu4g06230	integral to plasma membrane
Afu4g06230	fatty acid metabolic process
Afu4g06230	response to osmotic stress
Afu4g06250	RNA binding

Afu4g06250	nucleolus
Afu4g06250	rRNA processing
Afu4g06260	single-stranded DNA specific endodeoxyribonuclease activity
Afu4g06260	nucleotide-excision repair factor 1 complex
Afu4g06260	removal of nonhomologous ends
Afu4g06260	double-strand break repair via single-strand annealing, removal of nonhomologous ends
Afu4g06260	nucleotide-excision repair, DNA incision, 5'-to lesion
Afu4g06290	endoplasmic reticulum
Afu4g06290	aging
Afu4g06290	protein transporter activity
Afu4g06290	ceramide biosynthetic process
Afu4g06350	nucleus
Afu4g06350	nucleolus
Afu4g06350	ribosomal large subunit biogenesis
Afu4g06400	molecular function unknown
Afu4g06400	nucleus
Afu4g06400	cytoplasm
Afu4g06400	proteolysis
Afu4g06400	invasive growth
Afu4g06400	protein processing
Afu4g06400	sporulation resulting in formation of a cellular spore
Afu4g06420	transcription factor activity
Afu4g06420	regulation of transcription
Afu4g06460	3-dehydroquinate dehydratase activity
Afu4g06460	3-dehydroquinate synthase activity
Afu4g06460	3-phosphoshikimate 1-carboxyvinyltransferase activity
Afu4g06460	shikimate 5-dehydrogenase activity
Afu4g06460	shikimate kinase activity
Afu4g06460	cytoplasm
Afu4g06460	aromatic amino acid family biosynthetic process
Afu4g06490	molecular function unknown
Afu4g06490	nucleus
Afu4g06490	mismatch repair
Afu4g06490	reciprocal meiotic recombination
Afu4g06530	transcription factor activity
Afu4g06530	nucleus
Afu4g06530	transcription
Afu4g06530	regulation of sulfur metabolic process
Afu4g06540	condensed nuclear chromosome kinetochore
Afu4g06540	DNA binding
Afu4g06540	chromosome segregation
Afu4g06550	zinc ion binding
Afu4g06570	regulation of progression through cell cycle
Afu4g06570	Ras guanyl-nucleotide exchange factor activity
Afu4g06570	cytoplasm
Afu4g06570	plasma membrane
Afu4g06570	traversing start control point of mitotic cell cycle
Afu4g06570	Ras protein signal transduction
Afu4g06620	glutamate dehydrogenase (NADP+) activity
Afu4g06620	nucleus

Afu4g06620	cytoplasm
Afu4g06620	glutamate biosynthetic process
Afu4g06630	transporter activity
Afu4g06630	integral to plasma membrane
Afu4g06630	transport
Afu4g06640	lipid biosynthetic process
Afu4g06640	cyclopropane-fatty-acyl-phospholipid synthase activity
Afu4g06690	ribonucleoside-diphosphate reductase activity
Afu4g06690	cytoplasm
Afu4g06690	ribonucleoside-diphosphate reductase complex
Afu4g06690	DNA replication
Afu4g06690	deoxyribonucleoside diphosphate metabolic process
Afu4g06690	programmed cell death
Afu4g06710	biological process unknown
Afu4g06710	molecular function unknown
Afu4g06710	cellular component unknown
Afu4g06740	cytoplasm
Afu4g06740	dihydrofolate synthase activity
Afu4g06740	folic acid and derivative biosynthetic process
Afu4g06750	cytokinesis
Afu4g06750	protein kinase activity
Afu4g06750	spindle pole body
Afu4g06750	protein amino acid phosphorylation
Afu4g06750	regulation of exit from mitosis
Afu4g06760	biological process unknown
Afu4g06760	molecular function unknown
Afu4g06760	mitochondrion
Afu4g06770	molecular function unknown
Afu4g06770	mitochondrial matrix
Afu4g06770	cellular iron ion homeostasis
Afu4g06770	iron-sulfur cluster assembly
Afu4g06780	transporter activity
Afu4g06780	mitochondrial inner membrane
Afu4g06780	transport
Afu4g06790	mitochondrial respiratory chain complex III
Afu4g06790	mitochondrial electron transport, ubiquinol to cytochrome c
Afu4g06790	ubiquinol-cytochrome-c reductase activity
Afu4g06790	aerobic respiration
Afu4g06790	respiratory chain complex III assembly
Afu4g06800	alkylbase DNA N-glycosylase activity
Afu4g06800	nucleus
Afu4g06800	DNA dealkylation
Afu4g06820	plasma membrane
Afu4g06820	cell wall organization
Afu4g06830	mitotic spindle elongation
Afu4g06830	G2/M transition of mitotic cell cycle
Afu4g06830	nucleus
Afu4g06830	protein modification process
Afu4g06830	SUMO conjugating enzyme activity
Afu4g06840	RNA binding

Afu4g06850	biological process unknown
Afu4g06850	cytoplasm
Afu4g06850	peroxisomal membrane
Afu4g06850	peroxisomal matrix
Afu4g06850	AMP binding
Afu4g06870	mannosyltransferase activity
Afu4g06870	alpha-1,6-mannosyltransferase complex
Afu4g06870	Golgi cis cisterna
Afu4g06870	protein amino acid N-linked glycosylation
Afu4g06890	endoplasmic reticulum
Afu4g06890	ergosterol biosynthetic process
Afu4g06890	sterol 14-demethylase activity
Afu4g06900	asparagine synthase (glutamine-hydrolyzing) activity
Afu4g06900	cytoplasm
Afu4g06900	asparagine biosynthetic process
Afu4g06910	mitochondrial outer membrane
Afu4g06910	ion transport
Afu4g06910	mitochondrion organization
Afu4g06910	voltage-gated anion channel activity
Afu4g06910	aerobic respiration
Afu4g06930	methionyl aminopeptidase activity
Afu4g06930	cytoplasm
Afu4g06930	proteolysis
Afu4g06940	stearoyl-CoA 9-desaturase activity
Afu4g06940	fatty acid biosynthetic process
Afu4g06970	nuclear chromosome
Afu4g06970	meiotic DNA recombinase assembly
Afu4g06970	telomere maintenance via recombination
Afu4g06970	double-strand break repair via break-induced replication
Afu4g06970	DNA recombinase assembly
Afu4g06970	DNA strand annealing activity
Afu4g06970	nucleus
Afu4g06970	double-strand break repair via single-strand annealing
Afu4g06970	double-strand break repair via synthesis-dependent strand annealing
Afu4g06990	transporter activity
Afu4g06990	endoplasmic reticulum
Afu4g06990	transport
Afu4g07000	protein tyrosine phosphatase activity
Afu4g07000	cytoplasm
Afu4g07000	protein amino acid dephosphorylation
Afu4g07000	response to stress
Afu4g07010	biological process unknown
Afu4g07010	molecular function unknown
Afu4g07010	cytoplasm
Afu4g07020	L-lactate dehydrogenase (cytochrome) activity
Afu4g07020	mitochondrial intermembrane space
Afu4g07020	electron transport
Afu4g07040	cathepsin D activity
Afu4g07040	endocytic vesicle
Afu4g07040	protein catabolic process

Afu4g07050	L-lactate dehydrogenase (cytochrome) activity
Afu4g07050	mitochondrial intermembrane space
Afu4g07050	electron transport
Afu4g07080	protein tyrosine phosphatase activity
Afu4g07080	cytoplasm
Afu4g07080	meiosis
Afu4g07080	sporulation (sensu Saccharomyces)
Afu4g07090	DNA binding
Afu4g07090	nucleus
Afu4g07090	zinc ion binding
Afu4g07110	t-SNARE activity
Afu4g07110	endosome
Afu4g07110	Golgi apparatus
Afu4g07110	Golgi to vacuole transport
Afu4g07120	holocytochrome-c synthase activity
Afu4g07120	mitochondrial intermembrane space
Afu4g07120	cytochrome c-heme linkage
Afu4g07130	diphosphomevalonate decarboxylase activity
Afu4g07130	cytosol
Afu4g07130	ergosterol biosynthetic process
Afu4g07130	isoprenoid biosynthetic process
Afu4g07140	histone acetyltransferase activity
Afu4g07140	regulation of transcription from RNA polymerase II promoter
Afu4g07140	transcription elongation factor complex
Afu4g07140	DNA-directed RNA polymerase II, holoenzyme
Afu4g07140	RNA polymerase II transcription elongation factor activity
Afu4g07160	ATP-dependent RNA helicase activity
Afu4g07160	nucleolus
Afu4g07160	35S primary transcript processing
Afu4g07170	nucleus
Afu4g07170	ubiquitin-dependent protein catabolic process
Afu4g07170	chromosome segregation
Afu4g07190	ornithine carbamoyltransferase activity
Afu4g07190	cytosol
Afu4g07190	arginine biosynthetic process
Afu4g07190	ornithine metabolic process
Afu4g07210	acetolactate synthase activity
Afu4g07210	mitochondrion
Afu4g07210	branched chain family amino acid biosynthetic process
Afu4g07210	enzyme regulator activity
Afu4g07230	mitotic sister chromatid segregation
Afu4g07230	ATP-dependent DNA helicase activity
Afu4g07230	nucleolus
Afu4g07230	DNA unwinding during replication
Afu4g07230	chromosome organization and biogenesis (sensu Eukaryota)
Afu4g07230	meiotic chromosome segregation
Afu4g07250	structural constituent of ribosome
Afu4g07250	mitochondrial small ribosomal subunit
Afu4g07250	translation
Afu4g07260	cytoplasm

Afu4g07260	mating projection
Afu4g07270	carboxypeptidase D activity
Afu4g07270	trans-Golgi network
Afu4g07270	protein processing
Afu4g07280	molecular function unknown
Afu4g07280	nucleus
Afu4g07280	cAMP-mediated signaling
Afu4g07310	biological process unknown
Afu4g07310	molecular function unknown
Afu4g07310	cellular component unknown
Afu4g07330	biological process unknown
Afu4g07330	molecular function unknown
Afu4g07330	endoplasmic reticulum
Afu4g07330	endoplasmic reticulum membrane
Afu4g07340	ubiquitin conjugating enzyme activity
Afu4g07340	nucleus
Afu4g07340	cytoplasm
Afu4g07340	ubiquitin-dependent protein catabolic process
Afu4g07340	response to stress
Afu4g07360	5-methyltetrahydropteroyltriglutamate-homocysteine S-methyltransferase activity
Afu4g07360	cytoplasm
Afu4g07360	methionine biosynthetic process
Afu4g07380	nucleus
Afu4g07380	DNA metabolic process
Afu4g07390	molecular function unknown
Afu4g07390	integral to membrane
Afu4g07390	secretory pathway
Afu4g07400	two-component sensor activity
Afu4g07400	protein histidine kinase activity
Afu4g07400	protein amino acid phosphorylation
Afu4g07420	endopeptidase activity
Afu4g07420	proteasome core complex
Afu4g07420	ubiquitin-dependent protein catabolic process
Afu4g07420	proteasome core complex, beta-subunit complex
Afu4g07500	rRNA modification
Afu4g07500	small nucleolar ribonucleoprotein complex
Afu4g07500	35S primary transcript processing
Afu4g07500	maturation of SSU-rRNA
Afu4g07500	snoRNA binding
Afu4g07500	small nuclear ribonucleoprotein complex
Afu4g07510	endopeptidase activity
Afu4g07510	nucleus
Afu4g07510	proteasome core complex
Afu4g07510	ubiquitin-dependent protein catabolic process
Afu4g07510	response to stress
Afu4g07510	proteasome core complex, beta-subunit complex
Afu4g07520	nuclear mRNA splicing, via spliceosome
Afu4g07520	nucleus
Afu4g07520	pre-mRNA splicing factor activity
Afu4g07540	small nucleolar ribonucleoprotein complex

Afu4g07540	maturation of SSU-rRNA
Afu4g07540	snoRNA binding
Afu4g07550	nuclear mRNA splicing, via spliceosome
Afu4g07550	RNA binding
Afu4g07550	spliceosomal complex
Afu4g07560	biological process unknown
Afu4g07560	molecular function unknown
Afu4g07560	cellular component unknown
Afu4g07570	molecular function unknown
Afu4g07570	membrane fraction
Afu4g07570	virus-host interaction
Afu4g07570	ribosomal large subunit biogenesis
Afu4g07580	translation initiation factor activity
Afu4g07580	ribosome
Afu4g07580	translational initiation
Afu4g07590	conjugation with cellular fusion
Afu4g07590	metalloendopeptidase activity
Afu4g07590	peptide pheromone maturation
Afu4g07590	prenyl-dependent CAAX protease activity
Afu4g07590	integral to endoplasmic reticulum membrane
Afu4g07610	biological process unknown
Afu4g07610	molecular function unknown
Afu4g07610	cytoplasm
Afu4g07630	molecular function unknown
Afu4g07630	nucleus
Afu4g07630	nucleolus
Afu4g07630	chromosome organization and biogenesis (sensu Eukaryota)
Afu4g07630	ribosomal large subunit biogenesis
Afu4g07640	biological process unknown
Afu4g07640	molecular function unknown
Afu4g07640	cytoplasm
Afu4g07640	mitochondrion
Afu4g07650	histone deacetylase complex
Afu4g07650	peptidyl-prolyl cis-trans isomerase activity
Afu4g07650	protein metabolic process
Afu4g07660	RNA helicase activity
Afu4g07660	cytoplasm
Afu4g07660	translational initiation
Afu4g07670	molecular function unknown
Afu4g07670	nucleus
Afu4g07670	chromatin remodeling
Afu4g07670	chromatin remodeling complex
Afu4g07690	IMP cyclohydrolase activity
Afu4g07690	phosphoribosylaminoimidazolecarboxamide formyltransferase activity
Afu4g07690	cytosol
Afu4g07690	'de novo' IMP biosynthetic process
Afu4g07700	structural molecule activity
Afu4g07700	vesicle-mediated transport
Afu4g07700	clathrin vesicle coat
Afu4g07710	pyruvate carboxylase activity

Afu4g07710	cytosol
Afu4g07710	gluconeogenesis
Afu4g07710	NADPH regeneration
Afu4g07730	ribosomal large subunit assembly
Afu4g07730	structural constituent of ribosome
Afu4g07730	cytosolic large ribosomal subunit (sensu Eukaryota)
Afu4g07730	translation
Afu4g07740	nuclear mRNA splicing, via spliceosome
Afu4g07740	pre-mRNA splicing factor activity
Afu4g07740	small nuclear ribonucleoprotein complex
Afu4g07750	biological process unknown
Afu4g07750	molecular function unknown
Afu4g07750	mitochondrion
Afu4g07760	vacuole
Afu4g07760	neutral amino acid transmembrane transporter activity
Afu4g07760	neutral amino acid transport
Afu4g07770	ion transmembrane transporter activity
Afu4g07780	mevalonate kinase activity
Afu4g07780	cytosol
Afu4g07780	ergosterol biosynthetic process
Afu4g07800	conjugation with cellular fusion
Afu4g07800	protein farnesyltransferase activity
Afu4g07800	protein geranylgeranyltransferase activity
Afu4g07800	protein farnesyltransferase complex
Afu4g07800	peptide pheromone maturation
Afu4g07800	protein amino acid farnesylation
Afu4g07800	protein amino acid geranylgeranylation
Afu4g07810	biological process unknown
Afu4g07810	molecular function unknown
Afu4g07810	cellular component unknown
Afu4g07820	methionine-tRNA ligase activity
Afu4g07820	mitochondrion
Afu4g07820	methionyl-tRNA aminoacylation
Afu4g07845	structural constituent of ribosome
Afu4g07845	translation
Afu4g07845	ribosome biogenesis
Afu4g07910	metalloendopeptidase activity
Afu4g07910	pyruvate metabolic process
Afu4g07910	proteolysis
Afu4g07940	metabolic process
Afu4g07940	oxidoreductase activity
Afu4g07970	delta DNA polymerase activity
Afu4g07970	delta DNA polymerase complex
Afu4g07970	leading strand elongation
Afu4g07970	lagging strand elongation
Afu4g07970	mutagenesis
Afu4g07970	base-excision repair
Afu4g07970	nucleotide-excision repair
Afu4g07970	mismatch repair
Afu4g07970	postreplication repair

Afu4g07990	biological process unknown
Afu4g07990	molecular function unknown
Afu4g07990	cytoplasm
Afu4g08010	ornithine decarboxylase activity
Afu4g08010	cytoplasm
Afu4g08010	pantothenate biosynthetic process
Afu4g08030	biological process unknown
Afu4g08030	molecular function unknown
Afu4g08030	mitochondrion
Afu4g08040	GTPase activity
Afu4g08040	RAB small monomeric GTPase activity
Afu4g08040	late endosome
Afu4g08040	protein targeting to vacuole
Afu4g08040	endocytosis
Afu4g08050	inositol or phosphatidylinositol phosphatase activity
Afu4g08050	dephosphorylation
Afu4g08050	integral to Golgi membrane
Afu4g08050	integral to endoplasmic reticulum membrane
Afu4g08050	phosphoinositide metabolic process
Afu4g08060	tetrahydrofolylpolyglutamate synthase activity
Afu4g08060	cytoplasm
Afu4g08060	mitochondrion
Afu4g08060	one-carbon metabolic process
Afu4g08070	glycylpeptide N-tetradecanoyltransferase activity
Afu4g08070	cytosol
Afu4g08070	N-terminal peptidyl-glycine N-myristoylation
Afu4g08070	pheromone response (sensu Fungi)
Afu4g08110	translation elongation factor activity
Afu4g08110	mitochondrion
Afu4g08110	translational elongation
Afu4g08120	soluble fraction
Afu4g08120	lipid binding
Afu4g08120	regulation of proteolysis
Afu4g08120	peptidase inhibitor activity
Afu4g08130	biological process unknown
Afu4g08130	molecular function unknown
Afu4g08130	mitochondrion
Afu4g08140	L-threonine ammonia-lyase activity
Afu4g08140	mitochondrion
Afu4g08140	branched chain family amino acid biosynthetic process
Afu4g08170	cytoplasm
Afu4g08170	glutamate catabolic process
Afu4g08170	response to oxidative stress
Afu4g08170	succinate-semialdehyde dehydrogenase [NAD(P)+] activity
Afu4g08190	molecular function unknown
Afu4g08190	nucleus
Afu4g08190	nucleolus
Afu4g08190	maturation of SSU-rRNA
Afu4g08190	ribosomal large subunit biogenesis
Afu4g08200	GPI-anchor transamidase activity

Afu4g08200	cellular component unknown
Afu4g08200	attachment of GPI anchor to protein
Afu4g08210	N-acetyltransferase activity
Afu4g08210	metabolic process
Afu4g08230	aldo-keto reductase activity
Afu4g08230	cytoplasm
Afu4g08230	cellular aldehyde metabolic process
Afu4g08240	alcohol dehydrogenase (NAD) activity
Afu4g08240	soluble fraction
Afu4g08240	mitochondrial matrix
Afu4g08240	fermentation
Afu4g08280	proteolysis
Afu4g08280	metallopeptidase activity
Afu4g08280	cellular component unknown
Afu4g08300	mismatch repair
Afu4g08300	mismatch repair
Afu4g08320	tyrosine-tRNA ligase activity
Afu4g08320	mitochondrion
Afu4g08320	tRNA aminoacylation for protein translation
Afu4g08330	aspartate-tRNA ligase activity
Afu4g08330	mitochondrion
Afu4g08330	translation
Afu4g08340	mitochondrial inner membrane
Afu4g08340	heme a biosynthetic process
Afu4g08340	protoheme IX farnesyltransferase activity
Afu4g08360	mediator complex
Afu4g08360	transcription from RNA polymerase II promoter
Afu4g08360	RNA polymerase II transcription mediator activity
Afu4g08410	cell wall mannoprotein biosynthetic process
Afu4g08410	mannose-6-phosphate isomerase activity
Afu4g08410	nucleus
Afu4g08410	cytoplasm
Afu4g08410	protein amino acid glycosylation
Afu4g08410	GDP-mannose biosynthetic process
Afu4g08440	molecular function unknown
Afu4g08440	lipid particle
Afu4g08480	endopeptidase activity
Afu4g08480	receptor activity
Afu4g08480	proteasome regulatory particle
Afu4g08480	ubiquitin-dependent protein catabolic process
Afu4g08490	electron transporter activity
Afu4g08490	endoplasmic reticulum membrane
Afu4g08490	microsome
Afu4g08490	sterol biosynthetic process
Afu4g08500	nucleus
Afu4g08500	chromatin organization
Afu4g08500	regulation of transcription, DNA-dependent
Afu4g08500	RNA elongation from RNA polymerase II promoter
Afu4g08500	transcription elongation factor complex
Afu4g08500	RNA polymerase II transcription elongation factor activity

Afu4g08510	mRNA capping
Afu4g08510	nucleoside-triphosphatase activity
Afu4g08520	metabolic process
Afu4g08520	acyltransferase activity
Afu4g08530	biological process unknown
Afu4g08530	molecular function unknown
Afu4g08530	nucleus
Afu4g08530	cytoplasm
Afu4g08580	mitochondrion
Afu4g08580	response to oxidative stress
Afu4g08580	thioredoxin peroxidase activity
Afu4g08580	antioxidant activity
Afu4g08580	regulation of cell redox homeostasis
Afu4g08590	AT DNA binding
Afu4g08590	nucleus
Afu4g08590	programmed cell death
Afu4g08600	aldehyde dehydrogenase (NAD) activity
Afu4g08600	mitochondrion
Afu4g08600	ethanol metabolic process
Afu4g08600	fermentation
Afu4g08610	cellular component unknown
Afu4g08630	acid phosphatase activity
Afu4g08630	polyphosphate catabolic process
Afu4g08630	cell wall-bounded periplasmic space
Afu4g08650	signal transducer activity
Afu4g08650	plasma membrane
Afu4g08650	pseudohyphal growth
Afu4g08650	invasive growth
Afu4g08650	cell-cell adhesion
Afu4g08650	filamentous growth
Afu4g08660	dolichyl-diphosphooligosaccharide-protein glycotransferase activity
Afu4g08710	fatty acid catabolic process
Afu4g08720	lysophospholipase activity
Afu4g08720	glycerophospholipid metabolic process
Afu4g08720	fungal-type cell wall
Afu4g08740	transporter activity
Afu4g08740	transport
Afu4g08800	conjugation with cellular fusion
Afu4g08800	peptide pheromone export
Afu4g08800	ATP-binding cassette (ABC) transporter activity
Afu4g08800	integral to plasma membrane
Afu4g08810	biological process unknown
Afu4g08810	molecular function unknown
Afu4g08810	cytoplasm
Afu4g08830	telomere maintenance
Afu4g08830	nuclear telomere cap complex
Afu4g08830	protein binding
Afu4g08830	chromatin silencing at telomere
Afu4g08830	telomere maintenance via telomerase
Afu4g08830	regulation of meiosis

Afu4g08840	zinc ion binding
Afu4g08870	plasma membrane
Afu4g08870	choline transmembrane transporter activity
Afu4g08870	choline transport
Afu4g08880	biological process unknown
Afu4g08880	molecular function unknown
Afu4g08880	nucleus
Afu4g08880	cytoplasm
Afu4g08890	aldo-keto reductase activity
Afu4g08890	cellular aldehyde metabolic process
Afu4g08890	cellular component unknown
Afu4g08900	nucleotide-excision repair factor 3 complex
Afu4g08900	nucleotide-excision repair, DNA duplex unwinding
Afu4g08900	holo TFIIH complex
Afu4g08900	nucleotide-excision repair
Afu4g08900	transcription initiation from RNA polymerase II promoter
Afu4g08900	negative regulation of transcription from RNA polymerase II promoter, mitotic
Afu4g08900	general RNA polymerase II transcription factor activity
Afu4g08920	biological process unknown
Afu4g08920	protein kinase activity
Afu4g08920	cellular component unknown
Afu4g08930	ribosomal large subunit export from nucleus
Afu4g08930	GTPase activity
Afu4g08930	nucleus
Afu4g08930	nucleoplasm
Afu4g08930	nucleolus
Afu4g08970	fungal-type vacuole membrane
Afu4g08970	diacylglycerol pyrophosphate phosphatase activity
Afu4g08970	phospholipid metabolic process
Afu4g08970	phosphatidate phosphatase activity
Afu4g09010	commitment complex
Afu4g09010	nuclear mRNA splicing, via spliceosome
Afu4g09010	RNA binding
Afu4g09010	U1 snRNP
Afu4g09020	cis assembly of U2-type pre-catalytic spliceosome
Afu4g09020	ATP-dependent RNA helicase activity
Afu4g09020	spliceosomal complex
Afu4g09020	pre-mRNA splicing factor activity
Afu4g09030	leucyl aminopeptidase activity
Afu4g09030	cytoplasm
Afu4g09030	peptide metabolic process
Afu4g09030	cell wall-bounded periplasmic space
Afu4g09040	sulfur amino acid transport
Afu4g09040	L-methionine secondary active transmembrane transporter activity
Afu4g09040	integral to plasma membrane
Afu4g09050	protein serine/threonine kinase activity
Afu4g09050	cytosol
Afu4g09050	autophagy
Afu4g09070	endoribonuclease activity
Afu4g09070	cytoplasm

Afu4g09070	mRNA catabolic process
Afu4g09080	DNA binding
Afu4g09080	transcription factor activity
Afu4g09080	nucleus
Afu4g09080	response to osmotic stress
Afu4g09080	zinc ion binding
Afu4g09080	regulation of transcription
Afu4g09090	vacuole inheritance
Afu4g09090	fungal-type vacuole
Afu4g09090	cytosol
Afu4g09090	DNA-dependent DNA replication
Afu4g09090	response to oxidative stress
Afu4g09090	regulation of cell redox homeostasis
Afu4g09090	thiol-disulfide exchange intermediate activity
Afu4g09090	vacuole fusion, non-autophagic
Afu4g09110	cytochrome-c peroxidase activity
Afu4g09110	mitochondrion
Afu4g09110	mitochondrial intermembrane space
Afu4g09110	response to oxidative stress
Afu4g09120	regulation of progression through cell cycle
Afu4g09120	cell morphogenesis
Afu4g09120	chronological cell aging
Afu4g09120	molecular function unknown
Afu4g09120	nucleus
Afu4g09120	cytoplasm
Afu4g09120	multidrug transport
Afu4g09120	sporulation (sensu Saccharomyces)
Afu4g09120	ultradian rhythm
Afu4g09130	molecular function unknown
Afu4g09130	GPI anchor biosynthetic process
Afu4g09130	integral to membrane
Afu4g09140	ornithine-oxo-acid transaminase activity
Afu4g09140	nucleus
Afu4g09140	cytoplasm
Afu4g09140	arginine catabolic process
Afu4g09150	plasma membrane
Afu4g09150	xenobiotic-transporting ATPase activity
Afu4g09150	ABC-type efflux porter activity
Afu4g09150	drug transport
Afu4g09150	response to drug
Afu4g09170	membrane fraction
Afu4g09170	plasma membrane
Afu4g09170	transport
Afu4g09170	anion transmembrane transporter activity
Afu4g09190	sterol 24-C-methyltransferase activity
Afu4g09190	endoplasmic reticulum
Afu4g09190	lipid particle
Afu4g09190	ergosterol biosynthetic process
Afu4g09210	inorganic phosphate transmembrane transporter activity
Afu4g09210	integral to plasma membrane

Afu4g09210	phosphate transport
Afu4g09270	pheromone-dependent signal transduction involved in conjugation with cellular fusion
Afu4g09270	endocytosis
Afu4g09270	membrane
Afu4g09270	palmitoyltransferase activity
Afu4g09270	protein amino acid palmitoylation
Afu4g09320	aminopeptidase activity
Afu4g09320	proteolysis
Afu4g09320	serine-type peptidase activity
Afu4g09360	ATP synthesis coupled proton transport
Afu4g09360	proton-transporting two-sector ATPase complex
Afu4g09360	proton-transporting ATPase activity, rotational mechanism
Afu4g09400	aspartic-type endopeptidase activity
Afu4g09400	extracellular region
Afu4g09400	protein catabolic process
Afu4g09420	carbonate dehydratase activity
Afu4g09420	metabolic process
Afu4g09440	plasma membrane
Afu4g09440	sodium ion transport
Afu4g09440	ATPase activity, coupled to transmembrane movement of ions, phosphorylative mechanism
Afu4g09460	nucleotide binding
Afu4g09460	programmed cell death
Afu4g09470	metabolic process
Afu4g09470	oxidoreductase activity
Afu4g09480	polysaccharide catabolic process
Afu4g09480	hydrolase activity, acting on glycosyl bonds
Afu4g09500	molecular function unknown
Afu4g09500	cellular component unknown
Afu4g09500	virus-host interaction
Afu4g09520	v-SNARE activity
Afu4g09520	intra-Golgi vesicle-mediated transport
Afu4g09520	vesicle fusion
Afu4g09520	membrane
Afu4g09560	low-affinity zinc ion transmembrane transporter activity
Afu4g09560	plasma membrane
Afu4g09560	low-affinity zinc ion transport
Afu4g09580	biological process unknown
Afu4g09580	molecular function unknown
Afu4g09620	protein binding
Afu4g09640	condensed nuclear chromosome
Afu4g09640	molecular function unknown
Afu4g09640	reciprocal meiotic recombination
Afu4g09650	molecular function unknown
Afu4g09650	cellular component unknown
Afu4g09660	chaperone activity
Afu4g09660	amino acid transport
Afu4g09660	ER to Golgi vesicle-mediated transport
Afu4g09660	integral to endoplasmic reticulum membrane
Afu4g09710	transcription factor activity
Afu4g09710	sporocarp development

Afu4g09710	sporocarp development
Afu4g09710	regulation of developmental process
Afu4g09730	metalloendopeptidase activity
Afu4g09730	mitochondrion
Afu4g09730	proteolysis
Afu4g09730	membrane
Afu4g09740	chaperone activity
Afu4g09740	cytoplasm
Afu4g09740	cytoskeleton
Afu4g09740	protein folding
Afu4g09740	cytoskeleton organization
Afu4g09750	organellar large ribosomal subunit
Afu4g09750	structural constituent of ribosome
Afu4g09750	mitochondrion
Afu4g09750	translation
Afu4g09810	biological process unknown
Afu4g09810	molecular function unknown
Afu4g09810	mitochondrion
Afu4g09820	regulation of progression through cell cycle
Afu4g09820	histone acetyltransferase complex
Afu4g09820	histone acetyltransferase activity
Afu4g09820	regulation of transcription from RNA polymerase II promoter
Afu4g09820	microtubule depolymerization
Afu4g09820	histone acetylation
Afu4g09830	tryptophan 2,3-dioxygenase activity
Afu4g09830	cytoplasm
Afu4g09830	NAD biosynthetic process
Afu4g09840	nucleus
Afu4g09840	cytoplasm
Afu4g09840	NAD biosynthetic process
Afu4g09840	tryptophan catabolic process to kynurenine
Afu4g09840	kynureninase activity
Afu4g09860	transcription factor activity
Afu4g09860	nucleus
Afu4g09860	zinc ion binding
Afu4g09860	regulation of transcription
Afu4g09900	molecular function unknown
Afu4g09900	nucleus
Afu4g09900	cytoplasm
Afu4g09900	cell wall organization
Afu4g09940	chitin deacetylase activity
Afu4g09940	chitosan layer of spore wall
Afu4g09940	spore wall assembly (sensu Saccharomyces)
Afu4g09980	metabolic process
Afu4g09980	oxidoreductase activity
Afu4g09990	nucleoside transmembrane transporter activity
Afu4g09990	intracellular
Afu4g09990	nucleoside transport
Afu4g09990	membrane
Afu4g10000	ATP-binding cassette (ABC) transporter activity

Afu4g10000	mitochondrial inner membrane
Afu4g10000	oligopeptide transport
Afu4g10000	peptide-transporting ATPase activity
Afu4g10000	ATPase activity
Afu4g10010	regulation of progression through cell cycle
Afu4g10010	chaperone activity
Afu4g10010	cytoplasm
Afu4g10010	spindle pole body duplication in nuclear envelope
Afu4g10010	signal transduction
Afu4g10020	structural molecule activity
Afu4g10020	vesicle-mediated transport
Afu4g10020	clathrin vesicle coat
Afu4g10040	Golgi trans cisterna
Afu4g10040	v-SNARE activity
Afu4g10040	t-SNARE activity
Afu4g10040	early endosome
Afu4g10040	trans-Golgi network
Afu4g10040	vesicle fusion
Afu4g10050	incipient cellular bud site
Afu4g10050	calcium ion binding
Afu4g10050	cytoplasm
Afu4g10050	central plaque of spindle pole body
Afu4g10050	cellular bud tip
Afu4g10050	cellular bud neck
Afu4g10050	mating projection
Afu4g10050	cytoskeleton organization
Afu4g10050	mitosis
Afu4g10050	cell budding
Afu4g10070	mannosyl-oligosaccharide 1,2-alpha-mannosidase activity
Afu4g10070	endoplasmic reticulum
Afu4g10070	protein amino acid N-linked glycosylation
Afu4g10090	plasma membrane
Afu4g10090	choline transmembrane transporter activity
Afu4g10090	choline transport
Afu4g10110	specific RNA polymerase II transcription factor activity
Afu4g10110	nucleus
Afu4g10110	transcription initiation from RNA polymerase II promoter
Afu4g10110	cellular copper ion homeostasis
Afu4g10120	DNA binding
Afu4g10120	zinc ion binding
Afu4g10130	polysaccharide catabolic process
Afu4g10130	alpha-amylase activity
Afu4g10130	extracellular region
Afu4g10140	fungal-type vacuole
Afu4g10140	glucan 1,4-alpha-glucosidase activity
Afu4g10140	polysaccharide metabolic process
Afu4g10140	sporulation (sensu Saccharomyces)
Afu4g10140	hydrolase activity, acting on glycosyl bonds
Afu4g10150	alpha-glucosidase activity
Afu4g10150	endoplasmic reticulum

Afu4g10150	fungal-type cell wall biogenesis
Afu4g10160	transcription factor activity
Afu4g10160	nucleus
Afu4g10160	carbohydrate metabolic process
Afu4g10160	regulation of transcription, DNA-dependent
Afu4g10180	signal sequence binding
Afu4g10180	signal recognition particle, endoplasmic reticulum targeting
Afu4g10180	protein targeting to ER
Afu4g10190	metabolic process
Afu4g10190	oxidoreductase activity
Afu4g10210	phospholipid-translocating ATPase activity
Afu4g10210	intracellular protein transport
Afu4g10210	trans-Golgi network transport vesicle
Afu4g10220	histidine biosynthetic process
Afu4g10220	transcription factor activity
Afu4g10220	nucleus
Afu4g10220	transcription
Afu4g10220	purine base biosynthetic process
Afu4g10220	cellular response to phosphate starvation
Afu4g10230	biological process unknown
Afu4g10230	molecular function unknown
Afu4g10230	cellular component unknown
Afu4g10240	commitment complex
Afu4g10240	nuclear mRNA splicing, via spliceosome
Afu4g10240	mRNA binding
Afu4g10240	pre-mRNA splicing factor activity
Afu4g10240	small nuclear ribonucleoprotein complex
Afu4g10270	biological process unknown
Afu4g10270	fungal-type vacuole
Afu4g10270	molecular function unknown
Afu4g10270	endoplasmic reticulum
Afu4g10280	cytoplasm
Afu4g10280	response to osmotic stress
Afu4g10280	osmosensory signaling pathway via two-component system
Afu4g10280	transferase activity, transferring phosphorus-containing groups
Afu4g10330	conjugation with cellular fusion
Afu4g10330	protein farnesyltransferase activity
Afu4g10330	protein farnesyltransferase complex
Afu4g10330	a-factor processing (proteolytic)
Afu4g10330	protein amino acid farnesylation
Afu4g10340	DNA binding
Afu4g10340	zinc ion binding
Afu4g10350	structural constituent of ribosome
Afu4g10350	cytosolic large ribosomal subunit (sensu Eukaryota)
Afu4g10350	translation
Afu4g10350	ubiquitin-dependent protein catabolic process
Afu4g10350	protein tagging activity
Afu4g10360	biological process unknown
Afu4g10360	nuclear localization sequence binding
Afu4g10360	zinc ion binding

Afu4g10360	cellular component unknown
Afu4g10370	hexaprenyldihydroxybenzoate methyltransferase activity
Afu4g10370	mitochondrion
Afu4g10370	mitochondrial inner membrane
Afu4g10370	ubiquinone metabolic process
Afu4g10370	ubiquinone biosynthetic process
Afu4g10370	extrinsic to membrane
Afu4g10380	DNA binding
Afu4g10380	nucleus
Afu4g10380	zinc ion binding
Afu4g10390	biological process unknown
Afu4g10390	molecular function unknown
Afu4g10390	cytoplasm
Afu4g10410	L-aspartate:2-oxoglutarate aminotransferase activity
Afu4g10410	cytoplasm
Afu4g10410	peroxisome
Afu4g10410	aspartate biosynthetic process
Afu4g10410	aspartate catabolic process
Afu4g10410	glutamate metabolic process
Afu4g10410	nitrogen compound metabolic process
Afu4g10410	asparagine biosynthetic process from oxaloacetate
Afu4g10430	aminoacyl-tRNA hydrolase activity
Afu4g10430	cytoplasm
Afu4g10430	translation
Afu4g10460	homocitrate synthase activity
Afu4g10460	nucleus
Afu4g10460	lysine biosynthetic process via aminoadipic acid
Afu4g10470	endoplasmic reticulum
Afu4g10470	sphingolipid metabolic process
Afu4g10470	sphinganine-1-phosphate aldolase activity
Afu4g10470	cellular response to starvation
Afu4g10470	calcium-mediated signaling
Afu4g10480	structural constituent of ribosome
Afu4g10480	mitochondrial large ribosomal subunit
Afu4g10480	translation
Afu4g10490	actin cap (sensu Saccharomyces)
Afu4g10490	exocyst
Afu4g10490	establishment of cell polarity (sensu Saccharomyces)
Afu4g10490	cytokinesis
Afu4g10490	molecular function unknown
Afu4g10490	Golgi to plasma membrane transport
Afu4g10490	endocytosis
Afu4g10490	vesicle docking during exocytosis
Afu4g10490	vesicle fusion
Afu4g10490	bipolar cellular bud site selection
Afu4g10510	mitochondrion
Afu4g10510	oxygen and reactive oxygen species metabolic process
Afu4g10510	cellular iron ion homeostasis
Afu4g10510	iron incorporation into metallo-sulfur cluster
Afu4g10510	enzyme regulator activity

Afu4g10540	nucleus
Afu4g10540	sporulation (sensu Saccharomyces)
Afu4g10540	transcription regulator activity
Afu4g10550	small nucleolar ribonucleoprotein complex
Afu4g10550	maturation of SSU-rRNA
Afu4g10550	snoRNA binding
Afu4g10570	mitotic spindle elongation
Afu4g10570	mitotic sister chromatid segregation
Afu4g10570	anaphase-promoting complex
Afu4g10570	ubiquitin-dependent protein catabolic process
Afu4g10570	mitotic metaphase/anaphase transition
Afu4g10570	enzyme activator activity
Afu4g10570	cyclin catabolic process
Afu4g10580	Rab geranylgeranyltransferase activity
Afu4g10580	Rab-protein geranylgeranyltransferase complex
Afu4g10580	protein amino acid geranylgeranylation
Afu4g10600	Rab GTPase activator activity
Afu4g10600	soluble fraction
Afu4g10600	cytosol
Afu4g10600	vesicle-mediated transport
Afu4g10620	4-hydroxyphenylpyruvate dioxygenase activity
Afu4g10620	L-phenylalanine catabolic process
Afu4g10620	tyrosine catabolic process
Afu4g10660	histone acetyltransferase complex
Afu4g10660	histone acetyltransferase activity
Afu4g10660	regulation of transcription from RNA polymerase II promoter
Afu4g10660	histone acetylation
Afu4g10690	molecular function unknown
Afu4g10690	mitochondrial matrix
Afu4g10690	iron ion transport
Afu4g10700	biological process unknown
Afu4g10700	molecular function unknown
Afu4g10700	membrane
Afu4g10710	v-SNARE activity
Afu4g10710	intra-Golgi vesicle-mediated transport
Afu4g10710	Golgi to vacuole transport
Afu4g10710	vesicle fusion
Afu4g10710	endosome to lysosome transport
Afu4g10710	integral to Golgi membrane
Afu4g10730	nucleus
Afu4g10730	regulation of transcription from RNA polymerase II promoter
Afu4g10730	chromatin remodeling complex
Afu4g10730	ATPase activity
Afu4g10740	structural constituent of ribosome
Afu4g10740	mitochondrial large ribosomal subunit
Afu4g10740	translation
Afu4g10750	alpha-1,6-mannosyltransferase activity
Afu4g10750	cell wall mannoprotein biosynthetic process
Afu4g10750	alpha-1,6-mannosyltransferase complex
Afu4g10750	substituted mannan metabolic process

Afu4g10750	N-glycan processing
Afu4g10760	very-long-chain fatty acid metabolic process
Afu4g10760	endoplasmic reticulum membrane
Afu4g10760	oxidoreductase activity
Afu4g10780	protein polyubiquitination
Afu4g10780	ubiquitin-protein ligase activity
Afu4g10780	nucleus
Afu4g10780	nucleolus
Afu4g10780	protein monoubiquitination
Afu4g10780	nucleocytoplasmic transport
Afu4g10780	nucleus organization
Afu4g10780	mitosis
Afu4g10790	histidine biosynthetic process
Afu4g10790	tryptophan biosynthetic process
Afu4g10790	ribose phosphate diphosphokinase activity
Afu4g10790	cytoplasm
Afu4g10790	purine ribonucleoside salvage
Afu4g10790	'de novo' IMP biosynthetic process
Afu4g10790	'de novo' pyrimidine base biosynthetic process
Afu4g10800	structural constituent of ribosome
Afu4g10800	cytoplasm
Afu4g10800	cytosolic small ribosomal subunit (sensu Eukaryota)
Afu4g10800	translation
Afu4g10820	DNA binding
Afu4g10830	nucleotide-excision repair, DNA damage recognition
Afu4g10830	helicase activity
Afu4g10830	nucleus
Afu4g10830	DNA-dependent ATPase activity
Afu4g10840	biological process unknown
Afu4g10840	molecular function unknown
Afu4g10840	cytoplasm
Afu4g10910	nuclear nucleosome
Afu4g10910	chromatin silencing at telomere
Afu4g10910	acetyltransferase activity
Afu4g10910	chromatin modification
Afu4g10950	acetyl-CoA C-acyltransferase activity
Afu4g10950	peroxisomal matrix
Afu4g10950	fatty acid beta-oxidation
Afu4g10990	manganese ion transmembrane transporter activity
Afu4g10990	manganese ion transport
Afu4g10990	cytoplasmic membrane-bounded vesicle
Afu4g11000	biological process unknown
Afu4g11000	fungal-type vacuole membrane
Afu4g11000	molecular function unknown
Afu4g11000	cytoplasm
Afu4g11012	G1/S transition of mitotic cell cycle
Afu4g11012	protein serine/threonine phosphatase activity
Afu4g11012	cytoplasm
Afu4g11040	biological process unknown
Afu4g11040	molecular function unknown

Afu4g11040	nucleus
Afu4g11040	cytoplasm
Afu4g11060	transporter activity
Afu4g11060	integral to plasma membrane
Afu4g11060	transport
Afu4g11070	nuclear pore
Afu4g11070	mRNA export from nucleus
Afu4g11070	rRNA export from nucleus
Afu4g11070	snRNA export from nucleus
Afu4g11070	tRNA export from nucleus
Afu4g11070	protein import into nucleus
Afu4g11070	NLS-bearing substrate import into nucleus
Afu4g11070	snRNP protein import into nucleus
Afu4g11070	mRNA-binding (hnRNP) protein import into nucleus
Afu4g11070	ribosomal protein import into nucleus
Afu4g11070	protein export from nucleus
Afu4g11070	nuclear pore organization
Afu4g11070	nuclear pore organization
Afu4g11070	regulation of mitosis
Afu4g11080	acetate-CoA ligase activity
Afu4g11080	cytosol
Afu4g11080	acetyl-CoA biosynthetic process
Afu4g11110	biological process unknown
Afu4g11110	molecular function unknown
Afu4g11110	cellular component unknown
Afu4g11140	UV protection
Afu4g11160	structural constituent of cytoskeleton
Afu4g11160	nuclear pore
Afu4g11160	half bridge of spindle pole body
Afu4g11160	microtubule nucleation
Afu4g11160	spindle pole body duplication in nuclear envelope
Afu4g11180	helicase activity
Afu4g11180	nucleus
Afu4g11180	DNA replication
Afu4g11180	regulation of DNA replication
Afu4g11180	ATPase activity
Afu4g11190	arylformamidase activity
Afu4g11190	cytoplasm
Afu4g11190	mitochondrion
Afu4g11190	NAD biosynthetic process
Afu4g11210	molecular function unknown
Afu4g11210	mating projection
Afu4g11210	integral to membrane
Afu4g11210	plasma membrane fusion
Afu4g11220	electron transport
Afu4g11220	electron carrier activity
Afu4g11240	L-aminoadipate-semialdehyde dehydrogenase activity
Afu4g11240	cytoplasm
Afu4g11240	lysine biosynthetic process via aminoadipic acid
Afu4g11250	biological process unknown

Afu4g11250	molecular function unknown
Afu4g11250	nucleus
Afu4g11250	cytoplasm
Afu4g11260	aldo-keto reductase activity
Afu4g11260	cytoplasm
Afu4g11260	cellular aldehyde metabolic process
Afu4g11280	biological process unknown
Afu4g11280	molecular function unknown
Afu4g11280	cellular component unknown
Afu4g11290	DNA repair
Afu4g11290	proteasome activator complex
Afu4g11290	proteasome activator activity
Afu4g11300	vacuolar proton-transporting V-type ATPase, V0 domain
Afu4g11300	vacuole
Afu4g11300	polyphosphate metabolic process
Afu4g11300	vacuolar acidification
Afu4g11300	proton-transporting ATPase activity, rotational mechanism
Afu4g11310	cytosol
Afu4g11310	gluconeogenesis
Afu4g11310	fructose 1,6-bisphosphate 1-phosphatase activity
Afu4g11330	cytoplasm
Afu4g11330	protein folding
Afu4g11330	response to stress
Afu4g11330	chaperone activator activity
Afu4g11340	saccharopine dehydrogenase (NAD+, L-lysine-forming) activity
Afu4g11340	saccharopine dehydrogenase (NADP+, L-glutamate-forming) activity
Afu4g11340	cytoplasm
Afu4g11340	lysine biosynthetic process
Afu4g11340	lysine biosynthetic process via aminoadipic acid
Afu4g11350	prenyltransferase activity
Afu4g11350	endoplasmic reticulum
Afu4g11350	protein amino acid glycosylation
Afu4g11350	dolichol biosynthetic process
Afu4g11360	glycerol-3-phosphate O-acyltransferase activity
Afu4g11360	endoplasmic reticulum
Afu4g11360	phospholipid biosynthetic process
Afu4g11390	mitochondrion
Afu4g11390	mitochondrial respiratory chain complex III
Afu4g11390	mitochondrial electron transport, ubiquinol to cytochrome c
Afu4g11390	ubiquinol-cytochrome-c reductase activity
Afu4g11390	aerobic respiration
Afu4g11400	transporter activity
Afu4g11400	transport
Afu4g11440	nuclear ubiquitin ligase complex
Afu4g11440	protein binding
Afu4g11440	ubiquitin-dependent protein catabolic process
Afu4g11440	cell cycle
Afu4g11440	protein ubiquitination
Afu4g11440	SCF ubiquitin ligase complex
Afu4g11450	pheromone-dependent signal transduction involved in conjugation with cellular fusion

Afu4g11450	cellular morphogenesis during conjugation with cellular fusion
Afu4g11450	signal transducer activity
Afu4g11450	Rho guanyl-nucleotide exchange factor activity
Afu4g11450	nucleus
Afu4g11450	chitin localization
Afu4g11450	invasive growth
Afu4g11450	small GTPase mediated signal transduction
Afu4g11480	DNA binding
Afu4g11480	nucleus
Afu4g11480	zinc ion binding
Afu4g11500	3-keto sterol reductase activity
Afu4g11500	endoplasmic reticulum
Afu4g11500	endoplasmic reticulum membrane
Afu4g11500	ergosterol biosynthetic process
Afu4g11510	cell wall mannoprotein biosynthetic process
Afu4g11510	mannose-1-phosphate guanylyltransferase activity
Afu4g11510	cytoplasm
Afu4g11510	protein amino acid glycosylation
Afu4g11510	GDP-mannose biosynthetic process
Afu4g11530	ATP-dependent peptidase activity
Afu4g11530	mitochondrion
Afu4g11530	mitochondrial inner membrane
Afu4g11530	mitochondrion organization
Afu4g11540	glycerol kinase activity
Afu4g11540	cytoplasm
Afu4g11540	glycerol metabolic process
Afu4g11560	molecular function unknown
Afu4g11560	extrinsic to membrane
Afu4g11560	protein retention in Golgi apparatus
Afu4g11560	late endosome to vacuole transport
Afu4g11570	biological process unknown
Afu4g11570	RNA binding
Afu4g11570	nucleus
Afu4g11570	cytoplasm
Afu4g11580	mitochondrion
Afu4g11580	mitochondrial matrix
Afu4g11580	oxygen and reactive oxygen species metabolic process
Afu4g11580	manganese superoxide dismutase activity
Afu4g11620	GINS complex
Afu4g11620	DNA binding
Afu4g11620	DNA-dependent DNA replication
Afu4g11650	oxoglutarate dehydrogenase (succinyl-transferring) activity
Afu4g11650	mitochondrial matrix
Afu4g11650	tricarboxylic acid cycle
Afu4g11650	2-oxoglutarate metabolic process
Afu4g11660	DNA binding
Afu4g11660	nucleus
Afu4g11660	chromatin remodeling
Afu4g11660	zinc ion binding
Afu4g11690	nucleotide-excision repair factor 3 complex

Afu4g11690	nucleotide-excision repair, DNA duplex unwinding
Afu4g11690	holo TFIIH complex
Afu4g11690	nucleotide-excision repair
Afu4g11690	transcription initiation from RNA polymerase II promoter
Afu4g11690	negative regulation of transcription from RNA polymerase II promoter, mitotic
Afu4g11690	general RNA polymerase II transcription factor activity
Afu4g11700	biological process unknown
Afu4g11700	molecular function unknown
Afu4g11700	cellular component unknown
Afu4g11710	biological process unknown
Afu4g11710	molecular function unknown
Afu4g11710	cellular component unknown
Afu4g11720	biological process unknown
Afu4g11720	molecular function unknown
Afu4g11720	mitochondrion
Afu4g11730	cytoplasm
Afu4g11730	glycerol biosynthetic process
Afu4g11730	response to osmotic stress
Afu4g11730	glycerol dehydrogenase (NADP+) activity
Afu4g11780	drug transporter activity
Afu4g11780	drug transport
Afu4g11780	integral to membrane
Afu4g11800	extracellular region
Afu4g11800	proteolysis
Afu4g11800	serine-type peptidase activity
Afu4g11800	pathogenesis
Afu4g11820	ATP binding
Afu4g11820	molecular function unknown
Afu4g11820	cytoplasm
Afu4g11840	nucleus
Afu4g11840	cytoplasm
Afu4g11840	metabolic process
Afu4g11840	oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor
Afu4g11850	zinc ion binding
Afu4g11870	co-chaperone activity
Afu4g11870	post-chaperonin tubulin folding pathway
Afu4g11870	alpha-tubulin folding
Afu4g11870	cellular component unknown
Afu4g11880	spliceosome assembly
Afu4g11880	RNA binding
Afu4g11880	U2 snRNP
Afu4g11890	protein kinase activity
Afu4g11890	nucleus
Afu4g11890	cytoplasm
Afu4g11900	mitochondrial translocation
Afu4g11900	protein transporter activity
Afu4g11900	mitochondrial inner membrane protein insertion complex
Afu4g11910	peptide alpha-N-acetyltransferase activity
Afu4g11910	protein binding
Afu4g11910	intracellular

Afu4g11910	cytoplasm
Afu4g11910	protein amino acid acetylation
Afu4g11930	cytoplasm
Afu4g11930	DNA repair
Afu4g11930	oxidized purine base lesion DNA N-glycosylase activity
Afu4g11960	biological process unknown
Afu4g11960	cellular component unknown
Afu4g11960	iron hydrogenase activity
Afu4g11970	DNA-directed RNA polymerase activity
Afu4g11970	DNA-directed RNA polymerase II, core complex
Afu4g11970	DNA-directed RNA polymerase III complex
Afu4g11970	DNA-directed RNA polymerase I complex
Afu4g11970	transcription from RNA polymerase I promoter
Afu4g11970	transcription from RNA polymerase II promoter
Afu4g11970	transcription from RNA polymerase III promoter
Afu4g11980	tryptophan biosynthetic process
Afu4g11980	anthranilate phosphoribosyltransferase activity
Afu4g11980	nucleus
Afu4g11980	cytoplasm
Afu4g12010	molecular function unknown
Afu4g12010	mitochondrial matrix
Afu4g12010	tricarboxylic acid cycle
Afu4g12010	2-oxoglutarate metabolic process
Afu4g12040	lanosterol synthase activity
Afu4g12040	endoplasmic reticulum
Afu4g12040	lipid particle
Afu4g12040	plasma membrane
Afu4g12040	ergosterol biosynthetic process
Afu4g12050	biological process unknown
Afu4g12050	molecular function unknown
Afu4g12050	cytoplasm
Afu4g12060	molecular function unknown
Afu4g12060	endosome
Afu4g12060	retrograde transport, endosome to Golgi
Afu4g12060	protein retention in Golgi apparatus
Afu4g12070	endosome
Afu4g12070	protein targeting to vacuole
Afu4g12070	transport
Afu4g12080	ubiquitin conjugating enzyme activity
Afu4g12080	nucleus
Afu4g12080	cytoplasm
Afu4g12080	regulation of DNA repair
Afu4g12080	postreplication repair
Afu4g12080	ubiquitin-dependent protein catabolic process
Afu4g12080	ubiquitin cycle
Afu4g12110	protein binding
Afu4g12120	histone deacetylase complex
Afu4g12120	nucleus
Afu4g12120	transcriptional gene silencing
Afu4g12120	NAD-dependent histone deacetylase activity

Afu4g12120	NAD-independent histone deacetylase activity
Afu4g12140	biological process unknown
Afu4g12140	cytoplasm
Afu4g12140	S-adenosylmethionine-dependent methyltransferase activity
Afu4g12160	regulation of cyclin-dependent protein kinase activity
Afu4g12160	G2/M transition of mitotic cell cycle
Afu4g12160	nucleus
Afu4g12160	cytoplasm
Afu4g12160	cyclin-dependent protein kinase regulator activity
Afu4g12170	structural constituent of ribosome
Afu4g12170	mitochondrial large ribosomal subunit
Afu4g12170	translation
Afu4g12170	fatty acid metabolic process
Afu4g12180	transcription factor activity
Afu4g12180	nucleus
Afu4g12180	zinc ion binding
Afu4g12180	regulation of transcription
Afu4g12190	biological process unknown
Afu4g12190	molecular function unknown
Afu4g12190	cellular component unknown
Afu4g12210	single-stranded DNA specific endodeoxyribonuclease activity
Afu4g12210	ATP-dependent DNA helicase activity
Afu4g12210	nucleus
Afu4g12210	DNA-dependent DNA replication
Afu4g12210	lagging strand elongation
Afu4g12210	DNA repair
Afu4g12240	hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in other compounds
Afu4g12250	3'-5'-exoribonuclease activity
Afu4g12250	nuclear exosome (RNase complex)
Afu4g12250	cytoplasmic exosome (RNase complex)
Afu4g12250	35S primary transcript processing
Afu4g12250	mRNA catabolic process
Afu4g12260	transporter activity
Afu4g12260	transport
Afu4g12260	monocarboxylic acid transmembrane transporter activity
Afu4g12260	membrane
Afu4g12280	protein binding
Afu4g12280	nucleus
Afu4g12280	tRNA (guanine-N7-)-methyltransferase activity
Afu4g12280	tRNA methylation
Afu4g12290	molecular function unknown
Afu4g12290	endosome
Afu4g12290	protein targeting to vacuole
Afu4g12290	negative regulation of transcription by glucose
Afu4g12310	negative regulation of transposition, DNA-mediated
Afu4g12310	molecular function unknown
Afu4g12310	nucleus
Afu4g12330	endoplasmic reticulum
Afu4g12330	ceramide metabolic process
Afu4g12330	response to heat

Afu4g12330	ceramidase activity
Afu4g12340	transporter activity
Afu4g12340	mitochondrial inner membrane
Afu4g12340	transport
Afu4g12390	molecular function unknown
Afu4g12390	regulation of transcription from RNA polymerase II promoter
Afu4g12390	CCR4-NOT complex
Afu4g12400	DNA binding
Afu4g12400	nucleus
Afu4g12400	chromatin remodeling
Afu4g12400	regulation of transcription, DNA-dependent
Afu4g12400	zinc ion binding
Afu4g12410	DNA binding
Afu4g12430	GINS complex
Afu4g12430	DNA binding
Afu4g12430	DNA-dependent DNA replication
Afu4g12440	biological process unknown
Afu4g12440	fungal-type vacuole
Afu4g12440	molecular function unknown
Afu4g12470	transcription factor activity
Afu4g12470	nucleus
Afu4g12470	transcription
Afu4g12470	regulation of cellular amino acid metabolic process
Afu4g12470	pathogenesis
Afu4g12480	biological process unknown
Afu4g12480	molecular function unknown
Afu4g12480	cytoplasm
Afu4g12490	guanyl-nucleotide exchange factor activity
Afu4g12490	cytosol
Afu4g12490	protein targeting to vacuole
Afu4g12490	ubiquitin binding
Afu4g12530	membrane fraction
Afu4g12530	Golgi apparatus
Afu4g12530	cellular calcium ion homeostasis
Afu4g12530	cellular iron ion homeostasis
Afu4g12530	cellular manganese ion homeostasis
Afu4g12560	transcription factor activity
Afu4g12560	nucleus
Afu4g12560	regulation of transcription, DNA-dependent
Afu4g12570	transcription factor activity
Afu4g12570	nucleus
Afu4g12570	regulation of transcription, DNA-dependent
Afu4g12600	phosphoribosylaminoimidazole carboxylase activity
Afu4g12600	cytoplasm
Afu4g12600	purine base metabolic process
Afu4g12620	copper-exporting ATPase activity
Afu4g12620	trans-Golgi network
Afu4g12620	copper ion transport
Afu4g12620	intracellular copper ion transport
Afu4g12630	protein deneddylation

Afu4g12630	signalosome
Afu4g12630	ascospore formation
Afu4g12630	regulation of developmental process
Afu4g12640	cellular bud site selection
Afu4g12640	molecular function unknown
Afu4g12640	cellular component unknown
Afu4g12650	SAGA complex
Afu4g12650	histone acetyltransferase activity
Afu4g12650	chromatin modification
Afu4g12650	histone acetylation
Afu4g12680	meiotic DNA double-strand break processing
Afu4g12680	telomere maintenance via recombination
Afu4g12680	double-strand break repair via break-induced replication
Afu4g12680	double-stranded DNA binding
Afu4g12680	protein binding
Afu4g12680	nucleus
Afu4g12680	double-strand break repair via nonhomologous end joining
Afu4g12680	ATPase activity
Afu4g12680	meiotic DNA double-strand break formation
Afu4g12690	transcription factor activity
Afu4g12690	signal transducer activity
Afu4g12690	nucleus
Afu4g12690	zinc ion binding
Afu4g12690	response to light stimulus
Afu4g12690	blue light signaling pathway
Afu4g12690	regulation of transcription
Afu4g12720	phosphate metabolic process
Afu4g12720	cellular component unknown
Afu4g12720	phosphoric ester hydrolase activity
Afu4g12730	biological process unknown
Afu4g12730	molecular function unknown
Afu4g12730	nucleus
Afu4g12730	cytoplasm
Afu4g12750	3'-5'-exoribonuclease activity
Afu4g12750	nuclear-transcribed mRNA catabolic process, deadenylation-dependent decay
Afu4g12750	nuclear-transcribed mRNA poly(A) tail shortening
Afu4g12750	cytoplasm
Afu4g12750	regulation of transcription from RNA polymerase II promoter
Afu4g12750	CCR4-NOT core complex
Afu4g12790	molecular function unknown
Afu4g12790	membrane fraction
Afu4g12790	chromosome segregation
Afu4g12840	biological process unknown
Afu4g12840	molecular function unknown
Afu4g12840	cytoplasm
Afu4g12850	molecular function unknown
Afu4g12850	integral to endoplasmic reticulum membrane
Afu4g12850	ER-associated protein catabolic process
Afu4g12870	aldehyde dehydrogenase (NAD) activity
Afu4g12900	alpha-1,6-mannosyltransferase activity

Afu4g12900	endoplasmic reticulum membrane
Afu4g12900	protein amino acid glycosylation
Afu4g12900	dolichol-linked oligosaccharide biosynthetic process
Afu4g12910	ubiquitin-specific protease activity
Afu4g12910	cellular component unknown
Afu4g12920	histidine-tRNA ligase activity
Afu4g12920	cytoplasm
Afu4g12920	mitochondrion
Afu4g12920	histidyl-tRNA aminoacylation
Afu4g12930	mitochondrion
Afu4g12930	mitochondrial inner membrane
Afu4g12930	ubiquinone metabolic process
Afu4g12930	ubiquinone biosynthetic process monooxygenase activity
Afu4g12950	transport
Afu4g12950	autophagy
Afu4g12950	lipid binding
Afu4g12950	membrane
Afu4g12970	conjugation with cellular fusion
Afu4g12970	serine-type endopeptidase activity
Afu4g12970	trans-Golgi network
Afu4g12970	peptide pheromone maturation
Afu4g12980	biological process unknown
Afu4g12980	molecular function unknown
Afu4g12980	plasma membrane
Afu4g12990	thioredoxin-disulfide reductase activity
Afu4g12990	cytoplasm
Afu4g12990	regulation of cell redox homeostasis
Afu4g13010	biological process unknown
Afu4g13010	molecular function unknown
Afu4g13010	cytoplasm
Afu4g13040	biological process unknown
Afu4g13040	molecular function unknown
Afu4g13040	cytoplasm
Afu4g13060	transcription factor activity
Afu4g13060	cytoplasm
Afu4g13060	intracellular signaling cascade
Afu4g13060	zinc ion binding
Afu4g13060	conjugation (sensu Fungi)
Afu4g13070	metabolic process
Afu4g13070	hydrolase activity
Afu4g13080	transporter activity
Afu4g13080	transport
Afu4g13080	membrane
Afu4g13090	transporter activity
Afu4g13090	integral to plasma membrane
Afu4g13090	transport
Afu4g13120	glutamate-ammonia ligase activity
Afu4g13120	cytoplasm
Afu4g13120	glutamine biosynthetic process
Afu4g13120	nitrogen compound metabolic process

Afu4g13150	biological process unknown
Afu4g13150	molecular function unknown
Afu4g13150	nucleus
Afu4g13150	cytoplasm
Afu4g13160	biological process unknown
Afu4g13160	protein binding
Afu4g13170	cytoplasm
Afu4g13170	signal transduction
Afu4g13180	biological process unknown
Afu4g13180	molecular function unknown
Afu4g13180	mitochondrion
Afu4g13190	molecular function unknown
Afu4g13190	ER to Golgi vesicle-mediated transport
Afu4g13190	COPII-coated vesicle
Afu4g13250	actin binding
Afu4g13250	actin cross-linking activity
Afu4g13250	actin cortical patch (sensu Saccharomyces)
Afu4g13250	actin filament organization
Afu4g13270	molecular function unknown
Afu4g13270	endoplasmic reticulum
Afu4g13270	response to unfolded protein
Afu4g13280	molecular function unknown
Afu4g13280	nucleus
Afu4g13280	mRNA export from nucleus
Afu4g13290	nucleus
Afu4g13290	cytoplasm
Afu4g13290	metabolic process
Afu4g13290	hydrolase activity
Afu4g13310	catalytic activity
Afu4g13310	metabolic process
Afu4g13330	helicase activity
Afu4g13330	nuclear envelope
Afu4g13330	nucleolus
Afu4g13330	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process
Afu4g13340	biological process unknown
Afu4g13340	molecular function unknown
Afu4g13340	cytoplasm
Afu4g13360	hydrolase activity, hydrolyzing O-glycosyl compounds
Afu4g13360	1,3-beta-glucan metabolic process
Afu4g13360	fungal-type cell wall
Afu4g13390	mitochondrion inheritance
Afu4g13390	vacuole inheritance
Afu4g13390	histone acetyltransferase complex
Afu4g13390	establishment of mitotic spindle orientation
Afu4g13390	cytokinesis
Afu4g13390	structural constituent of cytoskeleton
Afu4g13390	actin filament
Afu4g13390	regulation of transcription from RNA polymerase II promoter
Afu4g13390	exocytosis
Afu4g13390	endocytosis

Afu4g13390	response to osmotic stress
Afu4g13390	cell wall organization
Afu4g13390	budding cell apical bud growth
Afu4g13390	budding cell isotropic bud growth
Afu4g13390	sporulation (sensu Saccharomyces)
Afu4g13390	protein secretion
Afu4g13390	histone acetylation
Afu4g13390	actin filament reorganization during cell cycle
Afu4g13390	vesicle transport along actin filament
Afu4g13400	biological process unknown
Afu4g13400	molecular function unknown
Afu4g13400	endoplasmic reticulum
Afu4g13410	structural constituent of ribosome
Afu4g13410	mitochondrial small ribosomal subunit
Afu4g13410	translation
Afu4g13410	aerobic respiration
Afu4g13440	DNA binding
Afu4g13440	nucleus
Afu4g13440	chromatin remodeling
Afu4g13440	regulation of transcription, DNA-dependent
Afu4g13440	RNA elongation from RNA polymerase II promoter
Afu4g13440	zinc ion binding
Afu4g13440	ATPase activity
Afu4g13450	rRNA modification
Afu4g13450	mitochondrion
Afu4g13450	rRNA (guanine-N1-)-methyltransferase activity
Afu4g13460	nucleus
Afu4g13460	chromatin remodeling
Afu4g13460	ATPase activity
Afu4g13460	negative regulation of transcription from RNA polymerase II promoter by pheromones
Afu4g13490	intracellular protein transport
Afu4g13490	AP-3 adaptor complex
Afu4g13490	clathrin vesicle coat
Afu4g13500	3-chloroallyl aldehyde dehydrogenase activity
Afu4g13500	cytosol
Afu4g13500	cellular aldehyde metabolic process
Afu4g13510	isocitrate lyase activity
Afu4g13510	glyoxylate cycle
Afu4g13510	cellular component unknown
Afu4g13530	alpha,alpha-trehalase activity
Afu4g13530	cytoplasm
Afu4g13530	cytosol
Afu4g13530	trehalose catabolic process
Afu4g13530	response to stress
Afu4g13540	plasma membrane
Afu4g13540	potassium ion transmembrane transporter activity
Afu4g13540	cellular potassium ion homeostasis
Afu4g13550	peroxisomal matrix
Afu4g13550	sporulation (sensu Saccharomyces)
Afu4g13550	2,4-dienoyl-CoA reductase (NADPH) activity

Afu4g13550	fatty acid catabolic process
Afu4g13560	cytoplasm
Afu4g13560	cysteine-type peptidase activity
Afu4g13560	protein catabolic process
Afu4g13600	DNA binding
Afu4g13600	nucleus
Afu4g13600	zinc ion binding
Afu4g13660	biological process unknown
Afu4g13660	molecular function unknown
Afu4g13660	cellular component unknown
Afu4g13670	transmembrane receptor activity
Afu4g13670	membrane fraction
Afu4g13670	cell wall organization
Afu4g13670	Rho protein signal transduction
Afu4g13670	response to heat
Afu4g13670	actin cytoskeleton organization
Afu4g13680	CDP-diacylglycerol-serine O-phosphatidyltransferase activity
Afu4g13680	endoplasmic reticulum
Afu4g13680	phosphatidylserine biosynthetic process
Afu4g13690	rRNA modification
Afu4g13690	RNA binding
Afu4g13690	nucleolus
Afu4g13690	small nucleolar ribonucleoprotein complex
Afu4g13690	35S primary transcript processing
Afu4g13700	threonine-tRNA ligase activity
Afu4g13700	cytoplasm
Afu4g13700	translation
Afu4g13720	MAP kinase activity
Afu4g13720	nucleus
Afu4g13720	cytoplasm
Afu4g13720	protein amino acid phosphorylation
Afu4g13720	cell wall organization
Afu4g13720	signal transduction
Afu4g13740	molecular function unknown
Afu4g13740	endoplasmic reticulum
Afu4g13740	protein targeting to vacuole
Afu4g13740	metal ion transport
Afu4g13770	hydrolase activity, hydrolyzing O-glycosyl compounds
Afu4g13770	carbohydrate metabolic process
Afu4g13820	transporter activity
Afu4g13820	transport
Afu4g13830	integral to plasma membrane
Afu4g13830	transport
Afu4g13830	response to toxin
Afu4g13830	multidrug transporter activity
Afu4g13850	metabolic process
Afu4g13850	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecu
Afu4g13860	monooxygenase activity
Afu4g13860	cellular aromatic compound metabolic process
Afu4g13900	integral to plasma membrane

Afu4g13900	nicotinamide mononucleotide permease activity
Afu4g13900	nicotinamide mononucleotide transport
Afu4g13920	polygalacturonase activity
Afu4g13920	extracellular region
Afu4g13920	pseudohyphal growth
Afu4g13920	pectin catabolic process
Afu4g13930	cytoplasm
Afu4g13930	microsome
Afu4g13930	cytosol
Afu4g13930	cell wall organization
Afu4g13930	phosphatidylinositol transporter activity
Afu4g13930	phospholipid transport
Afu4g13950	N-acetyltransferase activity
Afu4g13950	metabolic process
Afu4g13960	biological process unknown
Afu4g13960	molecular function unknown
Afu4g13960	nucleus
Afu4g13960	cytoplasm
Afu4g14000	serine-type endopeptidase activity
Afu4g14000	protein catabolic process
Afu4g14010	metabolic process
Afu4g14010	oxidoreductase activity
Afu4g14060	biological process unknown
Afu4g14060	cellular component unknown
Afu4g14070	transferase activity, transferring glycosyl groups
Afu4g14090	molecular function unknown
Afu4g14090	galactose metabolic process
Afu4g14090	cellular component unknown
Afu4g14130	peptide pheromone export
Afu4g14130	ATP-binding cassette (ABC) transporter activity
Afu4g14130	integral to plasma membrane
Afu4g14140	metabolic process
Afu4g14140	oxidoreductase activity
Afu4g14150	diacylglycerol O-acyltransferase activity
Afu4g14150	lipid particle
Afu4g14150	triglyceride biosynthetic process
Afu4g14150	lipid storage
Afu4g14200	biological process unknown
Afu4g14200	molecular function unknown
Afu4g14200	cellular component unknown
Afu4g14220	DNA binding
Afu4g14220	zinc ion binding
Afu4g14230	transporter activity
Afu4g14230	integral to plasma membrane
Afu4g14230	transport
Afu4g14240	O-methyltransferase activity
Afu4g14240	S-adenosylmethionine-dependent methyltransferase activity
Afu4g14260	transporter activity
Afu4g14260	transport
Afu4g14260	monocarboxylic acid transmembrane transporter activity

Afu4g14260	membrane
Afu4g14270	biosynthetic process
Afu4g14270	hydrolase activity, acting on ester bonds
Afu4g14290	biological process unknown
Afu4g14290	cellular component unknown
Afu4g14360	capsule (sensu Fungi)
Afu4g14360	capsule organization
Afu4g14400	DNA binding
Afu4g14400	nucleus
Afu4g14400	zinc ion binding
Afu4g14440	cytoplasm
Afu4g14440	CoA-ligase activity
Afu4g14440	nonribosomal peptide biosynthetic process
Afu4g14450	cellular component unknown
Afu4g14450	mannitol dehydrogenase activity
Afu4g14490	ferroxidase activity
Afu4g14490	plasma membrane
Afu4g14490	high-affinity iron ion transport
Afu4g14530	transcription corepressor activity
Afu4g14530	soluble fraction
Afu4g14530	regulation of nitrogen utilization
Afu4g14540	transcription factor activity
Afu4g14540	nucleus
Afu4g14540	regulation of transcription
Afu4g14560	polyketide synthase activity
Afu4g14570	catalytic activity
Afu4g14570	metabolic process
Afu4g14580	O-methyltransferase activity
Afu4g14590	transcription factor activity
Afu4g14590	nucleus
Afu4g14590	regulation of transcription
Afu4g14610	transporter activity
Afu4g14610	transport
Afu4g14610	membrane
Afu4g14640	low-affinity iron ion transport
Afu4g14640	iron ion transmembrane transporter activity
Afu4g14640	integral to plasma membrane
Afu4g14640	intracellular copper ion transport
Afu4g14650	ribokinase activity
Afu4g14650	ATP binding
Afu4g14650	nucleus
Afu4g14650	cytoplasm
Afu4g14650	D-ribose metabolic process
Afu4g14670	fructose transmembrane transporter activity
Afu4g14670	glucose transmembrane transporter activity
Afu4g14670	plasma membrane
Afu4g14670	hexose transport
Afu4g14670	mannose transmembrane transporter activity
Afu4g14700	lipase activity
Afu4g14730	N-acetyltransferase activity

Afu4g14730	metabolic process
Afu4g14740	protein kinase activity
Afu4g14740	kinetochore microtubule
Afu4g14740	spindle microtubule
Afu4g14740	chromosome segregation
Afu4g14770	lanosterol synthase activity
Afu4g14770	endoplasmic reticulum
Afu4g14770	lipid particle
Afu4g14770	plasma membrane
Afu4g14770	ergosterol biosynthetic process
Afu4g14780	metabolic process
Afu4g14780	oxidoreductase activity
Afu4g14790	metabolic process
Afu4g14790	oxidoreductase activity
Afu4g14800	metabolic process
Afu4g14800	oxidoreductase activity
Afu4g14810	metabolic process
Afu4g14810	oxidoreductase activity
Afu4g14830	metabolic process
Afu4g14830	oxidoreductase activity
Afu4g14850	cellular aromatic compound metabolic process
Afu5g00110	hopanoid biosynthetic process
Afu5g00110	squalene-hopene cyclase activity
Afu5g00120	metabolic process
Afu5g00120	oxidoreductase activity
Afu5g00130	capsule polysaccharide biosynthetic process
Afu5g00150	biosynthetic process
Afu5g00150	hydrolase activity, acting on ester bonds
Afu5g00160	drug transporter activity
Afu5g00160	drug transport
Afu5g00160	integral to membrane
Afu5g00260	transition metal ion transport
Afu5g00260	ferric-chelate reductase activity
Afu5g00260	integral to membrane
Afu5g00280	transporter activity
Afu5g00280	transport
Afu5g00280	membrane
Afu5g00300	metabolic process
Afu5g00300	zinc ion binding
Afu5g00300	cellular component unknown
Afu5g00300	oxidoreductase activity
Afu5g00340	transport
Afu5g00340	ABC-type efflux porter activity
Afu5g00370	plasma membrane
Afu5g00370	basic amino acid transmembrane transporter activity
Afu5g00370	basic amino acid transport
Afu5g00400	transaminase activity
Afu5g00420	transporter activity
Afu5g00420	transport
Afu5g00420	drug transporter activity

Afu5g00420	drug transport
Afu5g00420	integral to membrane
Afu5g00430	transporter activity
Afu5g00430	plasma membrane
Afu5g00430	transport
Afu5g00440	N-acetyltransferase activity
Afu5g00440	metabolic process
Afu5g00460	metabolic process
Afu5g00460	oxidoreductase activity
Afu5g00460	FAD binding
Afu5g00470	biological process unknown
Afu5g00470	amidase activity
Afu5g00470	cellular component unknown
Afu5g00480	beta-fructofuranosidase activity
Afu5g00480	extracellular region
Afu5g00480	cytoplasm
Afu5g00480	sucrose catabolic process
Afu5g00500	alpha-glucoside transport
Afu5g00500	alpha-glucoside:hydrogen symporter activity
Afu5g00500	maltose:hydrogen symporter activity
Afu5g00500	membrane fraction
Afu5g00500	trehalose transmembrane transporter activity
Afu5g00500	trehalose transport
Afu5g00520	transcription factor activity
Afu5g00520	nucleus
Afu5g00520	zinc ion binding
Afu5g00520	regulation of transcription
Afu5g00530	extracellular region
Afu5g00530	cytoplasm
Afu5g00530	sucrose catabolic process
Afu5g00550	polysaccharide catabolic process
Afu5g00550	hydrolase activity, hydrolyzing O-glycosyl compounds
Afu5g00600	pathogenesis
Afu5g00640	3-hydroxyacyl-CoA dehydrogenase activity
Afu5g00640	enoyl-CoA hydratase activity
Afu5g00640	peroxisomal matrix
Afu5g00640	fatty acid beta-oxidation
Afu5g00680	cytosol
Afu5g00680	Golgi to plasma membrane transport
Afu5g00680	phosphatidylinositol transporter activity
Afu5g00680	phospholipid transport
Afu5g00710	plasma membrane
Afu5g00710	choline transmembrane transporter activity
Afu5g00710	choline transport
Afu5g00720	N-acetyltransferase activity
Afu5g00720	metabolic process
Afu5g00730	calcium-transporting ATPase activity
Afu5g00730	Golgi apparatus
Afu5g00730	calcium ion transport
Afu5g00730	manganese ion transport

Afu5g00730	manganese-transporting ATPase activity
Afu5g00730	secretory pathway
Afu5g00760	cytokinesis
Afu5g00760	chitin synthase activity
Afu5g00760	chitin biosynthetic process
Afu5g00790	ATP-binding cassette (ABC) transporter activity
Afu5g00790	ATP binding
Afu5g00790	transport
Afu5g00920	beta-lactamase activity
Afu5g00920	polyketide biosynthetic process
Afu5g00930	plasma membrane
Afu5g00930	amino acid transport
Afu5g00930	amino acid transmembrane transporter activity
Afu5g00930	amino acid permease activity
Afu5g00950	RNA polymerase II transcription factor activity
Afu5g00950	nucleus
Afu5g00950	regulation of transcription
Afu5g00980	integral to plasma membrane
Afu5g00980	response to toxin
Afu5g00980	multidrug transporter activity
Afu5g01000	metabolic process
Afu5g01000	oxidoreductase activity
Afu5g01020	biological process unknown
Afu5g01020	cytoplasm
Afu5g01020	S-adenosylmethionine-dependent methyltransferase activity
Afu5g01030	glyceraldehyde-3-phosphate dehydrogenase (phosphorylating) activity
Afu5g01030	cytoplasm
Afu5g01030	lipid particle
Afu5g01030	cytosol
Afu5g01030	gluconeogenesis
Afu5g01030	glycolysis
Afu5g01030	fungal-type cell wall
Afu5g01070	transcription factor activity
Afu5g01070	nucleus
Afu5g01070	zinc ion binding
Afu5g01070	regulation of transcription
Afu5g01080	transporter activity
Afu5g01080	transport
Afu5g01080	membrane
Afu5g01160	fructose transmembrane transporter activity
Afu5g01160	glucose transmembrane transporter activity
Afu5g01160	plasma membrane
Afu5g01160	hexose transport
Afu5g01160	mannose transmembrane transporter activity
Afu5g01170	biological process unknown
Afu5g01170	molecular function unknown
Afu5g01170	cellular component unknown
Afu5g01180	RAN small monomeric GTPase activity
Afu5g01180	nucleus
Afu5g01180	nucleus organization

Afu5g01200	biological process unknown
Afu5g01200	fungal-type vacuole
Afu5g01200	carboxypeptidase C activity
Afu5g01230	phospholipid-translocating ATPase activity
Afu5g01230	endoplasmic reticulum
Afu5g01230	plasma membrane
Afu5g01230	fatty acid transport
Afu5g01230	integral to membrane
Afu5g01240	biological process unknown
Afu5g01240	amidase activity
Afu5g01240	cellular component unknown
Afu5g01272	transcription factor activity
Afu5g01272	nucleus
Afu5g01272	regulation of transcription
Afu5g01290	metabolic process
Afu5g01290	zinc ion binding
Afu5g01290	oxidoreductase activity
Afu5g01310	biological process unknown
Afu5g01310	molecular function unknown
Afu5g01310	integral to membrane
Afu5g01320	inorganic phosphate transmembrane transporter activity
Afu5g01320	integral to plasma membrane
Afu5g01320	phosphate transport
Afu5g01330	phosphate metabolic process
Afu5g01330	phosphoric ester hydrolase activity
Afu5g01340	lysophospholipase activity
Afu5g01340	extracellular region
Afu5g01340	plasma membrane
Afu5g01340	phosphatidylserine catabolic process
Afu5g01340	phosphoinositide metabolic process
Afu5g01350	drug transporter activity
Afu5g01350	drug transport
Afu5g01350	integral to membrane
Afu5g01400	chitinase activity
Afu5g01400	cell wall chitin catabolic process
Afu5g01400	chitin binding
Afu5g01400	fungal-type cell wall
Afu5g01430	biological process unknown
Afu5g01430	molecular function unknown
Afu5g01430	soluble fraction
Afu5g01440	cytoplasm
Afu5g01440	thioredoxin peroxidase activity
Afu5g01440	response to metal ion
Afu5g01440	regulation of cell redox homeostasis
Afu5g01450	biological process unknown
Afu5g01450	NADPH dehydrogenase activity
Afu5g01450	cellular component unknown
Afu5g01460	zinc ion binding
Afu5g01480	metabolic process
Afu5g01480	hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in linear amides

Afu5g01500	sulfur amino acid metabolic process
Afu5g01500	cytoplasm
Afu5g01500	homocysteine S-methyltransferase activity
Afu5g01510	plasma membrane
Afu5g01510	neutral amino acid transmembrane transporter activity
Afu5g01510	amino acid permease activity
Afu5g01510	neutral amino acid transport
Afu5g01520	transporter activity
Afu5g01520	transport
Afu5g01530	metabolic process
Afu5g01530	oxidoreductase activity
Afu5g01540	biological process unknown
Afu5g01540	molecular function unknown
Afu5g01540	cellular component unknown
Afu5g01550	transcription factor activity
Afu5g01550	nucleus
Afu5g01550	regulation of transcription
Afu5g01590	farnesyltranstransferase activity
Afu5g01590	mitochondrion
Afu5g01590	terpenoid biosynthetic process
Afu5g01630	drug transporter activity
Afu5g01630	drug transport
Afu5g01630	integral to membrane
Afu5g01650	transcription factor activity
Afu5g01650	nucleus
Afu5g01650	transcription
Afu5g01650	regulation of cellular amino acid metabolic process
Afu5g01680	integral to plasma membrane
Afu5g01700	transcription factor activity
Afu5g01700	nucleus
Afu5g01700	zinc ion binding
Afu5g01700	regulation of transcription
Afu5g01710	metabolic process
Afu5g01710	oxidoreductase activity
Afu5g01730	histone deacetylase complex
Afu5g01730	histone deacetylation
Afu5g01730	NAD-dependent histone deacetylase activity
Afu5g01730	NAD-independent histone deacetylase activity
Afu5g01730	negative regulation of meiosis
Afu5g01740	deoxyhypusine synthase activity
Afu5g01740	cytoplasm
Afu5g01740	peptidyl-lysine modification to hypusine
Afu5g01750	ubiquitin-specific protease activity
Afu5g01750	plasma membrane
Afu5g01750	protein deubiquitination
Afu5g01760	nucleolus
Afu5g01760	rRNA processing
Afu5g01760	RNA methyltransferase activity
Afu5g01760	S-adenosylmethionine-dependent methyltransferase activity
Afu5g01780	sexual reproduction

Afu5g01780	developmental process
Afu5g01800	nucleotide-excision repair factor 1 complex
Afu5g01800	nucleotide-excision repair, DNA damage recognition
Afu5g01800	damaged DNA binding
Afu5g01820	biological process unknown
Afu5g01820	fungal-type vacuole
Afu5g01820	molecular function unknown
Afu5g01840	biological process unknown
Afu5g01840	molecular function unknown
Afu5g01840	cytoplasm
Afu5g01850	nucleus
Afu5g01850	translational initiation
Afu5g01850	tRNA methyltransferase activity
Afu5g01850	tRNA methylation
Afu5g01860	structural constituent of cytoskeleton
Afu5g01860	Arp2/3 protein complex
Afu5g01860	actin filament organization
Afu5g01870	DNA clamp loader activity
Afu5g01870	nucleus
Afu5g01870	DNA replication factor C complex
Afu5g01870	leading strand elongation
Afu5g01870	mismatch repair
Afu5g01870	sister chromatid cohesion
Afu5g01870	ATPase activity
Afu5g01900	transcription factor activity
Afu5g01900	nucleus
Afu5g01900	regulation of transcription from RNA polymerase II promoter
Afu5g01900	response to stress
Afu5g01900	response to heat
Afu5g01910	aldo-keto reductase activity
Afu5g01910	cellular aldehyde metabolic process
Afu5g01940	single-stranded RNA binding
Afu5g01940	cytoplasm
Afu5g01950	nuclear chromatin
Afu5g01950	chromatin binding
Afu5g01950	chromatin assembly complex
Afu5g01950	regulation of transcription from RNA polymerase II promoter
Afu5g01960	phosphate transport
Afu5g01960	phosphate transmembrane transporter activity
Afu5g01960	membrane
Afu5g01970	glyceraldehyde-3-phosphate dehydrogenase (phosphorylating) activity
Afu5g01970	cytoplasm
Afu5g01970	lipid particle
Afu5g01970	cytosol
Afu5g01970	gluconeogenesis
Afu5g01970	glycolysis
Afu5g01970	fungal-type cell wall
Afu5g01980	histone deacetylase complex
Afu5g01980	loss of chromatin silencing during replicative cell aging
Afu5g01980	histone deacetylase activity

Afu5g01980	chromatin organization
Afu5g01980	regulation of transcription, DNA-dependent
Afu5g01980	protein amino acid deacetylation
Afu5g02010	conjugation with cellular fusion
Afu5g02010	proteolysis
Afu5g02010	peptide pheromone maturation
Afu5g02010	metallopeptidase activity
Afu5g02010	integral to membrane
Afu5g02020	aldo-keto reductase activity
Afu5g02020	cellular aldehyde metabolic process
Afu5g02020	cellular component unknown
Afu5g02060	dephospho-CoA kinase activity
Afu5g02060	intracellular
Afu5g02060	coenzyme A biosynthetic process
Afu5g02140	inositol-polyphosphate 5-phosphatase activity
Afu5g02140	membrane fraction
Afu5g02140	actin cortical patch (sensu Saccharomyces)
Afu5g02140	endocytosis
Afu5g02140	cell wall organization
Afu5g02140	dephosphorylation
Afu5g02150	endopeptidase activity
Afu5g02150	proteasome core complex
Afu5g02150	ubiquitin-dependent protein catabolic process
Afu5g02150	proteasome core complex, alpha-subunit complex
Afu5g02160	biological process unknown
Afu5g02160	molecular function unknown
Afu5g02160	cytoplasm
Afu5g02170	nuclear condensin complex
Afu5g02170	molecular function unknown
Afu5g02170	mitotic chromosome condensation
Afu5g02180	biological process unknown
Afu5g02180	cysteine synthase activity
Afu5g02180	mitochondrion
Afu5g02200	mitochondrial translocation
Afu5g02200	protein transporter activity
Afu5g02200	mitochondrial inner membrane protein insertion complex
Afu5g02220	protein serine/threonine kinase activity
Afu5g02220	nucleus
Afu5g02220	cytoplasm
Afu5g02220	protein amino acid phosphorylation
Afu5g02220	signal transduction
Afu5g02230	biological process unknown
Afu5g02230	D-lactate dehydrogenase (cytochrome) activity
Afu5g02230	mitochondrial matrix
Afu5g02260	plasma membrane
Afu5g02260	xenobiotic-transporting ATPase activity
Afu5g02260	drug transport
Afu5g02260	response to drug
Afu5g02280	hydrolase activity, hydrolyzing O-glycosyl compounds
Afu5g02280	1,3-beta-glucan metabolic process

Afu5g02280	fungal-type cell wall
Afu5g02290	plasma membrane
Afu5g02290	potassium ion transmembrane transporter activity
Afu5g02290	cellular potassium ion homeostasis
Afu5g02310	metabolic process
Afu5g02310	hydrolase activity
Afu5g02330	pathogenesis
Afu5g02360	GTPase activity
Afu5g02360	membrane fraction
Afu5g02360	protein targeting to vacuole
Afu5g02360	peroxisome organization
Afu5g02360	vacuolar transport
Afu5g02360	protein retention in Golgi apparatus
Afu5g02370	vacuolar proton-transporting V-type ATPase, V1 domain
Afu5g02370	fungal-type vacuole membrane
Afu5g02370	endodeoxyribonuclease activity
Afu5g02370	vacuolar acidification
Afu5g02370	protein metabolic process
Afu5g02370	proton-transporting ATPase activity, rotational mechanism
Afu5g02400	molecular function unknown
Afu5g02400	nucleus
Afu5g02400	cytoplasm
Afu5g02400	negative regulation of gluconeogenesis
Afu5g02410	ATP-dependent RNA helicase activity
Afu5g02410	nucleolus
Afu5g02410	35S primary transcript processing
Afu5g02420	nuclear mRNA splicing, via spliceosome
Afu5g02420	RNA binding
Afu5g02420	U2 snRNP
Afu5g02430	DNA ligase (ATP) activity
Afu5g02430	replication fork
Afu5g02430	DNA ligation
Afu5g02430	lagging strand elongation
Afu5g02430	base-excision repair
Afu5g02430	nucleotide-excision repair
Afu5g02430	DNA recombination
Afu5g02440	mitotic spindle elongation
Afu5g02440	mitotic sister chromatid segregation
Afu5g02440	ubiquitin-protein ligase activity
Afu5g02440	protein binding
Afu5g02440	anaphase-promoting complex
Afu5g02440	ubiquitin-dependent protein catabolic process
Afu5g02440	mitotic metaphase/anaphase transition
Afu5g02450	dimethylallyltranstransferase activity
Afu5g02450	geranyltranstransferase activity
Afu5g02450	cytosol
Afu5g02450	ergosterol biosynthetic process
Afu5g02450	isoprenoid biosynthetic process
Afu5g02450	farnesyl diphosphate biosynthetic process
Afu5g02470	molecular function unknown

Afu5g02470	cellular component unknown
Afu5g02470	thiamin biosynthetic process
Afu5g02480	glycogen (starch) synthase activity
Afu5g02480	cytoplasm
Afu5g02480	glycogen metabolic process
Afu5g02490	metabolic process
Afu5g02490	zinc ion binding
Afu5g02490	oxidoreductase activity
Afu5g02510	GARP complex
Afu5g02510	molecular function unknown
Afu5g02510	Golgi apparatus
Afu5g02510	Golgi to vacuole transport
Afu5g02520	chromatin binding
Afu5g02520	ATP-dependent DNA helicase activity
Afu5g02520	pre-replicative complex
Afu5g02520	replication fork
Afu5g02520	cytoplasm
Afu5g02520	pre-replicative complex assembly
Afu5g02520	DNA unwinding during replication
Afu5g02520	DNA replication initiation
Afu5g02520	establishment of chromatin silencing
Afu5g02530	ribokinase activity
Afu5g02530	ATP binding
Afu5g02530	nucleus
Afu5g02530	cytoplasm
Afu5g02530	D-ribose metabolic process
Afu5g02550	transcription factor TFIIIC complex
Afu5g02550	RNA polymerase III transcription factor activity
Afu5g02550	transcription initiation from RNA polymerase III promoter
Afu5g02560	protein phosphatase type 2A activity
Afu5g02560	protein phosphatase type 2A complex
Afu5g02560	nucleus
Afu5g02560	cytoplasm
Afu5g02560	spindle pole body
Afu5g02560	cellular bud neck
Afu5g02560	translation
Afu5g02560	protein amino acid dephosphorylation
Afu5g02570	histone acetyltransferase complex
Afu5g02570	histone acetyltransferase activity
Afu5g02570	regulation of transcription from RNA polymerase II promoter
Afu5g02570	histone acetylation
Afu5g02580	nuclear mRNA splicing, via spliceosome
Afu5g02580	molecular function unknown
Afu5g02580	nucleus
Afu5g02590	mitotic spindle elongation
Afu5g02590	mitotic sister chromatid segregation
Afu5g02590	ubiquitin-protein ligase activity
Afu5g02590	protein binding
Afu5g02590	anaphase-promoting complex
Afu5g02590	ubiquitin-dependent protein catabolic process

Afu5g02590	mitotic metaphase/anaphase transition
Afu5g02590	cyclin catabolic process
Afu5g02610	metabolic process
Afu5g02610	oxidoreductase activity
Afu5g02620	catalytic activity
Afu5g02620	spore wall assembly (sensu Saccharomyces)
Afu5g02620	metabolic process
Afu5g02620	cellular component unknown
Afu5g02620	oxidoreductase activity
Afu5g02640	O-methyltransferase activity
Afu5g02660	catalytic activity
Afu5g02660	spore wall assembly (sensu Saccharomyces)
Afu5g02660	cellular component unknown
Afu5g02690	transcription factor activity
Afu5g02690	nucleus
Afu5g02690	regulation of transcription
Afu5g02700	drug transporter activity
Afu5g02700	drug transport
Afu5g02700	integral to membrane
Afu5g02720	phosphoribosylformylglycinamidine synthase activity
Afu5g02720	cytoplasm
Afu5g02720	purine nucleotide biosynthetic process
Afu5g02730	gamma-tubulin complex
Afu5g02740	alpha-1,2-mannosyltransferase activity
Afu5g02740	Golgi apparatus
Afu5g02740	protein amino acid N-linked glycosylation
Afu5g02750	cytochrome-c oxidase activity
Afu5g02750	mitochondrial respiratory chain complex IV
Afu5g02750	aerobic respiration
Afu5g02760	endoplasmic reticulum
Afu5g02760	endoplasmic reticulum membrane
Afu5g02760	nonselective vesicle transport
Afu5g02760	fatty acid elongase activity
Afu5g02760	sphingolipid biosynthetic process
Afu5g02760	fatty acid elongation
Afu5g02780	NAD(P)+ transhydrogenase (B-specific) activity
Afu5g02780	electron transport
Afu5g02800	RNA polymerase II transcription factor activity
Afu5g02800	nucleus
Afu5g02800	zinc ion binding
Afu5g02800	regulation of transcription
Afu5g02840	transporter activity
Afu5g02840	integral to plasma membrane
Afu5g02840	transport
Afu5g02840	membrane
Afu5g02840	sugar transmembrane transporter activity
Afu5g02870	3-hydroxyacyl-CoA dehydrogenase activity
Afu5g02870	enoyl-CoA hydratase activity
Afu5g02870	peroxisomal matrix
Afu5g02870	fatty acid beta-oxidation

Afu5g02880	transcription factor activity
Afu5g02880	regulation of transcription
Afu5g02940	plasma membrane
Afu5g02940	choline transmembrane transporter activity
Afu5g02940	choline transport
Afu5g02970	biological process unknown
Afu5g02970	fungal-type vacuole
Afu5g02970	molecular function unknown
Afu5g02990	cytoplasm
Afu5g02990	aromatic-amino-acid:2-oxoglutarate aminotransferase activity
Afu5g02990	aromatic amino acid family metabolic process
Afu5g03000	nucleus
Afu5g03000	cytoplasm
Afu5g03000	regulation of cellular amino acid metabolic process
Afu5g03020	structural constituent of ribosome
Afu5g03020	cytosolic large ribosomal subunit (sensu Eukaryota)
Afu5g03020	translation
Afu5g03030	transcription factor activity
Afu5g03030	nucleus
Afu5g03030	zinc ion binding
Afu5g03030	regulation of transcription
Afu5g03050	nucleus
Afu5g03050	transcription activator activity
Afu5g03050	positive regulation of transcription from RNA polymerase II promoter
Afu5g03080	cellular bud neck septin ring
Afu5g03080	establishment of cell polarity (sensu Saccharomyces)
Afu5g03080	conjugation with cellular fusion
Afu5g03080	cell morphogenesis
Afu5g03080	cytokinesis
Afu5g03080	structural constituent of cytoskeleton
Afu5g03080	phosphatidylinositol binding
Afu5g03080	cytoplasm
Afu5g03080	cell wall organization
Afu5g03080	axial cellular bud site selection
Afu5g03080	bipolar cellular bud site selection
Afu5g03090	cytokinesis
Afu5g03090	small nucleolar ribonucleoprotein complex
Afu5g03090	cytoplasm
Afu5g03090	maturation of SSU-rRNA
Afu5g03090	snoRNA binding
Afu5g03100	metabolic process
Afu5g03100	oxidoreductase activity
Afu5g03120	recombinase activity
Afu5g03120	cytoplasmic mRNA processing body
Afu5g03120	5'-3' exoribonuclease activity
Afu5g03120	deoxyribonuclease activity
Afu5g03120	cytoplasm
Afu5g03120	35S primary transcript processing
Afu5g03120	mRNA catabolic process
Afu5g03120	filamentous growth

Afu5g03130	H3/H4 histone acetyltransferase activity
Afu5g03130	nucleus
Afu5g03130	cytoplasm
Afu5g03130	chromatin assembly or disassembly
Afu5g03130	chromatin silencing at telomere
Afu5g03140	GTP cyclohydrolase I activity
Afu5g03140	GTP cyclohydrolase I activity
Afu5g03140	nucleus
Afu5g03140	cytoplasm
Afu5g03140	folic acid and derivative biosynthetic process
Afu5g03160	protein kinase activity
Afu5g03160	cyclin-dependent protein kinase activity
Afu5g03160	nucleus
Afu5g03160	regulation of transcription from RNA polymerase II promoter
Afu5g03160	protein amino acid phosphorylation
Afu5g03180	regulation of progression through cell cycle
Afu5g03180	translation initiation factor activity
Afu5g03180	nucleus
Afu5g03180	cytoplasm
Afu5g03180	ribosome
Afu5g03180	translational initiation
Afu5g03200	nucleus
Afu5g03200	plasmid maintenance
Afu5g03200	mitotic cell cycle spindle assembly checkpoint
Afu5g03200	cysteine-type peptidase activity
Afu5g03200	protein desumoylation
Afu5g03200	SUMO-specific protease activity
Afu5g03230	response to stress
Afu5g03240	biological process unknown
Afu5g03240	protein kinase activity
Afu5g03240	mitochondrion
Afu5g03250	ubiquitin-specific protease activity
Afu5g03250	nucleus
Afu5g03250	ubiquitin-dependent protein catabolic process
Afu5g03250	programmed cell death
Afu5g03250	protein deubiquitination
Afu5g03260	molecular function unknown
Afu5g03260	integral to membrane
Afu5g03260	secretory pathway
Afu5g03320	nucleotide-excision repair factor 3 complex
Afu5g03320	nucleotide-excision repair, DNA duplex unwinding
Afu5g03320	DNA helicase activity
Afu5g03320	holo TFIIH complex
Afu5g03320	transcription initiation from RNA polymerase II promoter
Afu5g03320	negative regulation of transcription from RNA polymerase II promoter, mitotic
Afu5g03320	general RNA polymerase II transcription factor activity
Afu5g03350	biological process unknown
Afu5g03350	NAD+ synthase (glutamine-hydrolyzing) activity
Afu5g03350	nucleus
Afu5g03350	cytoplasm

Afu5g03350	hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in linear amides
Afu5g03360	NAD+ diphosphatase activity
Afu5g03360	cytoplasm
Afu5g03360	peroxisome
Afu5g03360	NADH metabolic process
Afu5g03380	monooxygenase activity
Afu5g03380	endoplasmic reticulum membrane
Afu5g03380	protein folding
Afu5g03400	cytokinesis
Afu5g03400	molecular function unknown
Afu5g03400	cytoplasm
Afu5g03400	cellular bud neck
Afu5g03410	exopolyphosphatase activity
Afu5g03410	cytoplasm
Afu5g03410	polyphosphate metabolic process
Afu5g03420	1-aminocyclopropane-1-carboxylate deaminase activity
Afu5g03420	1-aminocyclopropane-1-carboxylate catabolic process
Afu5g03430	DNA binding
Afu5g03430	transcription factor activity
Afu5g03430	nucleus
Afu5g03430	chromatin remodeling
Afu5g03430	zinc ion binding
Afu5g03450	molecular function unknown
Afu5g03450	DNA repair
Afu5g03450	cellular component unknown
Afu5g03460	thymidylate kinase activity
Afu5g03460	nucleus
Afu5g03460	cytoplasm
Afu5g03460	dTDP biosynthetic process
Afu5g03460	dTTP biosynthetic process
Afu5g03460	DNA-dependent DNA replication
Afu5g03460	plasmid maintenance
Afu5g03460	mutagenesis
Afu5g03460	DNA repair
Afu5g03480	methylenetetrahydrofolate reductase (NADPH) activity
Afu5g03480	cell
Afu5g03480	methionine metabolic process
Afu5g03490	nucleoside diphosphate kinase activity
Afu5g03490	mitochondrial intermembrane space
Afu5g03490	cytosol
Afu5g03490	purine nucleotide biosynthetic process
Afu5g03490	DNA metabolic process
Afu5g03490	nucleotide metabolic process
Afu5g03490	RNA metabolic process
Afu5g03500	alpha-glucosidase activity
Afu5g03500	endoplasmic reticulum
Afu5g03500	fungal-type cell wall biogenesis
Afu5g03510	biological process unknown
Afu5g03510	molecular function unknown
Afu5g03510	cytoplasm

Afu5g03530	chitinase activity
Afu5g03530	cell wall chitin catabolic process
Afu5g03530	fungal-type cell wall
Afu5g03550	fungal-type vacuole
Afu5g03550	endoplasmic reticulum
Afu5g03550	plasma membrane
Afu5g03550	regulation of pH
Afu5g03550	hydrogen-exporting ATPase activity, phosphorylative mechanism
Afu5g03550	proton transport
Afu5g03560	biological process unknown
Afu5g03560	glutathione transferase activity
Afu5g03560	glutamate-tRNA ligase activity
Afu5g03560	cytoplasm
Afu5g03570	structural constituent of ribosome
Afu5g03570	mitochondrial large ribosomal subunit
Afu5g03570	translation
Afu5g03570	aerobic respiration
Afu5g03600	molecular function unknown
Afu5g03600	cytoplasm
Afu5g03600	iron-sulfur cluster assembly
Afu5g03610	molecular function unknown
Afu5g03610	nucleus
Afu5g03610	cytoplasm
Afu5g03610	glycogen metabolic process
Afu5g03640	mitochondrial inner membrane
Afu5g03640	mitochondrial translocation
Afu5g03640	protein transporter activity
Afu5g03670	adenosylmethionine decarboxylase activity
Afu5g03670	nucleus
Afu5g03670	cytoplasm
Afu5g03670	pantothenate biosynthetic process
Afu5g03680	regulation of transcription involved in G1 phase of mitotic cell cycle
Afu5g03680	SAGA complex
Afu5g03680	transcription factor TFIID complex
Afu5g03680	chromatin organization
Afu5g03680	transcription initiation from RNA polymerase II promoter
Afu5g03680	protein amino acid acetylation
Afu5g03680	general RNA polymerase II transcription factor activity
Afu5g03680	chromatin modification
Afu5g03680	histone acetylation
Afu5g03690	microsome
Afu5g03690	cytosol
Afu5g03690	phosphatidylinositol transporter activity
Afu5g03690	phospholipid transport
Afu5g03740	secondary metabolic process
Afu5g03760	chitinase activity
Afu5g03760	cell wall chitin catabolic process
Afu5g03760	fungal-type cell wall
Afu5g03780	endoribonuclease activity
Afu5g03780	nucleus

Afu5g03780	cytoplasm
Afu5g03780	cytosol
Afu5g03780	mRNA catabolic process
Afu5g03790	ferroxidase activity
Afu5g03790	plasma membrane
Afu5g03790	high-affinity iron ion transport
Afu5g03800	iron ion transmembrane transporter activity
Afu5g03800	plasma membrane
Afu5g03800	high-affinity iron ion transport
Afu5g03820	structural constituent of cytoskeleton
Afu5g03820	inner plaque of spindle pole body
Afu5g03820	central plaque of spindle pole body
Afu5g03820	microtubule nucleation
Afu5g03850	chitinase activity
Afu5g03850	extracellular region
Afu5g03850	cell wall chitin catabolic process
Afu5g03850	cell wall organization
Afu5g03870	biological process unknown
Afu5g03870	molecular function unknown
Afu5g03870	nucleus
Afu5g03870	nucleolus
Afu5g03880	signal sequence binding
Afu5g03880	signal recognition particle, endoplasmic reticulum targeting
Afu5g03880	protein targeting to ER
Afu5g03910	transporter activity
Afu5g03910	mitochondrial outer membrane
Afu5g03910	transport
Afu5g03910	mitochondrial fusion
Afu5g03920	transcription factor activity
Afu5g03920	nucleus
Afu5g03920	transcription
Afu5g03930	monosaccharide metabolic process
Afu5g03930	cellular component unknown
Afu5g03930	D-xylulose reductase activity
Afu5g03940	hydrolase activity, hydrolyzing O-glycosyl compounds
Afu5g03940	cellular glucan metabolic process
Afu5g03940	fungal-type cell wall
Afu5g03950	protein serine/threonine kinase activity
Afu5g03950	protein amino acid phosphorylation
Afu5g03960	chitinase activity
Afu5g03960	extracellular region
Afu5g03960	chitin catabolic process
Afu5g03960	chitin binding
Afu5g03980	extracellular region
Afu5g03980	chitin binding
Afu5g03990	fungal-type vacuole
Afu5g03990	aminopeptidase I activity
Afu5g03990	vacuolar protein catabolic process
Afu5g04000	proteasome complex
Afu5g04000	chaperone activity

Afu5g04000	nucleus
Afu5g04000	protein complex assembly
Afu5g04000	ubiquitin-dependent protein catabolic process
Afu5g04010	tRNA-intron endonuclease activity
Afu5g04010	tRNA-intron endonuclease complex
Afu5g04010	nuclear inner membrane
Afu5g04010	tRNA splicing, via endonucleolytic cleavage and ligation
Afu5g04030	peptidyltransferase activity
Afu5g04030	structural constituent of ribosome
Afu5g04030	mitochondrial large ribosomal subunit
Afu5g04030	translation
Afu5g04050	biological process unknown
Afu5g04050	molecular function unknown
Afu5g04050	cellular component unknown
Afu5g04060	ubiquitin conjugating enzyme activity
Afu5g04060	endoplasmic reticulum
Afu5g04060	ubiquitin cycle
Afu5g04060	protein ubiquitination
Afu5g04060	ER-associated protein catabolic process
Afu5g04070	reciprocal meiotic recombination
Afu5g04080	lanosterol synthase activity
Afu5g04080	endoplasmic reticulum
Afu5g04080	lipid particle
Afu5g04080	plasma membrane
Afu5g04080	ergosterol biosynthetic process
Afu5g04090	centromere and kinetochore complex maturation
Afu5g04090	regulation of progression through cell cycle
Afu5g04090	ubiquitin ligase complex
Afu5g04090	co-chaperone activity
Afu5g04090	protein complex assembly
Afu5g04090	protein ubiquitination
Afu5g04090	cAMP-mediated signaling
Afu5g04100	biological process unknown
Afu5g04100	molecular function unknown
Afu5g04100	cellular component unknown
Afu5g04130	cyclin-dependent protein kinase activity
Afu5g04130	nucleus
Afu5g04130	protein amino acid phosphorylation
Afu5g04130	phosphate metabolic process
Afu5g04130	cell cycle
Afu5g04140	spindle pole
Afu5g04140	molecular function unknown
Afu5g04140	chromosome segregation
Afu5g04170	chaperonin ATPase activity
Afu5g04170	cytoplasm
Afu5g04170	protein folding
Afu5g04170	response to stress
Afu5g04170	signal transduction
Afu5g04190	transcription factor activity
Afu5g04190	nucleus

Afu5g04190	transcription
Afu5g04190	regulation of phosphorus utilization
Afu5g04190	response to stress
Afu5g04200	DNA-directed RNA polymerase activity
Afu5g04200	DNA-directed RNA polymerase III complex
Afu5g04200	transcription from RNA polymerase III promoter
Afu5g04210	mitochondrion
Afu5g04210	mitochondrial respiratory chain complex III
Afu5g04210	mitochondrial electron transport, ubiquinol to cytochrome c
Afu5g04210	ubiquinol-cytochrome-c reductase activity
Afu5g04210	aerobic respiration
Afu5g04220	mitochondrial inner membrane
Afu5g04230	citrate (Si)-synthase activity
Afu5g04230	mitochondrion
Afu5g04230	mitochondrial matrix
Afu5g04230	tricarboxylic acid cycle
Afu5g04230	citrate metabolic process
Afu5g04230	glutamate biosynthetic process
Afu5g04240	RNA binding
Afu5g04240	nucleus
Afu5g04240	termination of RNA polymerase II transcription, poly(A)-independent
Afu5g04250	O-acetylhomoserine aminocarboxypropyltransferase activity
Afu5g04250	cysteine synthase activity
Afu5g04250	cytoplasm
Afu5g04250	methionine metabolic process
Afu5g04260	arginine permease activity
Afu5g04260	lysine permease activity
Afu5g04260	plasma membrane
Afu5g04260	basic amino acid transmembrane transporter activity
Afu5g04260	basic amino acid transport
Afu5g04270	long-chain-fatty-acid-CoA ligase activity
Afu5g04270	peroxisome
Afu5g04270	N-terminal protein myristoylation
Afu5g04270	lipid metabolic process
Afu5g04310	mitochondrion
Afu5g04310	mitochondrial transport
Afu5g04310	FAD transmembrane transporter activity
Afu5g04320	Golgi membrane
Afu5g04320	RAB small monomeric GTPase activity
Afu5g04320	endoplasmic reticulum membrane
Afu5g04320	protein complex assembly
Afu5g04320	ER to Golgi vesicle-mediated transport
Afu5g04330	aminopeptidase activity
Afu5g04330	nucleus
Afu5g04330	cytoplasm
Afu5g04330	proteolysis
Afu5g04330	metallopeptidase activity
Afu5g04340	nuclear-transcribed mRNA catabolic process, deadenylation-dependent decay
Afu5g04340	mRNA binding
Afu5g04340	cytoplasm

Afu5g04360	molecular function unknown
Afu5g04360	endoplasmic reticulum
Afu5g04360	ER to Golgi vesicle-mediated transport
Afu5g04370	programmed cell death
Afu5g04420	spliceosome assembly
Afu5g04420	RNA binding
Afu5g04420	protein binding
Afu5g04420	U2 snRNP
Afu5g04440	ribonuclease III activity
Afu5g04440	nucleolus
Afu5g04440	35S primary transcript processing
Afu5g05450	structural constituent of ribosome
Afu5g05450	cytosolic small ribosomal subunit (sensu Eukaryota)
Afu5g05450	translation
Afu5g05460	uracil phosphoribosyltransferase activity
Afu5g05460	cellular component unknown
Afu5g05460	pyrimidine salvage
Afu5g05480	RHEB small monomeric GTPase activity
Afu5g05480	pathogenesis
Afu5g05480	detection of nutrient
Afu5g05480	nitrogen utilization
Afu5g05480	extrinsic to plasma membrane
Afu5g05490	serine-tRNA ligase activity
Afu5g05490	cytoplasm
Afu5g05490	tRNA aminoacylation for protein translation
Afu5g05500	phosphoglycerate dehydrogenase activity
Afu5g05500	cytoplasm
Afu5g05500	serine family amino acid biosynthetic process
Afu5g05510	cyclin-dependent protein kinase activity
Afu5g05510	nucleus
Afu5g05510	transcription
Afu5g05510	protein amino acid phosphorylation
Afu5g05520	metabolic process
Afu5g05520	membrane
Afu5g05520	ATPase activity, coupled to transmembrane movement of ions
Afu5g05540	M phase of mitotic cell cycle
Afu5g05540	protein binding
Afu5g05540	nucleus
Afu5g05540	nucleosome assembly
Afu5g05550	mitochondrion inheritance
Afu5g05550	vacuole inheritance
Afu5g05550	microfilament motor activity
Afu5g05550	endocytosis
Afu5g05550	vesicle-mediated transport
Afu5g05570	molecular function unknown
Afu5g05570	nucleus
Afu5g05570	response to oxidative stress
Afu5g05570	maturation of SSU-rRNA
Afu5g05590	aspartate kinase activity
Afu5g05590	cytoplasm

Afu5g05590	methionine metabolic process
Afu5g05590	threonine metabolic process
Afu5g05590	homoserine biosynthetic process
Afu5g05600	specific RNA polymerase II transcription factor activity
Afu5g05600	nucleus
Afu5g05600	transcription initiation from RNA polymerase II promoter
Afu5g05600	spindle organization
Afu5g05610	cellular bud site selection
Afu5g05610	molecular function unknown
Afu5g05610	nucleus
Afu5g05630	structural constituent of ribosome
Afu5g05630	cytosolic large ribosomal subunit (sensu Eukaryota)
Afu5g05630	translation
Afu5g05660	biological process unknown
Afu5g05660	molecular function unknown
Afu5g05660	nucleolus
Afu5g05670	vacuole
Afu5g05670	neutral amino acid transmembrane transporter activity
Afu5g05670	neutral amino acid transport
Afu5g05680	cytosol
Afu5g05680	translational termination
Afu5g05680	translation release factor activity, codon specific
Afu5g05690	prephenate dehydratase activity
Afu5g05690	cytoplasm
Afu5g05690	phenylalanine biosynthetic process, prephenate pathway
Afu5g05710	rRNA modification
Afu5g05710	pseudouridylate synthase activity
Afu5g05710	small nucleolar ribonucleoprotein complex
Afu5g05710	35S primary transcript processing
Afu5g05720	molecular function unknown
Afu5g05720	nucleus
Afu5g05720	cytoplasm
Afu5g05720	negative regulation of gluconeogenesis
Afu5g05730	biological process unknown
Afu5g05730	molecular function unknown
Afu5g05730	nucleus
Afu5g05730	nucleolus
Afu5g05740	nucleotide-sugar transmembrane transporter activity
Afu5g05740	Golgi apparatus
Afu5g05740	protein amino acid N-linked glycosylation
Afu5g05740	nucleotide-sugar transport
Afu5g05740	lipid glycosylation
Afu5g05750	protein kinase activity
Afu5g05750	cytoplasm
Afu5g05760	GTPase inhibitor activity
Afu5g05760	cytoplasm
Afu5g05760	positive regulation of transcription from RNA polymerase II promoter by pheromones
Afu5g05770	1,3-beta-glucan biosynthetic process
Afu5g05770	cell wall organization
Afu5g05790	G1/S transition of mitotic cell cycle

Afu5g05790	G2/M transition of mitotic cell cycle
Afu5g05790	nuclear ubiquitin ligase complex
Afu5g05790	ubiquitin-protein ligase activity
Afu5g05790	protein binding
Afu5g05790	nucleus
Afu5g05790	cytoplasm
Afu5g05790	ubiquitin-dependent protein catabolic process
Afu5g05820	homoserine kinase activity
Afu5g05820	isoleucine metabolic process
Afu5g05820	methionine metabolic process
Afu5g05820	threonine metabolic process
Afu5g05820	cellular component unknown
Afu5g05820	homoserine metabolic process
Afu5g05830	plasma membrane
Afu5g05830	di-, tri-valent inorganic cation transmembrane transporter activity
Afu5g05830	di-, tri-valent inorganic cation transport
Afu5g05830	magnesium ion transport
Afu5g05840	calcium channel activity
Afu5g05840	plasma membrane
Afu5g05840	calcium ion transport
Afu5g05870	nucleus
Afu5g05870	transcription from RNA polymerase II promoter
Afu5g05870	RNA elongation from RNA polymerase II promoter
Afu5g05870	chromosome segregation
Afu5g05870	transcription elongation factor complex
Afu5g05870	Cdc73/Paf1 complex
Afu5g05870	RNA polymerase II transcription elongation factor activity
Afu5g05870	triplex DNA binding
Afu5g05880	lipid particle
Afu5g05880	acyltransferase activity
Afu5g05880	phospholipid biosynthetic process
Afu5g05890	mitochondrial matrix
Afu5g05890	NADP biosynthetic process
Afu5g05890	response to oxidative stress
Afu5g05890	NADH kinase activity
Afu5g05900	cytokinesis
Afu5g05900	protein serine/threonine kinase activity
Afu5g05900	protein amino acid phosphorylation
Afu5g05920	glycine-tRNA ligase activity
Afu5g05920	cytoplasm
Afu5g05920	mitochondrion
Afu5g05920	transcription termination
Afu5g05920	glycyl-tRNA aminoacylation
Afu5g05930	ribosomal large subunit assembly
Afu5g05930	nucleolus
Afu5g05930	processing of 27S pre-rRNA
Afu5g05930	rRNA primary transcript binding
Afu5g05950	endocytosis
Afu5g05950	response to osmotic stress
Afu5g05950	bipolar cellular bud site selection

Afu5g05950	cytoskeletal protein binding
Afu5g05950	membrane raft
Afu5g05960	G1/S transition of mitotic cell cycle
Afu5g05960	protein kinase activity
Afu5g05960	cellular component unknown
Afu5g05960	cellular cation homeostasis
Afu5g05970	molecular function unknown
Afu5g05970	ER to Golgi vesicle-mediated transport
Afu5g05970	TRAPP complex
Afu5g05980	nuclear division
Afu5g05980	calcium- and calmodulin-dependent protein kinase activity
Afu5g05990	AT DNA binding
Afu5g06000	nucleus
Afu5g06000	RNA elongation
Afu5g06000	regulation of transcription, DNA-dependent
Afu5g06000	histone methylation
Afu5g06000	histone-lysine N-methyltransferase activity
Afu5g06010	molecular function unknown
Afu5g06010	nucleus
Afu5g06010	cytoplasm
Afu5g06010	processing of 27S pre-rRNA
Afu5g06010	ribosomal large subunit biogenesis
Afu5g06040	repairosome
Afu5g06040	nucleotide-excision repair factor 2 complex
Afu5g06040	nucleotide-excision repair, DNA damage recognition
Afu5g06040	damaged DNA binding
Afu5g06040	DNA repair protein
Afu5g06040	ubiquitin cycle
Afu5g06040	negative regulation of protein catabolic process
Afu5g06050	mannosyltransferase activity
Afu5g06060	G1/S transition of mitotic cell cycle
Afu5g06060	G2/M transition of mitotic cell cycle
Afu5g06060	nuclear ubiquitin ligase complex
Afu5g06060	kinetochore
Afu5g06060	ubiquitin-protein ligase activity
Afu5g06060	protein binding
Afu5g06060	nucleus
Afu5g06060	cytoplasm
Afu5g06060	ubiquitin-dependent protein catabolic process
Afu5g06060	SCF ubiquitin ligase complex
Afu5g06060	regulation of sulfur metabolic process
Afu5g06070	ATP-binding cassette (ABC) transporter activity
Afu5g06070	ATP-binding cassette (ABC) transporter activity
Afu5g06070	ATP binding
Afu5g06070	integral to plasma membrane
Afu5g06070	transport
Afu5g06070	transport
Afu5g06070	pathogenesis
Afu5g06090	biological process unknown
Afu5g06090	molecular function unknown

Afu5g06090	membrane
Afu5g06100	nucleus
Afu5g06100	protein sumoylation
Afu5g06100	SUMO activating enzyme activity
Afu5g06120	DNA damage checkpoint
Afu5g06120	negative regulation of transcription from RNA polymerase II promoter
Afu5g06120	nucleus
Afu5g06120	cytoplasm
Afu5g06120	specific transcriptional repressor activity
Afu5g06130	succinate-CoA ligase (ADP-forming) activity
Afu5g06130	mitochondrion
Afu5g06130	tricarboxylic acid cycle
Afu5g06130	succinyl-CoA metabolic process
Afu5g06140	histone acetyltransferase activity
Afu5g06140	regulation of transcription from RNA polymerase II promoter
Afu5g06140	transcription elongation factor complex
Afu5g06140	DNA-directed RNA polymerase II, holoenzyme
Afu5g06140	RNA polymerase II transcription elongation factor activity
Afu5g06160	histidine biosynthetic process
Afu5g06160	1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)methylideneamino]imidazole-4-carboxami
Afu5g06160	cell
Afu5g06190	response to pheromone during conjugation with cellular fusion
Afu5g06190	pheromone-dependent signal transduction involved in conjugation with cellular fusion
Afu5g06190	transcription factor activity
Afu5g06190	positive regulation of transcription from RNA polymerase II promoter by pheromones
Afu5g06190	sexual reproduction
Afu5g06220	late endosome
Afu5g06220	vacuolar acidification
Afu5g06220	monovalent inorganic cation transmembrane transporter activity
Afu5g06220	monovalent inorganic cation transport
Afu5g06220	endosome transport
Afu5g06220	cellular monovalent inorganic cation homeostasis
Afu5g06230	gamma-aminobutyric acid transporter activity
Afu5g06230	transport
Afu5g06230	membrane
Afu5g06240	alcohol dehydrogenase (NAD) activity
Afu5g06240	soluble fraction
Afu5g06240	mitochondrial matrix
Afu5g06240	fermentation
Afu5g06240	zinc ion binding
Afu5g06260	helicase activity
Afu5g06260	chromatin remodeling
Afu5g06260	transcription from RNA polymerase II promoter
Afu5g06260	chromatin remodeling complex
Afu5g06260	ATPase activity
Afu5g06270	5-aminolevulinate synthase activity
Afu5g06270	mitochondrial matrix
Afu5g06270	heme biosynthetic process
Afu5g06290	transporter activity
Afu5g06290	integral to plasma membrane

Afu5g06290	transport
Afu5g06290	nicotinamide mononucleotide permease activity
Afu5g06290	nicotinamide mononucleotide transport
Afu5g06300	molecular function unknown
Afu5g06300	peroxisomal membrane
Afu5g06300	protein targeting to peroxisome
Afu5g06300	peroxisome organization
Afu5g06320	molecular function unknown
Afu5g06320	membrane
Afu5g06320	membrane organization
Afu5g06330	DNA helicase activity
Afu5g06330	nucleus
Afu5g06330	chromatin remodeling
Afu5g06330	meiosis
Afu5g06330	ATPase activity
Afu5g06350	transcription factor activity
Afu5g06350	regulation of transcription, DNA-dependent
Afu5g06360	structural constituent of ribosome
Afu5g06360	cytosolic large ribosomal subunit (sensu Eukaryota)
Afu5g06360	translation
Afu5g06390	adenosine kinase activity
Afu5g06390	nucleus
Afu5g06390	cytoplasm
Afu5g06390	purine base metabolic process
Afu5g06410	negative regulation of transcription from RNA polymerase II promoter
Afu5g06410	RNA polymerase II transcription factor activity
Afu5g06410	nucleus
Afu5g06410	zinc ion binding
Afu5g06420	MAP kinase kinase kinase activity
Afu5g06420	cytoplasm
Afu5g06420	protein amino acid phosphorylation
Afu5g06430	structural constituent of ribosome
Afu5g06430	mitochondrial large ribosomal subunit
Afu5g06430	translation
Afu5g06450	extrinsic to vacuolar membrane
Afu5g06450	fungal-type vacuole membrane
Afu5g06450	protein binding
Afu5g06450	Golgi to endosome transport
Afu5g06450	vesicle docking during exocytosis
Afu5g06450	homotypic vacuole fusion, non-autophagic
Afu5g06450	late endosome to vacuole transport
Afu5g06460	zinc ion binding
Afu5g06470	protein serine/threonine kinase activity
Afu5g06470	nucleus
Afu5g06470	protein amino acid phosphorylation
Afu5g06480	biological process unknown
Afu5g06480	molecular function unknown
Afu5g06480	cellular component unknown
Afu5g06510	ribosomal subunit export from nucleus
Afu5g06510	conjugation with cellular fusion

Afu5g06510	GTPase activity
Afu5g06510	cytoplasm
Afu5g06520	biological process unknown
Afu5g06520	molecular function unknown
Afu5g06520	cytoplasm
Afu5g06530	mitochondrion
Afu5g06530	CDP-diacylglycerol-glycerol-3-phosphate 3-phosphatidyltransferase activity
Afu5g06530	phospholipid biosynthetic process
Afu5g06550	protein binding
Afu5g06580	drug transporter activity
Afu5g06580	drug transport
Afu5g06580	integral to membrane
Afu5g06590	repairosome
Afu5g06590	nucleotide-excision repair factor 4 complex
Afu5g06590	nucleotide-excision repair, DNA damage recognition
Afu5g06590	DNA-dependent ATPase activity
Afu5g06600	ATP-dependent DNA helicase activity
Afu5g06600	nucleus
Afu5g06600	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process
Afu5g06600	chromatin remodeling
Afu5g06600	regulation of transcription, DNA-dependent
Afu5g06610	glutathione synthase activity
Afu5g06610	intracellular
Afu5g06610	glutathione biosynthetic process
Afu5g06680	4-aminobutyrate transaminase activity
Afu5g06680	intracellular
Afu5g06680	nitrogen utilization
Afu5g06690	nucleus
Afu5g06690	chromatin organization
Afu5g06690	regulation of transcription, DNA-dependent
Afu5g06690	RNA elongation from RNA polymerase II promoter
Afu5g06690	chromosome segregation
Afu5g06690	transcription elongation factor complex
Afu5g06690	RNA polymerase II transcription elongation factor activity
Afu5g06700	protein serine/threonine phosphatase activity
Afu5g06700	nucleus
Afu5g06700	cytoplasm
Afu5g06700	protein amino acid phosphorylation
Afu5g06710	biological process unknown
Afu5g06710	molecular function unknown
Afu5g06710	nucleus
Afu5g06710	cytoplasm
Afu5g06720	transporter activity
Afu5g06720	transport
Afu5g06720	membrane
Afu5g06730	protein kinase activity
Afu5g06730	cytoplasm
Afu5g06750	protein kinase activity
Afu5g06750	cytosolic ribosome (sensu Eukaryota)
Afu5g06750	regulation of translational initiation

Afu5g06750	protein amino acid phosphorylation
Afu5g06750	cellular amino acid biosynthetic process
Afu5g06770	biological process unknown
Afu5g06770	GTP binding
Afu5g06770	cytoplasm
Afu5g06780	carbamoyl-phosphate synthase (glutamine-hydrolyzing) activity
Afu5g06780	cytosol
Afu5g06780	arginine biosynthetic process
Afu5g06800	transcription factor activity
Afu5g06800	nucleus
Afu5g06800	response to xenobiotic stimulus
Afu5g06800	regulation of transcription
Afu5g06840	chitinase activity
Afu5g06840	extracellular region
Afu5g06840	chitin catabolic process
Afu5g06840	chitin binding
Afu5g06940	biological process unknown
Afu5g06940	molecular function unknown
Afu5g06940	nucleus
Afu5g06940	cytoplasm
Afu5g06990	O-methyltransferase activity
Afu5g07000	metabolic process
Afu5g07000	oxidoreductase activity
Afu5g07020	ATP binding
Afu5g07020	cytoplasm
Afu5g07020	ribosome biogenesis
Afu5g07030	holo TFIIH complex
Afu5g07030	transcription initiation from RNA polymerase II promoter
Afu5g07030	negative regulation of transcription from RNA polymerase II promoter, mitotic
Afu5g07030	general RNA polymerase II transcription factor activity
Afu5g07030	cyclin-dependent protein kinase regulator activity
Afu5g07040	ubiquitin conjugating enzyme activity
Afu5g07040	protein modification process
Afu5g07040	ubiquitin-dependent protein catabolic process
Afu5g07040	ubiquitin cycle
Afu5g07040	ligase activity
Afu5g07050	endopeptidase activity
Afu5g07050	proteasome regulatory particle
Afu5g07050	ubiquitin-dependent protein catabolic process
Afu5g07050	ATPase activity
Afu5g07070	integral to membrane
Afu5g07080	hydrolase activity, hydrolyzing O-glycosyl compounds
Afu5g07080	carbohydrate metabolic process
Afu5g07130	actin binding
Afu5g07130	ER-Golgi intermediate compartment
Afu5g07130	cytoskeleton
Afu5g07130	ER to Golgi vesicle-mediated transport
Afu5g07130	retrograde vesicle-mediated transport, Golgi to ER
Afu5g07130	ARF GTPase activator activity
Afu5g07130	actin filament reorganization during cell cycle

Afu5g07140	translation elongation factor activity
Afu5g07140	mitochondrion
Afu5g07140	translational elongation
Afu5g07150	molecular function unknown
Afu5g07150	endosome
Afu5g07150	retrograde transport, endosome to Golgi
Afu5g07170	THO complex
Afu5g07170	nucleic acid binding
Afu5g07170	DNA recombination
Afu5g07170	RNA elongation from RNA polymerase II promoter
Afu5g07170	mRNA export from nucleus
Afu5g07210	homoserine O-acetyltransferase activity
Afu5g07210	cytoplasm
Afu5g07210	methionine biosynthetic process
Afu5g07210	homoserine metabolic process
Afu5g07260	protein deneddylation
Afu5g07260	signalosome
Afu5g07260	regulation of developmental process
Afu5g07290	biological process unknown
Afu5g07290	molecular function unknown
Afu5g07290	cellular component unknown
Afu5g07300	biological process unknown
Afu5g07300	molecular function unknown
Afu5g07300	mitochondrion
Afu5g07310	biological process unknown
Afu5g07310	molecular function unknown
Afu5g07310	cellular component unknown
Afu5g07320	nucleus
Afu5g07320	protein amino acid ADP-ribosylation
Afu5g07320	programmed cell death
Afu5g07320	ascospore formation
Afu5g07330	carboxypeptidase C activity
Afu5g07340	chaperone activity
Afu5g07340	cytosolic small ribosomal subunit (sensu Eukaryota)
Afu5g07340	translational initiation
Afu5g07370	3'-5'-exoribonuclease activity
Afu5g07370	nuclear-transcribed mRNA poly(A) tail shortening
Afu5g07370	cytoplasm
Afu5g07370	regulation of transcription from RNA polymerase II promoter
Afu5g07370	CCR4-NOT core complex
Afu5g07390	ribosomal large subunit assembly
Afu5g07390	molecular function unknown
Afu5g07390	cytoplasm
Afu5g07390	cytosol
Afu5g07390	cytosolic ribosome (sensu Eukaryota)
Afu5g07410	catalytic activity
Afu5g07410	metabolic process
Afu5g07430	signal transducer activity
Afu5g07430	Rho guanyl-nucleotide exchange factor activity
Afu5g07430	intracellular

Afu5g07430	actin filament organization
Afu5g07430	cell wall organization
Afu5g07430	small GTPase mediated signal transduction
Afu5g07440	Rab GTPase activator activity
Afu5g07440	soluble fraction
Afu5g07440	protein catabolic process
Afu5g07470	peroxisomal matrix
Afu5g07470	sporulation (sensu Saccharomyces)
Afu5g07470	2,4-dienoyl-CoA reductase (NADPH) activity
Afu5g07470	fatty acid catabolic process
Afu5g07510	transcription factor activity
Afu5g07510	nucleus
Afu5g07510	ethanol catabolic process
Afu5g07510	zinc ion binding
Afu5g07510	regulation of transcription
Afu5g07520	metabolic process
Afu5g07520	oxidoreductase activity
Afu5g07570	pyruvate carboxylase activity
Afu5g07570	cytosol
Afu5g07570	gluconeogenesis
Afu5g07570	NADPH regeneration
Afu5g07600	inositol-polyphosphate 5-phosphatase activity
Afu5g07600	membrane fraction
Afu5g07600	actin cortical patch (sensu Saccharomyces)
Afu5g07600	endocytosis
Afu5g07600	cell wall organization
Afu5g07600	dephosphorylation
Afu5g07620	conjugation with cellular fusion
Afu5g07620	molecular function unknown
Afu5g07620	integral to membrane
Afu5g07630	metabolic process
Afu5g07630	methyltransferase activity
Afu5g07640	RNA-3'-phosphate cyclase activity
Afu5g07640	RNA processing
Afu5g07670	endocytosis
Afu5g07670	response to osmotic stress
Afu5g07670	bipolar cellular bud site selection
Afu5g07670	cytoskeletal protein binding
Afu5g07710	microtubule cytoskeleton organization
Afu5g07710	cellular bud tip
Afu5g07710	cell cortex
Afu5g07710	tubulin binding
Afu5g07720	spliceosomal complex
Afu5g07740	telomere maintenance
Afu5g07740	double-strand break repair via homologous recombination
Afu5g07740	nuclear chromatin
Afu5g07740	damaged DNA binding
Afu5g07740	ATP-dependent DNA helicase activity
Afu5g07740	nuclear envelope
Afu5g07740	nuclear telomeric heterochromatin

Afu5g07740	DNA-dependent protein kinase-DNA ligase 4 complex
Afu5g07740	double-strand break repair via nonhomologous end joining
Afu5g07740	chromatin assembly or disassembly
Afu5g07740	transcriptional gene silencing
Afu5g07750	ferrochelatase activity
Afu5g07750	mitochondrial inner membrane
Afu5g07750	heme biosynthetic process
Afu5g07760	biological process unknown
Afu5g07760	molecular function unknown
Afu5g07760	cellular component unknown
Afu5g07780	squalene monooxygenase activity
Afu5g07780	endoplasmic reticulum
Afu5g07780	lipid particle
Afu5g07780	ergosterol biosynthetic process
Afu5g07830	biological process unknown
Afu5g07830	molecular function unknown
Afu5g07830	nucleus
Afu5g07840	biological process unknown
Afu5g07840	molecular function unknown
Afu5g07840	cytoplasm
Afu5g07860	inositol-polyphosphate 5-phosphatase activity
Afu5g07860	membrane fraction
Afu5g07860	endocytosis
Afu5g07860	cell wall organization
Afu5g07860	dephosphorylation
Afu5g07880	response to pheromone during conjugation with cellular fusion
Afu5g07880	pheromone-dependent signal transduction involved in conjugation with cellular fusion
Afu5g07880	mating-type a-factor pheromone receptor activity
Afu5g07880	integral to plasma membrane
Afu5g07890	single-stranded DNA binding
Afu5g07890	DNA replication
Afu5g07890	DNA repair
Afu5g07890	DNA recombination
Afu5g07890	transcription
Afu5g07930	molecular function unknown
Afu5g07930	intracellular protein transport
Afu5g07930	AP-2 adaptor complex
Afu5g07950	protein serine/threonine kinase activity
Afu5g07950	nucleus
Afu5g07950	protein amino acid phosphorylation
Afu5g07960	biological process unknown
Afu5g07960	protein binding
Afu5g07960	cytoplasm
Afu5g07960	zinc ion binding
Afu5g07970	vacuolar membrane
Afu5g07970	cadmium ion transmembrane transporter activity
Afu5g07970	arsenite transmembrane transporter activity
Afu5g07970	bilirubin transmembrane transporter activity
Afu5g07970	cadmium ion transport
Afu5g07970	arsenite transport

Afu5g07970	bilirubin transport
Afu5g07970	response to mercury ion
Afu5g08000	protein binding
Afu5g08000	mRNA export from nucleus
Afu5g08000	protein export from nucleus
Afu5g08000	mitosis
Afu5g08000	actin filament-based process
Afu5g08000	RNA nuclear export complex
Afu5g08010	mitochondrion
Afu5g08010	protein modification process
Afu5g08010	protein N-terminal asparagine amidohydrolase activity
Afu5g08010	protein catabolic process
Afu5g08020	chromosome, centromeric region
Afu5g08020	DNA binding
Afu5g08020	nucleus
Afu5g08020	transcription
Afu5g08030	cellulase activity
Afu5g08040	incipient cellular bud site
Afu5g08040	exocyst
Afu5g08040	cytokinesis
Afu5g08040	protein binding
Afu5g08040	cellular bud tip
Afu5g08040	Golgi to plasma membrane transport
Afu5g08040	vesicle docking during exocytosis
Afu5g08040	vesicle fusion
Afu5g08040	bipolar cellular bud site selection
Afu5g08050	cytoplasm
Afu5g08050	proteolysis
Afu5g08050	metallopeptidase activity
Afu5g08060	nuclear pore
Afu5g08060	cytoplasm
Afu5g08060	protein import into nucleus
Afu5g08060	protein transmembrane transporter activity
Afu5g08060	response to drug
Afu5g08090	protein binding
Afu5g08090	cellular component unknown
Afu5g08090	pyridoxine metabolic process
Afu5g08090	thiamin biosynthetic process
Afu5g08110	DNA replication origin binding
Afu5g08110	nuclear origin of replication recognition complex
Afu5g08110	pre-replicative complex assembly
Afu5g08110	DNA replication initiation
Afu5g08110	chromatin silencing at HML and HMR (sensu Saccharomyces)
Afu5g08120	acetyl-CoA:L-glutamate N-acetyltransferase activity
Afu5g08120	glutamate N-acetyltransferase activity
Afu5g08120	mitochondrial matrix
Afu5g08120	arginine biosynthetic process
Afu5g08120	ornithine biosynthetic process
Afu5g08120	cell wall organization
Afu5g08130	Sec61 translocon complex

Afu5g08130	endoplasmic reticulum lumen
Afu5g08130	SRP-dependent cotranslational protein targeting to membrane, translocation
Afu5g08130	intracellular protein transport
Afu5g08130	protein transporter activity
Afu5g08130	integral to endoplasmic reticulum membrane
Afu5g08130	protein targeting to ER
Afu5g08150	fungal-type vacuole
Afu5g08150	ATP-binding cassette (ABC) transporter activity
Afu5g08150	bile acid transmembrane transporter activity
Afu5g08150	bile acid and bile salt transport
Afu5g08170	cytoplasm
Afu5g08170	protein targeting to vacuole
Afu5g08170	autophagy
Afu5g08210	dolichyl-phosphate beta-glucosyltransferase activity
Afu5g08210	endoplasmic reticulum membrane
Afu5g08210	protein amino acid N-linked glycosylation
Afu5g08235	metabolic process
Afu5g08235	hydrolase activity
Afu5g08240	biological process unknown
Afu5g08240	phosphoribosyl-ATP diphosphatase activity
Afu5g08240	nucleus
Afu5g08240	cytoplasm
Afu5g08270	metabolic process
Afu5g08270	hydrolase activity
Afu5g08280	cytoplasm
Afu5g08280	transferase activity, transferring pentosyl groups
Afu5g08280	charged-tRNA amino acid modification
Afu5g08290	prostaglandin biosynthetic process
Afu5g08290	aldo-keto reductase activity
Afu5g08290	cytoplasm
Afu5g08290	prostaglandin-F synthase activity
Afu5g08330	RNA binding
Afu5g08330	cytoplasm
Afu5g08330	regulation of cell size
Afu5g08350	structural constituent of ribosome
Afu5g08350	mitochondrial small ribosomal subunit
Afu5g08350	translation
Afu5g08360	biological process unknown
Afu5g08360	molecular function unknown
Afu5g08360	cytoplasm
Afu5g08370	molecular function unknown
Afu5g08370	nucleus
Afu5g08370	cytoplasm
Afu5g08370	double-strand break repair via nonhomologous end joining
Afu5g08370	ubiquitin-dependent protein catabolic process
Afu5g08390	two-component response regulator activity
Afu5g08390	cytoplasm
Afu5g08390	osmosensory signaling pathway via two-component system
Afu5g08390	enzyme activator activity
Afu5g08410	biological process unknown

Afu5g08410	molecular function unknown
Afu5g08410	integral to membrane
Afu5g08420	osmosensor activity
Afu5g08420	plasma membrane
Afu5g08420	mating projection
Afu5g08420	pseudohyphal growth
Afu5g08420	osmosensory signaling pathway via Sho1 osmosensor
Afu5g08470	biological process unknown
Afu5g08470	cytoplasm
Afu5g08470	peroxisomal membrane
Afu5g08470	peroxisomal matrix
Afu5g08470	AMP binding
Afu5g08480	protein kinase activity
Afu5g08480	cellular component unknown
Afu5g08530	cytoplasm
Afu5g08530	phosphoinositide binding
Afu5g08540	conjugation with cellular fusion
Afu5g08540	cell morphogenesis
Afu5g08540	cytokinesis
Afu5g08540	structural constituent of cytoskeleton
Afu5g08540	phosphatidylinositol binding
Afu5g08540	ascospore wall
Afu5g08540	prospore membrane
Afu5g08540	mating projection
Afu5g08540	cell wall organization
Afu5g08540	axial cellular bud site selection
Afu5g08550	signal transducer activity
Afu5g08550	Rho guanyl-nucleotide exchange factor activity
Afu5g08550	actin filament organization
Afu5g08550	cell wall organization
Afu5g08550	small GTPase mediated signal transduction
Afu5g08560	vacuolar proton-transporting V-type ATPase, V0 domain
Afu5g08560	vacuolar acidification
Afu5g08560	proton-transporting ATPase activity, rotational mechanism
Afu5g08570	protein serine/threonine kinase activity
Afu5g08570	cAMP-dependent protein kinase activity
Afu5g08580	alpha-1,6-mannosyltransferase activity
Afu5g08580	cell wall mannoprotein biosynthetic process
Afu5g08580	alpha-1,6-mannosyltransferase complex
Afu5g08580	substituted mannan metabolic process
Afu5g08580	N-glycan processing
Afu5g08600	homoserine O-acetyltransferase activity
Afu5g08600	cytoplasm
Afu5g08600	methionine biosynthetic process
Afu5g08600	homoserine metabolic process
Afu5g08610	biological process unknown
Afu5g08610	coenzyme binding
Afu5g08620	biological process unknown
Afu5g08620	fungal-type vacuole
Afu5g08620	phosphatase activity

Afu5g08630	biological process unknown
Afu5g08630	fungal-type vacuole
Afu5g08630	molecular function unknown
Afu5g08660	nucleus
Afu5g08660	DNA repair
Afu5g08670	vacuole inheritance
Afu5g08670	protein kinase activity
Afu5g08670	membrane fraction
Afu5g08670	protein amino acid phosphorylation
Afu5g08670	protein targeting to vacuole
Afu5g08670	vacuolar transport
Afu5g08670	1-phosphatidylinositol-3-kinase activity
Afu5g08680	GTPase activity
Afu5g08680	mitochondrial inner membrane
Afu5g08680	translation
Afu5g08680	ribosome assembly
Afu5g08690	nuclear mRNA splicing, via spliceosome
Afu5g08690	spliceosomal complex
Afu5g08690	pre-mRNA splicing factor activity
Afu5g08700	microfilament motor activity
Afu5g08700	cytokinesis
Afu5g08700	response to osmotic stress
Afu5g08700	contractile ring (sensu Fungi)
Afu5g08740	biological process unknown
Afu5g08740	fungal-type vacuole
Afu5g08740	molecular function unknown
Afu5g08780	cellular glucan metabolic process
Afu5g08780	cell wall organization
Afu5g08780	fungal-type cell wall
Afu5g08810	metabolic process
Afu5g08810	hydrolase activity
Afu5g08840	DNA binding
Afu5g08840	nucleus
Afu5g08840	transcription factor binding
Afu5g08840	zinc ion binding
Afu5g08840	positive regulation of transcription
Afu5g08890	homoaconitate hydratase activity
Afu5g08890	peroxisome
Afu5g08890	pathogenesis
Afu5g08890	lysine biosynthetic process via aminoadipic acid
Afu5g08910	cytoplasm
Afu5g08910	leucine catabolic process
Afu5g08930	leucine catabolic process
Afu5g08930	isovaleryl-CoA dehydrogenase activity
Afu5g08950	small monomeric GTPase activity
Afu5g08950	RAS small monomeric GTPase activity
Afu5g08950	signal transducer activity
Afu5g08950	plasma membrane
Afu5g08950	small GTPase mediated signal transduction
Afu5g08960	lipid particle

Afu5g08960	lipid metabolic process
Afu5g08960	lipase activity
Afu5g08970	dolichyl-diphosphooligosaccharide-protein glycotransferase activity
Afu5g08970	protein amino acid N-linked glycosylation
Afu5g08970	cell cycle
Afu5g08970	oligosaccharyltransferase complex
Afu5g09000	replication fork
Afu5g09000	DNA replication
Afu5g09000	DNA repair
Afu5g09000	sister chromatid cohesion
Afu5g09000	eta DNA polymerase activity
Afu5g09000	translesion synthesis
Afu5g09020	transmembrane receptor activity
Afu5g09020	membrane fraction
Afu5g09020	cell wall organization
Afu5g09020	Rho protein signal transduction
Afu5g09020	response to heat
Afu5g09020	actin cytoskeleton organization
Afu5g09080	SAGA complex
Afu5g09080	transcription cofactor activity
Afu5g09080	nucleus
Afu5g09080	chromatin modification
Afu5g09080	histone acetylation
Afu5g09090	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
Afu5g09090	nucleic acid binding
Afu5g09090	cytoplasm
Afu5g09090	polysome
Afu5g09090	mRNA catabolic process
Afu5g09090	regulation of translational termination
Afu5g09090	ATP-dependent helicase activity
Afu5g09090	ATPase activity
Afu5g09100	MAP kinase activity
Afu5g09100	cytoplasm
Afu5g09100	protein amino acid phosphorylation
Afu5g09100	hyperosmotic response
Afu5g09140	amidase activity
Afu5g09140	mitochondrion
Afu5g09140	aerobic respiration
Afu5g09150	peroxisomal matrix
Afu5g09150	sporulation (sensu Saccharomyces)
Afu5g09150	2,4-dienoyl-CoA reductase (NADPH) activity
Afu5g09150	fatty acid catabolic process
Afu5g09170	transcription factor activity
Afu5g09170	nucleus
Afu5g09170	regulation of transcription, DNA-dependent
Afu5g09170	zinc ion binding
Afu5g09190	fungal-type vacuole
Afu5g09190	ATP-binding cassette (ABC) transporter activity
Afu5g09190	bile acid transmembrane transporter activity
Afu5g09190	bile acid and bile salt transport

Afu5g09200	G1/S transition of mitotic cell cycle
Afu5g09200	G2/M transition of mitotic cell cycle
Afu5g09200	nuclear ubiquitin ligase complex
Afu5g09200	ubiquitin conjugating enzyme activity
Afu5g09200	ubiquitin-protein ligase activity
Afu5g09200	nucleus
Afu5g09200	cytoplasm
Afu5g09200	ubiquitin-dependent protein catabolic process
Afu5g09210	fungal-type vacuole
Afu5g09210	serine-type endopeptidase activity
Afu5g09210	autophagy
Afu5g09210	vacuolar protein catabolic process
Afu5g09210	cellular response to starvation
Afu5g09210	programmed cell death
Afu5g09210	sporulation resulting in formation of a cellular spore
Afu5g09220	molecular function unknown
Afu5g09220	cellular component unknown
Afu5g09220	response to pH
Afu5g09230	transaldolase activity
Afu5g09230	cytoplasm
Afu5g09230	pentose-phosphate shunt
Afu5g09240	copper, zinc superoxide dismutase activity
Afu5g09240	mitochondrial intermembrane space
Afu5g09240	cytosol
Afu5g09240	superoxide metabolic process
Afu5g09240	cellular copper ion homeostasis
Afu5g09240	cellular zinc ion homeostasis
Afu5g09250	transcription cofactor activity
Afu5g09250	pathogenesis
Afu5g09260	cytosol
Afu5g09260	Golgi to plasma membrane transport
Afu5g09260	phosphatidylinositol transporter activity
Afu5g09260	phospholipid transport
Afu5g09270	biological process unknown
Afu5g09270	molecular function unknown
Afu5g09270	endoplasmic reticulum
Afu5g09290	metabolic process
Afu5g09290	oxidoreductase activity
Afu5g09300	vacuole
Afu5g09300	amino acid transport
Afu5g09300	amino acid transmembrane transporter activity
Afu5g09320	plasma membrane
Afu5g09320	signal transduction
Afu5g09360	adaptation to pheromone during conjugation with cellular fusion
Afu5g09360	calcium-dependent protein serine/threonine phosphatase activity
Afu5g09360	cytoplasm
Afu5g09360	cellular ion homeostasis
Afu5g09400	metabolic process
Afu5g09400	oxidoreductase activity
Afu5g09430	RNA-directed RNA polymerase activity

Afu5g09430	cytoplasm
Afu5g09430	posttranscriptional gene silencing
Afu5g09460	transporter activity
Afu5g09460	transport
Afu5g09480	ATP-binding cassette (ABC) transporter activity
Afu5g09480	transport
Afu5g09480	membrane
Afu5g09490	structural constituent of ribosome
Afu5g09490	mitochondrial ribosome
Afu5g09490	translation
Afu5g09560	biological process unknown
Afu5g09560	molecular function unknown
Afu5g09560	cytoplasm
Afu5g09580	cell wall organization
Afu5g09580	pathogenesis
Afu5g09610	cysteine-tRNA ligase activity
Afu5g09610	cytoplasm
Afu5g09610	cysteinyl-tRNA aminoacylation
Afu5g09610	cysteine metabolic process
Afu5g09620	nucleus
Afu5g09620	tRNA methyltransferase activity
Afu5g09620	tRNA methylation
Afu5g09630	molecular function unknown
Afu5g09630	endoplasmic reticulum membrane
Afu5g09630	endoplasmic reticulum organization
Afu5g09650	small monomeric GTPase activity
Afu5g09650	nucleus
Afu5g09650	cytoplasm
Afu5g09650	phosphate transport
Afu5g09660	vesicle-mediated transport
Afu5g09660	AP-1 adaptor complex
Afu5g09660	clathrin binding
Afu5g09680	biological process unknown
Afu5g09680	molecular function unknown
Afu5g09680	cellular component unknown
Afu5g09710	cysteine-type endopeptidase activity
Afu5g09710	nucleus
Afu5g09710	cytoplasm
Afu5g09710	spindle
Afu5g09710	regulation of exit from mitosis
Afu5g09710	mitotic sister chromatid separation
Afu5g09720	amine oxidase (flavin-containing) activity
Afu5g09720	cytoplasm
Afu5g09720	polyamine catabolic process
Afu5g09720	amine oxidase activity
Afu5g09720	pantothenate biosynthetic process
Afu5g09740	transcription factor activity
Afu5g09740	nucleus
Afu5g09740	regulation of transcription
Afu5g09750	nucleoside transmembrane transporter activity

Afu5g09750	nucleoside transport
Afu5g09780	drug transporter activity
Afu5g09780	drug transport
Afu5g09780	integral to membrane
Afu5g09830	molecular function unknown
Afu5g09830	mitochondrion
Afu5g09830	cellular iron ion homeostasis
Afu5g09830	integral to membrane
Afu5g09840	xylulokinase activity
Afu5g09840	cytoplasm
Afu5g09840	xylulose catabolic process
Afu5g09850	tRNA binding
Afu5g09850	tRNA splicing, via endonucleolytic cleavage and ligation
Afu5g09850	tRNA export from nucleus
Afu5g09850	Ran GTPase binding
Afu5g09850	nuclear matrix
Afu5g09860	carboxylesterase activity
Afu5g09860	cytosol
Afu5g09860	formaldehyde catabolic process
Afu5g09900	biological process unknown
Afu5g09900	molecular function unknown
Afu5g09900	integral to membrane
Afu5g09910	molecular function unknown
Afu5g09910	nucleus
Afu5g09910	cytoplasm
Afu5g09910	negative regulation of fatty acid metabolic process
Afu5g09920	proteolysis
Afu5g09920	metallopeptidase activity
Afu5g09940	biological process unknown
Afu5g09940	molecular function unknown
Afu5g09940	cellular component unknown
Afu5g09980	acyl-CoA dehydrogenase activity
Afu5g09980	fatty acid catabolic process
Afu5g09980	phospholipid catabolic process
Afu5g09990	transcription factor activity
Afu5g09990	regulation of transcription
Afu5g10040	transcription factor activity
Afu5g10040	nucleus
Afu5g10040	regulation of transcription
Afu5g10050	metabolic process
Afu5g10050	oxidoreductase activity
Afu5g10060	cytochrome-b5 reductase activity
Afu5g10060	microsome
Afu5g10060	electron transport
Afu5g10120	cytoplasm
Afu5g10120	oxidoreductase activity
Afu5g10120	nonribosomal peptide biosynthetic process
Afu5g10120	amino acid activation for nonribosomal peptide biosynthetic process
Afu5g10120	amino acid adenylylation by nonribosomal peptide synthase
Afu5g10130	transcription factor activity

Afu5g10130	nucleus
Afu5g10130	transcription
Afu5g10140	transporter activity
Afu5g10140	transport
Afu5g10180	FAD binding
Afu5g10220	biological process unknown
Afu5g10220	nucleus
Afu5g10220	cytoplasm
Afu5g10220	alcohol dehydrogenase (NADP+) activity
Afu5g10290	fructose-bisphosphate aldolase activity
Afu5g10290	glycolysis
Afu5g10310	DNA binding
Afu5g10310	transcription factor activity
Afu5g10310	nucleus
Afu5g10310	zinc ion binding
Afu5g10310	regulation of transcription
Afu5g10340	transporter activity
Afu5g10340	transport
Afu5g10340	membrane
Afu5g10370	mitochondrial respiratory chain complex II
Afu5g10370	tricarboxylic acid cycle
Afu5g10370	mitochondrial electron transport, succinate to ubiquinone
Afu5g10370	succinate dehydrogenase (ubiquinone) activity
Afu5g10380	pectin metabolic process
Afu5g10380	pectin lyase activity
Afu5g10420	biological process unknown
Afu5g10420	molecular function unknown
Afu5g10420	endoplasmic reticulum
Afu5g10480	cytoplasm
Afu5g10480	protein modification process
Afu5g10480	Mo-molybdopterin cofactor biosynthetic process
Afu5g10480	Mo-molybdopterin cofactor sulfurase activity
Afu5g10480	URM1 activating enzyme activity
Afu5g10490	amidase activity
Afu5g10510	ATP-binding cassette (ABC) transporter activity
Afu5g10510	transport
Afu5g10530	polygalacturonase activity
Afu5g10530	extracellular region
Afu5g10530	pseudohyphal growth
Afu5g10530	pectin catabolic process
Afu5g10540	1,4-alpha-glucan branching enzyme activity
Afu5g10540	cytoplasm
Afu5g10540	glycogen metabolic process
Afu5g10550	age-dependent general metabolic decline during replicative cell aging
Afu5g10550	soluble fraction
Afu5g10550	mitochondrial proton-transporting ATP synthase, catalytic core
Afu5g10550	ATP synthesis coupled proton transport
Afu5g10550	hydrogen ion transporting ATP synthase activity, rotational mechanism
Afu5g10560	cytochrome-c oxidase activity
Afu5g10560	mitochondrial respiratory chain complex IV

Afu5g10560	aerobic respiration
Afu5g10570	actin filament severing activity
Afu5g10570	actin cortical patch (sensu Saccharomyces)
Afu5g10570	actin filament organization
Afu5g10570	actin filament depolymerization
Afu5g10590	molecular function unknown
Afu5g10590	cytoplasm
Afu5g10590	response to stress
Afu5g10590	integral to membrane
Afu5g10600	molecular function unknown
Afu5g10600	mitochondrial inner membrane
Afu5g10600	mitochondrion organization
Afu5g10600	inner mitochondrial membrane organization
Afu5g10610	mitochondrial respiratory chain complex III
Afu5g10610	mitochondrial electron transport, ubiquinol to cytochrome c
Afu5g10610	ubiquinol-cytochrome-c reductase activity
Afu5g10610	aerobic respiration
Afu5g10630	voltage-gated chloride channel activity
Afu5g10630	Golgi-associated vesicle
Afu5g10630	cellular cation homeostasis
Afu5g10640	tyrosine-tRNA ligase activity
Afu5g10640	nucleus
Afu5g10640	cytoplasm
Afu5g10640	tRNA aminoacylation for protein translation
Afu5g10640	tyrosyl-tRNA aminoacylation
Afu5g10650	pyridoxamine-phosphate oxidase activity
Afu5g10650	fatty acid metabolic process
Afu5g10650	cellular component unknown
Afu5g10670	lipid metabolic process
Afu5g10680	phosphomevalonate kinase activity
Afu5g10680	cytosol
Afu5g10680	ergosterol biosynthetic process
Afu5g10680	isoprenoid biosynthetic process
Afu5g10690	transporter activity
Afu5g10690	transport
Afu5g10690	membrane
Afu5g10740	chaperone activity
Afu5g10740	proteasome core complex
Afu5g10740	proteasome activator activity
Afu5g10740	protein catabolic process
Afu5g10750	organellar small ribosomal subunit
Afu5g10750	structural constituent of ribosome
Afu5g10750	translation
Afu5g10760	alpha-1,2-mannosyltransferase activity
Afu5g10760	cell wall mannoprotein biosynthetic process
Afu5g10760	Golgi apparatus
Afu5g10760	N-glycan processing
Afu5g10760	protein amino acid O-linked glycosylation
Afu5g10770	cytoplasmic mRNA processing body
Afu5g10770	cytosolic small ribosomal subunit (sensu Eukaryota)

Afu5g10770	regulation of translational initiation
Afu5g10770	chromosome segregation
Afu5g10780	molecular function unknown
Afu5g10780	galactose metabolic process
Afu5g10780	cellular component unknown
Afu5g10790	endoplasmic reticulum
Afu5g10790	metabolic process
Afu5g10790	oxidoreductase activity, acting on CH or CH2 groups, NAD or NADP as acceptor
Afu5g10800	RNA binding
Afu5g10810	actin cap (sensu Saccharomyces)
Afu5g10810	SNARE binding
Afu5g10810	exocytosis
Afu5g10810	vesicle docking during exocytosis
Afu5g10810	vesicle fusion
Afu5g10820	ATP-dependent RNA helicase activity
Afu5g10820	mitochondrion
Afu5g10820	mitochondrial matrix
Afu5g10820	RNA catabolic process
Afu5g10830	U2-dependent spliceosome disassembly
Afu5g10830	ATP-dependent RNA helicase activity
Afu5g10830	spliceosomal complex
Afu5g10830	pre-mRNA splicing factor activity
Afu5g10840	molecular function unknown
Afu5g10840	nucleolus
Afu5g10840	rRNA processing
Afu5g10880	nucleotide-excision repair, DNA damage recognition
Afu5g10880	nucleus
Afu5g10880	chromatin remodeling
Afu5g10880	DNA-dependent ATPase activity
Afu5g10890	chromatin binding
Afu5g10890	ATP-dependent DNA helicase activity
Afu5g10890	nucleus
Afu5g10890	pre-replicative complex
Afu5g10890	cytoplasm
Afu5g10890	DNA unwinding during replication
Afu5g10890	DNA replication initiation
Afu5g10920	biological process unknown
Afu5g10920	fungal-type vacuole
Afu5g10920	molecular function unknown
Afu5g11000	nuclear mRNA splicing, via spliceosome
Afu5g11000	U2 snRNP
Afu5g11000	cytoplasm
Afu5g11000	pre-mRNA splicing factor activity
Afu5g11010	Golgi apparatus
Afu5g11010	protein amino acid glycosylation
Afu5g11010	nucleoside-diphosphatase activity
Afu5g11020	plasma membrane
Afu5g11020	ammonium transmembrane transporter activity
Afu5g11020	ammonium transport
Afu5g11030	metabolic process

Afu5g11030	acyltransferase activity
Afu5g11040	pantoate-beta-alanine ligase activity
Afu5g11040	nucleus
Afu5g11040	cytoplasm
Afu5g11040	pantothenate biosynthetic process
Afu5g11050	ribosomal large subunit assembly
Afu5g11050	ATP-dependent RNA helicase activity
Afu5g11050	nucleolus
Afu5g11050	35S primary transcript processing
Afu5g11070	transcription factor activity
Afu5g11070	nucleus
Afu5g11070	arginine catabolic process
Afu5g11070	regulation of transcription
Afu5g11080	transporter activity
Afu5g11080	integral to plasma membrane
Afu5g11080	transport
Afu5g11100	biological process unknown
Afu5g11100	molecular function unknown
Afu5g11100	nucleus
Afu5g11100	cytoplasm
Afu5g11110	biological process unknown
Afu5g11110	molecular function unknown
Afu5g11110	cellular component unknown
Afu5g11120	DNA-directed RNA polymerase activity
Afu5g11120	DNA-directed RNA polymerase II, core complex
Afu5g11120	DNA-directed RNA polymerase III complex
Afu5g11120	DNA-directed RNA polymerase I complex
Afu5g11120	transcription from RNA polymerase I promoter
Afu5g11120	transcription from RNA polymerase II promoter
Afu5g11120	transcription from RNA polymerase III promoter
Afu5g11130	cytoplasm
Afu5g11130	regulation of transcription from RNA polymerase II promoter
Afu5g11130	transcription elongation factor complex
Afu5g11130	RNA polymerase II transcription elongation factor activity
Afu5g11140	tRNA-intron endonuclease activity
Afu5g11140	tRNA-intron endonuclease complex
Afu5g11140	nuclear inner membrane
Afu5g11140	tRNA splicing, via endonucleolytic cleavage and ligation
Afu5g11150	ribonuclease MRP activity
Afu5g11150	ribonuclease MRP complex
Afu5g11150	ribonuclease P activity
Afu5g11150	nucleolar ribonuclease P complex
Afu5g11150	rRNA processing
Afu5g11150	tRNA processing
Afu5g11160	metabolic process
Afu5g11160	oxidoreductase activity
Afu5g11170	nucleoplasm
Afu5g11170	nucleosome remodeling complex
Afu5g11170	DNA replication-dependent nucleosome assembly
Afu5g11170	chromatin remodeling

Afu5g11170	ISW2 complex
Afu5g11170	NURF complex
Afu5g11170	ATPase activity
Afu5g11170	regulation of transcription
Afu5g11210	catalytic activity
Afu5g11210	nucleus
Afu5g11210	cytoplasm
Afu5g11210	Mo-molybdopterin cofactor biosynthetic process
Afu5g11230	replicative cell aging
Afu5g11230	RAS small monomeric GTPase activity
Afu5g11230	plasma membrane
Afu5g11230	activation of adenylate cyclase activity
Afu5g11230	Ras protein signal transduction
Afu5g11240	nucleus
Afu5g11240	cytoplasm
Afu5g11240	L-serine metabolic process
Afu5g11240	oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acc
Afu5g11260	negative regulation of transcription from RNA polymerase II promoter
Afu5g11260	specific RNA polymerase II transcription factor activity
Afu5g11260	nucleus
Afu5g11260	zinc ion binding
Afu5g11260	siderophore-iron transport
Afu5g11260	siderophore biosynthetic process
Afu5g11270	biological process unknown
Afu5g11270	molecular function unknown
Afu5g11270	COPI-coated vesicle
Afu5g11300	cysteine-type peptidase activity
Afu5g11300	protein catabolic process
Afu5g11320	vacuole inheritance
Afu5g11320	fungal-type vacuole
Afu5g11320	cytosol
Afu5g11320	DNA-dependent DNA replication
Afu5g11320	response to oxidative stress
Afu5g11320	regulation of cell redox homeostasis
Afu5g11320	thiol-disulfide exchange intermediate activity
Afu5g11320	vacuole fusion, non-autophagic
Afu5g11340	translation initiation factor activity
Afu5g11340	eukaryotic translation initiation factor 2B complex
Afu5g11340	translational initiation
Afu5g11360	transporter activity
Afu5g11360	coatomer
Afu5g11360	secretory vesicle membrane
Afu5g11360	post-Golgi vesicle-mediated transport
Afu5g11360	AP-3 adaptor complex
Afu5g11370	protein phosphatase type 2A activity
Afu5g11370	nucleus
Afu5g11370	cytoplasm
Afu5g11370	glycogen metabolic process
Afu5g11370	protein amino acid dephosphorylation
Afu5g11380	signal transducer activity

Afu5g11380	Rho GDP-dissociation inhibitor activity
Afu5g11380	cytosol
Afu5g11380	actin filament organization
Afu5g11380	small GTPase mediated signal transduction
Afu5g11400	mRNA cleavage factor complex
Afu5g11400	mRNA polyadenylation
Afu5g11400	mRNA cleavage
Afu5g11400	cleavage and polyadenylylation specificity factor activity
Afu5g11410	polysaccharide metabolic process
Afu5g11410	deacetylase activity
Afu5g11430	nucleus
Afu5g11430	cytoplasm
Afu5g11430	metabolic process
Afu5g11430	zinc ion binding
Afu5g11430	oxidoreductase activity
Afu5g11450	inositol or phosphatidylinositol kinase activity
Afu5g11450	nucleus
Afu5g11450	arginine metabolic process
Afu5g11450	phosphorylation
Afu5g11460	regulation of transcription involved in G1 phase of mitotic cell cycle
Afu5g11460	SAGA complex
Afu5g11460	transcription factor TFIID complex
Afu5g11460	chromatin organization
Afu5g11460	transcription initiation from RNA polymerase II promoter
Afu5g11460	protein amino acid acetylation
Afu5g11460	general RNA polymerase II transcription factor activity
Afu5g11460	chromatin modification
Afu5g11460	histone acetylation
Afu5g11470	nuclear chromosome
Afu5g11470	nuclear chromosome, telomeric region
Afu5g11470	DNA binding
Afu5g11470	transcription factor activity
Afu5g11470	nucleus
Afu5g11470	loss of chromatin silencing
Afu5g11520	protein kinase activity
Afu5g11520	cytoplasm
Afu5g11540	structural constituent of ribosome
Afu5g11540	mitochondrial ribosome
Afu5g11540	mitochondrial small ribosomal subunit
Afu5g11540	translation
Afu5g11550	tRNA modification
Afu5g11550	tRNA methyltransferase activity
Afu5g11550	cellular component unknown
Afu5g11560	actin binding
Afu5g11560	structural constituent of cytoskeleton
Afu5g11560	Arp2/3 protein complex
Afu5g11560	actin filament organization
Afu5g11580	holo TFIIH complex
Afu5g11580	transcription initiation from RNA polymerase II promoter
Afu5g11580	negative regulation of transcription from RNA polymerase II promoter, mitotic

Afu5g11580	general RNA polymerase II transcription factor activity
Afu5g11590	cytoplasm
Afu5g11590	glycerophosphodiester phosphodiesterase activity
Afu5g11590	phospholipid catabolic process
Afu5g11600	protein binding
Afu5g11600	cytoplasm
Afu5g11600	intracellular mRNA localization
Afu5g11600	actin cytoskeleton organization
Afu5g11610	regulation of progression through cell cycle
Afu5g11610	G2/M transition of mitotic cell cycle
Afu5g11610	cellular bud neck
Afu5g11610	protein-arginine N-methyltransferase activity
Afu5g11620	U2-dependent spliceosome disassembly
Afu5g11620	ATP-dependent RNA helicase activity
Afu5g11620	spliceosomal complex
Afu5g11620	pre-mRNA splicing factor activity
Afu5g11640	molecular function unknown
Afu5g11640	cytoplasm
Afu5g11640	protein secretion
Afu5g11650	biological process unknown
Afu5g11650	cytoplasm
Afu5g11650	S-adenosylmethionine-dependent methyltransferase activity
Afu5g11660	molecular function unknown
Afu5g11660	cytosol
Afu5g11660	protein targeting to vacuole
Afu5g11660	vacuolar protein processing
Afu5g11660	autophagy
Afu5g11670	biological process unknown
Afu5g11670	C-terminal protein carboxyl methyltransferase activity
Afu5g11670	cytoplasm
Afu5g11690	vitamin B12 reduction
Afu5g11690	regulation of S phase of mitotic cell cycle
Afu5g11690	protein tyrosine/threonine phosphatase activity
Afu5g11690	cellular component unknown
Afu5g11700	DNA binding
Afu5g11700	ATP binding
Afu5g11700	nucleus
Afu5g11700	reciprocal meiotic recombination
Afu5g11700	ATPase activity
Afu5g11720	endopeptidase activity
Afu5g11720	receptor activity
Afu5g11720	cytoplasm
Afu5g11720	endoplasmic reticulum
Afu5g11720	proteasome regulatory particle
Afu5g11720	ubiquitin-dependent protein catabolic process
Afu5g11730	protein kinase activity
Afu5g11730	nucleocytoplasmic transporter activity
Afu5g11730	nucleus
Afu5g11730	cytosol
Afu5g11730	maturation of SSU-rRNA

Afu5g11740	structural constituent of ribosome
Afu5g11740	mitochondrial large ribosomal subunit
Afu5g11740	translation
Afu5g11750	ATP-dependent peptidase activity
Afu5g11750	mitochondrial matrix
Afu5g11750	proteolysis
Afu5g11750	response to heat
Afu5g11760	hydroxymethylbilane synthase activity
Afu5g11760	nucleus
Afu5g11760	cytoplasm
Afu5g11760	heme biosynthetic process
Afu5g11780	protein binding
Afu5g11780	signal transduction
Afu5g11780	cell growth and/or maintenance
Afu5g11780	cellular component unknown
Afu5g11790	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process
Afu5g11790	ATP-dependent helicase activity
Afu5g11810	mitotic spindle elongation
Afu5g11810	nuclear migration (sensu Saccharomyces)
Afu5g11810	mitotic sister chromatid segregation
Afu5g11810	establishment of mitotic spindle orientation
Afu5g11810	motor activity
Afu5g11810	spindle pole body
Afu5g11810	cytoplasmic microtubule
Afu5g11820	nucleus
Afu5g11820	cytoplasm
Afu5g11830	structural constituent of ribosome
Afu5g11830	mitochondrial large ribosomal subunit
Afu5g11830	translation
Afu5g11840	protein kinase activity
Afu5g11840	cytoplasm
Afu5g11840	cellular ion homeostasis
Afu5g11850	S-adenosylmethionine transmembrane transporter activity
Afu5g11850	mitochondrion
Afu5g11850	mitochondrial inner membrane
Afu5g11850	S-adenosylmethionine transport
Afu5g11860	biological process unknown
Afu5g11860	molecular function unknown
Afu5g11860	nucleus
Afu5g11860	cytoplasm
Afu5g11870	biological process unknown
Afu5g11870	molecular function unknown
Afu5g11870	cytoplasm
Afu5g11890	Rho guanyl-nucleotide exchange factor activity
Afu5g11890	small GTPase mediated signal transduction
Afu5g11900	ARF guanyl-nucleotide exchange factor activity
Afu5g11900	Golgi-associated vesicle
Afu5g11900	ER to Golgi vesicle-mediated transport
Afu5g11900	intra-Golgi vesicle-mediated transport
Afu5g11910	nuclear mRNA splicing, via spliceosome

Afu5g11910	spliceosomal complex
Afu5g11910	cell cycle
Afu5g11920	vacuolar proton-transporting V-type ATPase, V1 domain
Afu5g11920	fungal-type vacuole membrane
Afu5g11920	vacuolar acidification
Afu5g11920	proton-transporting ATPase activity, rotational mechanism
Afu5g11950	ubiquitin-specific protease activity
Afu5g11950	cytoplasm
Afu5g11950	protein deubiquitination
Afu5g11970	protein kinase C activity
Afu5g11970	protein amino acid phosphorylation
Afu5g11970	actin filament organization
Afu5g11970	cell wall organization
Afu5g11970	signal transduction
Afu5g11970	protein kinase cascade
Afu5g11980	transporter activity
Afu5g11980	transport
Afu5g11980	clathrin-coated vesicle
Afu5g11980	COPI-coated vesicle
Afu5g11990	alpha-1,3-mannosyltransferase activity
Afu5g11990	endoplasmic reticulum
Afu5g11990	protein amino acid glycosylation
Afu5g11990	dolichol-linked oligosaccharide biosynthetic process
Afu5g12010	protein phosphatase type 2A activity
Afu5g12010	nucleus
Afu5g12010	cytoplasm
Afu5g12010	protein amino acid dephosphorylation
Afu5g12010	nitrogen compound metabolic process
Afu5g12020	transcription factor activity
Afu5g12020	nucleus
Afu5g12020	regulation of transcription, DNA-dependent
Afu5g12020	cellular amino acid catabolic process
Afu5g12050	DNA ligase (ATP) activity
Afu5g12050	nucleus
Afu5g12050	double-strand break repair via nonhomologous end joining
Afu5g12060	transcription factor activity
Afu5g12060	nucleus
Afu5g12060	regulation of transcription, DNA-dependent
Afu5g12060	zinc ion binding
Afu5g12070	biological process unknown
Afu5g12070	molecular function unknown
Afu5g12070	cellular component unknown
Afu5g12090	biological process unknown
Afu5g12090	molecular function unknown
Afu5g12090	cellular component unknown
Afu5g12100	nucleus
Afu5g12100	nucleolus
Afu5g12100	rRNA processing
Afu5g12100	RNA methyltransferase activity
Afu5g12130	vacuole inheritance

Afu5g12130	RAB small monomeric GTPase activity
Afu5g12130	vacuole
Afu5g12130	Golgi to vacuole transport
Afu5g12130	vesicle-mediated transport
Afu5g12140	biological process unknown
Afu5g12140	fungal-type vacuole membrane
Afu5g12140	molecular function unknown
Afu5g12160	alpha-1,2-mannosyltransferase activity
Afu5g12160	Golgi apparatus
Afu5g12160	protein amino acid N-linked glycosylation
Afu5g12160	cell wall organization
Afu5g12180	G1/S transition of mitotic cell cycle
Afu5g12180	nucleus
Afu5g12180	cytoplasm
Afu5g12180	RNA export from nucleus
Afu5g12180	ubiquitin-dependent protein catabolic process
Afu5g12180	protein import into nucleus
Afu5g12180	Ran GTPase binding
Afu5g12190	regulation of transcription involved in G1 phase of mitotic cell cycle
Afu5g12190	cell morphogenesis
Afu5g12190	transcription factor TFIID complex
Afu5g12190	transcription factor TFIIF complex
Afu5g12190	nucleosome remodeling complex
Afu5g12190	chromatin remodeling
Afu5g12190	transcription initiation from RNA polymerase II promoter
Afu5g12190	general RNA polymerase II transcription factor activity
Afu5g12190	SWI/SNF complex
Afu5g12190	chromatin remodeling complex
Afu5g12210	response to pheromone during conjugation with cellular fusion
Afu5g12210	pheromone-dependent signal transduction involved in conjugation with cellular fusion
Afu5g12210	heterotrimeric G-protein GTPase activity
Afu5g12210	heterotrimeric G-protein complex
Afu5g12210	plasma membrane
Afu5g12210	response to stress
Afu5g12210	regulation of sporulation resulting in formation of a cellular spore
Afu5g12230	nucleus
Afu5g12230	regulation of transcription, DNA-dependent
Afu5g12230	zinc ion binding
Afu5g12230	anatomical structure morphogenesis
Afu5g12230	chromatin modification
Afu5g12242	metabolic process
Afu5g12242	oxidoreductase activity
Afu5g12250	cytoplasm
Afu5g12250	viral reproduction
Afu5g12260	protein disulfide isomerase activity
Afu5g12260	endoplasmic reticulum lumen
Afu5g12260	protein folding
Afu5g12270	molecular function unknown
Afu5g12270	nucleolus
Afu5g12270	rRNA processing

Afu5g12310	pseudouridylate synthase activity
Afu5g12310	nucleus
Afu5g12310	mitochondrion
Afu5g12310	tRNA modification
Afu5g12320	signal transducer activity
Afu5g12320	plasma membrane
Afu5g12320	cell-cell adhesion
Afu5g12320	filamentous growth
Afu5g12330	biological process unknown
Afu5g12330	molecular function unknown
Afu5g12330	cellular component unknown
Afu5g12350	ribonucleoside-diphosphate reductase activity
Afu5g12350	nucleus
Afu5g12350	cytoplasm
Afu5g12350	DNA replication
Afu5g12360	oxaloacetate secondary active transmembrane transporter activity
Afu5g12360	mitochondrial inner membrane
Afu5g12360	secondary active sulfate transmembrane transporter activity
Afu5g12360	sulfate transport
Afu5g12360	oxaloacetate transport
Afu5g12370	mRNA cleavage and polyadenylation specificity factor complex
Afu5g12370	histone methylation
Afu5g12370	histone-lysine N-methyltransferase activity
Afu5g12370	termination of RNA polymerase II transcription, poly(A)-coupled
Afu5g12370	termination of RNA polymerase II transcription, poly(A)-independent
Afu5g12390	biological process unknown
Afu5g12390	molecular function unknown
Afu5g12390	cellular component unknown
Afu5g12400	biological process unknown
Afu5g12400	molecular function unknown
Afu5g12400	cytoplasm
Afu5g12420	deadenylation-dependent decapping of nuclear-transcribed mRNA
Afu5g12420	cytoplasmic mRNA processing body
Afu5g12420	mRNA binding
Afu5g12420	nucleus
Afu5g12420	cytoplasm
Afu5g12420	mRNA catabolic process
Afu5g12420	enzyme activator activity
Afu5g12420	hydrolase activity
Afu5g12430	aminomethyltransferase activity
Afu5g12430	mitochondrion
Afu5g12510	cytoplasm
Afu5g12510	AMP binding
Afu5g12530	biological process unknown
Afu5g12530	molecular function unknown
Afu5g12530	cytoplasm
Afu5g12530	clathrin-coated vesicle
Afu5g12550	N-acetylglucosaminylphosphatidylinositol deacetylase activity
Afu5g12550	endoplasmic reticulum membrane
Afu5g12550	GPI anchor biosynthetic process

Afu5g12580	translation elongation factor activity
Afu5g12580	ribosome
Afu5g12580	translational elongation
Afu5g12600	nuclear chromatin
Afu5g12600	DNA repair
Afu5g12600	ATPase activity
Afu5g12640	gamma DNA-directed DNA polymerase activity
Afu5g12640	mitochondrion
Afu5g12640	DNA-dependent DNA replication
Afu5g12650	biological process unknown
Afu5g12650	molecular function unknown
Afu5g12650	cellular component unknown
Afu5g12660	inositol or phosphatidylinositol kinase activity
Afu5g12660	nucleus
Afu5g12660	response to DNA damage stimulus
Afu5g12660	telomere maintenance via telomerase
Afu5g12670	nuclear pore
Afu5g12670	nuclear pore organization
Afu5g12670	structural constituent of nuclear pore
Afu5g12680	ubiquitin ligase complex
Afu5g12680	ubiquitin-protein ligase activity
Afu5g12680	protein binding
Afu5g12680	ubiquitin-dependent protein catabolic process
Afu5g12680	SCF ubiquitin ligase complex
Afu5g12690	glycerone kinase activity
Afu5g12690	cytoplasm
Afu5g12690	response to stress
Afu5g12690	glycerol catabolic process
Afu5g12720	ATP-binding cassette (ABC) transporter activity
Afu5g12720	transport
Afu5g12730	catalytic activity
Afu5g12730	nonribosomal peptide biosynthetic process
Afu5g12730	amino acid adenylylation by nonribosomal peptide synthase
Afu5g12740	transporter activity
Afu5g12740	transport
Afu5g12790	3-hydroxyisobutyryl-CoA hydrolase activity
Afu5g12790	mitochondrion
Afu5g12790	fatty acid beta-oxidation
Afu5g12790	endocytosis
Afu5g12800	ribosomal large subunit assembly
Afu5g12800	structural constituent of ribosome
Afu5g12800	mitochondrial large ribosomal subunit
Afu5g12800	translation
Afu5g12810	structural constituent of ribosome
Afu5g12810	mitochondrial large ribosomal subunit
Afu5g12810	translation
Afu5g12820	mitochondrial protein processing during import
Afu5g12820	peptidase activity
Afu5g12820	protein secretion
Afu5g12820	mitochondrial inner membrane peptidase complex

Afu5g12840	hydroxyacylglutathione hydrolase activity
Afu5g12840	cytoplasm
Afu5g12840	carbohydrate metabolic process
Afu5g12850	establishment of cell polarity (sensu Saccharomyces)
Afu5g12850	nucleus
Afu5g12850	budding cell bud growth
Afu5g12870	NAD+ kinase activity
Afu5g12870	nucleus
Afu5g12870	cytoplasm
Afu5g12870	cellular iron ion homeostasis
Afu5g12870	NAD phosphorylation and dephosphorylation
Afu5g12880	molecular function unknown
Afu5g12880	ER to Golgi vesicle-mediated transport
Afu5g12880	TRAPP complex
Afu5g12900	chromosome, centromeric region
Afu5g12900	regulation of chromatin assembly or disassembly
Afu5g12900	transcription factor activity
Afu5g12900	nucleus
Afu5g12900	transcription
Afu5g12900	zinc ion binding
Afu5g12900	centromeric DNA binding
Afu5g12910	nuclear mRNA splicing, via spliceosome
Afu5g12910	pre-mRNA splicing factor activity
Afu5g12910	small nuclear ribonucleoprotein complex
Afu5g12950	fructose transmembrane transporter activity
Afu5g12950	glucose transmembrane transporter activity
Afu5g12950	plasma membrane
Afu5g12950	hexose transport
Afu5g12950	mannose transmembrane transporter activity
Afu5g12960	transcription factor activity
Afu5g12960	nucleus
Afu5g12960	transcription
Afu5g12960	response to stress
Afu5g12990	nucleus
Afu5g12990	cytoplasm
Afu5g12990	plasma membrane
Afu5g12990	regulation of transcription from RNA polymerase II promoter
Afu5g12990	peroxisome organization
Afu5g12990	protein kinase activator activity
Afu5g13000	cytoplasm
Afu5g13000	microsome
Afu5g13000	lipid particle
Afu5g13000	phosphatidylinositol transporter activity
Afu5g13000	phospholipid transport
Afu5g13000	sterol biosynthetic process
Afu5g13000	response to drug
Afu5g13020	alpha DNA polymerase activity
Afu5g13020	alpha DNA polymerase:primase complex
Afu5g13020	DNA replication, synthesis of RNA primer
Afu5g13020	DNA replication initiation

Afu5g13020	lagging strand elongation
Afu5g13040	translation initiation factor activity
Afu5g13040	ribosome
Afu5g13040	eukaryotic translation initiation factor 2B complex
Afu5g13040	translational initiation
Afu5g13050	establishment of mitotic spindle orientation
Afu5g13050	microtubule motor activity
Afu5g13050	kinesin complex
Afu5g13050	nuclear microtubule
Afu5g13050	cytoplasmic microtubule
Afu5g13050	microtubule depolymerization
Afu5g13060	integral to membrane
Afu5g13090	alpha-1,2-mannosyltransferase activity
Afu5g13090	Golgi apparatus
Afu5g13090	protein amino acid glycosylation
Afu5g13120	biological process unknown
Afu5g13120	molecular function unknown
Afu5g13120	nucleus
Afu5g13120	cytoplasm
Afu5g13130	chorismate mutase activity
Afu5g13130	nucleus
Afu5g13130	cytoplasm
Afu5g13130	aromatic amino acid family biosynthetic process
Afu5g13140	mitochondrial genome maintenance
Afu5g13140	mitochondrial fission
Afu5g13140	molecular function unknown
Afu5g13140	mitochondrial outer membrane
Afu5g13160	transporter activity
Afu5g13160	plasma membrane
Afu5g13160	transport
Afu5g13170	biological process unknown
Afu5g13170	molecular function unknown
Afu5g13170	cellular component unknown
Afu5g13190	establishment of mitotic spindle orientation
Afu5g13190	microtubule motor activity
Afu5g13190	kinesin complex
Afu5g13190	nuclear microtubule
Afu5g13190	cytoplasmic microtubule
Afu5g13190	microtubule depolymerization
Afu5g13190	mitotic spindle organization in nucleus
Afu5g13190	nuclear migration along microtubule
Afu5g13210	alpha-1,2-mannosyltransferase activity
Afu5g13210	endoplasmic reticulum
Afu5g13210	oligosaccharide-lipid intermediate assembly
Afu5g13230	transporter activity
Afu5g13230	transport
Afu5g13230	monocarboxylic acid transmembrane transporter activity
Afu5g13230	membrane
Afu5g13240	inositol or phosphatidylinositol kinase activity
Afu5g13240	cytoplasm

Afu5g13240	response to stress
Afu5g13240	vacuole organization
Afu5g13290	integral to plasma membrane
Afu5g13290	nicotinamide mononucleotide permease activity
Afu5g13290	nicotinamide mononucleotide transport
Afu5g13300	aspartic-type endopeptidase activity
Afu5g13300	extracellular region
Afu5g13300	pathogenesis
Afu5g13300	protein catabolic process
Afu5g13310	specific RNA polymerase II transcription factor activity
Afu5g13310	nucleus
Afu5g13310	positive regulation of transcription from RNA polymerase II promoter
Afu5g13320	programmed cell death
Afu5g13340	mitochondrion inheritance
Afu5g13340	nucleus
Afu5g13340	cytoplasm
Afu5g13340	tRNA splicing, via endonucleolytic cleavage and ligation
Afu5g13340	protein amino acid dephosphorylation
Afu5g13340	response to osmotic stress
Afu5g13340	protein phosphatase type 2C activity
Afu5g13350	peptidyl-prolyl cis-trans isomerase activity
Afu5g13350	mitochondrion
Afu5g13350	protein folding
Afu5g13360	biological process unknown
Afu5g13360	molecular function unknown
Afu5g13360	cytoplasm
Afu5g13370	telomere maintenance
Afu5g13370	DNA helicase activity
Afu5g13370	nucleus
Afu5g13370	mitochondrion
Afu5g13370	DNA recombination
Afu5g13370	chromosome organization and biogenesis (sensu Eukaryota)
Afu5g13392	GTPase activity
Afu5g13392	mitochondrial outer membrane
Afu5g13392	mitochondrion organization
Afu5g13392	mitochondrial fusion
Afu5g13410	protein binding
Afu5g13410	cytoplasm
Afu5g13410	endosome
Afu5g13410	protein retention in Golgi apparatus
Afu5g13410	late endosome to vacuole transport
Afu5g13420	protein kinase activity
Afu5g13450	triose-phosphate isomerase activity
Afu5g13450	cytoplasm
Afu5g13450	cytosol
Afu5g13450	gluconeogenesis
Afu5g13450	glycolysis
Afu5g13460	mitochondrion inheritance
Afu5g13460	mitochondrial genome maintenance
Afu5g13460	molecular function unknown

Afu5g13460	mitochondrial outer membrane
Afu5g13460	mitochondrion organization
Afu5g13470	molecular function unknown
Afu5g13470	nucleus
Afu5g13470	nucleolus
Afu5g13470	rRNA processing
Afu5g13470	ribosomal large subunit biogenesis
Afu5g13480	commitment complex
Afu5g13480	nuclear mRNA splicing, via spliceosome
Afu5g13480	mRNA binding
Afu5g13480	U1 snRNP
Afu5g13490	structural constituent of ribosome
Afu5g13490	mitochondrial large ribosomal subunit
Afu5g13490	translation
Afu5g13490	aerobic respiration
Afu5g13500	zinc ion binding
Afu5g13510	nuclear mRNA splicing, via spliceosome
Afu5g13510	nucleus
Afu5g13510	spliceosomal complex
Afu5g13510	cytoplasm
Afu5g13510	pre-mRNA splicing factor activity
Afu5g13520	translation elongation factor activity
Afu5g13520	cytoplasm
Afu5g13520	ribosome biogenesis
Afu5g13530	3'-5'-exoribonuclease activity
Afu5g13530	nuclear exosome (RNase complex)
Afu5g13530	cytoplasmic exosome (RNase complex)
Afu5g13530	35S primary transcript processing
Afu5g13530	mRNA catabolic process
Afu5g13540	vacuole inheritance
Afu5g13540	fungal-type vacuole
Afu5g13540	protein binding
Afu5g13540	protein targeting to vacuole
Afu5g13540	microautophagy
Afu5g13540	homotypic vacuole fusion, non-autophagic
Afu5g13560	biological process unknown
Afu5g13560	molecular function unknown
Afu5g13560	cytoplasm
Afu5g13600	fungal-type vacuole membrane
Afu5g13600	molecular function unknown
Afu5g13600	insoluble fraction
Afu5g13600	vacuolar membrane
Afu5g13600	protein targeting to vacuole
Afu5g13600	Golgi to endosome transport
Afu5g13600	vacuole organization
Afu5g13600	homotypic vacuole fusion, non-autophagic
Afu5g13600	late endosome to vacuole transport
Afu5g13620	ubiquitin-specific protease activity
Afu5g13620	cytoplasm
Afu5g13620	protein deubiquitination

Afu5g13730	host-pathogen interaction
Afu5g13790	transcription factor activity
Afu5g13790	nucleus
Afu5g13790	regulation of transcription
Afu5g13810	cystathionine beta-lyase activity
Afu5g13810	cytoplasm
Afu5g13810	sulfur metabolic process
Afu5g13850	endoplasmic reticulum
Afu5g13850	integral to plasma membrane
Afu5g13850	sulfur metabolic process
Afu5g13850	oligopeptide transporter activity
Afu5g13890	molecular function unknown
Afu5g13890	cytoplasm
Afu5g13890	endosome
Afu5g13890	late endosome to vacuole transport
Afu5g13920	co-chaperone activity
Afu5g13920	nucleus
Afu5g13920	cytoplasm
Afu5g13920	protein folding
Afu5g13930	biological process unknown
Afu5g13930	DNA binding
Afu5g13930	cytoplasm
Afu5g13990	hydrolase activity, hydrolyzing O-glycosyl compounds
Afu5g13990	1,3-beta-glucan metabolic process
Afu5g13990	fungal-type cell wall
Afu5g13995	hydrolase activity, hydrolyzing O-glycosyl compounds
Afu5g13995	carbohydrate metabolic process
Afu5g14010	nucleic acid binding
Afu5g14010	nucleus
Afu5g14010	cytoplasm
Afu5g14010	zinc ion binding
Afu5g14010	snoRNA metabolic process
Afu5g14030	hydrolase activity, hydrolyzing O-glycosyl compounds
Afu5g14030	1,3-beta-glucan metabolic process
Afu5g14030	cell wall organization
Afu5g14030	fungal-type cell wall
Afu5g14040	G2/M transition of mitotic cell cycle
Afu5g14040	nuclear envelope
Afu5g14040	nuclear pore
Afu5g14040	cysteine-type peptidase activity
Afu5g14040	protein desumoylation
Afu5g14040	SUMO-specific protease activity
Afu5g14050	endoplasmic reticulum
Afu5g14050	sphingolipid biosynthetic process
Afu5g14050	sphingosine-1-phosphate phosphatase activity
Afu5g14060	1,3-beta-glucan synthase complex
Afu5g14060	establishment of cell polarity (sensu Saccharomyces)
Afu5g14060	Rho small monomeric GTPase activity
Afu5g14060	signal transducer activity
Afu5g14060	cellular bud tip

Afu5g14060	cellular bud neck
Afu5g14060	mating projection
Afu5g14060	actin filament organization
Afu5g14060	cell wall organization
Afu5g14060	budding cell bud growth
Afu5g14060	small GTPase mediated signal transduction
Afu5g14230	DNA binding
Afu5g14230	nucleus
Afu5g14230	zinc ion binding
Afu5g14250	metabolic process
Afu5g14250	oxidoreductase activity
Afu5g14260	electron transporter activity
Afu5g14260	endoplasmic reticulum membrane
Afu5g14260	microsome
Afu5g14260	sterol biosynthetic process
Afu5g14270	cytoplasm
Afu5g14270	peroxisomal membrane
Afu5g14270	peroxisomal matrix
Afu5g14270	AMP binding
Afu5g14290	transcription factor activity
Afu5g14290	nucleus
Afu5g14290	zinc ion binding
Afu5g14290	regulation of transcription
Afu5g14300	alpha,alpha-trehalose-phosphate synthase (UDP-forming) activity
Afu5g14300	cytoplasm
Afu5g14300	alpha,alpha-trehalose-phosphate synthase complex (UDP-forming)
Afu5g14300	carbohydrate metabolic process
Afu5g14300	trehalose biosynthetic process
Afu5g14300	response to stress
Afu5g14310	metabolic process
Afu5g14310	oxidoreductase activity
Afu5g14330	biological process unknown
Afu5g14330	NADPH dehydrogenase activity
Afu5g14330	nucleus
Afu5g14330	cytoplasm
Afu5g14340	peroxisomal matrix
Afu5g14340	sporulation (sensu Saccharomyces)
Afu5g14340	2,4-dienoyl-CoA reductase (NADPH) activity
Afu5g14340	fatty acid catabolic process
Afu5g14350	delta24(24-1) sterol reductase activity
Afu5g14350	endoplasmic reticulum
Afu5g14350	ergosterol biosynthetic process
Afu5g14360	transcription factor activity
Afu5g14360	regulation of transcription
Afu5g14390	transcription factor activity
Afu5g14390	nucleus
Afu5g14390	zinc ion binding
Afu5g14390	regulation of transcription
Afu5g14490	transporter activity
Afu5g14490	integral to plasma membrane

Afu5g14490	transport
Afu5g14500	integral to plasma membrane
Afu5g14510	beta-lactamase activity
Afu5g14510	beta-lactam antibiotic catabolic process
Afu5g14510	response to antibiotic
Afu5g14540	fructose transmembrane transporter activity
Afu5g14540	glucose transmembrane transporter activity
Afu5g14540	plasma membrane
Afu5g14540	hexose transport
Afu5g14540	mannose transmembrane transporter activity
Afu5g14582	nucleotide binding
Afu5g14610	biological process unknown
Afu5g14610	fungal-type vacuole
Afu5g14610	carboxypeptidase C activity
Afu5g14660	plasma membrane
Afu5g14660	choline transmembrane transporter activity
Afu5g14660	choline transport
Afu5g14730	aldo-keto reductase activity
Afu5g14730	nucleus
Afu5g14730	cytoplasm
Afu5g14730	cellular aldehyde metabolic process
Afu5g14770	pyrroline-5-carboxylate reductase activity
Afu5g14770	cytoplasm
Afu5g14770	proline biosynthetic process
Afu5g14780	trehalose biosynthetic process
Afu5g14780	response to stress
Afu5g14780	transferase activity, transferring glycosyl groups
Afu5g14790	gluconeogenesis
Afu5g14790	pyruvate, water dikinase activity
Afu5g14790	phosphoenolpyruvate-dependent sugar phosphotransferase system
Afu5g14810	pyruvate decarboxylase activity
Afu5g14810	nucleus
Afu5g14810	cytoplasm
Afu5g14810	pyruvate metabolic process
Afu5g14810	glucose catabolic process to ethanol
Afu5g14820	DNA clamp loader activity
Afu5g14820	nucleus
Afu5g14820	DNA replication factor C complex
Afu5g14820	leading strand elongation
Afu5g14820	mismatch repair
Afu5g14820	sister chromatid cohesion
Afu5g14820	ATPase activity
Afu5g14830	catalytic activity
Afu5g14830	metabolic process
Afu5g14870	protein kinase activity
Afu5g14870	cytoplasm
Afu5g14880	biological process unknown
Afu5g14880	molecular function unknown
Afu5g14880	mitochondrion
Afu5g14940	ferric-chelate reductase activity

Afu5g14940	integral to plasma membrane
Afu5g14940	cellular iron ion homeostasis
Afu5g14940	ferrous iron transport
Afu5g15000	cytoplasm
Afu5g15000	arsenite transport
Afu5g15000	arsenate reductase activity
Afu5g15000	response to arsenic
Afu5g15010	integral to plasma membrane
Afu5g15010	arsenite transmembrane transporter activity
Afu5g15010	arsenite transport
Afu5g15010	response to arsenic
Afu5g15020	cytoplasm
Afu5g15020	S-adenosylmethionine-dependent methyltransferase activity
Afu5g15020	response to arsenic
Afu5g15030	response to arsenic
Afu5g15070	mitochondrion
Afu5g15070	response to oxidative stress
Afu5g15070	thioredoxin peroxidase activity
Afu5g15070	antioxidant activity
Afu5g15070	regulation of cell redox homeostasis
Afu6g00120	transcription factor activity
Afu6g00120	nucleus
Afu6g00120	zinc ion binding
Afu6g00120	regulation of transcription
Afu6g00130	transporter activity
Afu6g00130	integral to plasma membrane
Afu6g00130	transport
Afu6g00160	fungal-type vacuole
Afu6g00160	phosphate metabolic process
Afu6g00160	phosphoric ester hydrolase activity
Afu6g00200	transcription factor activity
Afu6g00200	nucleus
Afu6g00200	zinc ion binding
Afu6g00200	regulation of transcription
Afu6g00210	fungal-type vacuole membrane
Afu6g00210	transporter activity
Afu6g00210	transport
Afu6g00210	monocarboxylic acid transmembrane transporter activity
Afu6g00220	transcription factor activity
Afu6g00220	nucleus
Afu6g00220	regulation of transcription
Afu6g00260	phosphatidylserine decarboxylase activity
Afu6g00260	phosphatidylserine catabolic process
Afu6g00290	arylformamidase activity
Afu6g00290	cytoplasm
Afu6g00290	mitochondrion
Afu6g00290	NAD biosynthetic process
Afu6g00300	serine C-palmitoyltransferase activity
Afu6g00300	membrane fraction
Afu6g00300	microsome

Afu6g00300	serine C-palmitoyltransferase complex
Afu6g00300	sphingolipid biosynthetic process
Afu6g00310	biological process unknown
Afu6g00310	fungal-type vacuole
Afu6g00310	carboxypeptidase C activity
Afu6g00370	biological process unknown
Afu6g00370	molecular function unknown
Afu6g00370	nucleus
Afu6g00370	cytoplasm
Afu6g00390	arylformamidase activity
Afu6g00390	cytoplasm
Afu6g00390	mitochondrion
Afu6g00390	NAD biosynthetic process
Afu6g00412	plasma membrane
Afu6g00412	choline transmembrane transporter activity
Afu6g00412	choline transport
Afu6g00440	cation transport
Afu6g00440	cation transmembrane transporter activity
Afu6g00440	efflux transmembrane transporter activity
Afu6g00470	high affinity zinc uptake transmembrane transporter activity
Afu6g00470	integral to plasma membrane
Afu6g00470	high-affinity zinc ion transport
Afu6g00510	soluble fraction
Afu6g00510	alcohol metabolic process
Afu6g00510	alcohol dehydrogenase (NADP+) activity
Afu6g00630	transporter activity
Afu6g00630	transport
Afu6g00630	integral to membrane
Afu6g00710	integral to plasma membrane
Afu6g00710	nicotinamide mononucleotide permease activity
Afu6g00710	nicotinamide mononucleotide transport
Afu6g00720	chitin binding
Afu6g00750	pyruvate decarboxylase activity
Afu6g00750	cytoplasm
Afu6g00750	ethanol metabolic process
Afu6g00770	metabolic process
Afu6g00770	hydrolase activity, hydrolyzing N-glycosyl compounds
Afu6g01810	metabolic process
Afu6g01810	oxidoreductase activity
Afu6g01820	plasma membrane
Afu6g01820	allantoate transmembrane transporter activity
Afu6g01820	allantoate transport
Afu6g01840	transcription factor activity
Afu6g01840	regulation of transcription
Afu6g01860	fructose transmembrane transporter activity
Afu6g01860	glucose transmembrane transporter activity
Afu6g01860	plasma membrane
Afu6g01860	hexose transport
Afu6g01860	mannose transmembrane transporter activity
Afu6g01910	DNA binding

Afu6g01910	nucleus
Afu6g01910	zinc ion binding
Afu6g01930	transporter activity
Afu6g01930	transport
Afu6g01930	membrane
Afu6g01960	zinc ion binding
Afu6g01970	specific RNA polymerase II transcription factor activity
Afu6g01970	nucleus
Afu6g01970	transcription initiation from RNA polymerase II promoter
Afu6g01970	regulation of nitrogen utilization
Afu6g01970	zinc ion binding
Afu6g01980	biological process unknown
Afu6g01980	molecular function unknown
Afu6g01980	integral to membrane
Afu6g01990	ribosomal large subunit assembly
Afu6g01990	nucleus
Afu6g01990	rRNA processing
Afu6g02000	allantoin uptake transmembrane transporter activity
Afu6g02000	allantoin transport
Afu6g02000	membrane
Afu6g02060	ATP-dependent RNA helicase activity
Afu6g02060	nucleolus
Afu6g02060	35S primary transcript processing
Afu6g02070	phospholipid-translocating ATPase activity
Afu6g02070	plasma membrane
Afu6g02070	intracellular protein transport
Afu6g02090	vacuolar proton-transporting V-type ATPase, V1 domain
Afu6g02090	fungal-type vacuole membrane
Afu6g02090	vacuolar acidification
Afu6g02090	proton-transporting ATPase activity, rotational mechanism
Afu6g02110	response to pheromone during conjugation without cellular fusion
Afu6g02110	nuclear chromatin
Afu6g02110	DNA binding
Afu6g02110	DNA replication origin binding
Afu6g02110	RNA polymerase II transcription factor activity
Afu6g02110	nucleus
Afu6g02110	DNA replication initiation
Afu6g02110	regulation of transcription from RNA polymerase II promoter
Afu6g02130	Rab escort protein activity
Afu6g02130	cytoplasm
Afu6g02130	intracellular protein transport
Afu6g02130	membrane
Afu6g02140	peptidyl-prolyl cis-trans isomerase activity
Afu6g02140	mitochondrion
Afu6g02140	protein folding
Afu6g02170	plasma membrane
Afu6g02170	copper ion import
Afu6g02170	oxidoreductase activity, oxidizing metal ions
Afu6g02180	N-acetyltransferase activity
Afu6g02180	metabolic process

Afu6g02190	transcription factor activity
Afu6g02190	nucleus
Afu6g02190	regulation of transcription
Afu6g02200	biological process unknown
Afu6g02200	molecular function unknown
Afu6g02200	cytoplasm
Afu6g02210	metabolic process
Afu6g02210	oxidoreductase activity
Afu6g02220	transporter activity
Afu6g02220	integral to plasma membrane
Afu6g02220	transport
Afu6g02230	glucokinase activity
Afu6g02230	cytosol
Afu6g02230	carbohydrate metabolic process
Afu6g02270	ribonuclease MRP activity
Afu6g02270	ribonuclease MRP complex
Afu6g02270	ribonuclease P activity
Afu6g02270	nucleolar ribonuclease P complex
Afu6g02270	rRNA processing
Afu6g02270	tRNA processing
Afu6g02280	cytoplasm
Afu6g02280	thioredoxin peroxidase activity
Afu6g02280	pathogenesis
Afu6g02280	response to metal ion
Afu6g02280	regulation of cell redox homeostasis
Afu6g02300	septin checkpoint
Afu6g02300	septin ring assembly
Afu6g02300	protein kinase activity
Afu6g02300	protein amino acid phosphorylation
Afu6g02350	biological process unknown
Afu6g02350	molecular function unknown
Afu6g02350	cellular component unknown
Afu6g02370	actin cortical patch assembly
Afu6g02370	structural molecule activity
Afu6g02370	Arp2/3 protein complex
Afu6g02380	ubiquitin-specific protease activity
Afu6g02380	protein tagging activity
Afu6g02380	protein deubiquitination
Afu6g02390	mitochondrion
Afu6g02390	fatty acid metabolic process
Afu6g02390	CoA hydrolase activity
Afu6g02400	transporter activity
Afu6g02400	transport
Afu6g02410	biological process unknown
Afu6g02410	fungal-type vacuole membrane
Afu6g02410	molecular function unknown
Afu6g02420	protein polyubiquitination
Afu6g02420	ubiquitin conjugating enzyme activity
Afu6g02420	nucleus
Afu6g02420	cytoplasm

Afu6g02420	postreplication repair
Afu6g02420	ubiquitin cycle
Afu6g02420	protein monoubiquitination
Afu6g02440	RNA binding
Afu6g02440	structural constituent of ribosome
Afu6g02440	cytosolic large ribosomal subunit (sensu Eukaryota)
Afu6g02440	translation
Afu6g02450	structural constituent of ribosome
Afu6g02450	cytosolic small ribosomal subunit (sensu Eukaryota)
Afu6g02450	translation
Afu6g02460	glucosamine 6-phosphate N-acetyltransferase activity
Afu6g02460	nucleus
Afu6g02460	cytoplasm
Afu6g02460	UDP-N-acetylglucosamine biosynthetic process
Afu6g02470	fumarate hydratase activity
Afu6g02470	mitochondrial matrix
Afu6g02470	cytosol
Afu6g02470	tricarboxylic acid cycle
Afu6g02470	fumarate metabolic process
Afu6g02490	L-aspartate:2-oxoglutarate aminotransferase activity
Afu6g02490	cytoplasm
Afu6g02490	peroxisome
Afu6g02490	aspartate biosynthetic process
Afu6g02490	aspartate catabolic process
Afu6g02490	glutamate metabolic process
Afu6g02490	nitrogen compound metabolic process
Afu6g02490	asparagine biosynthetic process from oxaloacetate
Afu6g02510	conjugation with cellular fusion
Afu6g02510	cytoplasm
Afu6g02510	cell wall chitin biosynthetic process
Afu6g02510	Golgi to plasma membrane transport
Afu6g02510	ascospore wall assembly
Afu6g02520	translation initiation factor activity
Afu6g02520	ribosome
Afu6g02520	translational initiation
Afu6g02530	single-stranded DNA specific endodeoxyribonuclease activity
Afu6g02530	nucleotide-excision repair factor 1 complex
Afu6g02530	removal of nonhomologous ends
Afu6g02530	double-strand break repair via single-strand annealing, removal of nonhomologous ends
Afu6g02530	nucleotide-excision repair, DNA incision, 5'-to lesion
Afu6g02540	cytokinesis
Afu6g02540	cytoplasm
Afu6g02540	endocytosis
Afu6g02540	response to osmotic stress
Afu6g02540	actin filament organization
Afu6g02540	cytoskeletal protein binding
Afu6g02540	actin polymerization or depolymerization
Afu6g02550	Group II intron splicing
Afu6g02550	mitochondrial inner membrane
Afu6g02550	magnesium ion transmembrane transporter activity

Afu6g02550	mitochondrial magnesium ion transport
Afu6g02570	biological process unknown
Afu6g02570	molecular function unknown
Afu6g02570	cytoplasm
Afu6g02590	protein kinase activity
Afu6g02590	cytoplasm
Afu6g02600	biological process unknown
Afu6g02600	molecular function unknown
Afu6g02600	nucleus
Afu6g02600	cytoplasm
Afu6g02620	molecular function unknown
Afu6g02620	cytoplasm
Afu6g02620	cellular bud
Afu6g02620	cellular bud neck
Afu6g02620	endocytosis
Afu6g02630	transcription export complex
Afu6g02630	U2-type nuclear mRNA branch site recognition
Afu6g02630	ATP-dependent RNA helicase activity
Afu6g02630	protein binding
Afu6g02630	nucleus
Afu6g02630	spliceosomal complex
Afu6g02630	mRNA export from nucleus
Afu6g02630	pre-mRNA splicing factor activity
Afu6g02670	regulation of transcription involved in G2-phase of mitotic cell cycle
Afu6g02670	protein kinase activity
Afu6g02670	chromosome segregation
Afu6g02680	biological process unknown
Afu6g02680	molecular function unknown
Afu6g02680	cytoplasm
Afu6g02690	DNA binding
Afu6g02690	nucleus
Afu6g02690	zinc ion binding
Afu6g02700	nucleus
Afu6g02700	DNA repair
Afu6g02700	cell proliferation
Afu6g02700	Smc5-Smc6 complex
Afu6g02720	L-lactate dehydrogenase (cytochrome) activity
Afu6g02720	mitochondrial intermembrane space
Afu6g02720	electron transport
Afu6g02730	integral to plasma membrane
Afu6g02730	nicotinamide mononucleotide permease activity
Afu6g02730	nicotinamide mononucleotide transport
Afu6g02750	chaperone activity
Afu6g02750	nascent polypeptide-associated complex
Afu6g02750	nascent polypeptide association
Afu6g02770	biological process unknown
Afu6g02770	lipid particle
Afu6g02770	oxidoreductase activity
Afu6g02780	biological process unknown
Afu6g02780	nucleus

Afu6g02780	cytoplasm
Afu6g02780	hydrolase activity, acting on ester bonds
Afu6g02820	transition metal ion transport
Afu6g02820	cellular iron ion homeostasis
Afu6g02820	integral to membrane
Afu6g02820	oxidoreductase activity, oxidizing metal ions, NAD or NADP as acceptor
Afu6g02840	protein serine/threonine kinase activity
Afu6g02840	cytoplasm
Afu6g02840	protein amino acid phosphorylation
Afu6g02840	cell cycle
Afu6g02850	transcription factor activity
Afu6g02850	nucleus
Afu6g02850	zinc ion binding
Afu6g02850	regulation of transcription
Afu6g02860	mitochondrial matrix
Afu6g02860	threonine catabolic process
Afu6g02860	propionate metabolic process
Afu6g02860	methylisocitrate lyase activity
Afu6g02910	N-acetyl-gamma-glutamyl-phosphate reductase activity
Afu6g02910	acetylglutamate kinase activity
Afu6g02910	mitochondrial matrix
Afu6g02910	arginine biosynthetic process
Afu6g02910	ornithine biosynthetic process
Afu6g02920	v-SNARE activity
Afu6g02920	Golgi to plasma membrane transport
Afu6g02920	endocytosis
Afu6g02920	vesicle fusion
Afu6g02920	transport vesicle
Afu6g02940	cytokinesis
Afu6g02940	cell wall chitin biosynthetic process
Afu6g02940	response to osmotic stress
Afu6g02940	enzyme activator activity
Afu6g02970	biological process unknown
Afu6g02970	molecular function unknown
Afu6g02970	mitochondrion
Afu6g02980	polygalacturonase activity
Afu6g02980	extracellular region
Afu6g02980	pseudohyphal growth
Afu6g02980	pectin catabolic process
Afu6g03010	DNA binding
Afu6g03010	nucleus
Afu6g03010	zinc ion binding
Afu6g03030	FAD binding
Afu6g03040	drug transporter activity
Afu6g03040	drug transport
Afu6g03040	integral to membrane
Afu6g03060	receptor activity
Afu6g03060	glucose transmembrane transporter activity
Afu6g03060	glucose binding
Afu6g03060	plasma membrane

Afu6g03060	signal transduction
Afu6g03060	response to glucose stimulus
Afu6g03080	ATP-binding cassette (ABC) transporter activity
Afu6g03080	ATP binding
Afu6g03080	transport
Afu6g03110	transcription factor activity
Afu6g03110	nucleus
Afu6g03110	regulation of transcription
Afu6g03140	integral to plasma membrane
Afu6g03140	oligopeptide transport
Afu6g03140	oligopeptide transporter activity
Afu6g03160	nucleotide binding
Afu6g03160	signal transduction
Afu6g03200	plasma membrane
Afu6g03200	urea transmembrane transporter activity
Afu6g03200	urea transport
Afu6g03230	hydrolase activity, hydrolyzing O-glycosyl compounds
Afu6g03230	cellular glucan metabolic process
Afu6g03230	fungal-type cell wall
Afu6g03252	protein kinase activity
Afu6g03260	aspartic-type endopeptidase activity
Afu6g03260	protein metabolic process
Afu6g03290	isocitrate dehydrogenase activity
Afu6g03290	metabolic process
Afu6g03290	hydrolase activity
Afu6g03320	multidrug transport
Afu6g03320	multidrug efflux pump activity
Afu6g03320	response to drug
Afu6g03350	N-acetyltransferase activity
Afu6g03350	metabolic process
Afu6g03360	biological process unknown
Afu6g03360	nucleus
Afu6g03360	cytoplasm
Afu6g03360	alcohol dehydrogenase (NADP+) activity
Afu6g03370	acylglycerone-phosphate reductase activity
Afu6g03370	cytoplasm
Afu6g03370	endoplasmic reticulum
Afu6g03370	lipid particle
Afu6g03370	phosphatidic acid biosynthetic process
Afu6g03430	DNA binding
Afu6g03450	secondary metabolic process
Afu6g03470	ATP-binding cassette (ABC) transporter activity
Afu6g03470	integral to plasma membrane
Afu6g03470	transport
Afu6g03480	cytoplasm
Afu6g03480	transaminase activity
Afu6g03480	nonribosomal peptide biosynthetic process
Afu6g03480	secondary metabolic process
Afu6g03480	secondary metabolic process
Afu6g03480	amino acid activation for nonribosomal peptide biosynthetic process

Afu6g03480	amino acid adenylylation by nonribosomal peptide synthase
Afu6g03490	monooxygenase activity
Afu6g03490	cellular aromatic compound metabolic process
Afu6g03530	glutamate-ammonia ligase activity
Afu6g03530	glutamine biosynthetic process
Afu6g03540	allantoin catabolic process
Afu6g03540	malate synthase activity
Afu6g03540	cytoplasm
Afu6g03580	cytoplasm
Afu6g03580	mRNA export from nucleus
Afu6g03580	ATPase activity
Afu6g03590	mitochondrion
Afu6g03590	mitochondrial matrix
Afu6g03590	propionate metabolic process, methylcitrate cycle
Afu6g03590	2-methylcitrate synthase activity
Afu6g03620	FAD binding
Afu6g03630	very-long-chain fatty acid metabolic process
Afu6g03630	long-chain-fatty-acid-CoA ligase activity
Afu6g03630	long-chain fatty acid transporter activity
Afu6g03630	peroxisome
Afu6g03630	microsome
Afu6g03630	lipid particle
Afu6g03630	plasma membrane
Afu6g03630	lipid transport
Afu6g03640	serine C-palmitoyltransferase activity
Afu6g03640	membrane fraction
Afu6g03640	microsome
Afu6g03640	serine C-palmitoyltransferase complex
Afu6g03640	sphingolipid biosynthetic process
Afu6g03660	adenosylmethionine-8-amino-7-oxononanoate transaminase activity
Afu6g03660	cytoplasm
Afu6g03660	biotin biosynthetic process
Afu6g03670	biotin synthase activity
Afu6g03670	mitochondrion
Afu6g03670	biotin biosynthetic process
Afu6g03690	plasma membrane
Afu6g03690	sodium ion transport
Afu6g03690	ATPase activity, coupled to transmembrane movement of ions, phosphorylative mechanism
Afu6g03710	carboxypeptidase activity
Afu6g03710	proteolysis
Afu6g03720	plasma membrane
Afu6g03720	allantoate transmembrane transporter activity
Afu6g03720	allantoate transport
Afu6g03730	cytoplasm
Afu6g03730	mitochondrion
Afu6g03730	propionate metabolic process
Afu6g03730	2-methylcitrate dehydratase activity
Afu6g03740	DNA (cytosine-5-)-methyltransferase activity
Afu6g03740	DNA modification
Afu6g03750	amidophosphoribosyltransferase activity

Afu6g03750	cytoplasm
Afu6g03750	purine base metabolic process
Afu6g03770	endoplasmic reticulum
Afu6g03770	reciprocal meiotic recombination
Afu6g03770	oxidoreductase activity
Afu6g03810	mitochondrial proton-transporting ATP synthase, stator stalk
Afu6g03810	structural molecule activity
Afu6g03810	protein complex assembly
Afu6g03810	ATP synthesis coupled proton transport
Afu6g03810	hydrogen ion transporting ATP synthase activity, rotational mechanism
Afu6g03820	chaperone activity
Afu6g03820	nascent polypeptide-associated complex
Afu6g03820	nascent polypeptide association
Afu6g03830	RNA binding
Afu6g03830	structural constituent of ribosome
Afu6g03830	cytosolic large ribosomal subunit (sensu Eukaryota)
Afu6g03830	translation
Afu6g03840	molecular function unknown
Afu6g03840	ER to Golgi vesicle-mediated transport
Afu6g03840	COPII-coated vesicle
Afu6g03850	signal recognition particle binding
Afu6g03850	endoplasmic reticulum membrane
Afu6g03850	protein targeting to ER
Afu6g03860	transporter activity
Afu6g03860	transport
Afu6g03890	catalase activity
Afu6g03890	cytoplasm
Afu6g03890	response to oxidative stress
Afu6g03890	intracellular immature spore
Afu6g03910	biological process unknown
Afu6g03910	molecular function unknown
Afu6g03910	cellular component unknown
Afu6g03920	electron transport
Afu6g03920	electron carrier activity
Afu6g03940	Rab GTPase activator activity
Afu6g03940	cytoplasm
Afu6g03940	vesicle-mediated transport
Afu6g03950	phospholipid-translocating ATPase activity
Afu6g03950	calcium-transporting ATPase activity
Afu6g03950	intracellular protein transport
Afu6g03960	vesicle-mediated transport
Afu6g03980	hexokinase activity
Afu6g03980	nucleus
Afu6g03980	cytosol
Afu6g03980	fructose metabolic process
Afu6g04000	regulation of progression through cell cycle
Afu6g04000	chaperone activity
Afu6g04000	GTPase activator activity
Afu6g04000	protein binding
Afu6g04000	cytosol

Afu6g04000	arginine metabolic process
Afu6g04010	nuclear envelope
Afu6g04010	protein export from nucleus
Afu6g04010	importin-alpha export receptor activity
Afu6g04010	programmed cell death
Afu6g04020	aminoacyl-tRNA hydrolase activity
Afu6g04020	mitochondrion
Afu6g04020	translational termination
Afu6g04040	dodecenoyl-CoA delta-isomerase activity
Afu6g04040	peroxisome
Afu6g04040	fatty acid beta-oxidation
Afu6g04050	molecular function unknown
Afu6g04050	cytoplasm
Afu6g04050	regulation of mitotic cell cycle
Afu6g04080	biological process unknown
Afu6g04080	molecular function unknown
Afu6g04090	biological process unknown
Afu6g04090	molecular function unknown
Afu6g04090	mitochondrion
Afu6g04120	metabolic process
Afu6g04120	oxidoreductase activity
Afu6g04150	v-SNARE activity
Afu6g04150	endoplasmic reticulum
Afu6g04150	Golgi apparatus
Afu6g04150	ER to Golgi vesicle-mediated transport
Afu6g04150	retrograde vesicle-mediated transport, Golgi to ER
Afu6g04150	intra-Golgi vesicle-mediated transport
Afu6g04150	vesicle fusion
Afu6g04150	integral to membrane
Afu6g04210	mannosyl-oligosaccharide glucosidase activity
Afu6g04210	extracellular region
Afu6g04210	cell wall organization
Afu6g04220	biological process unknown
Afu6g04220	molecular function unknown
Afu6g04220	cytoplasm
Afu6g04230	molecular function unknown
Afu6g04230	regulation of translational termination
Afu6g04230	cellular component unknown
Afu6g04240	protein amino acid N-linked glycosylation
Afu6g04240	lipid biosynthetic process
Afu6g04240	pyrophosphatase activity
Afu6g04240	integral to endoplasmic reticulum membrane
Afu6g04250	sexual reproduction
Afu6g04260	nucleolus
Afu6g04260	virus-host interaction
Afu6g04260	ribosomal large subunit biogenesis
Afu6g04270	myo-inositol transmembrane transporter activity
Afu6g04270	myo-inositol transport
Afu6g04270	membrane
Afu6g04290	phosphoethanolamine N-methyltransferase activity

Afu6g04290	endoplasmic reticulum
Afu6g04290	GPI anchor biosynthetic process
Afu6g04310	nuclear-transcribed mRNA catabolic process, deadenylation-dependent decay
Afu6g04310	mRNA binding
Afu6g04310	cytoplasm
Afu6g04330	RNA helicase activity
Afu6g04330	nucleolus
Afu6g04330	small nucleolar ribonucleoprotein complex
Afu6g04330	ribosome biogenesis
Afu6g04330	maturation of SSU-rRNA
Afu6g04360	plasma membrane
Afu6g04360	multidrug transport
Afu6g04360	xenobiotic-transporting ATPase activity
Afu6g04360	ABC-type efflux porter activity
Afu6g04360	response to drug
Afu6g04380	chaperone activity
Afu6g04380	mitochondrion
Afu6g04380	mitochondrial electron transport, ubiquinol to cytochrome c
Afu6g04390	ubiquitin-protein ligase activity
Afu6g04390	nucleus
Afu6g04390	chromatin silencing at telomere
Afu6g04390	protein monoubiquitination
Afu6g04390	histone methylation
Afu6g04390	histone ubiquitination
Afu6g04400	transcription factor TFIIIB complex
Afu6g04400	RNA polymerase III transcription factor activity
Afu6g04400	transcription initiation from RNA polymerase III promoter
Afu6g04420	mitochondrial genome maintenance
Afu6g04420	molecular function unknown
Afu6g04420	mitochondrial outer membrane
Afu6g04420	mitochondrion organization
Afu6g04430	biological process unknown
Afu6g04430	molecular function unknown
Afu6g04430	nucleus
Afu6g04430	cytoplasm
Afu6g04440	molecular function unknown
Afu6g04440	mitochondrion
Afu6g04440	tRNA modification
Afu6g04440	translation
Afu6g04450	alpha-1,2-mannosyltransferase activity
Afu6g04450	Golgi apparatus
Afu6g04450	protein amino acid glycosylation
Afu6g04460	mitochondrial envelope
Afu6g04460	mitochondrial membrane organization
Afu6g04460	CDP-diacylglycerol-glycerol-3-phosphate 3-phosphatidyltransferase activity
Afu6g04460	lipid biosynthetic process
Afu6g04460	phospholipid biosynthetic process
Afu6g04460	cardiolipin synthase activity
Afu6g04460	CDP-alcohol phosphatidyltransferase activity
Afu6g04490	biological process unknown

Afu6g04490	molecular function unknown
Afu6g04490	nucleus
Afu6g04490	cytoplasm
Afu6g04500	AMP-activated protein kinase activity
Afu6g04500	nucleus
Afu6g04500	protein amino acid phosphorylation
Afu6g04500	cell adhesion
Afu6g04500	signal transduction
Afu6g04500	filamentous growth
Afu6g04510	biological process unknown
Afu6g04510	molecular function unknown
Afu6g04510	nucleus
Afu6g04510	cytoplasm
Afu6g04520	biological process unknown
Afu6g04520	molecular function unknown
Afu6g04520	nucleus
Afu6g04530	histone acetyltransferase complex
Afu6g04530	histone acetyltransferase activity
Afu6g04530	regulation of transcription from RNA polymerase II promoter
Afu6g04530	histone acetylation
Afu6g04540	adaptation to pheromone during conjugation with cellular fusion
Afu6g04540	calcium-dependent protein serine/threonine phosphatase activity
Afu6g04540	cytoplasm
Afu6g04540	cellular ion homeostasis
Afu6g04540	cell wall organization
Afu6g04560	structural constituent of ribosome
Afu6g04560	mitochondrial small ribosomal subunit
Afu6g04560	translation
Afu6g04570	translation elongation factor activity
Afu6g04570	cytosolic ribosome (sensu Eukaryota)
Afu6g04570	regulation of translational elongation
Afu6g04590	molecular function unknown
Afu6g04590	cellular component unknown
Afu6g04590	maturation of SSU-rRNA
Afu6g04610	DNA-directed RNA polymerase activity
Afu6g04610	DNA-directed RNA polymerase III complex
Afu6g04610	DNA-directed RNA polymerase I complex
Afu6g04610	transcription from RNA polymerase I promoter
Afu6g04610	transcription from RNA polymerase III promoter
Afu6g04640	metabolic process
Afu6g04640	cellular component unknown
Afu6g04640	hydrolase activity
Afu6g04660	nuclear nucleosome
Afu6g04660	DNA binding
Afu6g04660	nucleus
Afu6g04660	chromatin assembly or disassembly
Afu6g04680	mannose inositol phosphoceramide metabolic process
Afu6g04680	transferase activity, transferring glycosyl groups
Afu6g04680	sphingolipid biosynthetic process
Afu6g04700	histidine biosynthetic process

Afu6g04700	imidazoleglycerol-phosphate dehydratase activity
Afu6g04700	cell
Afu6g04720	molecular function unknown
Afu6g04720	mitochondrial envelope
Afu6g04720	RNA processing
Afu6g04730	phosphoribosylamine-glycine ligase activity
Afu6g04730	phosphoribosylformylglycinamidine cyclo-ligase activity
Afu6g04730	cytoplasm
Afu6g04730	purine base metabolic process
Afu6g04740	mitochondrion inheritance
Afu6g04740	vacuole inheritance
Afu6g04740	histone acetyltransferase complex
Afu6g04740	establishment of mitotic spindle orientation
Afu6g04740	cytokinesis
Afu6g04740	structural constituent of cytoskeleton
Afu6g04740	actin filament
Afu6g04740	regulation of transcription from RNA polymerase II promoter
Afu6g04740	exocytosis
Afu6g04740	endocytosis
Afu6g04740	response to osmotic stress
Afu6g04740	cell wall organization
Afu6g04740	budding cell apical bud growth
Afu6g04740	budding cell isotropic bud growth
Afu6g04740	protein secretion
Afu6g04740	histone acetylation
Afu6g04740	actin filament reorganization during cell cycle
Afu6g04740	vesicle transport along actin filament
Afu6g04750	adenyl-nucleotide exchange factor activity
Afu6g04750	cytosol
Afu6g04750	cytosolic ribosome (sensu Eukaryota)
Afu6g04750	translation
Afu6g04780	molecular function unknown
Afu6g04780	late endosome
Afu6g04780	late endosome to vacuole transport
Afu6g04790	endopeptidase activity
Afu6g04790	proteasome core complex
Afu6g04790	ubiquitin-dependent protein catabolic process
Afu6g04790	proteasome core complex, alpha-subunit complex
Afu6g04800	biological process unknown
Afu6g04800	molecular function unknown
Afu6g04800	nucleus
Afu6g04800	cytoplasm
Afu6g04810	mediator complex
Afu6g04810	transcription from RNA polymerase II promoter
Afu6g04810	RNA polymerase II transcription mediator activity
Afu6g04820	cytoplasm
Afu6g04820	pathogenesis
Afu6g04820	para-aminobenzoic acid metabolic process
Afu6g04820	folic acid biosynthetic process
Afu6g04820	4-amino-4-deoxychorismate synthase activity

Afu6g04830	ATP binding
Afu6g04840	molecular function unknown
Afu6g04840	ER to Golgi vesicle-mediated transport
Afu6g04840	TRAPP complex
Afu6g04850	nucleus
Afu6g04850	cytoplasm
Afu6g04850	metabolic process
Afu6g04850	oxidoreductase activity
Afu6g04860	transporter activity
Afu6g04860	transport
Afu6g04860	membrane
Afu6g04870	Golgi membrane
Afu6g04870	chaperone activity
Afu6g04870	cytosol
Afu6g04870	protein complex assembly
Afu6g04870	Golgi to vacuole transport
Afu6g04870	vacuole organization
Afu6g04870	osmoregulation
Afu6g04870	extrinsic to membrane
Afu6g04890	conjugation with cellular fusion
Afu6g04890	peptide pheromone maturation
Afu6g04890	prenyl-dependent CAAX protease activity
Afu6g04890	protein processing
Afu6g04890	integral to endoplasmic reticulum membrane
Afu6g04900	nucleus
Afu6g04900	cytoplasm
Afu6g04910	Group I intron splicing
Afu6g04910	mRNA binding
Afu6g04910	leucine-tRNA ligase activity
Afu6g04910	mitochondrion
Afu6g04910	leucyl-tRNA aminoacylation
Afu6g04920	cytosol
Afu6g04920	acetate metabolic process
Afu6g04920	NADH regeneration
Afu6g04920	formate dehydrogenase activity
Afu6g04920	formate catabolic process
Afu6g04940	establishment of mitotic spindle orientation
Afu6g04940	polarisome
Afu6g04940	cytoskeletal regulatory protein binding
Afu6g04940	actin filament
Afu6g04940	actin filament organization
Afu6g04940	Rho protein signal transduction
Afu6g04940	Rho protein signal transduction
Afu6g04940	spore germination
Afu6g04940	cell septum
Afu6g04940	hyphal growth
Afu6g04940	establishment of cell polarity (sensu Fungi)
Afu6g04940	actin nucleation
Afu6g04950	GTP binding
Afu6g04950	mitochondrial inner membrane

Afu6g04950	translation
Afu6g04970	O-phospho-L-serine:2-oxoglutarate aminotransferase activity
Afu6g04970	cytoplasm
Afu6g04970	L-serine biosynthetic process
Afu6g04970	serine family amino acid biosynthetic process
Afu6g04970	purine base biosynthetic process
Afu6g04980	molecular function unknown
Afu6g04980	mitochondrion
Afu6g04980	mitochondrial membrane organization
Afu6g04980	protein import into mitochondrial intermembrane space
Afu6g04990	sulfur amino acid transport
Afu6g04990	L-methionine secondary active transmembrane transporter activity
Afu6g04990	integral to plasma membrane
Afu6g05000	beta-fructofuranosidase activity
Afu6g05000	extracellular region
Afu6g05000	cytoplasm
Afu6g05000	sucrose catabolic process
Afu6g05010	transcription factor activity
Afu6g05010	regulation of transcription
Afu6g05020	biological process unknown
Afu6g05020	amidase activity
Afu6g05020	cellular component unknown
Afu6g05040	DNA clamp loader activity
Afu6g05040	DNA replication factor C complex
Afu6g05040	leading strand elongation
Afu6g05040	mismatch repair
Afu6g05040	sister chromatid cohesion
Afu6g05040	purine nucleotide binding
Afu6g05050	biological process unknown
Afu6g05050	molecular function unknown
Afu6g05050	cytoplasm
Afu6g05060	nucleus
Afu6g05060	RNA catabolic process
Afu6g05060	enzyme regulator activity
Afu6g05060	processing of 27S pre-rRNA
Afu6g05070	tRNA isopentenyltransferase activity
Afu6g05070	mitochondrion
Afu6g05070	cytosol
Afu6g05070	tRNA modification
Afu6g05080	ATP-binding cassette (ABC) transporter activity
Afu6g05080	cytoplasm
Afu6g05080	regulation of transcription, DNA-dependent
Afu6g05080	CCR4-NOT complex
Afu6g05090	regulation of transcription from RNA polymerase II promoter
Afu6g05090	transcription elongation factor complex
Afu6g05090	RNA polymerase II transcription elongation factor activity
Afu6g05100	biological process unknown
Afu6g05100	molecular function unknown
Afu6g05100	cytoplasm
Afu6g05110	mitochondrion

Afu6g05110	mitochondrial outer membrane translocase complex
Afu6g05110	mitochondrial translocation
Afu6g05110	protein transporter activity
Afu6g05120	glycogen synthase kinase 3 activity
Afu6g05120	cytoplasm
Afu6g05120	protein amino acid phosphorylation
Afu6g05120	proteolysis
Afu6g05120	response to stress
Afu6g05120	sporulation (sensu Saccharomyces)
Afu6g05130	commitment complex
Afu6g05130	nuclear mRNA splicing, via spliceosome
Afu6g05130	mRNA binding
Afu6g05130	nuclear cap binding complex
Afu6g05140	C-5 sterol desaturase activity
Afu6g05140	endoplasmic reticulum
Afu6g05140	ergosterol biosynthetic process
Afu6g05150	nucleus
Afu6g05150	negative regulation of transcription
Afu6g05150	general transcriptional repressor activity
Afu6g05160	nucleus
Afu6g05160	regulation of transcription, DNA-dependent
Afu6g05160	zinc ion binding
Afu6g05160	response to carbohydrate stimulus
Afu6g05160	transcription activator activity
Afu6g05170	mitochondrion
Afu6g05170	mitochondrial transport
Afu6g05170	FAD transmembrane transporter activity
Afu6g05180	nuclear mRNA splicing, via spliceosome
Afu6g05180	RNA binding
Afu6g05180	U2 snRNP
Afu6g05200	structural constituent of ribosome
Afu6g05200	translation
Afu6g05200	ribosome biogenesis
Afu6g05210	mitochondrial matrix
Afu6g05210	tricarboxylic acid cycle
Afu6g05210	malate metabolic process
Afu6g05210	L-malate dehydrogenase activity
Afu6g05240	nucleus
Afu6g05240	cytoplasm
Afu6g05240	SUMO ligase activity
Afu6g05240	chromosome condensation
Afu6g05260	integral to plasma membrane
Afu6g05260	GPI anchor biosynthetic process
Afu6g05260	transferase activity
Afu6g05260	integral to endoplasmic reticulum membrane
Afu6g05290	exocyst
Afu6g05290	cytokinesis
Afu6g05290	protein binding
Afu6g05290	Golgi to plasma membrane transport
Afu6g05290	vesicle docking during exocytosis

Afu6g05290	vesicle fusion
Afu6g05300	regulation of carbohydrate metabolic process
Afu6g05300	transcription
Afu6g05300	transcription activator activity
Afu6g05300	CCAAT-binding factor complex
Afu6g05310	biological process unknown
Afu6g05310	molecular function unknown
Afu6g05310	nucleolus
Afu6g05320	purine-nucleoside phosphorylase activity
Afu6g05320	purine nucleoside catabolic process
Afu6g05320	cellular component unknown
Afu6g05340	tryptophan-tRNA ligase activity
Afu6g05340	mitochondrion
Afu6g05340	tryptophanyl-tRNA aminoacylation
Afu6g05350	aspartic-type endopeptidase activity
Afu6g05350	protein catabolic process
Afu6g05350	cell wall-bounded periplasmic space
Afu6g06330	tRNA methylation
Afu6g06340	glutamine-fructose-6-phosphate transaminase (isomerizing) activity
Afu6g06340	amino sugar metabolic process
Afu6g06360	conjugation with cellular fusion
Afu6g06360	pheromone-dependent signal transduction involved in conjugation with cellular fusion
Afu6g06360	mating pheromone activity
Afu6g06360	extracellular region
Afu6g06370	isocitrate dehydrogenase (NAD+) activity
Afu6g06370	mitochondrial matrix
Afu6g06370	tricarboxylic acid cycle
Afu6g06370	isocitrate metabolic process
Afu6g06370	glutamate biosynthetic process
Afu6g06380	cellular bud site selection
Afu6g06380	nucleus
Afu6g06380	cytoplasm
Afu6g06380	S-adenosylmethionine-dependent methyltransferase activity
Afu6g06400	septin ring assembly
Afu6g06400	signal transducer activity
Afu6g06400	Rho GTPase activator activity
Afu6g06400	intracellular
Afu6g06400	small GTPase mediated signal transduction
Afu6g06400	establishment of cell polarity (sensu Fungi)
Afu6g06420	molecular function unknown
Afu6g06420	nucleus
Afu6g06420	mitochondrion organization
Afu6g06430	chaperone activity
Afu6g06430	nucleus
Afu6g06430	nucleolus
Afu6g06430	rRNA processing
Afu6g06430	35S primary transcript processing
Afu6g06430	protein complex assembly
Afu6g06440	endopeptidase activity
Afu6g06440	proteasome core complex

Afu6g06440	ubiquitin-dependent protein catabolic process
Afu6g06450	endopeptidase activity
Afu6g06450	proteasome core complex
Afu6g06450	ubiquitin-dependent protein catabolic process
Afu6g06450	proteasome core complex, beta-subunit complex
Afu6g06460	catalytic activity
Afu6g06460	metabolic process
Afu6g06500	structural constituent of cytoskeleton
Afu6g06500	Arp2/3 protein complex
Afu6g06500	actin filament organization
Afu6g06510	biological process unknown
Afu6g06510	cellular component unknown
Afu6g06510	lipase activity
Afu6g06520	biological process unknown
Afu6g06520	molecular function unknown
Afu6g06520	plasma membrane
Afu6g06540	proteasome complex
Afu6g06540	protein binding
Afu6g06540	protein catabolic process
Afu6g06550	helicase activity
Afu6g06550	nucleus
Afu6g06570	biological process unknown
Afu6g06570	molecular function unknown
Afu6g06570	mitochondrion
Afu6g06580	phosphomannomutase activity
Afu6g06580	cytosol
Afu6g06580	protein targeting to ER
Afu6g06590	biological process unknown
Afu6g06590	cellular component unknown
Afu6g06590	chaperone regulator activity
Afu6g06610	protein binding
Afu6g06610	protein folding
Afu6g06620	molecular function unknown
Afu6g06620	ER to Golgi vesicle-mediated transport
Afu6g06620	COPII-coated vesicle
Afu6g06680	transporter activity
Afu6g06680	plasma membrane
Afu6g06680	transport
Afu6g06710	establishment of cell polarity (sensu Saccharomyces)
Afu6g06710	protein geranylgeranyltransferase activity
Afu6g06710	signal transducer activity
Afu6g06710	intracellular
Afu6g06710	cellular calcium ion homeostasis
Afu6g06710	small GTPase mediated signal transduction
Afu6g06710	protein amino acid geranylgeranylation
Afu6g06720	biological process unknown
Afu6g06720	protein kinase activity
Afu6g06720	cellular component unknown
Afu6g06740	calcium-transporting ATPase activity
Afu6g06740	Golgi apparatus

Afu6g06740	calcium ion transport
Afu6g06740	manganese ion transport
Afu6g06740	manganese-transporting ATPase activity
Afu6g06740	secretory pathway
Afu6g06750	activation of MAPK (pseudohyphal growth)
Afu6g06750	DNA binding
Afu6g06750	protein binding
Afu6g06750	nucleus
Afu6g06750	glycogen metabolic process
Afu6g06750	pseudohyphal growth
Afu6g06750	Ras protein signal transduction
Afu6g06760	translation initiation factor activity
Afu6g06760	eukaryotic translation initiation factor 3 complex
Afu6g06760	translational initiation
Afu6g06770	phosphopyruvate hydratase complex
Afu6g06770	phosphopyruvate hydratase activity
Afu6g06770	cytoplasm
Afu6g06770	gluconeogenesis
Afu6g06770	glycolysis
Afu6g06770	pathogenesis
Afu6g06780	endopeptidase activity
Afu6g06780	nucleus
Afu6g06780	proteasome regulatory particle
Afu6g06780	ubiquitin-dependent protein catabolic process
Afu6g06780	proteasome regulatory particle, base subcomplex
Afu6g06780	ATPase activity
Afu6g06790	mannosyl-oligosaccharide 1,2-alpha-mannosidase activity
Afu6g06790	endoplasmic reticulum
Afu6g06790	protein amino acid N-linked glycosylation
Afu6g06820	single strand break repair
Afu6g06820	polynucleotide 3'-phosphatase activity
Afu6g06860	sexual reproduction
Afu6g06870	cell morphogenesis
Afu6g06870	cytokinesis
Afu6g06870	casein kinase I activity
Afu6g06870	plasma membrane
Afu6g06870	protein amino acid phosphorylation
Afu6g06870	endocytosis
Afu6g06880	negative regulation of transposition, DNA-mediated
Afu6g06880	molecular function unknown
Afu6g06880	nucleus
Afu6g06900	1,3-beta-glucan synthase complex
Afu6g06900	Rho small monomeric GTPase activity
Afu6g06900	signal transducer activity
Afu6g06900	actin filament organization
Afu6g06900	cell wall organization
Afu6g06900	small GTPase mediated signal transduction
Afu6g06960	fructose transmembrane transporter activity
Afu6g06960	galactose transmembrane transporter activity
Afu6g06960	glucose transmembrane transporter activity

Afu6g06960	plasma membrane
Afu6g06960	hexose transport
Afu6g06960	mannose transmembrane transporter activity
Afu6g07010	transcription factor activity
Afu6g07010	sporocarp development
Afu6g07010	regulation of transcription
Afu6g07010	regulation of developmental process
Afu6g07020	cell morphogenesis
Afu6g07020	phospholipid binding
Afu6g07020	Rho protein signal transduction
Afu6g07050	monovalent cation:hydrogen antiporter activity
Afu6g07050	integral to membrane
Afu6g07060	metabolic process
Afu6g07060	hydrolase activity
Afu6g07080	biological process unknown
Afu6g07080	molecular function unknown
Afu6g07080	nucleus
Afu6g07080	nucleolus
Afu6g07090	alcohol dehydrogenase activity, zinc-dependent
Afu6g07090	mitochondrion
Afu6g07090	fermentation
Afu6g07100	molecular function unknown
Afu6g07100	cytoplasm
Afu6g07100	peptidyl-diphthamide biosynthetic process from peptidyl-histidine
Afu6g07120	nuclear migration
Afu6g07130	RNA polymerase II transcription factor activity
Afu6g07130	nucleus
Afu6g07130	cytoplasm
Afu6g07130	zinc ion binding
Afu6g07130	regulation of transcription
Afu6g07150	actin cross-linking activity
Afu6g07150	actin filament
Afu6g07150	S-adenosylmethionine-dependent methyltransferase activity
Afu6g07150	actin cytoskeleton organization
Afu6g07160	nonselective channel activity
Afu6g07210	structural constituent of ribosome
Afu6g07210	mitochondrial small ribosomal subunit
Afu6g07210	translation
Afu6g07240	prenyltransferase activity
Afu6g07240	carrier activity
Afu6g07240	mitochondrial inner membrane
Afu6g07240	ubiquinone metabolic process
Afu6g07240	isoprenoid binding
Afu6g07260	plasma membrane
Afu6g07260	vitamin or cofactor transporter activity
Afu6g07260	vitamin or cofactor transport
Afu6g07270	very-long-chain fatty acid metabolic process
Afu6g07270	long-chain-fatty-acid-CoA ligase activity
Afu6g07270	long-chain fatty acid transporter activity
Afu6g07270	peroxisome

Afu6g07270	microsome
Afu6g07270	lipid particle
Afu6g07270	plasma membrane
Afu6g07270	lipid transport
Afu6g07280	ATP-binding cassette (ABC) transporter activity
Afu6g07280	cytoplasm
Afu6g07280	endoplasmic reticulum
Afu6g07280	transport
Afu6g07280	integral to membrane
Afu6g07290	molecular function unknown
Afu6g07290	endoplasmic reticulum membrane
Afu6g07290	ER to Golgi vesicle-mediated transport
Afu6g07290	COPII-coated vesicle
Afu6g07300	S phase of mitotic cell cycle
Afu6g07300	nuclear mRNA splicing, via spliceosome
Afu6g07300	nucleic acid binding
Afu6g07300	nuclear envelope
Afu6g07300	nuclear pore
Afu6g07300	spliceosomal complex
Afu6g07300	DNA replication
Afu6g07300	pre-mRNA splicing factor activity
Afu6g07330	methionyl aminopeptidase activity
Afu6g07330	cytosolic ribosome (sensu Eukaryota)
Afu6g07330	proteolysis
Afu6g07340	kynurenine 3-monooxygenase activity
Afu6g07340	mitochondrion
Afu6g07340	NAD biosynthetic process
Afu6g07360	structural constituent of ribosome
Afu6g07360	mitochondrial small ribosomal subunit
Afu6g07360	translation
Afu6g07390	isocitrate dehydrogenase activity
Afu6g07390	cytoplasm
Afu6g07390	mitochondrion
Afu6g07390	lysine biosynthetic process
Afu6g07430	pyruvate kinase activity
Afu6g07430	cytosol
Afu6g07430	pyruvate metabolic process
Afu6g07430	glycolysis
Afu6g07440	1-phosphatidylinositol-3-phosphate 5-kinase activity
Afu6g07440	vacuolar membrane
Afu6g07440	phospholipid metabolic process
Afu6g07440	response to stress
Afu6g07440	vacuole organization
Afu6g07480	polysaccharide catabolic process
Afu6g07480	hydrolase activity, hydrolyzing O-glycosyl compounds
Afu6g07490	biological process unknown
Afu6g07490	molecular function unknown
Afu6g07490	cytoplasm
Afu6g07500	single-stranded DNA specific endodeoxyribonuclease activity
Afu6g07500	nucleotide-excision repair factor 3 complex

Afu6g07500	nucleotide-excision repair, DNA incision, 3'-to lesion
Afu6g07530	transcription factor activity
Afu6g07530	nucleus
Afu6g07530	transcription
Afu6g07540	chaperone activity
Afu6g07540	cytoplasm
Afu6g07540	cytoskeleton
Afu6g07540	protein folding
Afu6g07540	cytoskeleton organization
Afu6g07570	biological process unknown
Afu6g07570	molecular function unknown
Afu6g07570	integral to membrane
Afu6g07580	biological process unknown
Afu6g07580	molecular function unknown
Afu6g07580	cytoplasm
Afu6g07590	biological process unknown
Afu6g07590	molecular function unknown
Afu6g07590	cellular component unknown
Afu6g07620	cell wall mannoprotein biosynthetic process
Afu6g07620	mannose-1-phosphate guanylyltransferase activity
Afu6g07620	cytoplasm
Afu6g07620	protein amino acid glycosylation
Afu6g07620	GDP-mannose biosynthetic process
Afu6g07630	GTPase activity
Afu6g07630	membrane fraction
Afu6g07630	protein targeting to vacuole
Afu6g07630	peroxisome organization
Afu6g07630	vacuolar transport
Afu6g07630	protein retention in Golgi apparatus
Afu6g07640	lysine-tRNA ligase activity
Afu6g07640	cytoplasm
Afu6g07640	lysyl-tRNA aminoacylation
Afu6g07670	molecular function unknown
Afu6g07670	mitochondrial inner membrane
Afu6g07670	heme a biosynthetic process
Afu6g07670	respiratory chain complex IV assembly
Afu6g07690	mRNA (guanine-N7-)-methyltransferase activity
Afu6g07690	nucleus
Afu6g07690	mRNA capping
Afu6g07690	DNA-directed RNA polymerase II, holoenzyme
Afu6g07710	dicarboxylic acid transmembrane transporter activity
Afu6g07710	mitochondrial envelope
Afu6g07710	dicarboxylic acid transport
Afu6g07720	phosphoenolpyruvate carboxykinase (ATP) activity
Afu6g07720	cytosol
Afu6g07720	gluconeogenesis
Afu6g07730	plasma membrane
Afu6g07730	cation:cation antiporter activity
Afu6g07730	cellular monovalent inorganic cation homeostasis
Afu6g07740	molecular function unknown

Afu6g07740	peroxisomal membrane
Afu6g07740	peroxisome organization
Afu6g07750	phospholipid transporter activity
Afu6g07750	plasma membrane
Afu6g07750	phospholipid transport
Afu6g07760	endopeptidase activity
Afu6g07760	ubiquitin-dependent protein catabolic process
Afu6g07760	proteasome regulatory particle, lid subcomplex
Afu6g07770	biological process unknown
Afu6g07770	cellular component unknown
Afu6g07770	transaminase activity
Afu6g07780	ligand-regulated transcription factor activity
Afu6g07780	nucleus
Afu6g07780	transcription initiation from RNA polymerase II promoter
Afu6g07780	response to copper ion
Afu6g07800	DNA binding
Afu6g07800	RNA polymerase II transcription factor activity
Afu6g07800	nucleus
Afu6g07800	zinc ion binding
Afu6g07810	chromatin binding
Afu6g07810	chromatin remodeling
Afu6g07810	regulation of transcription from RNA polymerase II promoter
Afu6g07810	rRNA transcription
Afu6g07810	chromatin remodeling complex
Afu6g07830	ER to Golgi vesicle-mediated transport
Afu6g07830	intra-Golgi vesicle-mediated transport
Afu6g07830	ARF GTPase activator activity
Afu6g07830	clathrin-coated vesicle
Afu6g07840	protein-methionine-R-oxide reductase activity
Afu6g07840	response to oxidative stress
Afu6g07840	cellular component unknown
Afu6g07860	negative regulation of transcription by carbon catabolites
Afu6g07870	GTP binding
Afu6g07870	programmed cell death
Afu6g07870	integral to membrane
Afu6g07870	vesicle-mediated transport
Afu6g07880	biological process unknown
Afu6g07880	molecular function unknown
Afu6g07880	cellular component unknown
Afu6g07900	molecular function unknown
Afu6g07900	cellular component unknown
Afu6g07900	protein deubiquitination
Afu6g07910	biological process unknown
Afu6g07910	molecular function unknown
Afu6g07910	cellular component unknown
Afu6g07940	lactoylglutathione lyase activity
Afu6g07940	nucleus
Afu6g07940	cytoplasm
Afu6g07940	glutathione metabolic process
Afu6g07950	DNA binding

Afu6g07950	nucleus
Afu6g07950	transcription
Afu6g07980	regulation of progression through cell cycle
Afu6g07980	cyclin-dependent protein kinase activity
Afu6g07980	nucleus
Afu6g07980	cytoplasm
Afu6g07980	protein amino acid phosphorylation
Afu6g08000	biological process unknown
Afu6g08000	amidase activity
Afu6g08000	cellular component unknown
Afu6g08020	ATP-binding cassette (ABC) transporter activity
Afu6g08020	transport
Afu6g08020	integral to membrane
Afu6g08050	phosphogluconate dehydrogenase (decarboxylating) activity
Afu6g08050	cytoplasm
Afu6g08050	glucose metabolic process
Afu6g08070	biological process unknown
Afu6g08070	molecular function unknown
Afu6g08070	nucleus
Afu6g08070	cytoplasm
Afu6g08080	polysaccharide metabolic process
Afu6g08080	hydrolase activity, acting on glycosyl bonds
Afu6g08110	DNA-(apurinic or apyrimidinic site) lyase activity
Afu6g08110	nucleus
Afu6g08110	mitochondrion
Afu6g08110	DNA repair
Afu6g08110	base-excision repair
Afu6g08120	kinetochore
Afu6g08120	condensed nuclear chromosome kinetochore
Afu6g08120	protein kinase activity
Afu6g08120	protein binding
Afu6g08120	nucleus
Afu6g08120	protein amino acid phosphorylation
Afu6g08120	mitotic cell cycle spindle assembly checkpoint
Afu6g08140	metabolic process
Afu6g08140	oxidoreductase activity
Afu6g08170	DNA-directed DNA polymerase activity
Afu6g08170	nucleolus
Afu6g08170	DNA-dependent DNA replication
Afu6g08200	regulation of cyclin-dependent protein kinase activity
Afu6g08200	G2/M transition of mitotic cell cycle
Afu6g08200	protein tyrosine phosphatase activity
Afu6g08200	nucleus
Afu6g08200	cytoplasm
Afu6g08220	G1/S transition of mitotic cell cycle
Afu6g08220	G2/M transition of mitotic cell cycle
Afu6g08220	nuclear ubiquitin ligase complex
Afu6g08220	ubiquitin-protein ligase activity
Afu6g08220	structural molecule activity
Afu6g08220	ubiquitin-dependent protein catabolic process

Afu6g08220	SCF ubiquitin ligase complex
Afu6g08230	mitochondrion
Afu6g08230	protein folding
Afu6g08230	protein import into mitochondrial matrix
Afu6g08240	negative regulation of cell proliferation
Afu6g08250	biological process unknown
Afu6g08250	molecular function unknown
Afu6g08250	nucleus
Afu6g08290	ARF small monomeric GTPase activity
Afu6g08290	Golgi-associated vesicle
Afu6g08290	cytosol
Afu6g08290	ER to Golgi vesicle-mediated transport
Afu6g08290	intra-Golgi vesicle-mediated transport
Afu6g08300	DNA-directed RNA polymerase activity
Afu6g08300	DNA-directed RNA polymerase I complex
Afu6g08300	transcription from RNA polymerase I promoter
Afu6g08310	endopeptidase activity
Afu6g08310	proteasome core complex
Afu6g08310	ubiquitin-dependent protein catabolic process
Afu6g08310	proteasome core complex, beta-subunit complex
Afu6g08320	biological process unknown
Afu6g08320	molecular function unknown
Afu6g08320	cytoplasm
Afu6g08340	transporter activity
Afu6g08340	integral to plasma membrane
Afu6g08340	transport
Afu6g08340	nicotinamide mononucleotide permease activity
Afu6g08350	cytoplasm
Afu6g08350	intracellular signaling cascade
Afu6g08350	transcription regulator activity
Afu6g08360	molecular function unknown
Afu6g08360	mitochondrion
Afu6g08360	DNA repair
Afu6g08360	thiamin biosynthetic process
Afu6g08370	phospholipase C activity
Afu6g08370	cellular component unknown
Afu6g08370	response to salt stress
Afu6g08370	sphingolipid catabolic process
Afu6g08380	nuclear chromatin
Afu6g08380	chromatin binding
Afu6g08380	chromatin silencing at telomere
Afu6g08380	histone methylation
Afu6g08380	histone-lysine N-methyltransferase activity
Afu6g08420	protein polyubiquitination
Afu6g08420	proteasome complex
Afu6g08420	ubiquitin-protein ligase activity
Afu6g08420	protein monoubiquitination
Afu6g08430	RNA metabolic process
Afu6g08440	oxygen-dependent protoporphyrinogen oxidase activity
Afu6g08440	mitochondrion

Afu6g08440	porphyrin biosynthetic process
Afu6g08440	heme biosynthetic process
Afu6g08450	nucleus
Afu6g08450	cytoplasm
Afu6g08450	mRNA polyadenylation
Afu6g08450	poly(A) RNA binding
Afu6g08450	poly(A)+ mRNA export from nucleus
Afu6g08470	glycerol kinase activity
Afu6g08470	cytoplasm
Afu6g08470	glycerol metabolic process
Afu6g08480	water transport
Afu6g08480	water channel activity
Afu6g08480	glycerol channel activity
Afu6g08480	glycerol transport
Afu6g08480	integral to membrane
Afu6g08490	inorganic diphosphatase activity
Afu6g08490	cytosol
Afu6g08490	phosphate metabolic process
Afu6g08500	biological process unknown
Afu6g08500	molecular function unknown
Afu6g08500	nucleus
Afu6g08500	cytoplasm
Afu6g08510	hydrolase activity, hydrolyzing O-glycosyl compounds
Afu6g08510	cellular glucan metabolic process
Afu6g08510	fungal-type cell wall
Afu6g08520	adenylate cyclase activity
Afu6g08520	G-protein signaling, coupled to cAMP nucleotide second messenger
Afu6g08520	pathogenesis
Afu6g08530	molecular function unknown
Afu6g08530	cellular component unknown
Afu6g08530	mitotic sister chromatid separation
Afu6g08540	DNA binding
Afu6g08540	zinc ion binding
Afu6g08550	transcription factor activity
Afu6g08550	nucleus
Afu6g08550	regulation of transcription
Afu6g08560	cytoplasm
Afu6g08560	oxidoreductase activity
Afu6g08560	nonribosomal peptide biosynthetic process
Afu6g08560	amino acid activation for nonribosomal peptide biosynthetic process
Afu6g08560	amino acid adenylylation by nonribosomal peptide synthase
Afu6g08570	DNA-directed DNA polymerase activity
Afu6g08570	nucleus
Afu6g08570	DNA-dependent DNA replication
Afu6g08570	DNA repair
Afu6g08580	peptidyl-prolyl cis-trans isomerase activity
Afu6g08580	FK506 binding
Afu6g08580	nucleolus
Afu6g08580	protein folding
Afu6g08590	response to pheromone during conjugation with cellular fusion

Afu6g08590	cellular morphogenesis during conjugation with cellular fusion
Afu6g08590	protein kinase activity
Afu6g08590	nucleus
Afu6g08590	cytoplasm
Afu6g08590	regulation of exit from mitosis
Afu6g08590	establishment and/or maintenance of cell polarity (sensu Saccharomyces)
Afu6g08600	regulation of transcription involved in G1 phase of mitotic cell cycle
Afu6g08600	histone acetyltransferase activity
Afu6g08600	protein serine/threonine kinase activity
Afu6g08600	transcription factor TFIID complex
Afu6g08600	transcription initiation from RNA polymerase II promoter
Afu6g08600	protein amino acid phosphorylation
Afu6g08600	general RNA polymerase II transcription factor activity
Afu6g08610	nucleolus
Afu6g08610	snRNA capping
Afu6g08610	RNA methyltransferase activity
Afu6g08620	molecular function unknown
Afu6g08620	cytoplasm
Afu6g08620	mitotic cell cycle spindle assembly checkpoint
Afu6g08630	biological process unknown
Afu6g08630	molecular function unknown
Afu6g08630	mitochondrion
Afu6g08640	mitochondrion
Afu6g08640	mitochondrial protein processing during import
Afu6g08640	cellular iron ion homeostasis
Afu6g08640	metallopeptidase activity
Afu6g08680	cell fraction
Afu6g08680	cytosol
Afu6g08680	DNA repair
Afu6g08680	response to osmotic stress
Afu6g08680	mitotic spindle organization
Afu6g08680	protein phosphatase type 2A regulator activity
Afu6g08700	hydrolase activity, hydrolyzing O-glycosyl compounds
Afu6g08700	carbohydrate metabolic process
Afu6g08720	phosphorylase activity
Afu6g08720	cytoplasm
Afu6g08720	L-methionine salvage from methylthioadenosine
Afu6g08730	phosphogluconate dehydrogenase (decarboxylating) activity
Afu6g08730	cytoplasm
Afu6g08730	glucose metabolic process
Afu6g08750	1-pyrroline-5-carboxylate dehydrogenase activity
Afu6g08750	mitochondrion
Afu6g08750	glutamate biosynthetic process
Afu6g08750	proline catabolic process
Afu6g08760	proline dehydrogenase activity
Afu6g08760	proline catabolic process
Afu6g08780	biological process unknown
Afu6g08780	molecular function unknown
Afu6g08780	cellular component unknown
Afu6g08790	transcription factor activity

Afu6g08790	nucleus
Afu6g08790	regulation of transcription, DNA-dependent
Afu6g08790	proline catabolic process
Afu6g08790	zinc ion binding
Afu6g08800	cellular bud site selection
Afu6g08800	molecular function unknown
Afu6g08800	nucleus
Afu6g08820	3'-5'-exoribonuclease activity
Afu6g08820	nuclear-transcribed mRNA poly(A) tail shortening
Afu6g08820	conjugation with cellular fusion
Afu6g08820	cytoplasm
Afu6g08820	regulation of transcription from RNA polymerase II promoter
Afu6g08820	transcription repressor activity
Afu6g08820	CCR4-NOT core complex
Afu6g08830	mitochondrion
Afu6g08830	pyruvate metabolic process
Afu6g08850	mitochondrion
Afu6g08850	ubiquinone metabolic process
Afu6g08850	2-polyprenyl-6-methoxy-1,4-benzoquinone methyltransferase activity
Afu6g08850	aerobic respiration
Afu6g08870	nicotinate-nucleotide adenylyltransferase activity
Afu6g08870	nucleus
Afu6g08870	NAD metabolic process
Afu6g08880	protein polyubiquitination
Afu6g08880	ubiquitin-protein ligase activity
Afu6g08880	ubiquitin-protein ligase activity
Afu6g08880	cytoplasm
Afu6g08880	protein monoubiquitination
Afu6g08890	fatty acid metabolic process
Afu6g08890	CoA hydrolase activity
Afu6g08900	ribosomal large subunit assembly
Afu6g08900	ATP-dependent RNA helicase activity
Afu6g08900	nucleus
Afu6g08900	rRNA processing
Afu6g08910	cytoplasm
Afu6g08910	translation
Afu6g08910	tRNA methyltransferase activity
Afu6g08910	tRNA methylation
Afu6g08920	sulfate assimilation
Afu6g08920	sulfite reductase (NADPH) activity
Afu6g08920	sulfite reductase complex (NADPH)
Afu6g08930	biological process unknown
Afu6g08930	molecular function unknown
Afu6g08930	endoplasmic reticulum
Afu6g08960	endopeptidase activity
Afu6g08960	proteasome core complex
Afu6g08960	ubiquitin-dependent protein catabolic process
Afu6g09000	DNA binding
Afu6g09000	nucleus
Afu6g09000	chromatin remodeling

Afu6g09000	zinc ion binding
Afu6g09010	mRNA binding
Afu6g09010	U1 snRNP
Afu6g09010	mRNA splice site selection
Afu6g09020	GPI-anchor transamidase activity
Afu6g09020	attachment of GPI anchor to protein
Afu6g09020	integral to endoplasmic reticulum membrane
Afu6g09020	GPI-anchor transamidase complex
Afu6g09060	structural constituent of ribosome
Afu6g09060	mitochondrial large ribosomal subunit
Afu6g09060	translation
Afu6g09070	sulfate assimilation
Afu6g09070	cytoplasm
Afu6g09070	3'(2'),5'-bisphosphate nucleotidase activity
Afu6g09070	methionine biosynthetic process
Afu6g09070	hyperosmotic salinity response
Afu6g09080	molecular function unknown
Afu6g09080	cell cortex
Afu6g09080	endocytosis
Afu6g09080	actin filament organization
Afu6g09110	integral to plasma membrane
Afu6g09110	multidrug transport
Afu6g09110	multidrug efflux pump activity
Afu6g09110	response to drug
Afu6g09140	biological process unknown
Afu6g09140	molecular function unknown
Afu6g09140	cytoplasm
Afu6g09160	protein polyubiquitination
Afu6g09160	ubiquitin conjugating enzyme activity
Afu6g09160	cytoplasm
Afu6g09160	protein monoubiquitination
Afu6g09160	negative regulation of gluconeogenesis
Afu6g09170	3-methyl-2-oxobutanoate hydroxymethyltransferase activity
Afu6g09170	mitochondrion
Afu6g09170	pantothenate biosynthetic process
Afu6g09180	protein serine/threonine kinase activity
Afu6g09180	nucleoplasm
Afu6g09180	DNA replication initiation
Afu6g09180	regulation of DNA replication
Afu6g09180	protein amino acid phosphorylation
Afu6g09190	mitochondrion
Afu6g09190	proteolysis
Afu6g09190	X-Pro aminopeptidase activity
Afu6g09210	histone deacetylase complex
Afu6g09210	nucleus
Afu6g09210	transcriptional gene silencing
Afu6g09210	NAD-dependent histone deacetylase activity
Afu6g09210	NAD-independent histone deacetylase activity
Afu6g09220	nucleus
Afu6g09220	chromatin assembly or disassembly

Afu6g09220	mating type switching
Afu6g09220	DNA-dependent ATPase activity
Afu6g09240	protein kinase activity
Afu6g09240	nucleus
Afu6g09240	cytoplasm
Afu6g09240	protein amino acid phosphorylation
Afu6g09250	glucan 1,3-beta-glucosidase activity
Afu6g09250	1,3-beta-glucan metabolic process
Afu6g09250	cell wall organization
Afu6g09250	fungal-type cell wall
Afu6g09260	two-component sensor activity
Afu6g09260	protein histidine kinase activity
Afu6g09260	protein amino acid phosphorylation
Afu6g09310	chitinase activity
Afu6g09310	chitin catabolic process
Afu6g09320	chitin binding
Afu6g09350	zinc ion binding
Afu6g09440	tetrahydrofolylpolyglutamate synthase activity
Afu6g09440	cytoplasm
Afu6g09440	folic acid and derivative metabolic process
Afu6g09440	dihydrofolate synthase activity
Afu6g09440	tetrahydrofolate biosynthetic process
Afu6g09450	nucleotide binding
Afu6g09450	cellular component unknown
Afu6g09500	protein binding
Afu6g09500	protein folding
Afu6g09550	biological process unknown
Afu6g09550	molecular function unknown
Afu6g09550	integral to membrane
Afu6g09590	metabolic process
Afu6g09590	zinc ion binding
Afu6g09590	oxidoreductase activity
Afu6g09600	carboxypeptidase activity
Afu6g09600	proteolysis
Afu6g09600	metallopeptidase activity
Afu6g09610	pathogenesis
Afu6g09610	nonribosomal peptide biosynthetic process
Afu6g09640	transaminase activity
Afu6g09640	secondary metabolic process
Afu6g09660	catalytic activity
Afu6g09660	nonribosomal peptide biosynthetic process
Afu6g09660	secondary metabolic process
Afu6g09660	secondary metabolic process
Afu6g09660	peptide antibiotic biosynthetic process
Afu6g09660	amino acid adenylylation by nonribosomal peptide synthase
Afu6g09670	metabolic process
Afu6g09670	oxidoreductase activity
Afu6g09680	O-methyltransferase activity
Afu6g09680	S-adenosylmethionine-dependent methyltransferase activity
Afu6g09710	transporter activity

Afu6g09710	transport
Afu6g09730	metabolic process
Afu6g09730	oxidoreductase activity
Afu6g09740	secondary metabolic process
Afu6g09760	metabolic process
Afu6g09760	oxidoreductase activity
Afu6g09770	farnesyltranstransferase activity
Afu6g09770	mitochondrion
Afu6g09770	terpenoid biosynthetic process
Afu6g09780	chitinase activity
Afu6g09780	chitin catabolic process
Afu6g09790	chitin binding
Afu6g09810	biological process unknown
Afu6g09810	nucleus
Afu6g09810	ATPase activity
Afu6g09820	nucleolus
Afu6g09820	ER to Golgi vesicle-mediated transport
Afu6g09880	transporter activity
Afu6g09880	transport
Afu6g09880	monocarboxylic acid transmembrane transporter activity
Afu6g09880	membrane
Afu6g09900	metabolic process
Afu6g09900	oxidoreductase activity
Afu6g09930	transcription factor activity
Afu6g09930	nucleus
Afu6g09930	cytoplasm
Afu6g09930	transcription
Afu6g09930	response to oxidative stress
Afu6g09930	response to drug
Afu6g09980	fungal-type vacuole membrane
Afu6g09980	sphingolipid metabolic process
Afu6g09980	sphingolipid transporter activity
Afu6g09990	nucleus
Afu6g09990	nuclear pore
Afu6g09990	cytoplasm
Afu6g09990	protein import into nucleus
Afu6g09990	protein transmembrane transporter activity
Afu6g10010	transcription factor activity
Afu6g10010	regulation of transcription
Afu6g10020	mediator complex
Afu6g10020	transcription from RNA polymerase II promoter
Afu6g10020	RNA polymerase II transcription mediator activity
Afu6g10030	fungal-type vacuole membrane
Afu6g10030	diacylglycerol pyrophosphate phosphatase activity
Afu6g10030	phospholipid metabolic process
Afu6g10030	phosphatidate phosphatase activity
Afu6g10040	extracellular region
Afu6g10040	cellular amino acid metabolic process
Afu6g10040	oxidoreductase activity
Afu6g10050	endoplasmic reticulum

Afu6g10050	integral to plasma membrane
Afu6g10050	sulfur metabolic process
Afu6g10050	oligopeptide transporter activity
Afu6g10060	F-actin capping activity
Afu6g10060	endocytosis
Afu6g10060	response to osmotic stress
Afu6g10060	actin filament organization
Afu6g10060	cell wall organization
Afu6g10060	F-actin capping protein complex
Afu6g10090	cytosol
Afu6g10090	NADH regeneration
Afu6g10090	formate dehydrogenase activity
Afu6g10090	formate catabolic process
Afu6g10100	transporter activity
Afu6g10100	mitochondrion
Afu6g10100	transport
Afu6g10100	monocarboxylic acid transmembrane transporter activity
Afu6g10100	membrane
Afu6g10120	nucleus
Afu6g10120	cytoplasm
Afu6g10120	alcohol dehydrogenase (NADP+) activity
Afu6g10120	metabolic process
Afu6g10120	zinc ion binding
Afu6g10140	transcription factor activity
Afu6g10140	nucleus
Afu6g10140	regulation of transcription
Afu6g10210	cytoplasm
Afu6g10210	hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in linear amides
Afu6g10210	guanine metabolic process
Afu6g10220	endoplasmic reticulum
Afu6g10220	integral to plasma membrane
Afu6g10220	sulfur metabolic process
Afu6g10220	oligopeptide transporter activity
Afu6g10240	two-component sensor activity
Afu6g10240	protein histidine kinase activity
Afu6g10240	protein amino acid phosphorylation
Afu6g10240	pathogenesis
Afu6g10250	serine-type endopeptidase activity
Afu6g10250	protein catabolic process
Afu6g10260	aldehyde reductase activity
Afu6g10260	nucleus
Afu6g10260	cytoplasm
Afu6g10260	cellular aldehyde metabolic process
Afu6g10300	vacuole inheritance
Afu6g10300	fungal-type vacuole
Afu6g10300	cytosol
Afu6g10300	DNA-dependent DNA replication
Afu6g10300	response to oxidative stress
Afu6g10300	regulation of cell redox homeostasis
Afu6g10300	thiol-disulfide exchange intermediate activity

Afu6g10300	vacuole fusion, non-autophagic
Afu6g10320	molecular function unknown
Afu6g10320	nucleolus
Afu6g10320	ribosome biogenesis
Afu6g10330	M phase of mitotic cell cycle
Afu6g10330	small monomeric GTPase activity
Afu6g10330	protein binding
Afu6g10330	spindle pole body
Afu6g10330	signal transduction
Afu6g10360	biological process unknown
Afu6g10360	molecular function unknown
Afu6g10360	cellular component unknown
Afu6g10370	nucleus
Afu6g10370	RNA catabolic process
Afu6g10370	RNA lariat debranching enzyme activity
Afu6g10370	snoRNA metabolic process
Afu6g10380	protein binding
Afu6g10380	nucleus
Afu6g10380	ubiquitin cycle
Afu6g10390	protein binding
Afu6g10410	fungal-type vacuole membrane
Afu6g10410	molecular function unknown
Afu6g10410	Golgi to endosome transport
Afu6g10410	vesicle docking during exocytosis
Afu6g10410	homotypic vacuole fusion, non-autophagic
Afu6g10410	late endosome to vacuole transport
Afu6g10430	chitin deacetylase activity
Afu6g10430	chitosan layer of spore wall
Afu6g10430	chitin metabolic process
Afu6g10430	chitin binding
Afu6g10460	replicative cell aging
Afu6g10460	endoplasmic reticulum
Afu6g10460	protein transporter activity
Afu6g10460	ceramide biosynthetic process
Afu6g10470	regulation of progression through cell cycle
Afu6g10470	protein binding
Afu6g10470	nucleolus
Afu6g10470	cytoplasm
Afu6g10480	peptidyl-prolyl cis-trans isomerase activity
Afu6g10480	mitochondrion
Afu6g10480	protein folding
Afu6g10510	nucleus
Afu6g10510	ligase activity
Afu6g10510	protein sumoylation
Afu6g10510	SUMO activating enzyme activity
Afu6g10510	SMT3-dependent protein catabolic process
Afu6g10530	transcription elongation regulator activity
Afu6g10530	RNA elongation from RNA polymerase II promoter
Afu6g10530	transcription elongation factor complex
Afu6g10540	tRNA-intron endonuclease activity

Afu6g10540	tRNA-intron endonuclease complex
Afu6g10540	nuclear inner membrane
Afu6g10540	tRNA splicing, via endonucleolytic cleavage and ligation
Afu6g10590	ubiquitin-protein ligase activity
Afu6g10590	endoplasmic reticulum membrane
Afu6g10590	ubiquitin-dependent protein catabolic process
Afu6g10600	nucleus
Afu6g10600	NEDD8 activating enzyme activity
Afu6g10600	amyloid precursor protein metabolic process
Afu6g10610	ribose-5-phosphate isomerase activity
Afu6g10610	nucleus
Afu6g10610	cytoplasm
Afu6g10610	pentose-phosphate shunt
Afu6g10620	structural molecule activity
Afu6g10620	nuclear pore
Afu6g10620	mRNA export from nucleus
Afu6g10620	rRNA export from nucleus
Afu6g10620	snRNA export from nucleus
Afu6g10620	tRNA export from nucleus
Afu6g10620	protein import into nucleus
Afu6g10620	NLS-bearing substrate import into nucleus
Afu6g10620	snRNP protein import into nucleus
Afu6g10620	mRNA-binding (hnRNP) protein import into nucleus
Afu6g10620	ribosomal protein import into nucleus
Afu6g10620	protein export from nucleus
Afu6g10620	nuclear envelope organization
Afu6g10620	nuclear pore organization
Afu6g10630	ATP binding
Afu6g10630	molecular function unknown
Afu6g10630	cytoplasm
Afu6g10650	ATP citrate synthase activity
Afu6g10690	mRNA cleavage and polyadenylation specificity factor complex
Afu6g10690	mRNA polyadenylation
Afu6g10690	mRNA cleavage
Afu6g10690	cleavage and polyadenylylation specificity factor activity
Afu6g10700	chaperone activity
Afu6g10700	mitochondrial matrix
Afu6g10700	protein folding
Afu6g10720	sulfonate dioxygenase activity
Afu6g10720	sulfur metabolic process
Afu6g10720	cellular component unknown
Afu6g10760	metabolic process
Afu6g10760	hydrolase activity
Afu6g10770	protein binding
Afu6g10810	homogentisate 1,2-dioxygenase activity
Afu6g10810	L-phenylalanine catabolic process
Afu6g10810	tyrosine catabolic process
Afu6g10830	G1/S transition of mitotic cell cycle
Afu6g10830	protein phosphatase type 2A activity
Afu6g10830	protein phosphatase type 2A complex

Afu6g10830	translation
Afu6g10830	protein amino acid dephosphorylation
Afu6g10830	actin filament organization
Afu6g10830	mitotic cell cycle spindle assembly checkpoint
Afu6g10830	budding cell bud growth
Afu6g10880	electron transporter activity
Afu6g10880	endoplasmic reticulum membrane
Afu6g10880	microsome
Afu6g10880	sterol biosynthetic process
Afu6g10890	actin cortical patch (sensu Saccharomyces)
Afu6g10890	actin filament organization
Afu6g10890	actin cytoskeleton
Afu6g10890	actin cytoskeleton organization
Afu6g10990	electron transporter activity
Afu6g10990	microsome
Afu6g10990	ergosterol biosynthetic process
Afu6g11010	regulation of progression through cell cycle
Afu6g11010	cell morphogenesis
Afu6g11010	protein binding
Afu6g11010	signal transduction
Afu6g11020	valine catabolic process
Afu6g11020	3-hydroxyisobutyrate dehydrogenase activity
Afu6g11040	FMN adenylyltransferase activity
Afu6g11040	cytoplasm
Afu6g11040	FAD biosynthetic process
Afu6g11070	ATP-dependent RNA helicase activity
Afu6g11070	nucleolus
Afu6g11070	35S primary transcript processing
Afu6g11100	plasma membrane
Afu6g11100	basic amino acid transmembrane transporter activity
Afu6g11100	basic amino acid transport
Afu6g11110	DNA binding
Afu6g11110	nucleus
Afu6g11110	zinc ion binding
Afu6g11120	ribosomal large subunit assembly
Afu6g11120	ATP-dependent RNA helicase activity
Afu6g11120	nucleolus
Afu6g11120	35S primary transcript processing
Afu6g11130	DNA binding
Afu6g11130	DNA replication factor A complex
Afu6g11130	DNA unwinding during replication
Afu6g11130	DNA replication, synthesis of RNA primer
Afu6g11130	DNA strand elongation during DNA replication
Afu6g11130	nucleotide-excision repair
Afu6g11130	postreplication repair
Afu6g11130	double-strand break repair
Afu6g11130	DNA recombination
Afu6g11140	biological process unknown
Afu6g11140	molecular function unknown
Afu6g11140	cellular component unknown

Afu6g11160	isopentenyl-diphosphate delta-isomerase activity
Afu6g11160	cytosol
Afu6g11160	ergosterol biosynthetic process
Afu6g11170	DNA binding
Afu6g11170	nucleus
Afu6g11170	zinc ion binding
Afu6g11190	Golgi membrane
Afu6g11190	protein serine/threonine kinase activity
Afu6g11190	protein binding
Afu6g11190	protein amino acid phosphorylation
Afu6g11190	protein targeting to vacuole
Afu6g11190	vacuolar transport
Afu6g11190	protein retention in Golgi apparatus
Afu6g11220	biological process unknown
Afu6g11220	Rab GTPase activator activity
Afu6g11220	soluble fraction
Afu6g11230	transcription factor activity
Afu6g11230	nucleus
Afu6g11230	zinc ion binding
Afu6g11230	regulation of transcription
Afu6g11260	RNA binding
Afu6g11260	structural constituent of ribosome
Afu6g11260	cytosolic large ribosomal subunit (sensu Eukaryota)
Afu6g11260	translation
Afu6g11270	v-SNARE activity
Afu6g11270	Golgi to plasma membrane transport
Afu6g11270	endocytosis
Afu6g11270	vesicle fusion
Afu6g11270	transport vesicle
Afu6g11300	ion channel activity
Afu6g11300	transport
Afu6g11300	integral to membrane
Afu6g11310	aspartate carbamoyltransferase activity
Afu6g11310	carbamoyl-phosphate synthase activity
Afu6g11310	cytoplasm
Afu6g11310	membrane
Afu6g11310	pyrimidine base biosynthetic process
Afu6g11320	transporter activity
Afu6g11320	integral to plasma membrane
Afu6g11320	transport
Afu6g11330	acid phosphatase activity
Afu6g11330	thiamin transport
Afu6g11330	cell wall-bounded periplasmic space
Afu6g11340	biological process unknown
Afu6g11340	cytoplasm
Afu6g11340	peroxisomal membrane
Afu6g11340	peroxisomal matrix
Afu6g11340	AMP binding
Afu6g11360	biological process unknown
Afu6g11360	ATP-binding cassette (ABC) transporter activity

Afu6g11360	mitochondrion
Afu6g11370	actin cap (sensu Saccharomyces)
Afu6g11370	exocyst
Afu6g11370	establishment of cell polarity (sensu Saccharomyces)
Afu6g11370	nuclear mRNA splicing, via spliceosome
Afu6g11370	cytokinesis
Afu6g11370	molecular function unknown
Afu6g11370	Golgi to plasma membrane transport
Afu6g11370	vesicle docking during exocytosis
Afu6g11370	vesicle fusion
Afu6g11370	bipolar cellular bud site selection
Afu6g11380	mitochondrial outer membrane translocase complex
Afu6g11380	mitochondrial translocation
Afu6g11380	protein transporter activity
Afu6g11390	cell wall organization
Afu6g11390	fungal-type cell wall
Afu6g11390	1,3-beta-glucanosyltransferase activity
Afu6g11410	meiotic DNA double-strand break processing
Afu6g11410	double-strand break repair via break-induced replication
Afu6g11410	endonuclease activity
Afu6g11410	protein binding
Afu6g11410	nucleus
Afu6g11410	DNA repair
Afu6g11410	double-strand break repair via nonhomologous end joining
Afu6g11410	3'-5' exonuclease activity
Afu6g11410	meiotic DNA double-strand break formation
Afu6g11430	aldehyde dehydrogenase (NAD) activity
Afu6g11430	mitochondrion
Afu6g11430	ethanol metabolic process
Afu6g11470	G1/S transition of mitotic cell cycle
Afu6g11470	protein serine/threonine phosphatase activity
Afu6g11470	nucleus
Afu6g11470	cytoplasm
Afu6g11470	protein amino acid phosphorylation
Afu6g11470	cell wall organization
Afu6g11470	protein kinase cascade
Afu6g11470	actin cytoskeleton organization
Afu6g11510	catalytic activity
Afu6g11510	electron transporter activity
Afu6g11510	endoplasmic reticulum
Afu6g11510	electron transport
Afu6g11540	biological process unknown
Afu6g11540	molecular function unknown
Afu6g11540	mitochondrion
Afu6g11570	metabolic process
Afu6g11570	hydrolase activity
Afu6g11590	catechol catabolic process
Afu6g11590	4-carboxymuconolactone decarboxylase activity
Afu6g11620	formyltetrahydrofolate deformylase activity
Afu6g11620	purine ribonucleotide biosynthetic process

Afu6g11630	FAD binding
Afu6g11650	metabolic process
Afu6g11650	oxidoreductase activity
Afu6g11660	carboxypeptidase activity
Afu6g11660	proteolysis
Afu6g11750	transcription factor activity
Afu6g11750	nucleus
Afu6g11750	regulation of transcription
Afu6g11800	biological process unknown
Afu6g11800	molecular function unknown
Afu6g11800	integral to membrane
Afu6g11810	biological process unknown
Afu6g11810	molecular function unknown
Afu6g11810	integral to membrane
Afu6g11820	polysaccharide catabolic process
Afu6g11820	hydrolase activity, acting on glycosyl bonds
Afu6g11890	mitochondrial fission
Afu6g11890	GTPase activity
Afu6g11890	mitochondrial outer membrane
Afu6g11910	hydrolase activity, hydrolyzing O-glycosyl compounds
Afu6g11910	carbohydrate metabolic process
Afu6g11920	alpha-glucoside transport
Afu6g11920	alpha-glucoside:hydrogen symporter activity
Afu6g11920	maltose:hydrogen symporter activity
Afu6g11920	membrane fraction
Afu6g11920	trehalose transmembrane transporter activity
Afu6g11920	trehalose transport
Afu6g11980	hydrolase activity, hydrolyzing O-glycosyl compounds
Afu6g11980	1,3-beta-glucan metabolic process
Afu6g11980	fungal-type cell wall
Afu6g12010	hydrolase activity, hydrolyzing O-glycosyl compounds
Afu6g12010	carbohydrate metabolic process
Afu6g12020	DNA binding
Afu6g12020	nucleus
Afu6g12020	zinc ion binding
Afu6g12040	alpha-glucoside transport
Afu6g12040	alpha-glucoside:hydrogen symporter activity
Afu6g12040	maltose:hydrogen symporter activity
Afu6g12040	membrane fraction
Afu6g12040	trehalose transmembrane transporter activity
Afu6g12040	trehalose transport
Afu6g12050	catalytic activity
Afu6g12050	nonribosomal peptide biosynthetic process
Afu6g12050	amino acid adenylylation by nonribosomal peptide synthase
Afu6g12060	monooxygenase activity
Afu6g12060	cellular aromatic compound metabolic process
Afu6g12070	FAD binding
Afu6g12080	catalytic activity
Afu6g12080	nonribosomal peptide biosynthetic process
Afu6g12080	amino acid adenylylation by nonribosomal peptide synthase

Afu6g12090	programmed cell death
Afu6g12100	biological process unknown
Afu6g12100	cellular component unknown
Afu6g12100	hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in other compounds
Afu6g12110	tryptophan biosynthetic process
Afu6g12110	anthranilate synthase activity
Afu6g12110	cytoplasm
Afu6g12130	nucleus
Afu6g12130	galactose metabolic process
Afu6g12130	regulation of transcription, DNA-dependent
Afu6g12130	transcription activator activity
Afu6g12150	transcription factor activity
Afu6g12150	nucleus
Afu6g12150	transcription
Afu6g12160	transcription factor activity
Afu6g12160	nucleus
Afu6g12160	regulation of transcription
Afu6g12170	peptidyl-prolyl cis-trans isomerase activity
Afu6g12170	nucleus
Afu6g12170	cytoplasm
Afu6g12170	ribosome assembly
Afu6g12210	xylan metabolic process
Afu6g12250	3-oxoacid CoA-transferase activity
Afu6g12250	ketone body catabolic process
Afu6g12270	ubiquitin-specific protease activity
Afu6g12270	cytoplasm
Afu6g12270	protein deubiquitination
Afu6g12290	biological process unknown
Afu6g12290	molecular function unknown
Afu6g12290	cytoplasm
Afu6g12300	nucleus
Afu6g12300	cytoplasm
Afu6g12300	protein import into nucleus
Afu6g12300	heterogeneous nuclear ribonucleoprotein complex
Afu6g12330	biological process unknown
Afu6g12330	molecular function unknown
Afu6g12330	nucleus
Afu6g12330	cytoplasm
Afu6g12340	signal transducer activity
Afu6g12340	GTPase activator activity
Afu6g12340	Ras GTPase activator activity
Afu6g12340	intracellular
Afu6g12340	small GTPase mediated signal transduction
Afu6g12350	autophagic vacuole formation
Afu6g12350	molecular function unknown
Afu6g12350	membrane fraction
Afu6g12350	cytoplasm
Afu6g12350	protein targeting to vacuole
Afu6g12350	autophagy
Afu6g12350	integral to membrane

Afu6g12360	cell wall mannoprotein biosynthetic process
Afu6g12360	mannosyl-oligosaccharide 1,2-alpha-mannosidase activity
Afu6g12360	endoplasmic reticulum
Afu6g12360	protein amino acid N-linked glycosylation
Afu6g12370	biological process unknown
Afu6g12370	molecular function unknown
Afu6g12370	cytoplasm
Afu6g12380	conjugation with cellular fusion
Afu6g12380	hydrolase activity, hydrolyzing O-glycosyl compounds
Afu6g12380	cellular glucan metabolic process
Afu6g12380	fungal-type cell wall biogenesis
Afu6g12380	fungal-type cell wall
Afu6g12390	serine C-palmitoyltransferase activity
Afu6g12390	membrane fraction
Afu6g12390	microsome
Afu6g12390	serine C-palmitoyltransferase complex
Afu6g12390	sphingolipid biosynthetic process
Afu6g12400	1,3-beta-glucan synthase complex
Afu6g12400	1,3-beta-glucan synthase activity
Afu6g12400	integral to plasma membrane
Afu6g12400	1,3-beta-glucan biosynthetic process
Afu6g12400	cell wall organization
Afu6g12410	plasma membrane
Afu6g12410	cell wall organization
Afu6g12410	1,3-beta-glucanosyltransferase activity
Afu6g12450	heat shock protein activity
Afu6g12450	nucleus
Afu6g12450	cytoplasm
Afu6g12450	hyperosmotic response
Afu6g12450	response to oxidative stress
Afu6g12450	cell adhesion
Afu6g12450	response to desiccation
Afu6g12450	response to heat
Afu6g12470	molecular function unknown
Afu6g12470	intra-Golgi vesicle-mediated transport
Afu6g12470	Golgi transport complex
Afu6g12480	cytoplasm
Afu6g12480	mitochondrion
Afu6g12490	biological process unknown
Afu6g12490	molecular function unknown
Afu6g12490	nucleus
Afu6g12490	cytoplasm
Afu6g12500	cytoplasm
Afu6g12500	thioredoxin peroxidase activity
Afu6g12500	response to metal ion
Afu6g12500	regulation of cell redox homeostasis
Afu6g12522	two-component response regulator activity
Afu6g12522	transcription factor activity
Afu6g12522	nucleus
Afu6g12522	transcription

Afu6g12522	response to osmotic stress
Afu6g12522	response to oxidative stress
Afu6g12530	translation initiation factor activity
Afu6g12530	ribosome
Afu6g12530	eukaryotic translation initiation factor 2B complex
Afu6g12530	translational initiation
Afu6g12530	acyltransferase activity
Afu6g12540	biological process unknown
Afu6g12540	molecular function unknown
Afu6g12540	cellular component unknown
Afu6g12550	carrier activity
Afu6g12550	mitochondrion
Afu6g12550	transport
Afu6g12550	RNA splicing
Afu6g12560	cytoplasm
Afu6g12560	ATPase activity
Afu6g12560	protein metabolic process
Afu6g12570	actin cortical patch assembly
Afu6g12570	actin cortical patch (sensu Saccharomyces)
Afu6g12570	endocytosis
Afu6g12570	actin filament organization
Afu6g12570	cytoskeletal adaptor activity
Afu6g12580	tryptophan biosynthetic process
Afu6g12580	anthranilate synthase activity
Afu6g12580	cytoplasm
Afu6g12610	biological process unknown
Afu6g12610	molecular function unknown
Afu6g12610	Golgi apparatus
Afu6g12610	COPI-coated vesicle
Afu6g12630	leucine-tRNA ligase activity
Afu6g12630	cytoplasm
Afu6g12630	leucyl-tRNA aminoacylation
Afu6g12660	structural constituent of ribosome
Afu6g12660	cytosolic small ribosomal subunit (sensu Eukaryota)
Afu6g12660	translation
Afu6g12680	nucleotide binding
Afu6g12680	nucleus
Afu6g12680	cytoplasm
Afu6g12680	nucleotide metabolic process
Afu6g12680	hydrolase activity
Afu6g12690	cytoplasm
Afu6g12690	microsome
Afu6g12690	cytosol
Afu6g12690	cell wall organization
Afu6g12690	phosphatidylinositol transporter activity
Afu6g12690	phospholipid transport
Afu6g12720	structural constituent of ribosome
Afu6g12720	cytosolic small ribosomal subunit (sensu Eukaryota)
Afu6g12720	translation
Afu6g12730	biological process unknown

Afu6g12730	molecular function unknown
Afu6g12730	cytoplasm
Afu6g12740	molecular function unknown
Afu6g12740	cytoplasm
Afu6g12740	aromatic compound catabolic process
Afu6g12750	Golgi apparatus
Afu6g12750	serine-type peptidase activity
Afu6g12750	integral to membrane
Afu6g12750	protein processing
Afu6g12750	COPI-coated vesicle
Afu6g12760	GPI-anchor transamidase activity
Afu6g12760	attachment of GPI anchor to protein
Afu6g12760	integral to endoplasmic reticulum membrane
Afu6g12770	endopeptidase activity
Afu6g12770	ubiquitin-dependent protein catabolic process
Afu6g12770	proteasome regulatory particle, lid subcomplex
Afu6g12800	uroporphyrinogen-III synthase activity
Afu6g12800	heme biosynthetic process
Afu6g12800	cellular component unknown
Afu6g12820	pheromone-dependent signal transduction involved in conjugation with cellular fusion
Afu6g12820	response to pheromone during conjugation without cellular fusion
Afu6g12820	MAP kinase activity
Afu6g12820	nucleus
Afu6g12820	cytoplasm
Afu6g12820	protein amino acid phosphorylation
Afu6g12820	response to osmotic stress
Afu6g12820	cell cycle arrest
Afu6g12830	protein binding
Afu6g12830	ER to Golgi vesicle-mediated transport
Afu6g12830	autophagy
Afu6g12830	COPII vesicle coat
Afu6g12840	establishment of mitotic spindle orientation
Afu6g12840	microtubule motor activity
Afu6g12840	kinesin complex
Afu6g12840	nuclear microtubule
Afu6g12840	cytoplasmic microtubule
Afu6g12840	microtubule depolymerization
Afu6g12870	ATP-binding cassette (ABC) transporter activity
Afu6g12870	mitochondrial inner membrane
Afu6g12870	cellular iron ion homeostasis
Afu6g12870	iron-sulfur cluster assembly
Afu6g12870	ATPase activity
Afu6g12870	mitochondrial iron ion transport
Afu6g12890	vacuole inheritance
Afu6g12890	vacuole
Afu6g12890	phospholipid metabolic process
Afu6g12890	enzyme activator activity
Afu6g12900	carnitine:acyl carnitine antiporter activity
Afu6g12900	mitochondrion
Afu6g12900	mitochondrial inner membrane

Afu6g12900	fatty acid metabolic process
Afu6g12910	telomere maintenance via recombination
Afu6g12910	double-strand break repair via break-induced replication
Afu6g12910	nucleus
Afu6g12910	chromatin remodeling
Afu6g12910	DNA-dependent ATPase activity
Afu6g12910	DNA supercoiling activity
Afu6g12910	heteroduplex formation
Afu6g12910	double-strand break repair via single-strand annealing
Afu6g12910	double-strand break repair via synthesis-dependent strand annealing
Afu6g12920	molecular function unknown
Afu6g12920	nucleus
Afu6g12930	aconitate hydratase activity
Afu6g12930	mitochondrial matrix
Afu6g12930	cytosol
Afu6g12930	tricarboxylic acid cycle
Afu6g12930	citrate metabolic process
Afu6g12930	glutamate biosynthetic process
Afu6g12930	propionate metabolic process
Afu6g12940	catalytic activity
Afu6g12940	metabolic process
Afu6g12950	alpha,alpha-trehalose-phosphate synthase (UDP-forming) activity
Afu6g12950	cytoplasm
Afu6g12950	alpha,alpha-trehalose-phosphate synthase complex (UDP-forming)
Afu6g12950	carbohydrate metabolic process
Afu6g12950	trehalose biosynthetic process
Afu6g12950	response to stress
Afu6g12970	biological process unknown
Afu6g12970	molecular function unknown
Afu6g12970	cellular component unknown
Afu6g12980	structural constituent of cytoskeleton
Afu6g12980	spindle pole body
Afu6g12980	microtubule nucleation
Afu6g12980	microtubule binding
Afu6g12990	structural constituent of ribosome
Afu6g12990	cytosolic large ribosomal subunit (sensu Eukaryota)
Afu6g12990	translation
Afu6g13020	molecular function unknown
Afu6g13020	Golgi to vacuole transport
Afu6g13020	AP-3 adaptor complex
Afu6g13030	G1/S transition of mitotic cell cycle
Afu6g13030	G2/M transition of mitotic cell cycle
Afu6g13030	ubiquitin ligase complex
Afu6g13030	ubiquitin-protein ligase activity
Afu6g13030	protein binding
Afu6g13030	nucleus
Afu6g13030	ubiquitin-dependent protein catabolic process
Afu6g13080	DNA helicase activity
Afu6g13080	nucleus
Afu6g13080	DNA unwinding during replication

Afu6g13080	meiosis
Afu6g13100	biological process unknown
Afu6g13100	molecular function unknown
Afu6g13100	nucleus
Afu6g13100	cytoplasm
Afu6g13120	molecular function unknown
Afu6g13120	nuclear envelope
Afu6g13120	nuclear pore
Afu6g13120	nucleoplasm
Afu6g13120	protein import into nucleus
Afu6g13130	transcription factor TFIIE complex
Afu6g13130	transcription initiation from RNA polymerase II promoter
Afu6g13130	general RNA polymerase II transcription factor activity
Afu6g13140	mitochondrial intermembrane space
Afu6g13140	cytosol
Afu6g13140	3,4-dihydroxy-2-butanone-4-phosphate synthase activity
Afu6g13140	aerobic respiration
Afu6g13140	riboflavin biosynthetic process
Afu6g13160	DNA damage checkpoint
Afu6g13160	protein kinase activity
Afu6g13160	nucleus
Afu6g13160	protein amino acid phosphorylation
Afu6g13170	protein polyubiquitination
Afu6g13170	ubiquitin conjugating enzyme activity
Afu6g13170	cytoplasm
Afu6g13170	ubiquitin-dependent protein catabolic process
Afu6g13170	protein monoubiquitination
Afu6g13170	mitotic metaphase/anaphase transition
Afu6g13190	nucleoside transmembrane transporter activity
Afu6g13190	integral to plasma membrane
Afu6g13190	nucleoside transport
Afu6g13200	autophagic vacuole fusion
Afu6g13200	fungal-type vacuole
Afu6g13200	molecular function unknown
Afu6g13200	cytosol
Afu6g13200	autophagy
Afu6g13200	peroxisome degradation
Afu6g13210	metabolic process
Afu6g13210	oxidoreductase activity
Afu6g13230	cytoplasm
Afu6g13230	mitochondrion
Afu6g13230	hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in other compounds
Afu6g13250	structural constituent of ribosome
Afu6g13250	cytosolic large ribosomal subunit (sensu Eukaryota)
Afu6g13250	translation
Afu6g13260	cell-cell adhesion
Afu6g13270	glucan 1,3-beta-glucosidase activity
Afu6g13270	1,3-beta-glucan metabolic process
Afu6g13270	fungal-type cell wall
Afu6g13290	nucleus

Afu6g13290	chromatin assembly or disassembly
Afu6g13290	mating type switching
Afu6g13290	DNA-dependent ATPase activity
Afu6g13300	RAN small monomeric GTPase activity
Afu6g13300	nucleus
Afu6g13300	cytoplasm
Afu6g13300	rRNA processing
Afu6g13300	nucleocytoplasmic transport
Afu6g13300	nucleus organization
Afu6g13310	molecular function unknown
Afu6g13310	cytoplasm
Afu6g13310	ubiquitin-dependent protein catabolic process
Afu6g13320	Rho guanyl-nucleotide exchange factor activity
Afu6g13320	small GTPase mediated signal transduction
Afu6g13350	sporocarp development involved in sexual reproduction
Afu6g13350	oxygen and reactive oxygen species metabolic process
Afu6g13350	integral to membrane
Afu6g13350	oxidoreductase activity, oxidizing metal ions
Afu6g13370	small nucleolar ribonucleoprotein complex
Afu6g13370	maturation of SSU-rRNA
Afu6g13370	snoRNA binding
Afu6g13390	metabolic process
Afu6g13390	oxidoreductase activity
Afu6g13390	FAD binding
Afu6g13400	arsenite transport
Afu6g13400	arsenate reductase activity
Afu6g13400	response to arsenic
Afu6g13410	spliceosome assembly
Afu6g13410	nuclear mRNA splicing, via spliceosome
Afu6g13410	U2 snRNP
Afu6g13410	U2 snRNA binding
Afu6g13420	protein degradation tagging activity
Afu6g13420	nucleus
Afu6g13420	modification-dependent protein catabolic process
Afu6g13430	transporter activity
Afu6g13430	membrane fraction
Afu6g13430	endosome
Afu6g13430	transport
Afu6g13440	metabolic process
Afu6g13440	sulfuric ester hydrolase activity
Afu6g13450	biological process unknown
Afu6g13450	molecular function unknown
Afu6g13450	cellular component unknown
Afu6g13490	glutamate decarboxylase activity
Afu6g13490	cytoplasm
Afu6g13490	glutamate catabolic process
Afu6g13490	response to oxidative stress
Afu6g13520	tryptophan biosynthetic process
Afu6g13520	tryptophan synthase activity
Afu6g13520	nucleus

Afu6g13520	cytoplasm
Afu6g13530	molecular function unknown
Afu6g13530	nucleus
Afu6g13530	cytoplasm
Afu6g13530	35S primary transcript processing
Afu6g13540	fungal-type vacuole
Afu6g13540	carboxypeptidase C activity
Afu6g13540	cytoplasm
Afu6g13540	endoplasmic reticulum
Afu6g13540	vacuolar protein catabolic process
Afu6g13550	structural constituent of ribosome
Afu6g13550	cytosolic small ribosomal subunit (sensu Eukaryota)
Afu6g13550	translation
Afu6g13570	cytochrome-c peroxidase activity
Afu6g13570	mitochondrion
Afu6g13570	mitochondrial intermembrane space
Afu6g13570	response to oxidative stress
Afu6g13590	3-isopropylmalate dehydrogenase activity
Afu6g13590	cytosol
Afu6g13590	leucine biosynthetic process
Afu6g13600	chaperone activity
Afu6g13600	cytoplasm
Afu6g13600	protein folding
Afu6g13630	biological process unknown
Afu6g13630	molecular function unknown
Afu6g13630	cellular component unknown
Afu6g13650	nucleus
Afu6g13650	signal transduction
Afu6g13650	programmed cell death
Afu6g13670	biological process unknown
Afu6g13670	molecular function unknown
Afu6g13670	endoplasmic reticulum
Afu6g13690	regulation of mitotic recombination
Afu6g13690	synaptonemal complex
Afu6g13690	DNA topoisomerase (ATP-hydrolyzing) activity
Afu6g13690	nucleus
Afu6g13690	DNA topological change
Afu6g13690	DNA strand elongation during DNA replication
Afu6g13690	chromatin assembly or disassembly
Afu6g13690	reciprocal meiotic recombination
Afu6g13720	chitinase activity
Afu6g13720	extracellular region
Afu6g13720	chitin catabolic process
Afu6g13720	chitin binding
Afu6g13750	transition metal ion transport
Afu6g13750	ferric-chelate reductase activity
Afu6g13750	integral to membrane
Afu6g13770	zinc ion binding
Afu6g13780	integral to plasma membrane
Afu6g13780	response to toxin

Afu6g13780	multidrug transporter activity
Afu6g13830	peroxisomal matrix
Afu6g13830	sporulation (sensu Saccharomyces)
Afu6g13830	2,4-dienoyl-CoA reductase (NADPH) activity
Afu6g13830	fatty acid catabolic process
Afu6g13850	Rab GTPase activator activity
Afu6g13850	cytosol
Afu6g13880	transporter activity
Afu6g13880	plasma membrane
Afu6g13880	transport
Afu6g13920	acetate-CoA ligase activity
Afu6g13920	cytosol
Afu6g13930	3-oxoacyl-[acyl-carrier-protein] synthase activity
Afu6g13930	polyketide synthase activity
Afu6g13940	oxidoreductase activity
Afu6g13940	secondary metabolic process
Afu6g13945	metabolic process
Afu6g13945	oxidoreductase activity
Afu6g13970	monooxygenase activity
Afu6g13970	cellular aromatic compound metabolic process
Afu6g13970	toxin biosynthetic process
Afu6g13970	pathogenesis
Afu6g13980	prenyltransferase activity
Afu6g13980	coenzyme and prosthetic group biosynthetic process
Afu6g13990	pathogenesis
Afu6g14000	secondary metabolic process
Afu6g14030	metabolic process
Afu6g14030	acyltransferase activity
Afu6g14040	cell wall mannoprotein biosynthetic process
Afu6g14040	substituted mannan metabolic process
Afu6g14040	N-glycan processing
Afu6g14040	transferase activity, transferring glycosyl groups
Afu6g14100	carnitine:acyl carnitine antiporter activity
Afu6g14100	mitochondrion
Afu6g14100	mitochondrial inner membrane
Afu6g14100	fatty acid metabolic process
Afu6g14130	ubiquitin conjugating enzyme activity
Afu6g14130	ubiquitin-protein ligase activity
Afu6g14130	endoplasmic reticulum
Afu6g14130	ER-associated protein catabolic process
Afu6g14140	phospholipid-translocating ATPase activity
Afu6g14140	endoplasmic reticulum
Afu6g14140	plasma membrane
Afu6g14140	fatty acid transport
Afu6g14140	integral to membrane
Afu6g14150	RNA polymerase II transcription factor activity
Afu6g14150	nucleus
Afu6g14170	nucleus
Afu6g14170	endoplasmic reticulum
Afu6g14170	cellular zinc ion homeostasis

Afu6g14170	cation:cation antiporter activity
Afu6g14170	membrane
Afu6g14180	protein amino acid N-linked glycosylation
Afu6g14180	integral to membrane
Afu6g14180	beta-1,4-mannosyltransferase activity
Afu6g14200	acetyl-CoA C-acetyltransferase activity
Afu6g14200	cytosol
Afu6g14200	ergosterol biosynthetic process
Afu6g14210	proteasome complex
Afu6g14210	ubiquitin conjugating enzyme activity
Afu6g14210	nucleus
Afu6g14210	cytoplasm
Afu6g14210	DNA repair
Afu6g14210	ubiquitin-dependent protein catabolic process
Afu6g14210	protein monoubiquitination
Afu6g14210	histone ubiquitination
Afu6g14220	nuclear migration (sensu Saccharomyces)
Afu6g14220	mitotic spindle assembly (sensu Saccharomyces)
Afu6g14220	establishment of mitotic spindle orientation
Afu6g14220	microtubule motor activity
Afu6g14220	kinesin complex
Afu6g14220	nuclear microtubule
Afu6g14220	cytoplasmic microtubule
Afu6g14220	microtubule depolymerization
Afu6g14240	calcium ion binding
Afu6g14240	detection of calcium ion
Afu6g14240	calcium ion transport
Afu6g14240	extrinsic to plasma membrane
Afu6g14240	ascospore formation
Afu6g14240	regulation of protein kinase activity
Afu6g14250	biological process unknown
Afu6g14250	molecular function unknown
Afu6g14250	membrane fraction
Afu6g14310	5'-nucleotidase activity
Afu6g14330	biological process unknown
Afu6g14330	cytoplasm
Afu6g14330	5-oxoprolinase (ATP-hydrolyzing) activity
Afu6g14350	specific RNA polymerase II transcription factor activity
Afu6g14350	nucleus
Afu6g14350	positive regulation of transcription from RNA polymerase II promoter
Afu6g14410	amidase activity
Afu6g14410	mitochondrion
Afu6g14410	aerobic respiration
Afu6g14442	receptor activity
Afu6g14442	glucose transmembrane transporter activity
Afu6g14442	glucose binding
Afu6g14442	plasma membrane
Afu6g14442	signal transduction
Afu6g14442	response to glucose stimulus
Afu6g14460	xenobiotic metabolic process

Afu6g14460	(S)-2-haloacid dehalogenase activity
Afu6g14480	mannosyltransferase activity
Afu6g14480	cell wall mannoprotein biosynthetic process
Afu6g14480	protein amino acid O-linked glycosylation
Afu6g14480	cellular component unknown
Afu6g14490	hydrolase activity, hydrolyzing O-glycosyl compounds
Afu6g14490	carbohydrate metabolic process
Afu6g14500	fructose transmembrane transporter activity
Afu6g14500	glucose transmembrane transporter activity
Afu6g14500	plasma membrane
Afu6g14500	hexose transport
Afu6g14500	mannose transmembrane transporter activity
Afu6g14510	monooxygenase activity
Afu6g14510	cellular aromatic compound metabolic process
Afu6g14520	plasma membrane
Afu6g14520	peptide transporter activity
Afu6g14520	peptide transport
Afu6g14530	L-cystine transmembrane transporter activity
Afu6g14530	L-cystine transport
Afu6g14530	integral to membrane
Afu6g14540	hydrolase activity, hydrolyzing O-glycosyl compounds
Afu6g14540	1,3-beta-glucan metabolic process
Afu6g14540	fungal-type cell wall
Afu6g14550	carbohydrate metabolic process
Afu6g14550	hydrolase activity, hydrolyzing N-glycosyl compounds
Afu6g14560	transporter activity
Afu6g14560	transport
Afu6g14560	membrane
Afu6g14580	zinc ion binding
Afu6g14590	alpha-glucoside transport
Afu6g14590	alpha-glucoside:hydrogen symporter activity
Afu6g14590	membrane fraction
Afu6g14640	transporter activity
Afu6g14640	integral to plasma membrane
Afu6g14640	drug transport
Afu6g14640	response to drug
Afu7g00090	telomere maintenance
Afu7g00090	helicase activity
Afu7g00090	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process
Afu7g00120	catalytic activity
Afu7g00120	metabolic process
Afu7g00130	transcription factor activity
Afu7g00130	nucleus
Afu7g00130	regulation of transcription
Afu7g00150	monooxygenase activity
Afu7g00150	cellular aromatic compound metabolic process
Afu7g00160	3-oxoacyl-[acyl-carrier-protein] synthase activity
Afu7g00160	polyketide synthase activity
Afu7g00170	tryptophan dimethylallyltransferase activity
Afu7g00180	biological process unknown

Afu7g00180	molecular function unknown
Afu7g00180	cellular component unknown
Afu7g00210	zinc ion binding
Afu7g00220	fructose transmembrane transporter activity
Afu7g00220	galactose transmembrane transporter activity
Afu7g00220	glucose transmembrane transporter activity
Afu7g00220	plasma membrane
Afu7g00220	hexose transport
Afu7g00220	mannose transmembrane transporter activity
Afu7g00230	integral to plasma membrane
Afu7g00230	response to toxin
Afu7g00230	multidrug transporter activity
Afu7g00240	hydrolase activity, hydrolyzing O-glycosyl compounds
Afu7g00240	carbohydrate metabolic process
Afu7g00250	nuclear migration (sensu Saccharomyces)
Afu7g00250	mitotic sister chromatid segregation
Afu7g00250	nuclear migration during conjugation with cellular fusion
Afu7g00250	structural constituent of cytoskeleton
Afu7g00250	spindle pole body
Afu7g00250	polar microtubule
Afu7g00250	kinetochore microtubule
Afu7g00250	nuclear microtubule
Afu7g00250	cytoplasmic microtubule
Afu7g00250	homologous chromosome segregation
Afu7g00260	lanosterol synthase activity
Afu7g00260	endoplasmic reticulum
Afu7g00260	lipid particle
Afu7g00260	plasma membrane
Afu7g00260	ergosterol biosynthetic process
Afu7g00260	hopanoid biosynthetic process
Afu7g00260	squalene-hopene cyclase activity
Afu7g00270	monooxygenase activity
Afu7g00270	cellular aromatic compound metabolic process
Afu7g00280	biological process unknown
Afu7g00280	molecular function unknown
Afu7g00280	clathrin-coated vesicle
Afu7g00280	COPI-coated vesicle
Afu7g00290	metabolic process
Afu7g00290	oxidoreductase activity
Afu7g00340	catalytic activity
Afu7g00340	metabolic process
Afu7g00390	drug transporter activity
Afu7g00390	drug transport
Afu7g00390	integral to membrane
Afu7g00410	DNA binding
Afu7g00410	zinc ion binding
Afu7g00440	plasma membrane
Afu7g00440	choline transmembrane transporter activity
Afu7g00440	choline transport
Afu7g00480	ATP-binding cassette (ABC) transporter activity

Afu7g00480	ATP-binding cassette (ABC) transporter activity
Afu7g00480	ATP binding
Afu7g00480	transport
Afu7g00480	transport
Afu7g00530	protein binding
Afu7g00530	GTP binding
Afu7g00530	signal transduction
Afu7g00550	nucleotide binding
Afu7g00550	protein binding
Afu7g00550	cellular component unknown
Afu7g00550	programmed cell death
Afu7g00590	FAD binding
Afu7g00690	cytoplasm
Afu7g00690	transaminase activity
Afu7g00690	NAD biosynthetic process
Afu7g00700	aldo-keto reductase activity
Afu7g00700	nucleus
Afu7g00700	cytoplasm
Afu7g00700	cellular aldehyde metabolic process
Afu7g00710	transporter activity
Afu7g00710	transport
Afu7g00710	monocarboxylic acid transmembrane transporter activity
Afu7g00710	membrane
Afu7g00730	sulfur amino acid transport
Afu7g00730	L-methionine secondary active transmembrane transporter activity
Afu7g00730	integral to plasma membrane
Afu7g00740	protein kinase activity
Afu7g00740	cytoplasm
Afu7g00770	RNA polymerase II transcription factor activity
Afu7g00770	nucleus
Afu7g00770	regulation of transcription
Afu7g00780	fungal-type vacuole membrane
Afu7g00780	transporter activity
Afu7g00780	transport
Afu7g00780	monocarboxylic acid transmembrane transporter activity
Afu7g00800	phosphate metabolic process
Afu7g00800	phosphoric ester hydrolase activity
Afu7g00830	metabolic process
Afu7g00830	hydrolase activity
Afu7g00840	metabolic process
Afu7g00840	oxidoreductase activity
Afu7g00850	N-acetyltransferase activity
Afu7g00850	metabolic process
Afu7g00850	cellular component unknown
Afu7g00870	nucleus
Afu7g00870	cytoplasm
Afu7g00870	RNA processing
Afu7g00870	3'-5' exonuclease activity
Afu7g00910	endoplasmic reticulum
Afu7g00910	integral to plasma membrane

Afu7g00910	sulfur metabolic process
Afu7g00910	oligopeptide transporter activity
Afu7g00920	carboxy-lyase activity
Afu7g00950	fructose transmembrane transporter activity
Afu7g00950	glucose transmembrane transporter activity
Afu7g00950	plasma membrane
Afu7g00950	hexose transport
Afu7g00950	mannose transmembrane transporter activity
Afu7g01000	aldehyde dehydrogenase (NAD) activity
Afu7g01000	mitochondrion
Afu7g01000	ethanol metabolic process
Afu7g01000	fermentation
Afu7g01010	alcohol dehydrogenase (NAD) activity
Afu7g01010	soluble fraction
Afu7g01010	mitochondrial matrix
Afu7g01010	fermentation
Afu7g01010	zinc ion binding
Afu7g01030	fungal-type vacuole membrane
Afu7g01030	calcium-transporting ATPase activity
Afu7g01030	calcium ion transport
Afu7g01030	cellular calcium ion homeostasis
Afu7g01040	zinc ion binding
Afu7g01050	FAD binding
Afu7g01090	plasma membrane
Afu7g01090	neutral amino acid transmembrane transporter activity
Afu7g01090	amino acid permease activity
Afu7g01090	neutral amino acid transport
Afu7g01150	nucleotide binding
Afu7g01150	cellular component unknown
Afu7g01160	metabolic process
Afu7g01160	oxidoreductase activity
Afu7g01190	plasma membrane
Afu7g01190	allantoate transmembrane transporter activity
Afu7g01190	allantoate transport
Afu7g01220	farnesyl-diphosphate farnesyltransferase activity
Afu7g01220	endoplasmic reticulum
Afu7g01220	ergosterol biosynthetic process
Afu7g01230	co-chaperone activity
Afu7g01230	cytosol
Afu7g01230	protein import into peroxisome matrix
Afu7g01240	fungal-type vacuole
Afu7g01240	acid phosphatase activity
Afu7g01300	mannosyltransferase activity
Afu7g01300	endoplasmic reticulum membrane
Afu7g01300	GPI anchor biosynthetic process
Afu7g01370	biological process unknown
Afu7g01370	thiosulfate sulfurtransferase activity
Afu7g01370	cytoplasm
Afu7g01380	mitotic spindle elongation
Afu7g01380	mitotic sister chromatid segregation

Afu7g01380	ubiquitin-protein ligase activity
Afu7g01380	protein binding
Afu7g01380	anaphase-promoting complex
Afu7g01380	ubiquitin-dependent protein catabolic process
Afu7g01380	mitotic metaphase/anaphase transition
Afu7g01380	cyclin catabolic process
Afu7g01380	zinc ion binding
Afu7g01400	mitotic sister chromatid segregation
Afu7g01400	mitotic anaphase B
Afu7g01400	microtubule motor activity
Afu7g01400	kinesin complex
Afu7g01400	spindle microtubule
Afu7g01400	ATPase activity
Afu7g01400	mitotic spindle organization in nucleus
Afu7g01420	isoleucine-tRNA ligase activity
Afu7g01420	mitochondrion
Afu7g01420	translation
Afu7g01420	isoleucyl-tRNA aminoacylation
Afu7g01450	metabolic process
Afu7g01450	oxidoreductase activity
Afu7g01460	structural constituent of ribosome
Afu7g01460	cytosolic small ribosomal subunit (sensu Eukaryota)
Afu7g01460	translation
Afu7g01460	regulation of translational fidelity
Afu7g01470	biological process unknown
Afu7g01470	molecular function unknown
Afu7g01470	cellular component unknown
Afu7g01480	regulation of progression through cell cycle
Afu7g01480	translation initiation factor activity
Afu7g01480	nucleus
Afu7g01480	cytoplasm
Afu7g01480	ribosome
Afu7g01480	translational initiation
Afu7g01490	plasma membrane
Afu7g01490	peptide transporter activity
Afu7g01490	peptide transport
Afu7g01510	t-SNARE activity
Afu7g01510	cytoplasm
Afu7g01510	endoplasmic reticulum
Afu7g01510	integral to plasma membrane
Afu7g01510	Golgi to plasma membrane transport
Afu7g01510	vesicle fusion
Afu7g01530	biological process unknown
Afu7g01530	cytoplasm
Afu7g01530	peroxisomal membrane
Afu7g01530	peroxisomal matrix
Afu7g01530	AMP binding
Afu7g01550	mitochondrion
Afu7g01550	mitochondrial matrix
Afu7g01550	RNA catabolic process

Afu7g01550	exoribonuclease II activity
Afu7g01560	oxidoreductase activity
Afu7g01590	cystathionine beta-lyase activity
Afu7g01590	cytoplasm
Afu7g01590	sulfur metabolic process
Afu7g01640	response to acid
Afu7g01640	transcription factor activity
Afu7g01640	nucleus
Afu7g01640	regulation of transcription
Afu7g01670	fungal-type vacuole
Afu7g01670	transporter activity
Afu7g01670	transport
Afu7g01690	biological process unknown
Afu7g01690	amidase activity
Afu7g01690	cellular component unknown
Afu7g01730	phosphatidylserine decarboxylase activity
Afu7g01730	phosphatidylserine catabolic process
Afu7g01790	sulfite transport
Afu7g01790	sulfite transmembrane transporter activity
Afu7g01790	plasma membrane
Afu7g01810	nucleus
Afu7g01810	galactose metabolic process
Afu7g01810	regulation of transcription, DNA-dependent
Afu7g01810	transcription activator activity
Afu7g01820	DNA binding
Afu7g01830	UTP:glucose-1-phosphate uridylyltransferase activity
Afu7g01830	cytoplasm
Afu7g01830	UDP-glucose metabolic process
Afu7g01830	protein amino acid glycosylation
Afu7g01840	biological process unknown
Afu7g01840	calcium ion binding
Afu7g01840	membrane
Afu7g01860	chaperone activity
Afu7g01860	enzyme inhibitor activity
Afu7g01860	cytoplasm
Afu7g01860	protein folding
Afu7g01870	DNA binding
Afu7g01870	nucleus
Afu7g01870	chromatin remodeling
Afu7g01870	regulation of transcription, DNA-dependent
Afu7g01870	zinc ion binding
Afu7g01880	chromatin silencing at rDNA
Afu7g01880	nicotinate phosphoribosyltransferase activity
Afu7g01880	nucleus
Afu7g01880	chromatin silencing at telomere
Afu7g01880	nicotinate nucleotide salvage
Afu7g01890	transcription factor activity
Afu7g01890	regulation of transcription
Afu7g01900	mitochondrial outer membrane translocase complex
Afu7g01900	protein import into mitochondrial outer membrane

Afu7g01920	DNA-directed RNA polymerase activity
Afu7g01920	DNA-directed RNA polymerase II, core complex
Afu7g01920	transcription from RNA polymerase II promoter
Afu7g01930	GTP binding
Afu7g01970	biological process unknown
Afu7g01970	molecular function unknown
Afu7g01970	integral to membrane
Afu7g01980	soluble fraction
Afu7g01980	alcohol metabolic process
Afu7g01980	cellular aldehyde metabolic process
Afu7g01980	alcohol dehydrogenase (NADP+) activity
Afu7g02010	tryptophan 2,3-dioxygenase activity
Afu7g02010	cytoplasm
Afu7g02010	NAD biosynthetic process
Afu7g02040	triglyceride lipase activity
Afu7g02040	lipid metabolic process
Afu7g02040	cellular component unknown
Afu7g02070	electron transport
Afu7g02070	electron carrier activity
Afu7g02070	oxidoreductase activity
Afu7g02070	coenzyme binding
Afu7g02140	structural constituent of ribosome
Afu7g02140	cytosolic small ribosomal subunit (sensu Eukaryota)
Afu7g02140	translation
Afu7g02170	RNA binding
Afu7g02180	UDP-N-acetylglucosamine diphosphorylase activity
Afu7g02180	nucleus
Afu7g02180	cytoplasm
Afu7g02180	UDP-N-acetylglucosamine biosynthetic process
Afu7g02190	transcription factor activity
Afu7g02190	cytoplasm
Afu7g02190	intracellular signaling cascade
Afu7g02200	meiotic joint molecule formation
Afu7g02200	condensed nuclear chromosome
Afu7g02200	double-stranded DNA binding
Afu7g02200	single-stranded DNA binding
Afu7g02200	nucleus
Afu7g02200	meiosis
Afu7g02200	reciprocal meiotic recombination
Afu7g02210	ribosomal small subunit assembly
Afu7g02210	molecular function unknown
Afu7g02210	nucleus
Afu7g02210	nucleolus
Afu7g02210	35S primary transcript processing
Afu7g02230	commitment complex
Afu7g02230	nuclear mRNA splicing, via spliceosome
Afu7g02230	RNA binding
Afu7g02230	mRNA binding
Afu7g02230	U1 snRNP
Afu7g02230	mRNA splice site selection

Afu7g02270	molecular function unknown
Afu7g02270	ER to Golgi vesicle-mediated transport
Afu7g02270	TRAPP complex
Afu7g02280	establishment of cell polarity (sensu Saccharomyces)
Afu7g02280	cytokinesis
Afu7g02280	small nucleolar ribonucleoprotein complex
Afu7g02280	cytoplasm
Afu7g02280	maturation of SSU-rRNA
Afu7g02280	snoRNA binding
Afu7g02290	endoplasmic reticulum
Afu7g02290	carbohydrate binding
Afu7g02290	ER-associated protein catabolic process
Afu7g02310	adenine phosphoribosyltransferase activity
Afu7g02310	nucleus
Afu7g02310	cytoplasm
Afu7g02310	AMP biosynthetic process
Afu7g02340	biological process unknown
Afu7g02340	molecular function unknown
Afu7g02340	nucleus
Afu7g02340	cytoplasm
Afu7g02340	cytosol
Afu7g02350	biological process unknown
Afu7g02350	molecular function unknown
Afu7g02350	cytoplasm
Afu7g02370	Swr1 complex
Afu7g02370	helicase activity
Afu7g02370	nucleus
Afu7g02370	chromatin remodeling
Afu7g02370	ATPase activity
Afu7g02400	biological process unknown
Afu7g02400	molecular function unknown
Afu7g02400	nucleus
Afu7g02400	cytoplasm
Afu7g02420	mitochondrion
Afu7g02420	pyruvate metabolic process
Afu7g02420	cellular amino acid metabolic process
Afu7g02420	malate dehydrogenase (oxaloacetate-decarboxylating) activity
Afu7g02470	molecular function unknown
Afu7g02470	mitochondrion
Afu7g02470	mRNA processing
Afu7g02470	translation
Afu7g02480	Golgi trans cisterna
Afu7g02480	phosphatidylinositol binding
Afu7g02480	early endosome
Afu7g02480	endoplasmic reticulum
Afu7g02480	steroid biosynthetic process
Afu7g02480	oxysterol binding
Afu7g02490	chaperone activity
Afu7g02490	mitochondrial matrix
Afu7g02490	protein complex assembly

Afu7g02500	carbohydrate metabolic process
Afu7g02500	transferase activity, transferring glycosyl groups
Afu7g02540	GTP binding
Afu7g02550	L-iditol 2-dehydrogenase activity
Afu7g02550	fructose metabolic process
Afu7g02550	mannose metabolic process
Afu7g02550	cellular component unknown
Afu7g02560	D-lactate dehydrogenase (cytochrome) activity
Afu7g02560	mitochondrial inner membrane
Afu7g02560	carbohydrate metabolic process
Afu7g02560	aerobic respiration
Afu7g02570	signal transduction
Afu7g02620	DNA-directed RNA polymerase activity
Afu7g02620	DNA-directed RNA polymerase II, core complex
Afu7g02620	DNA-directed RNA polymerase III complex
Afu7g02620	DNA-directed RNA polymerase I complex
Afu7g02620	transcription from RNA polymerase I promoter
Afu7g02620	transcription from RNA polymerase II promoter
Afu7g02620	transcription from RNA polymerase III promoter
Afu7g03640	transporter activity
Afu7g03640	Golgi apparatus
Afu7g03640	Golgi to vacuole transport
Afu7g03640	nonselective vesicle transport
Afu7g03640	AP-3 adaptor complex
Afu7g03660	translation elongation factor activity
Afu7g03660	cytosolic ribosome (sensu Eukaryota)
Afu7g03660	translational elongation
Afu7g03660	ATPase activity
Afu7g03690	RNA binding
Afu7g03690	nucleolus
Afu7g03690	35S primary transcript processing
Afu7g03690	snRNA processing
Afu7g03700	diacylglycerol O-acyltransferase activity
Afu7g03700	lipid particle
Afu7g03700	triglyceride biosynthetic process
Afu7g03700	lipid storage
Afu7g03710	mitotic anaphase B
Afu7g03710	microtubule motor activity
Afu7g03710	kinesin complex
Afu7g03710	cytoplasmic microtubule
Afu7g03710	negative regulation of microtubule depolymerization
Afu7g03720	cyclin-dependent protein kinase activity
Afu7g03720	holo TFIIH complex
Afu7g03720	transcription initiation from RNA polymerase II promoter
Afu7g03720	protein amino acid phosphorylation
Afu7g03720	negative regulation of transcription from RNA polymerase II promoter, mitotic
Afu7g03720	general RNA polymerase II transcription factor activity
Afu7g03740	endoplasmic reticulum
Afu7g03740	ergosterol biosynthetic process
Afu7g03740	sterol 14-demethylase activity

Afu7g03750	cell cycle checkpoint
Afu7g03750	DNA damage checkpoint
Afu7g03750	protein kinase activity
Afu7g03750	nucleus
Afu7g03750	protein amino acid phosphorylation
Afu7g03760	MAPKKK cascade
Afu7g03760	1-phosphatidylinositol 4-kinase activity
Afu7g03760	plasma membrane
Afu7g03760	phosphatidylethanolamine biosynthetic process
Afu7g03760	protein secretion
Afu7g03760	actin cytoskeleton organization
Afu7g03790	cytoplasm
Afu7g03790	ER to Golgi vesicle-mediated transport
Afu7g03790	intra-Golgi vesicle-mediated transport
Afu7g03790	ARF GTPase activator activity
Afu7g03820	repairosome
Afu7g03820	nucleotide-excision repair factor 4 complex
Afu7g03820	nucleotide-excision repair, DNA damage recognition
Afu7g03820	DNA-dependent ATPase activity
Afu7g03830	repairosome
Afu7g03830	nucleotide-excision repair factor 4 complex
Afu7g03830	nucleotide-excision repair, DNA damage recognition
Afu7g03830	DNA binding
Afu7g03830	DNA-dependent ATPase activity
Afu7g03850	metabolic process
Afu7g03850	oxidoreductase activity
Afu7g03860	DNA-directed RNA polymerase activity
Afu7g03860	DNA-directed RNA polymerase II, core complex
Afu7g03860	transcription from RNA polymerase II promoter
Afu7g03870	actin cortical patch assembly
Afu7g03870	cytokinesis
Afu7g03870	actin cortical patch (sensu Saccharomyces)
Afu7g03870	plasma membrane
Afu7g03870	endocytosis
Afu7g03870	axial cellular bud site selection
Afu7g03870	bipolar cellular bud site selection
Afu7g03870	cytoskeletal adaptor activity
Afu7g03880	biological process unknown
Afu7g03880	molecular function unknown
Afu7g03880	cellular component unknown
Afu7g03890	mitotic sister chromatid segregation
Afu7g03890	nuclear condensin complex
Afu7g03890	molecular function unknown
Afu7g03890	nucleus
Afu7g03890	mitotic chromosome condensation
Afu7g03910	transcription factor activity
Afu7g03910	nucleus
Afu7g03910	cytoplasm
Afu7g03910	regulation of transcription, DNA-dependent
Afu7g03910	calcium-mediated signaling

Afu7g03940	alpha,alpha-trehalose-phosphate synthase (UDP-forming) activity
Afu7g03940	trehalose-phosphatase activity
Afu7g03940	alpha,alpha-trehalose-phosphate synthase complex (UDP-forming)
Afu7g03940	trehalose biosynthetic process
Afu7g03940	response to stress
Afu7g03960	fatty acid metabolic process
Afu7g03960	CoA hydrolase activity
Afu7g03990	uridine kinase activity
Afu7g03990	nucleus
Afu7g03990	cytoplasm
Afu7g03990	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process
Afu7g04040	hexokinase activity
Afu7g04040	cytosol
Afu7g04040	fructose metabolic process
Afu7g04070	3-deoxy-7-phosphoheptulonate synthase activity
Afu7g04070	nucleus
Afu7g04070	cytoplasm
Afu7g04070	aromatic amino acid family biosynthetic process
Afu7g04080	acetyl-CoA C-acetyltransferase activity
Afu7g04080	peroxisomal matrix
Afu7g04080	fatty acid metabolic process
Afu7g04110	biological process unknown
Afu7g04110	molecular function unknown
Afu7g04110	endoplasmic reticulum
Afu7g04130	DNA-directed DNA polymerase activity
Afu7g04130	nucleus
Afu7g04130	sister chromatid cohesion
Afu7g04140	cytoplasm
Afu7g04140	galactose 1-dehydrogenase activity
Afu7g04140	L-ascorbic acid metabolic process
Afu7g04150	molecular function unknown
Afu7g04150	mitochondrion
Afu7g04150	protein import into mitochondrial matrix
Afu7g04160	biological process unknown
Afu7g04160	molecular function unknown
Afu7g04160	peroxisome
Afu7g04190	lipid biosynthetic process
Afu7g04190	cyclopropane-fatty-acyl-phospholipid synthase activity
Afu7g04210	mitochondrion inheritance
Afu7g04210	vacuole inheritance
Afu7g04210	actin lateral binding
Afu7g04210	exocytosis
Afu7g04210	actin filament organization
Afu7g04210	actin polymerization or depolymerization
Afu7g04210	intracellular mRNA localization
Afu7g04210	vesicle-mediated transport
Afu7g04210	actin cable formation
Afu7g04250	protein retention in ER lumen
Afu7g04250	integral to membrane
Afu7g04260	protein binding

Afu7g04260	peroxisomal membrane
Afu7g04260	peroxisome organization
Afu7g04280	nuclear mRNA splicing, via spliceosome
Afu7g04280	rRNA processing
Afu7g04280	pre-mRNA splicing factor activity
Afu7g04280	small nuclear ribonucleoprotein complex
Afu7g04290	general amino acid permease activity
Afu7g04290	integral to plasma membrane
Afu7g04290	amino acid transport
Afu7g04300	Rho GTPase activator activity
Afu7g04300	cytoplasm
Afu7g04300	cellular bud neck
Afu7g04300	small GTPase mediated signal transduction
Afu7g04310	DNA clamp loader activity
Afu7g04310	protein binding
Afu7g04310	pre-replicative complex
Afu7g04310	pre-replicative complex assembly
Afu7g04310	ATPase activity
Afu7g04310	ATPase activity
Afu7g04310	protein metabolic process
Afu7g04320	molecular function unknown
Afu7g04320	nucleus
Afu7g04320	cytoplasm
Afu7g04320	ubiquitin-dependent protein catabolic process
Afu7g04330	protein serine/threonine kinase activity
Afu7g04330	nucleus
Afu7g04330	cytoplasm
Afu7g04330	protein amino acid phosphorylation
Afu7g04340	transcription factor activity
Afu7g04340	nucleus
Afu7g04340	regulation of transcription
Afu7g04350	isomerase activity
Afu7g04350	aromatic compound catabolic process
Afu7g04360	peroxisomal matrix
Afu7g04360	sporulation (sensu Saccharomyces)
Afu7g04360	2,4-dienoyl-CoA reductase (NADPH) activity
Afu7g04360	fatty acid catabolic process
Afu7g04380	alcohol dehydrogenase (NAD) activity
Afu7g04380	cytosol
Afu7g04380	fermentation
Afu7g04380	zinc ion binding
Afu7g04420	nucleotide binding
Afu7g04420	mitochondrial matrix
Afu7g04420	mitochondrial ribosome
Afu7g04420	programmed cell death
Afu7g04420	translation
Afu7g04430	molecular function unknown
Afu7g04430	nucleus
Afu7g04430	rRNA processing
Afu7g04430	ribosome biogenesis

Afu7g04450	signal transducer activity
Afu7g04450	Rho GTPase activator activity
Afu7g04450	intracellular
Afu7g04450	budding cell apical bud growth
Afu7g04450	budding cell isotropic bud growth
Afu7g04450	pseudohyphal growth
Afu7g04450	invasive growth
Afu7g04450	small GTPase mediated signal transduction
Afu7g04460	Rab geranylgeranyltransferase activity
Afu7g04460	Rab-protein geranylgeranyltransferase complex
Afu7g04460	protein amino acid geranylgeranylation
Afu7g04480	nuclear chromosome
Afu7g04480	removal of nonhomologous ends
Afu7g04480	damaged DNA binding
Afu7g04480	mismatch repair
Afu7g04480	DNA recombination
Afu7g04480	mitotic recombination
Afu7g04490	structural constituent of ribosome
Afu7g04490	cytosolic small ribosomal subunit (sensu Eukaryota)
Afu7g04490	translation
Afu7g04500	histidine biosynthetic process
Afu7g04500	ATP phosphoribosyltransferase activity
Afu7g04500	cell
Afu7g04510	biological process unknown
Afu7g04510	molecular function unknown
Afu7g04510	cytoplasm
Afu7g04530	biological process unknown
Afu7g04530	molecular function unknown
Afu7g04530	cytoplasm
Afu7g04550	protein kinase activity
Afu7g04550	cellular component unknown
Afu7g04570	calcium-transporting ATPase activity
Afu7g04570	Golgi apparatus
Afu7g04570	calcium ion transport
Afu7g04570	manganese ion transport
Afu7g04570	manganese-transporting ATPase activity
Afu7g04570	secretory pathway
Afu7g04590	telomerase catalytic core complex
Afu7g04590	telomeric template RNA reverse transcriptase activity
Afu7g04590	nucleus
Afu7g04590	telomerase holoenzyme complex
Afu7g04590	nucleolus
Afu7g04590	telomere maintenance via telomerase
Afu7g04600	Rho guanyl-nucleotide exchange factor activity
Afu7g04600	small GTPase mediated signal transduction
Afu7g04640	cyclin-dependent protein kinase holoenzyme complex
Afu7g04640	regulation of glycogen biosynthetic process
Afu7g04640	regulation of glycogen catabolic process
Afu7g04640	cyclin-dependent protein kinase regulator activity
Afu7g04650	endopeptidase activity

Afu7g04650	proteasome core complex
Afu7g04650	ubiquitin-dependent protein catabolic process
Afu7g04650	response to stress
Afu7g04650	sporulation (sensu Saccharomyces)
Afu7g04650	proteasome core complex, beta-subunit complex
Afu7g04660	biological process unknown
Afu7g04660	molecular function unknown
Afu7g04660	cellular component unknown
Afu7g04670	chaperone activity
Afu7g04670	mitochondrial matrix
Afu7g04670	protein complex assembly
Afu7g04690	microsome
Afu7g04690	protein thiol-disulfide exchange
Afu7g04690	thiol oxidase activity
Afu7g04700	biological process unknown
Afu7g04700	molecular function unknown
Afu7g04700	nucleolus
Afu7g04710	single-stranded DNA binding
Afu7g04710	transcription factor activity
Afu7g04710	nucleus
Afu7g04710	zinc ion binding
Afu7g04730	endosome
Afu7g04730	cellular iron ion homeostasis
Afu7g04730	siderophore-iron (ferrioxamine) uptake transmembrane transporter activity
Afu7g04730	siderophore-iron transport
Afu7g04730	cytoplasmic membrane-bounded vesicle
Afu7g04760	protein-glutamine gamma-glutamyltransferase activity
Afu7g04760	intracellular
Afu7g04760	glutathione catabolic process
Afu7g04760	cell wall organization
Afu7g04850	aldo-keto reductase activity
Afu7g04850	cellular aldehyde metabolic process
Afu7g04850	cellular component unknown
Afu7g04860	rRNA modification
Afu7g04860	rRNA (adenine-N6,N6-)-dimethyltransferase activity
Afu7g04860	nucleolus
Afu7g04860	35S primary transcript processing
Afu7g04880	cytoplasm
Afu7g04880	sterol metabolic process
Afu7g04880	sterol 3-beta-glucosyltransferase activity
Afu7g04890	transcription factor activity
Afu7g04890	nucleus
Afu7g04890	regulation of transcription
Afu7g04900	integral to plasma membrane
Afu7g04900	transport
Afu7g04900	response to toxin
Afu7g04900	multidrug transporter activity
Afu7g04930	peptidase activity
Afu7g04930	cellular component unknown
Afu7g04930	protein catabolic process

Afu7g04960	N-acetyltransferase activity
Afu7g04960	metabolic process
Afu7g04970	ferric-chelate reductase activity
Afu7g04970	plasma membrane
Afu7g04970	iron ion transport
Afu7g04970	copper ion import
Afu7g04980	acylglycerone-phosphate reductase activity
Afu7g04980	cytoplasm
Afu7g04980	endoplasmic reticulum
Afu7g04980	lipid particle
Afu7g04980	phosphatidic acid biosynthetic process
Afu7g04990	dUTP diphosphatase activity
Afu7g04990	2'-deoxyribonucleotide metabolic process
Afu7g04990	uracil metabolic process
Afu7g05010	catalytic activity
Afu7g05010	metabolic process
Afu7g05040	GTP binding
Afu7g05060	pathogenesis
Afu7g05070	cytoplasm
Afu7g05070	metabolic process
Afu7g05070	fumarate reductase (NADH) activity
Afu7g05100	fructose transmembrane transporter activity
Afu7g05100	glucose transmembrane transporter activity
Afu7g05100	plasma membrane
Afu7g05100	hexose transport
Afu7g05100	mannose transmembrane transporter activity
Afu7g05140	chitinase activity
Afu7g05140	extracellular region
Afu7g05140	cell wall chitin catabolic process
Afu7g05140	cytokinesis, completion of separation
Afu7g05140	fungal-type cell wall
Afu7g05160	catalytic activity
Afu7g05160	metabolic process
Afu7g05190	alpha-glucoside transport
Afu7g05190	alpha-glucoside:hydrogen symporter activity
Afu7g05190	membrane fraction
Afu7g05210	CTP synthase activity
Afu7g05210	cytosol
Afu7g05210	CTP biosynthetic process
Afu7g05210	phospholipid biosynthetic process
Afu7g05210	pyrimidine base biosynthetic process
Afu7g05220	transporter activity
Afu7g05220	mitochondrial inner membrane
Afu7g05220	transport
Afu7g05240	biological process unknown
Afu7g05240	molecular function unknown
Afu7g05240	mitochondrion
Afu7g05250	histone acetyltransferase complex
Afu7g05250	DNA binding
Afu7g05250	histone acetyltransferase activity

Afu7g05250	nucleus
Afu7g05250	regulation of transcription, DNA-dependent
Afu7g05250	zinc ion binding
Afu7g05250	chromatin modification
Afu7g05270	nuclear chromatin
Afu7g05270	chromatin binding
Afu7g05270	chromatin silencing at telomere
Afu7g05270	histone methylation
Afu7g05270	histone-lysine N-methyltransferase activity
Afu7g05290	structural constituent of ribosome
Afu7g05290	cytosolic small ribosomal subunit (sensu Eukaryota)
Afu7g05290	translation
Afu7g05320	mitochondrion
Afu7g05320	DNA repair
Afu7g05320	base-excision repair, AP site formation
Afu7g05320	oxidized purine base lesion DNA N-glycosylase activity
Afu7g05340	cellular bud site selection
Afu7g05340	molecular function unknown
Afu7g05340	cellular bud scar
Afu7g05340	cellular bud neck
Afu7g05340	membrane
Afu7g05360	chromatin binding
Afu7g05360	nucleus
Afu7g05360	DNA-dependent DNA replication
Afu7g05360	chromatin assembly or disassembly
Afu7g05360	chromatin remodeling
Afu7g05370	cell morphogenesis
Afu7g05370	cytokinesis
Afu7g05370	structural constituent of cytoskeleton
Afu7g05370	phosphatidylinositol binding
Afu7g05370	ascospore wall
Afu7g05370	prospore membrane
Afu7g05370	mating projection
Afu7g05370	cell wall organization
Afu7g05370	axial cellular bud site selection
Afu7g05380	biological process unknown
Afu7g05380	molecular function unknown
Afu7g05380	endoplasmic reticulum
Afu7g05390	transporter activity
Afu7g05390	mitochondrial inner membrane
Afu7g05390	transport
Afu7g05410	thiamin diphosphokinase activity
Afu7g05410	thiamin metabolic process
Afu7g05420	mitochondrion
Afu7g05420	protein targeting
Afu7g05420	protein import into mitochondrial intermembrane space
Afu7g05430	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
Afu7g05430	protein binding
Afu7g05430	cytoplasm
Afu7g05430	polysome

Afu7g05430	mRNA catabolic process
Afu7g05440	biological process unknown
Afu7g05440	transcription factor activity
Afu7g05440	nucleus
Afu7g05440	cytoplasm
Afu7g05450	barrier septum formation
Afu7g05450	mitochondrial outer membrane
Afu7g05450	apoptosis
Afu7g05450	response to oxidative stress
Afu7g05450	mitochondrion organization
Afu7g05450	cell wall organization
Afu7g05450	beta-glucosidase activity
Afu7g05450	fungal-type cell wall
Afu7g05450	autophagic cell death
Afu7g05470	mitochondrion
Afu7g05470	electron transport
Afu7g05470	electron carrier activity
Afu7g05480	molecular function unknown
Afu7g05480	DNA replication factor C complex
Afu7g05480	sister chromatid cohesion
Afu7g05500	transcription corepressor activity
Afu7g05500	soluble fraction
Afu7g05500	regulation of nitrogen utilization
Afu7g05510	DNA binding
Afu7g05510	protein binding
Afu7g05510	chromatin remodeling
Afu7g05510	cell cycle
Afu7g05510	general RNA polymerase II transcription factor activity
Afu7g05510	RSC complex
Afu7g05510	regulation of transcription
Afu7g05530	biological process unknown
Afu7g05530	helicase activity
Afu7g05530	mitochondrion
Afu7g05540	molecular function unknown
Afu7g05540	endoplasmic reticulum
Afu7g05540	integral to membrane
Afu7g05540	vesicle organization
Afu7g05540	ER-associated protein catabolic process
Afu7g05550	plasma membrane
Afu7g05550	lactate transmembrane transporter activity
Afu7g05550	lactate transport
Afu7g05580	phospholipase D activity
Afu7g05580	phospholipid metabolic process
Afu7g05580	response to osmotic stress
Afu7g05600	biological process unknown
Afu7g05600	protein binding
Afu7g05600	nucleus
Afu7g05600	cytoplasm
Afu7g05620	regulation of progression through cell cycle
Afu7g05620	DNA binding

Afu7g05620	transcription factor activity
Afu7g05620	nucleus
Afu7g05620	DNA replication
Afu7g05660	translation elongation factor activity
Afu7g05660	cytosolic ribosome (sensu Eukaryota)
Afu7g05660	translational elongation
Afu7g05660	ATPase activity
Afu7g05670	histidine biosynthetic process
Afu7g05670	tryptophan biosynthetic process
Afu7g05670	ribose phosphate diphosphokinase activity
Afu7g05670	cytoplasm
Afu7g05670	purine ribonucleoside salvage
Afu7g05670	'de novo' IMP biosynthetic process
Afu7g05670	'de novo' pyrimidine base biosynthetic process
Afu7g05680	sulfate assimilation
Afu7g05680	ferrochelatase activity
Afu7g05680	cellular component unknown
Afu7g05680	siroheme synthase activity
Afu7g05680	siroheme biosynthetic process
Afu7g05700	ARF guanyl-nucleotide exchange factor activity
Afu7g05700	late endosome
Afu7g05700	Golgi-associated vesicle
Afu7g05700	cytosol
Afu7g05700	ER to Golgi vesicle-mediated transport
Afu7g05700	intra-Golgi vesicle-mediated transport
Afu7g05720	dihydrolipoyllysine-residue acetyltransferase activity
Afu7g05720	mitochondrion
Afu7g05720	pyruvate metabolic process
Afu7g05740	mitochondrial matrix
Afu7g05740	tricarboxylic acid cycle
Afu7g05740	malate metabolic process
Afu7g05740	L-malate dehydrogenase activity
Afu7g05790	fungal-type vacuole
Afu7g05790	vacuolar membrane
Afu7g05790	vacuole organization
Afu7g05790	Rab guanyl-nucleotide exchange factor activity
Afu7g05790	homotypic vacuole fusion, non-autophagic
Afu7g05800	6-phosphofructo-2-kinase activity
Afu7g05800	fructose-2,6-bisphosphate 2-phosphatase activity
Afu7g05800	cytosol
Afu7g05800	gluconeogenesis
Afu7g05830	fructose transmembrane transporter activity
Afu7g05830	glucose transmembrane transporter activity
Afu7g05830	plasma membrane
Afu7g05830	hexose transport
Afu7g05830	mannose transmembrane transporter activity
Afu7g05870	endopeptidase activity
Afu7g05870	proteasome core complex
Afu7g05870	ubiquitin-dependent protein catabolic process
Afu7g05920	mitochondrion inheritance

Afu7g05920	stearoyl-CoA 9-desaturase activity
Afu7g05920	endoplasmic reticulum membrane
Afu7g05920	unsaturated fatty acid biosynthetic process
Afu7g05930	metalloendopeptidase activity
Afu7g05930	cytoplasm
Afu7g05930	mitochondrial intermembrane space
Afu7g05930	proteolysis
Afu7g05950	mitochondrion inheritance
Afu7g05950	vacuole inheritance
Afu7g05950	actin cap (sensu Saccharomyces)
Afu7g05950	microfilament motor activity
Afu7g05950	establishment of cell polarity (sensu Saccharomyces)
Afu7g05950	cytokinesis
Afu7g05950	endocytosis
Afu7g05950	budding cell apical bud growth
Afu7g05950	budding cell isotropic bud growth
Afu7g05950	vesicle-mediated transport
Afu7g05960	DNA binding
Afu7g05960	nucleus
Afu7g05960	cytoplasm
Afu7g05960	zinc ion binding
Afu7g05970	nucleus
Afu7g05970	cytoplasm
Afu7g05970	RNA localization
Afu7g05970	protein import into nucleus
Afu7g05970	mRNA-binding (hnRNP) protein import into nucleus
Afu7g05970	nuclear localization sequence binding
Afu7g05980	nuclear mRNA splicing, via spliceosome
Afu7g05980	pre-mRNA splicing factor activity
Afu7g05980	small nuclear ribonucleoprotein complex
Afu7g05990	cellular component unknown
Afu7g05990	folic acid and derivative biosynthetic process
Afu7g05990	5-formyltetrahydrofolate cyclo-ligase activity
Afu7g06020	protein import into nucleus, docking
Afu7g06020	structural molecule activity
Afu7g06020	nuclear pore
Afu7g06020	mRNA export from nucleus
Afu7g06020	rRNA export from nucleus
Afu7g06020	snRNA export from nucleus
Afu7g06020	tRNA export from nucleus
Afu7g06020	NLS-bearing substrate import into nucleus
Afu7g06020	snRNP protein import into nucleus
Afu7g06020	mRNA-binding (hnRNP) protein import into nucleus
Afu7g06020	ribosomal protein import into nucleus
Afu7g06020	protein export from nucleus
Afu7g06020	nuclear pore organization
Afu7g06020	chromosome segregation
Afu7g06030	sulfonate dioxygenase activity
Afu7g06030	sulfur metabolic process
Afu7g06030	cellular component unknown

Afu7g06050	SNARE binding
Afu7g06050	plasma membrane
Afu7g06050	ubiquitin-dependent protein catabolic process
Afu7g06050	protein tagging activity
Afu7g06050	vesicle-mediated transport
Afu7g06060	endosome
Afu7g06060	cellular iron ion homeostasis
Afu7g06060	response to stress
Afu7g06060	siderophore-iron (ferrioxamine) uptake transmembrane transporter activity
Afu7g06060	siderophore-iron transport
Afu7g06060	integral to membrane
Afu7g06060	cytoplasmic membrane-bounded vesicle
Afu7g06080	metabolic process
Afu7g06080	methyltransferase activity
Afu7g06090	acyl-CoA oxidase activity
Afu7g06090	peroxisomal matrix
Afu7g06090	fatty acid beta-oxidation
Afu7g06100	acyl-CoA oxidase activity
Afu7g06100	peroxisomal matrix
Afu7g06100	fatty acid beta-oxidation
Afu7g06110	metabolic process
Afu7g06110	hydrolase activity, hydrolyzing N-glycosyl compounds
Afu7g06120	integral to plasma membrane
Afu7g06120	nicotinamide mononucleotide permease activity
Afu7g06120	nicotinamide mononucleotide transport
Afu7g06170	biological process unknown
Afu7g06170	molecular function unknown
Afu7g06170	cellular component unknown
Afu7g06260	metabolic process
Afu7g06260	zinc ion binding
Afu7g06260	oxidoreductase activity
Afu7g06270	molecular function unknown
Afu7g06270	cellular component unknown
Afu7g06290	purine-nucleoside phosphorylase activity
Afu7g06290	protein binding
Afu7g06290	GTP binding
Afu7g06290	programmed cell death
Afu7g06320	transcription factor activity
Afu7g06350	plasma membrane
Afu7g06350	phosphate transport
Afu7g06350	sodium:inorganic phosphate symporter activity
Afu7g06370	transcription factor activity
Afu7g06370	nucleus
Afu7g06370	carbohydrate metabolic process
Afu7g06370	regulation of transcription, DNA-dependent
Afu7g06380	maltose catabolic process
Afu7g06380	alpha-glucosidase activity
Afu7g06380	cellular component unknown
Afu7g06390	alpha-glucoside transport
Afu7g06390	alpha-glucoside:hydrogen symporter activity

Afu7g06390	membrane fraction
Afu7g06420	biological process unknown
Afu7g06420	NADPH dehydrogenase activity
Afu7g06420	nucleus
Afu7g06420	cytoplasm
Afu7g06460	molecular function unknown
Afu7g06460	cytoplasm
Afu7g06460	cell wall organization
Afu7g06500	transcription factor activity
Afu7g06500	nucleus
Afu7g06500	regulation of transcription, DNA-dependent
Afu7g06570	fungal-type vacuole
Afu7g06570	zinc ion transmembrane transporter activity
Afu7g06570	glutathione metabolic process
Afu7g06570	cobalt ion transport
Afu7g06570	zinc ion transport
Afu7g06570	cellular zinc ion homeostasis
Afu7g06570	di-, tri-valent inorganic cation transmembrane transporter activity
Afu7g06580	FAD binding
Afu7g06600	nucleus
Afu7g06600	cytoplasm
Afu7g06600	electron transport
Afu7g06600	FMN reductase activity
Afu7g06630	metabolic process
Afu7g06630	oxidoreductase activity
Afu7g06670	nucleotide binding
Afu7g06670	protein binding
Afu7g06670	programmed cell death
Afu7g06700	electron transport
Afu7g06700	electron carrier activity
Afu7g06760	cytoplasm
Afu7g06760	microsome
Afu7g06760	cytosol
Afu7g06760	cell wall organization
Afu7g06760	phosphatidylinositol transporter activity
Afu7g06760	phospholipid transport
Afu7g06790	biological process unknown
Afu7g06790	endoplasmic reticulum
Afu7g06790	ion transmembrane transporter activity
Afu7g06830	transporter activity
Afu7g06830	transport
Afu7g06830	clathrin-coated vesicle
Afu7g06830	COPI-coated vesicle
Afu7g06840	ornithine-oxo-acid transaminase activity
Afu7g06840	nucleus
Afu7g06840	cytoplasm
Afu7g06840	arginine catabolic process
Afu7g06850	nucleus
Afu7g06850	cytoplasm
Afu7g06850	metabolic process

Afu7g06850	hydrolase activity
Afu7g06960	monooxygenase activity
Afu7g06960	cellular aromatic compound metabolic process
Afu7g07000	catalytic activity
Afu7g07000	metabolic process
Afu7g07030	biological process unknown
Afu7g07030	molecular function unknown
Afu7g07030	cellular component unknown
Afu7g07100	purine-nucleoside phosphorylase activity
Afu7g07100	GTP binding
Afu7g07100	cellular component unknown
Afu7g07100	programmed cell death
Afu7g07120	ferric-chelate reductase activity
Afu7g08290	cellular component unknown
Afu7g08340	proteolysis
Afu7g08340	serine-type peptidase activity
Afu7g08350	hydrolase activity, hydrolyzing O-glycosyl compounds
Afu7g08350	cellular glucan metabolic process
Afu7g08350	fungal-type cell wall
Afu7g08450	ornithine decarboxylase activity
Afu7g08450	cytoplasm
Afu7g08450	pantothenate biosynthetic process
Afu7g08460	transporter activity
Afu7g08460	transport
Afu7g08480	nucleus
Afu7g08480	chromatin assembly or disassembly
Afu7g08480	mating type switching
Afu7g08480	DNA-dependent ATPase activity
Afu7g08490	chitinase activity
Afu7g08490	cell wall chitin catabolic process
Afu7g08490	fungal-type cell wall
Afu7g08500	GTP binding
Afu7g08500	programmed cell death
Afu7g08510	hydrolase activity, hydrolyzing O-glycosyl compounds
Afu7g08510	cellular glucan metabolic process
Afu7g08510	fungal-type cell wall
Afu7g08580	GTPase activity
Afu7g08580	membrane fraction
Afu7g08580	protein targeting to vacuole
Afu7g08580	peroxisome organization
Afu7g08580	vacuolar transport
Afu7g08580	protein retention in Golgi apparatus
Afu7g08650	biological process unknown
Afu7g08650	cellular component unknown
Afu8g00100	aspartate-tRNA ligase activity
Afu8g00100	cytoplasm
Afu8g00100	translation
Afu8g00110	metabolic process
Afu8g00110	oxidoreductase activity
Afu8g00140	transporter activity

Afu8g00140	transport
Afu8g00170	catalytic activity
Afu8g00170	nonribosomal peptide biosynthetic process
Afu8g00170	amino acid adenylylation by nonribosomal peptide synthase
Afu8g00190	metabolic process
Afu8g00190	oxidoreductase activity
Afu8g00200	O-methyltransferase activity
Afu8g00200	S-adenosylmethionine-dependent methyltransferase activity
Afu8g00220	metabolic process
Afu8g00220	oxidoreductase activity
Afu8g00240	GTP binding
Afu8g00240	metabolic process
Afu8g00240	oxidoreductase activity
Afu8g00280	lipid particle
Afu8g00280	metabolic process
Afu8g00280	oxidoreductase activity
Afu8g00370	3-oxoacyl-[acyl-carrier-protein] synthase activity
Afu8g00370	polyketide synthase activity
Afu8g00390	O-methyltransferase activity
Afu8g00390	S-adenosylmethionine-dependent methyltransferase activity
Afu8g00410	methionyl aminopeptidase activity
Afu8g00410	cytoplasm
Afu8g00410	proteolysis
Afu8g00420	DNA binding
Afu8g00460	methionyl aminopeptidase activity
Afu8g00460	cytosolic ribosome (sensu Eukaryota)
Afu8g00460	proteolysis
Afu8g00500	acetate-CoA ligase activity
Afu8g00500	cytosol
Afu8g00500	acetyl-CoA biosynthetic process
Afu8g00510	metabolic process
Afu8g00510	oxidoreductase activity
Afu8g00540	polyketide synthase activity
Afu8g00560	metabolic process
Afu8g00560	oxidoreductase activity
Afu8g00580	translation elongation factor activity
Afu8g00580	cytosolic ribosome (sensu Eukaryota)
Afu8g00580	regulation of translational elongation
Afu8g00590	stearoyl-CoA 9-desaturase activity
Afu8g00590	fatty acid biosynthetic process
Afu8g00600	nucleotide-sugar metabolic process
Afu8g00600	NAD or NADH binding
Afu8g00650	lipopolysaccharide biosynthetic process
Afu8g00650	transferase activity, transferring glycosyl groups
Afu8g00660	transporter activity
Afu8g00660	transport
Afu8g00660	integral to membrane
Afu8g00680	carbohydrate metabolic process
Afu8g00680	transferase activity, transferring glycosyl groups
Afu8g00700	chitinase activity

Afu8g00700	cell wall chitin catabolic process
Afu8g00700	fungal-type cell wall
Afu8g00730	cytoplasm
Afu8g00730	intracellular signaling cascade
Afu8g00730	transcription regulator activity
Afu8g00750	transcription factor activity
Afu8g00750	nucleus
Afu8g00750	regulation of transcription, DNA-dependent
Afu8g00750	zinc ion binding
Afu8g00760	metabolic process
Afu8g00760	oxidoreductase activity
Afu8g00770	plasma membrane
Afu8g00770	lactate transmembrane transporter activity
Afu8g00770	lactate transport
Afu8g00800	general amino acid permease activity
Afu8g00800	integral to plasma membrane
Afu8g00800	amino acid transport
Afu8g00840	plasma membrane
Afu8g00840	choline transmembrane transporter activity
Afu8g00840	choline transport
Afu8g00850	dihydroorotase activity
Afu8g00850	nucleus
Afu8g00850	cytoplasm
Afu8g00850	pyrimidine nucleotide biosynthetic process
Afu8g00890	fructose transmembrane transporter activity
Afu8g00890	glucose transmembrane transporter activity
Afu8g00890	plasma membrane
Afu8g00890	hexose transport
Afu8g00890	mannose transmembrane transporter activity
Afu8g00940	integral to plasma membrane
Afu8g00940	multidrug transport
Afu8g00940	multidrug efflux pump activity
Afu8g00940	response to drug
Afu8g01020	programmed cell death
Afu8g01070	C-5 sterol desaturase activity
Afu8g01070	endoplasmic reticulum
Afu8g01070	ergosterol biosynthetic process
Afu8g01090	vacuole inheritance
Afu8g01090	fungal-type vacuole
Afu8g01090	cytosol
Afu8g01090	DNA-dependent DNA replication
Afu8g01090	response to oxidative stress
Afu8g01090	regulation of cell redox homeostasis
Afu8g01090	thiol-disulfide exchange intermediate activity
Afu8g01090	vacuole fusion, non-autophagic
Afu8g01140	transcription factor activity
Afu8g01140	nucleus
Afu8g01140	zinc ion binding
Afu8g01140	regulation of transcription
Afu8g01150	transcription factor activity

Afu8g01150	nucleus
Afu8g01150	regulation of transcription
Afu8g01160	isocitrate dehydrogenase activity
Afu8g01160	cytoplasm
Afu8g01160	mitochondrion
Afu8g01160	lysine biosynthetic process
Afu8g01180	transporter activity
Afu8g01180	transport
Afu8g01180	membrane
Afu8g01210	3-hydroxyisobutyryl-CoA hydrolase activity
Afu8g01210	mitochondrion
Afu8g01210	fatty acid beta-oxidation
Afu8g01210	endocytosis
Afu8g01240	transcription factor activity
Afu8g01240	nucleus
Afu8g01240	response to xenobiotic stimulus
Afu8g01240	regulation of transcription
Afu8g01250	N-acetyltransferase activity
Afu8g01250	metabolic process
Afu8g01310	transition metal ion transport
Afu8g01310	ferric-chelate reductase activity
Afu8g01310	plasma membrane
Afu8g01310	cellular iron ion homeostasis
Afu8g01310	integral to membrane
Afu8g01340	alpha-glucoside transport
Afu8g01340	alpha-glucoside:hydrogen symporter activity
Afu8g01340	membrane fraction
Afu8g01380	nucleotide binding
Afu8g01380	protein binding
Afu8g01380	cellular component unknown
Afu8g01390	polysaccharide metabolic process
Afu8g01390	hydrolase activity, acting on glycosyl bonds
Afu8g01400	S-adenosylmethionine transmembrane transporter activity
Afu8g01400	mitochondrion
Afu8g01400	mitochondrial inner membrane
Afu8g01400	S-adenosylmethionine transport
Afu8g01410	chitinase activity
Afu8g01410	cell wall
Afu8g01410	cell wall chitin catabolic process
Afu8g01420	metabolic process
Afu8g01420	zinc ion binding
Afu8g01420	oxidoreductase activity
Afu8g01430	metabolic process
Afu8g01430	zinc ion binding
Afu8g01430	cellular component unknown
Afu8g01430	oxidoreductase activity
Afu8g01440	DNA binding
Afu8g01450	plasma membrane
Afu8g01450	choline transmembrane transporter activity
Afu8g01450	choline transport

Afu8g01480	potassium channel activity
Afu8g01480	plasma membrane
Afu8g01480	cellular potassium ion homeostasis
Afu8g01500	purine-nucleoside phosphorylase activity
Afu8g01550	peroxisomal matrix
Afu8g01550	sporulation (sensu Saccharomyces)
Afu8g01550	2,4-dienoyl-CoA reductase (NADPH) activity
Afu8g01550	fatty acid catabolic process
Afu8g01560	aldo-keto reductase activity
Afu8g01560	nucleus
Afu8g01560	cytoplasm
Afu8g01560	cellular aldehyde metabolic process
Afu8g01580	arylformamidase activity
Afu8g01580	cytoplasm
Afu8g01580	mitochondrion
Afu8g01580	NAD biosynthetic process
Afu8g01630	electron transport
Afu8g01630	oxidoreductase activity
Afu8g01630	coenzyme binding
Afu8g01640	nonribosomal peptide biosynthetic process
Afu8g01670	mitochondrial intermembrane space
Afu8g01670	response to oxidative stress
Afu8g01670	pathogenesis
Afu8g01670	bacterial catalase-peroxidase activity
Afu8g01780	biological process unknown
Afu8g01780	molecular function unknown
Afu8g01780	cellular component unknown
Afu8g01800	biological process unknown
Afu8g01800	thiosulfate sulfurtransferase activity
Afu8g01800	cytoplasm
Afu8g01850	plasma membrane
Afu8g01850	phosphate transport
Afu8g01850	sodium:inorganic phosphate symporter activity
Afu8g01910	acid phosphatase activity
Afu8g01910	thiamin transport
Afu8g01910	cell wall-bounded periplasmic space
Afu8g01940	DNA binding
Afu8g01940	zinc ion binding
Afu8g01970	polygalacturonase activity
Afu8g01970	extracellular region
Afu8g01970	pseudohyphal growth
Afu8g01970	pectin catabolic process
Afu8g01990	transcription factor activity
Afu8g01990	nucleus
Afu8g01990	regulation of transcription
Afu8g02000	monosaccharide metabolic process
Afu8g02000	cellular component unknown
Afu8g02000	D-xylulose reductase activity
Afu8g02010	transporter activity
Afu8g02010	transport

Afu8g02010	membrane
Afu8g02020	carbohydrate metabolic process
Afu8g02020	transferase activity, transferring glycosyl groups
Afu8g02040	N-linked glycoprotein maturation
Afu8g02040	transferase activity, transferring glycosyl groups
Afu8g02060	endoplasmic reticulum
Afu8g02060	hydrolase activity
Afu8g02070	biological process unknown
Afu8g02070	fungal-type vacuole
Afu8g02070	transferase activity, transferring glycosyl groups
Afu8g02090	integral to plasma membrane
Afu8g02130	cellular glucan metabolic process
Afu8g02130	cell wall organization
Afu8g02130	1,3-beta-glucanosyltransferase activity
Afu8g02130	anchored to plasma membrane
Afu8g02140	molecular function unknown
Afu8g02150	ornithine-oxo-acid transaminase activity
Afu8g02150	nucleus
Afu8g02150	cytoplasm
Afu8g02150	arginine catabolic process
Afu8g02160	aldehyde dehydrogenase (NAD) activity
Afu8g02160	mitochondrion
Afu8g02160	ethanol metabolic process
Afu8g02170	DNA binding
Afu8g02170	zinc ion binding
Afu8g02200	plasma membrane
Afu8g02200	amino acid transport
Afu8g02200	amino acid transmembrane transporter activity
Afu8g02200	amino acid permease activity
Afu8g02210	sulfonate dioxygenase activity
Afu8g02210	sulfur metabolic process
Afu8g02210	cellular component unknown
Afu8g02280	transcription cofactor activity
Afu8g02280	nucleus
Afu8g02280	regulation of transcription
Afu8g02300	L-lactate dehydrogenase (cytochrome) activity
Afu8g02300	mitochondrial intermembrane space
Afu8g02300	electron transport
Afu8g02310	3-chloroallyl aldehyde dehydrogenase activity
Afu8g02310	cytoplasm
Afu8g02310	cellular aldehyde metabolic process
Afu8g02310	polyamine catabolic process
Afu8g02310	beta-alanine biosynthetic process
Afu8g02320	carbohydrate metabolic process
Afu8g02320	transferase activity, transferring glycosyl groups
Afu8g02350	polyketide synthase activity
Afu8g02350	secondary metabolic process
Afu8g02380	monooxygenase activity
Afu8g02380	cellular aromatic compound metabolic process
Afu8g02380	pathogenesis

Afu8g02400	farnesyltranstransferase activity
Afu8g02400	terpenoid biosynthetic process
Afu8g02410	prenyltransferase activity
Afu8g02410	carrier activity
Afu8g02410	secondary metabolic process
Afu8g02410	isoprenoid binding
Afu8g02430	soluble fraction
Afu8g02430	alcohol metabolic process
Afu8g02430	alcohol dehydrogenase (NADP+) activity
Afu8g02430	zinc ion binding
Afu8g02440	C-4 methylsterol oxidase activity
Afu8g02440	endoplasmic reticulum membrane
Afu8g02440	plasma membrane
Afu8g02440	ergosterol biosynthetic process
Afu8g02500	glutathione transferase activity
Afu8g02500	endoplasmic reticulum
Afu8g02500	glutathione metabolic process
Afu8g02510	carbohydrate metabolic process
Afu8g02510	hydrolase activity, hydrolyzing N-glycosyl compounds
Afu8g02520	sulfur metabolic process
Afu8g02520	sulfuric ester hydrolase activity
Afu8g02550	plasma membrane
Afu8g02550	peptide transporter activity
Afu8g02550	peptide transport
Afu8g02560	glyceraldehyde-3-phosphate dehydrogenase (phosphorylating) activity
Afu8g02560	cytoplasm
Afu8g02560	lipid particle
Afu8g02560	cytosol
Afu8g02560	gluconeogenesis
Afu8g02560	glycolysis
Afu8g02560	fungal-type cell wall
Afu8g02600	biological process unknown
Afu8g02600	molecular function unknown
Afu8g02600	cellular component unknown
Afu8g02610	metabolic process
Afu8g02610	oxidoreductase activity
Afu8g02620	biological process unknown
Afu8g02620	molecular function unknown
Afu8g02620	cytoplasm
Afu8g02620	cobalamin biosynthetic process
Afu8g02630	polygalacturonase activity
Afu8g02630	extracellular region
Afu8g02630	pseudohyphal growth
Afu8g02630	pectin catabolic process
Afu8g02640	transcription factor activity
Afu8g02640	nucleus
Afu8g02640	regulation of transcription
Afu8g02650	ATP-binding cassette (ABC) transporter activity
Afu8g02650	transport
Afu8g02650	membrane

Afu8g02660	chromate transmembrane transporter activity
Afu8g02660	chromate transport
Afu8g02690	Golgi medial cisterna
Afu8g02690	protein amino acid N-linked glycosylation
Afu8g02690	acetylglucosaminyltransferase activity
Afu8g02700	3-dehydroquinate dehydratase activity
Afu8g02700	3-dehydroquinate synthase activity
Afu8g02700	3-phosphoshikimate 1-carboxyvinyltransferase activity
Afu8g02700	shikimate 5-dehydrogenase activity
Afu8g02700	shikimate kinase activity
Afu8g02700	cytoplasm
Afu8g02700	aromatic amino acid family biosynthetic process
Afu8g02710	transcription factor activity
Afu8g02710	nucleus
Afu8g02710	regulation of transcription
Afu8g02720	negative regulation of transcription from RNA polymerase II promoter
Afu8g02720	protein phosphatase type 1 activity
Afu8g02720	protein phosphatase type 1 complex
Afu8g02720	cytoplasm
Afu8g02720	glycogen metabolic process
Afu8g02720	regulation of carbohydrate metabolic process
Afu8g02720	cell growth and/or maintenance
Afu8g02720	protein phosphatase type 1 regulator activity
Afu8g02730	biological process unknown
Afu8g02730	RNA binding
Afu8g02730	cytoplasm
Afu8g02750	nucleolus
Afu8g02750	ribosome biogenesis
Afu8g02750	pathogenesis
Afu8g02750	growth or development of symbiont in host
Afu8g02760	L-ornithine transmembrane transporter activity
Afu8g02760	mitochondrial ornithine transport
Afu8g02760	mitochondrial envelope
Afu8g02760	arginine biosynthetic process
Afu8g02770	cytidine deaminase activity
Afu8g02770	nucleus
Afu8g02770	cytoplasm
Afu8g02770	cytidine catabolic process
Afu8g02770	deoxycytidine catabolic process
Afu8g02770	zinc ion binding
Afu8g02780	signal sequence binding
Afu8g02780	Golgi apparatus
Afu8g02780	protein targeting to vacuole
Afu8g02780	vacuolar transport
Afu8g02790	actin cap (sensu Saccharomyces)
Afu8g02790	exocyst
Afu8g02790	establishment of cell polarity (sensu Saccharomyces)
Afu8g02790	cytokinesis
Afu8g02790	protein binding
Afu8g02790	Golgi to plasma membrane transport

Afu8g02790	vesicle docking during exocytosis
Afu8g02790	vesicle fusion
Afu8g02790	bipolar cellular bud site selection
Afu8g02800	biological process unknown
Afu8g02800	molecular function unknown
Afu8g02800	endoplasmic reticulum
Afu8g02800	lipid particle
Afu8g02830	UDP-N-acetylglucosamine transmembrane transporter activity
Afu8g02830	cell wall chitin biosynthetic process
Afu8g02830	UDP-N-acetylglucosamine transport
Afu8g02830	integral to endoplasmic reticulum membrane
Afu8g02840	mitochondrial fission
Afu8g02840	GTPase activity
Afu8g02840	mitochondrial outer membrane
Afu8g02850	actin cortical patch assembly
Afu8g02850	protein binding
Afu8g02850	cytoplasm
Afu8g02850	cytoskeleton
Afu8g02850	cell cortex
Afu8g02860	AMP deaminase activity
Afu8g02860	cytoplasm
Afu8g02860	purine nucleotide metabolic process
Afu8g03880	alanine-tRNA ligase activity
Afu8g03880	cytoplasm
Afu8g03880	alanyl-tRNA aminoacylation
Afu8g03890	peptidyl-prolyl cis-trans isomerase activity
Afu8g03890	mitochondrion
Afu8g03890	protein folding
Afu8g03900	zinc ion binding
Afu8g03920	regulation of progression through cell cycle
Afu8g03930	chaperone activity
Afu8g03930	cytoplasm
Afu8g03930	polysome
Afu8g03930	translation
Afu8g03930	ATPase activity
Afu8g03940	translation
Afu8g03940	translation factor activity, nucleic acid binding
Afu8g03970	DNA binding
Afu8g03980	cytoplasm
Afu8g03980	transcription
Afu8g03990	GTPase activity
Afu8g03990	protein binding
Afu8g03990	spliceosomal complex
Afu8g03990	U5 snRNP
Afu8g03990	mRNA processing
Afu8g03990	pre-mRNA splicing factor activity
Afu8g04000	acetyl-CoA C-acetyltransferase activity
Afu8g04000	cytosol
Afu8g04000	ergosterol biosynthetic process
Afu8g04010	low-affinity zinc ion transmembrane transporter activity

Afu8g04010	plasma membrane
Afu8g04010	low-affinity zinc ion transport
Afu8g04030	integral to membrane
Afu8g04040	RNA binding
Afu8g04040	mRNA cleavage and polyadenylation specificity factor complex
Afu8g04040	termination of RNA polymerase II transcription
Afu8g04040	mRNA polyadenylation
Afu8g04040	mRNA cleavage
Afu8g04040	cleavage and polyadenylylation specificity factor activity
Afu8g04060	N-acetylglucosamine catabolic process
Afu8g04060	beta-N-acetylglucosaminidase activity
Afu8g04070	glucosamine-6-phosphate deaminase activity
Afu8g04070	N-acetylglucosamine catabolic process
Afu8g04080	cytoplasm
Afu8g04080	betaine biosynthetic process
Afu8g04080	betaine-aldehyde dehydrogenase activity
Afu8g04080	response to salt stress
Afu8g04080	choline catabolic process
Afu8g04090	response to cold
Afu8g04090	response to salt stress
Afu8g04090	oxidoreductase activity
Afu8g04090	glycine betaine biosynthetic process from choline
Afu8g04090	choline catabolic process
Afu8g04100	amino sugar metabolic process
Afu8g04100	N-acetylglucosamine catabolic process
Afu8g04100	N-acetylglucosamine-6-phosphate deacetylase activity
Afu8g04110	integral to membrane
Afu8g04120	serine-type carboxypeptidase activity
Afu8g04120	proteolysis
Afu8g04130	transcription factor activity
Afu8g04130	regulation of transcription
Afu8g04160	tetrahydrofolylpolyglutamate synthase activity
Afu8g04160	cytoplasm
Afu8g04160	mitochondrion
Afu8g04160	one-carbon metabolic process
Afu8g04180	molecular function unknown
Afu8g04180	cytoplasm
Afu8g04180	cellular response to glucose starvation
Afu8g04200	RNA binding
Afu8g04220	nucleus
Afu8g04220	nucleolus
Afu8g04220	small nucleolar ribonucleoprotein complex
Afu8g04220	maturation of SSU-rRNA
Afu8g04220	snoRNA binding
Afu8g04260	endoplasmic reticulum membrane
Afu8g04260	SRP-dependent cotranslational protein targeting to membrane, translocation
Afu8g04260	protein transporter activity
Afu8g04270	nucleus
Afu8g04270	ATPase activity
Afu8g04270	protein catabolic process

Afu8g04300	DNA binding
Afu8g04300	nucleus
Afu8g04300	zinc ion binding
Afu8g04330	biological process unknown
Afu8g04330	nucleus
Afu8g04330	cytoplasm
Afu8g04330	S-adenosylmethionine-dependent methyltransferase activity
Afu8g04340	sulfur amino acid metabolic process
Afu8g04340	cystathionine gamma-lyase activity
Afu8g04340	cytoplasm
Afu8g04340	cysteine metabolic process
Afu8g04340	transsulfuration
Afu8g04400	RNA binding
Afu8g04400	nucleolus
Afu8g04400	rRNA metabolic process
Afu8g04420	mRNA cleavage and polyadenylation specificity factor complex
Afu8g04420	mRNA cleavage factor complex
Afu8g04420	mRNA polyadenylation
Afu8g04420	mRNA cleavage
Afu8g04420	tRNA processing
Afu8g04420	cleavage and polyadenylylation specificity factor activity
Afu8g04420	termination of RNA polymerase II transcription, poly(A)-coupled
Afu8g04420	termination of RNA polymerase II transcription, poly(A)-independent
Afu8g04430	dolichyl-diphosphooligosaccharide-protein glycotransferase activity
Afu8g04430	protein amino acid N-linked glycosylation
Afu8g04430	oligosaccharyltransferase complex
Afu8g04440	protein deneddylation
Afu8g04440	signalosome
Afu8g04440	regulation of developmental process
Afu8g04460	microtubule motor activity
Afu8g04460	cytoplasm
Afu8g04460	microtubule-based movement
Afu8g04470	integral to plasma membrane
Afu8g04470	nicotinamide mononucleotide permease activity
Afu8g04470	nicotinamide mononucleotide transport
Afu8g04480	transporter activity
Afu8g04480	transport
Afu8g04480	membrane
Afu8g04500	dolichyl-phosphate-mannose-protein mannosyltransferase activity
Afu8g04500	endoplasmic reticulum
Afu8g04500	protein amino acid O-linked glycosylation
Afu8g04510	transcription cofactor activity
Afu8g04510	iron ion binding
Afu8g04510	nucleus
Afu8g04510	transcription from RNA polymerase II promoter
Afu8g04520	actin cortical patch assembly
Afu8g04520	actin cortical patch (sensu Saccharomyces)
Afu8g04520	endocytosis
Afu8g04520	actin filament organization
Afu8g04520	cell wall organization

Afu8g04520	bipolar cellular bud site selection
Afu8g04520	cytoskeletal protein binding
Afu8g04540	transcription factor activity
Afu8g04540	nucleus
Afu8g04540	zinc ion binding
Afu8g04540	regulation of transcription
Afu8g04580	biological process unknown
Afu8g04580	mitochondrion
Afu8g04580	protein phosphatase type 2C activity
Afu8g04590	nuclear mRNA splicing, via spliceosome
Afu8g04590	pre-mRNA splicing factor activity
Afu8g04590	small nuclear ribonucleoprotein complex
Afu8g04610	co-chaperone activity
Afu8g04610	mitochondrion
Afu8g04610	aerobic respiration
Afu8g04610	iron-sulfur cluster assembly
Afu8g04640	RNA-3'-phosphate cyclase activity
Afu8g04640	molecular function unknown
Afu8g04640	nucleolus
Afu8g04640	rRNA processing
Afu8g04650	3-hydroxyanthranilate 3,4-dioxygenase activity
Afu8g04650	cytoplasm
Afu8g04650	NAD biosynthetic process
Afu8g04660	mitotic anaphase B
Afu8g04660	spindle pole body
Afu8g04660	spindle microtubule
Afu8g04660	mitotic spindle organization
Afu8g04660	microtubule binding
Afu8g04670	biological process unknown
Afu8g04670	protein kinase activity
Afu8g04702	transporter activity
Afu8g04702	plasma membrane
Afu8g04702	transport
Afu8g04710	carbohydrate metabolic process
Afu8g04710	hydrolase activity, hydrolyzing N-glycosyl compounds
Afu8g04740	U2-type spliceosome conformational change to release U4 and U1
Afu8g04740	ATP-dependent RNA helicase activity
Afu8g04740	U5 snRNP
Afu8g04740	pre-mRNA splicing factor activity
Afu8g04740	U4/U6 x U5 tri-snRNP complex
Afu8g04750	ATP binding
Afu8g04750	mitochondrion
Afu8g04750	DNA repair
Afu8g04760	allantoin catabolic process
Afu8g04760	ureidoglycolate hydrolase activity
Afu8g04760	membrane
Afu8g04770	acetate-CoA ligase activity
Afu8g04770	cytosol
Afu8g04770	acetyl-CoA biosynthetic process
Afu8g04790	ribosomal large subunit assembly

Afu8g04790	nucleolus
Afu8g04790	5S rRNA binding
Afu8g04790	7S RNA binding
Afu8g04790	rRNA binding
Afu8g04790	processing of 27S pre-rRNA
Afu8g04800	valine-tRNA ligase activity
Afu8g04800	cytoplasm
Afu8g04800	mitochondrion
Afu8g04800	valyl-tRNA aminoacylation
Afu8g04810	G1/S transition of mitotic cell cycle
Afu8g04810	G2/M transition of mitotic cell cycle
Afu8g04810	flocculation
Afu8g04810	establishment of cell polarity (sensu Saccharomyces)
Afu8g04810	protein kinase CK2 activity
Afu8g04810	protein kinase CK2 complex
Afu8g04810	regulation of transcription from RNA polymerase I promoter
Afu8g04810	regulation of transcription from RNA polymerase III promoter
Afu8g04810	protein amino acid phosphorylation
Afu8g04810	cellular ion homeostasis
Afu8g04810	response to DNA damage stimulus
Afu8g04820	ribonuclease MRP activity
Afu8g04820	ribonuclease MRP complex
Afu8g04820	ribonuclease P activity
Afu8g04820	nucleolar ribonuclease P complex
Afu8g04820	rRNA processing
Afu8g04820	tRNA processing
Afu8g04840	ubiquitin-protein ligase activity
Afu8g04840	endoplasmic reticulum membrane
Afu8g04840	ER-associated protein catabolic process
Afu8g04870	metabolic process
Afu8g04870	oxidoreductase activity
Afu8g04880	protein deneddylation
Afu8g04880	signalosome
Afu8g04880	regulation of developmental process
Afu8g04910	plasma membrane
Afu8g04910	choline transmembrane transporter activity
Afu8g04910	choline transport
Afu8g04940	diacylglycerol cholinephosphotransferase activity
Afu8g04940	endoplasmic reticulum
Afu8g04940	phosphatidylcholine biosynthetic process
Afu8g04950	regulation of transcription involved in G1 phase of mitotic cell cycle
Afu8g04950	transcription factor TFIID complex
Afu8g04950	transcription initiation from RNA polymerase II promoter
Afu8g04950	general RNA polymerase II transcription factor activity
Afu8g04960	nuclear mRNA splicing, via spliceosome
Afu8g04960	pre-mRNA splicing factor activity
Afu8g04960	small nuclear ribonucleoprotein complex
Afu8g05000	bis(5'-nucleosyl)-tetraphosphatase (asymmetrical) activity
Afu8g05000	nucleus
Afu8g05000	cytoplasm

Afu8g05000	bis(5'-nucleosyl)-tetraphosphatase activity
Afu8g05000	nucleotide metabolic process
Afu8g05010	DNA binding
Afu8g05010	nucleus
Afu8g05010	zinc ion binding
Afu8g05020	beta-N-acetylhexosaminidase activity
Afu8g05020	cell wall chitin metabolic process
Afu8g05020	fungal-type cell wall
Afu8g05090	transporter activity
Afu8g05090	transport
Afu8g05140	endoplasmic reticulum
Afu8g05140	protein folding
Afu8g05140	protein thiol-disulfide exchange
Afu8g05140	electron carrier activity
Afu8g05160	protein binding
Afu8g05160	peroxisomal membrane
Afu8g05160	protein targeting to peroxisome
Afu8g05160	peroxisome organization
Afu8g05170	molecular function unknown
Afu8g05170	membrane fraction
Afu8g05170	protein targeting to vacuole
Afu8g05170	autophagy
Afu8g05200	biological process unknown
Afu8g05200	cysteine synthase activity
Afu8g05200	mitochondrion
Afu8g05220	biological process unknown
Afu8g05220	amidase activity
Afu8g05220	cellular component unknown
Afu8g05230	biological process unknown
Afu8g05230	molecular function unknown
Afu8g05230	cytoplasm
Afu8g05240	peroxisome targeting sequence binding
Afu8g05240	peroxisome targeting signal receptor activity
Afu8g05240	peroxisome matrix targeting signal-1 binding
Afu8g05240	protein binding
Afu8g05240	peroxisome
Afu8g05240	cytosol
Afu8g05240	protein targeting to peroxisome
Afu8g05240	peroxisome organization
Afu8g05260	ribosomal small subunit assembly
Afu8g05260	single-stranded DNA binding
Afu8g05260	RNA binding
Afu8g05260	nucleus
Afu8g05260	nucleolus
Afu8g05260	rRNA processing
Afu8g05300	DNA-directed RNA polymerase activity
Afu8g05300	DNA-directed RNA polymerase II, core complex
Afu8g05300	transcription from RNA polymerase II promoter
Afu8g05310	biological process unknown
Afu8g05310	molecular function unknown

Afu8g05310	endoplasmic reticulum
Afu8g05320	mitochondrial proton-transporting ATP synthase, catalytic core
Afu8g05320	ATP synthesis coupled proton transport
Afu8g05320	hydrogen ion transporting ATP synthase activity, rotational mechanism
Afu8g05330	methylenetetrahydrofolate dehydrogenase (NAD+) activity
Afu8g05330	cytosol
Afu8g05330	one-carbon metabolic process
Afu8g05330	purine base biosynthetic process
Afu8g05340	protein binding
Afu8g05340	signal peptidase complex
Afu8g05340	signal peptide processing
Afu8g05350	biological process unknown
Afu8g05350	molecular function unknown
Afu8g05350	cellular component unknown
Afu8g05370	RNA polymerase II transcription factor activity
Afu8g05370	nucleoplasm
Afu8g05370	nucleotide-excision repair
Afu8g05370	transcription from RNA polymerase II promoter
Afu8g05370	methionine metabolic process
Afu8g05430	nucleus
Afu8g05430	ribosome biogenesis
Afu8g05430	maturation of SSU-rRNA
Afu8g05430	snoRNA binding
Afu8g05440	mitochondrial proton-transporting ATP synthase, stator stalk
Afu8g05440	structural molecule activity
Afu8g05440	programmed cell death
Afu8g05440	ATP synthesis coupled proton transport
Afu8g05440	hydrogen ion transporting ATP synthase activity, rotational mechanism
Afu8g05460	transcription factor activity
Afu8g05460	transcription
Afu8g05490	transcription factor TFIIF complex
Afu8g05490	transcription initiation from RNA polymerase II promoter
Afu8g05490	general RNA polymerase II transcription factor activity
Afu8g05500	signalosome
Afu8g05500	sporocarp development
Afu8g05500	regulation of developmental process
Afu8g05520	aldehyde dehydrogenase (NAD) activity
Afu8g05520	mitochondrion
Afu8g05520	ethanol metabolic process
Afu8g05530	cytoplasm
Afu8g05530	metabolic process
Afu8g05530	fumarate reductase (NADH) activity
Afu8g05560	protein phosphatase type 2A activity
Afu8g05560	protein phosphatase type 2A complex
Afu8g05560	translation
Afu8g05560	protein amino acid dephosphorylation
Afu8g05560	actin filament organization
Afu8g05560	mitotic cell cycle spindle assembly checkpoint
Afu8g05560	budding cell bud growth
Afu8g05560	pseudohyphal growth

Afu8g05570	histone deacetylase complex
Afu8g05570	chromatin silencing at rDNA
Afu8g05570	histone deacetylase activity
Afu8g05570	chromatin silencing at HML and HMR (sensu Saccharomyces)
Afu8g05570	chromatin silencing at telomere
Afu8g05570	regulation of transcription from RNA polymerase II promoter
Afu8g05580	acetyl-CoA hydrolase activity
Afu8g05580	mitochondrion
Afu8g05580	cytosol
Afu8g05580	acetate metabolic process
Afu8g05580	acetyl-CoA metabolic process
Afu8g05610	hydrolase activity, hydrolyzing O-glycosyl compounds
Afu8g05610	cellular glucan metabolic process
Afu8g05610	cytokinesis, completion of separation
Afu8g05610	fungal-type cell wall
Afu8g05620	cytokinesis
Afu8g05620	cell wall chitin biosynthetic process
Afu8g05620	response to osmotic stress
Afu8g05620	enzyme activator activity
Afu8g05630	chitin synthase activity
Afu8g05630	integral to plasma membrane
Afu8g05630	chitin biosynthetic process
Afu8g05660	microfilament motor activity
Afu8g05660	actin cortical patch (sensu Saccharomyces)
Afu8g05660	exocytosis
Afu8g05660	endocytosis
Afu8g05660	response to osmotic stress
Afu8g05660	cell wall organization
Afu8g05660	bipolar cellular bud site selection
Afu8g05660	response to salt stress
Afu8g05680	spindle pole
Afu8g05680	protein serine/threonine kinase activity
Afu8g05680	nucleus
Afu8g05680	DNA-dependent DNA replication
Afu8g05680	protein amino acid phosphorylation
Afu8g05710	transporter activity
Afu8g05710	transport
Afu8g05710	membrane
Afu8g05740	biological process unknown
Afu8g05740	molecular function unknown
Afu8g05740	integral to membrane
Afu8g05750	DNA binding
Afu8g05760	nucleus
Afu8g05760	cytoplasm
Afu8g05760	metabolic process
Afu8g05760	oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor
Afu8g05780	protein binding
Afu8g05780	GTP binding
Afu8g05820	DNA binding
Afu8g05820	ATP binding

Afu8g05820	nucleus
Afu8g05820	reciprocal meiotic recombination
Afu8g05820	ATPase activity
Afu8g05840	transcription factor activity
Afu8g05840	regulation of transcription
Afu8g05860	plasma membrane
Afu8g05860	amino acid transport
Afu8g05860	amino acid transmembrane transporter activity
Afu8g05860	amino acid permease activity
Afu8g05880	protein folding
Afu8g05880	chaperone regulator activity
Afu8g05880	chaperone binding
Afu8g05975	transferase activity, transferring phosphorus-containing groups
Afu8g05980	protein kinase activity
Afu8g05980	cytoplasm
Afu8g06000	L-lactate dehydrogenase (cytochrome) activity
Afu8g06000	mitochondrial intermembrane space
Afu8g06000	electron transport
Afu8g06000	oxidoreductase activity
Afu8g06010	transcription factor activity
Afu8g06010	nucleus
Afu8g06010	zinc ion binding
Afu8g06010	regulation of transcription
Afu8g06020	glutamate decarboxylase activity
Afu8g06020	cytoplasm
Afu8g06020	glutamate catabolic process
Afu8g06020	response to oxidative stress
Afu8g06030	hydrolase activity, hydrolyzing O-glycosyl compounds
Afu8g06030	cellular glucan metabolic process
Afu8g06030	fungal-type cell wall
Afu8g06060	biological process unknown
Afu8g06060	molecular function unknown
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Afu8g06080	cytoplasm
Afu8g06080	response to stress
Afu8g06080	metabolic process
Afu8g06080	oxidoreductase activity, acting on NADH or NADPH
Afu8g06090	plasma membrane
Afu8g06090	choline transmembrane transporter activity
Afu8g06090	choline transport
Afu8g06140	two-component sensor activity
Afu8g06140	protein histidine kinase activity
Afu8g06140	protein amino acid phosphorylation
Afu8g06180	nucleic acid binding
Afu8g06180	catalytic activity
Afu8g06180	programmed cell death
Afu8g06210	ferric-chelate reductase activity
Afu8g06360	hydrolase activity, hydrolyzing O-glycosyl compounds
Afu8g06360	cellular glucan metabolic process
Afu8g06360	fungal-type cell wall

Afu8g06370	monooxygenase activity
Afu8g06370	cellular aromatic compound metabolic process
Afu8g06400	nucleotide binding
Afu8g06400	purine-nucleoside phosphorylase activity
Afu8g06400	protein binding
Afu8g06400	cellular component unknown
Afu8g06400	programmed cell death
Afu8g06410	transporter activity
Afu8g06410	transport
Afu8g06470	aminomethyltransferase activity
Afu8g06530	transporter activity
Afu8g06530	transport
Afu8g06540	ornithine decarboxylase activity
Afu8g06540	cytoplasm
Afu8g06540	pantothenate biosynthetic process
Afu8g06550	biological process unknown
Afu8g06550	molecular function unknown
Afu8g06550	nucleus
Afu8g06550	cytoplasm
Afu8g06554	carbonate dehydratase activity
Afu8g06554	metabolic process
Afu8g06580	plasma membrane
Afu8g06580	choline transmembrane transporter activity
Afu8g06580	choline transport
Afu8g06600	cellular component unknown
Afu8g06610	transporter activity
Afu8g06610	transport
Afu8g06610	monocarboxylic acid transmembrane transporter activity
Afu8g06610	membrane
Afu8g06640	metabolic process
Afu8g06640	methyltransferase activity
Afu8g06680	acyl-CoA metabolic process
Afu8g06680	acyl-CoA thioesterase activity
Afu8g06750	cytoplasm
Afu8g06750	sterol metabolic process
Afu8g06750	sterol 3-beta-glucosyltransferase activity
Afu8g06760	transporter activity
Afu8g06760	integral to plasma membrane
Afu8g06760	transport
Afu8g06840	metabolic process
Afu8g06840	oxidoreductase activity
Afu8g06870	fructose transmembrane transporter activity
Afu8g06870	glucose transmembrane transporter activity
Afu8g06870	plasma membrane
Afu8g06870	hexose transport
Afu8g06870	mannose transmembrane transporter activity
Afu8g06880	pectinesterase activity
Afu8g06880	pectin catabolic process
Afu8g06890	polygalacturonase activity
Afu8g06890	extracellular region

Afu8g06890	pectin catabolic process
Afu8g06920	membrane
Afu8g07000	transcription factor activity
Afu8g07000	nucleus
Afu8g07000	zinc ion binding
Afu8g07000	regulation of transcription
Afu8g07020	monooxygenase activity
Afu8g07020	cellular aromatic compound metabolic process
Afu8g07060	cell wall organization
Afu8g07070	cellular component unknown
Afu8g07080	endopeptidase activity
Afu8g07080	pathogenesis
Afu8g07130	mitochondrion
Afu8g07130	thioredoxin peroxidase activity
Afu8g07130	regulation of cell redox homeostasis
Afu8g07140	cytosol
Afu8g07150	electron transport
Afu8g07150	FMN reductase activity
Afu8g07180	transcription factor activity
Afu8g07180	nucleus
Afu8g07180	zinc ion binding
Afu8g07180	response to xenobiotic stimulus
Afu8g07180	regulation of transcription
Afu8g07210	hydroxymethylglutaryl-CoA synthase activity
Afu8g07210	mitochondrion
Afu8g07210	endoplasmic reticulum
Afu8g07210	ergosterol biosynthetic process
Afu8g07230	transcription factor activity
Afu8g07230	nucleus
Afu8g07230	carbohydrate metabolic process
Afu8g07230	regulation of transcription, DNA-dependent
Afu8g07240	alpha-glucoside transport
Afu8g07240	transporter activity
Afu8g07240	alpha-glucoside:hydrogen symporter activity
Afu8g07240	membrane fraction
Afu8g07240	transport
Afu8g07300	biological process unknown
Afu8g07300	molecular function unknown
Afu8g07300	mitochondrion
Afu8g07360	transcription factor activity
Afu8g07360	nucleus
Afu8g07360	zinc ion binding
Afu8g07360	regulation of transcription
Afu8g07370	transporter activity
Afu8g07370	plasma membrane
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Afu1g12250	In vitro pH response DOWN
Afu1g12530	In vitro pH response DOWN
Afu1g13480	In vitro pH response DOWN
Afu1g13800	In vitro pH response DOWN

Afu1g15140	In vitro pH response DOWN
Afu1g15230	In vitro pH response DOWN
Afu1g15290	In vitro pH response DOWN
Afu1g15490	In vitro pH response DOWN
Afu1g16290	In vitro pH response DOWN
Afu1g16340	In vitro pH response DOWN
Afu1g16710	In vitro pH response DOWN
Afu2g00180	In vitro pH response DOWN
Afu2g01100	In vitro pH response DOWN
Afu2g01480	In vitro pH response DOWN
Afu2g01750	In vitro pH response DOWN
Afu2g02380	In vitro pH response DOWN
Afu2g03010	In vitro pH response DOWN
Afu2g03510	In vitro pH response DOWN
Afu2g03610	In vitro pH response DOWN
Afu2g04080	In vitro pH response DOWN
Afu2g04710	In vitro pH response DOWN
Afu2g04780	In vitro pH response DOWN
Afu2g05480	In vitro pH response DOWN
Afu2g05560	In vitro pH response DOWN
Afu2g05690	In vitro pH response DOWN
Afu2g05910	In vitro pH response DOWN
Afu2g07810	In vitro pH response DOWN
Afu2g08680	In vitro pH response DOWN
Afu2g09860	In vitro pH response DOWN
Afu2g09890	In vitro pH response DOWN
Afu2g10230	In vitro pH response DOWN
Afu2g10690	In vitro pH response DOWN
Afu2g11260	In vitro pH response DOWN
Afu2g11550	In vitro pH response DOWN
Afu2g12880	In vitro pH response DOWN
Afu2g13000	In vitro pH response DOWN
Afu2g13010	In vitro pH response DOWN
Afu2g13110	In vitro pH response DOWN
Afu2g13850	In vitro pH response DOWN
Afu2g14020	In vitro pH response DOWN
Afu2g14490	In vitro pH response DOWN
Afu2g14590	In vitro pH response DOWN
Afu2g16340	In vitro pH response DOWN
Afu2g17050	In vitro pH response DOWN
Afu2g17060	In vitro pH response DOWN
Afu2g17830	In vitro pH response DOWN
Afu2g17840	In vitro pH response DOWN
Afu3g00590	In vitro pH response DOWN
Afu3g00770	In vitro pH response DOWN
Afu3g04220	In vitro pH response DOWN
Afu3g06070	In vitro pH response DOWN
Afu3g06190	In vitro pH response DOWN
Afu3g06410	In vitro pH response DOWN
Afu3g06460	In vitro pH response DOWN

Afu3g06820	In vitro pH response DOWN
Afu3g07640	In vitro pH response DOWN
Afu3g07810	In vitro pH response DOWN
Afu3g08110	In vitro pH response DOWN
Afu3g09640	In vitro pH response DOWN
Afu3g11880	In vitro pH response DOWN
Afu3g14440	In vitro pH response DOWN
Afu3g14640	In vitro pH response DOWN
Afu3g14660	In vitro pH response DOWN
Afu4g05880	In vitro pH response DOWN
Afu4g06250	In vitro pH response DOWN
Afu4g06620	In vitro pH response DOWN
Afu4g06670	In vitro pH response DOWN
Afu4g06790	In vitro pH response DOWN
Afu4g06910	In vitro pH response DOWN
Afu4g07810	In vitro pH response DOWN
Afu4g08190	In vitro pH response DOWN
Afu4g08270	In vitro pH response DOWN
Afu4g08930	In vitro pH response DOWN
Afu4g09510	In vitro pH response DOWN
Afu4g09870	In vitro pH response DOWN
Afu4g10110	In vitro pH response DOWN
Afu4g10550	In vitro pH response DOWN
Afu4g11080	In vitro pH response DOWN
Afu4g11390	In vitro pH response DOWN
Afu4g11480	In vitro pH response DOWN
Afu4g12530	In vitro pH response DOWN
Afu4g14000	In vitro pH response DOWN
Afu4g14240	In vitro pH response DOWN
Afu4g14250	In vitro pH response DOWN
Afu4g14380	In vitro pH response DOWN
Afu5g00700	In vitro pH response DOWN
Afu5g00710	In vitro pH response DOWN
Afu5g00720	In vitro pH response DOWN
Afu5g01970	In vitro pH response DOWN
Afu5g02290	In vitro pH response DOWN
Afu5g02700	In vitro pH response DOWN
Afu5g02750	In vitro pH response DOWN
Afu5g03010	In vitro pH response DOWN
Afu5g03090	In vitro pH response DOWN
Afu5g03550	In vitro pH response DOWN
Afu5g03750	In vitro pH response DOWN
Afu5g04220	In vitro pH response DOWN
Afu5g04230	In vitro pH response DOWN
Afu5g06240	In vitro pH response DOWN
Afu5g08830	In vitro pH response DOWN
Afu5g09330	In vitro pH response DOWN
Afu5g09400	In vitro pH response DOWN
Afu5g09680	In vitro pH response DOWN
Afu5g09910	In vitro pH response DOWN

Afu5g10560	In vitro pH response DOWN
Afu5g10610	In vitro pH response DOWN
Afu5g10780	In vitro pH response DOWN
Afu5g11040	In vitro pH response DOWN
Afu5g12100	In vitro pH response DOWN
Afu5g13610	In vitro pH response DOWN
Afu5g14680	In vitro pH response DOWN
Afu6g00640	In vitro pH response DOWN
Afu6g00650	In vitro pH response DOWN
Afu6g02470	In vitro pH response DOWN
Afu6g03400	In vitro pH response DOWN
Afu6g03750	In vitro pH response DOWN
Afu6g04030	In vitro pH response DOWN
Afu6g06460	In vitro pH response DOWN
Afu6g06840	In vitro pH response DOWN
Afu6g07750	In vitro pH response DOWN
Afu6g09820	In vitro pH response DOWN
Afu6g09990	In vitro pH response DOWN
Afu6g10650	In vitro pH response DOWN
Afu6g10660	In vitro pH response DOWN
Afu6g11200	In vitro pH response DOWN
Afu6g11850	In vitro pH response DOWN
Afu6g12740	In vitro pH response DOWN
Afu6g12930	In vitro pH response DOWN
Afu6g14090	In vitro pH response DOWN
Afu6g14260	In vitro pH response DOWN
Afu7g00930	In vitro pH response DOWN
Afu7g01490	In vitro pH response DOWN
Afu7g02340	In vitro pH response DOWN
Afu7g03690	In vitro pH response DOWN
Afu7g04290	In vitro pH response DOWN
Afu7g04820	In vitro pH response DOWN
Afu7g05210	In vitro pH response DOWN
Afu7g05460	In vitro pH response DOWN
Afu7g05670	In vitro pH response DOWN
Afu7g05920	In vitro pH response DOWN
Afu8g00790	In vitro pH response DOWN
Afu8g01260	In vitro pH response DOWN
Afu8g01710	In vitro pH response DOWN
Afu8g04110	In vitro pH response DOWN
Afu8g04790	In vitro pH response DOWN
Afu8g05010	In vitro pH response DOWN
Afu8g05430	In vitro pH response DOWN
Afu8g05530	In vitro pH response DOWN
Afu8g05990	In vitro pH response DOWN
Afu8g06350	In vitro pH response DOWN
Afu8g06360	In vitro pH response DOWN

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lar oxygen, 2-oxoglutarate as one donor, and incorporation of one atom each of oxygen into both donor

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