

GO-Stats Results

Your dataset contains **884** annotated gene products.

You can download a tabulated text output file [here](#), for use with a spreadsheet application.

Color codes			
E	The term is enriched in your gene set.	D	The term is depleted in your gene set.
	P-value < 0.01		0.01 < P-value < 0.05
RO	Number of genes annotated for this term in the reference set.	RF	Frequency of genes annotated for this term in the reference set.
DO	Number of genes annotated for this term in your gene set.	DF	Frequency of genes annotated for this term in your gene set.

The terms are ranked according to the P-value column representing their statistical relevance. The 'level' column describes the depth at which a given GO term is found in the GO hierarchy (note that some terms can be found at several levels simultaneously). The last column indicates whether a given GO term is enriched (E) or depleted (D), based on the term frequency ratio (DF/RF). To visualize the hierarchy between these terms, you can click on the radio button close to a GO ID, and all its parent terms in the list are highlighted in orange. When moving the mouse pointer on the GO ID column will make all the genes associated with a given GO term appear in a box. The terms are hyperlinked to the QuickGO EBI browser.

GO ID	Level	GO Term	RO	RF	DO	DF	P-value	E/D
<input type="radio"/> GO:0022613	4	ribonucleoprotein complex biogenesis and assembly	483	0.0746	174	0.1968	8.523846E-36	E
<input type="radio"/> GO:0042254	5	ribosome biogenesis and assembly	410	0.0633	154	0.1742	1.267881E-33	E
<input type="radio"/> GO:0006139	4	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	1532	0.2366	345	0.3903	1.463957E-25	E
<input type="radio"/> GO:0009987	2	cellular process	4654	0.7187	764	0.8643	2.406776E-25	E
<input type="radio"/> GO:0016070	5	RNA metabolic process	1058	0.1634	263	0.2975	1.491867E-24	E
<input type="radio"/> GO:0016043	3	cellular component organization and biogenesis	2264	0.3496	448	0.5068	2.533545E-22	E
<input type="radio"/> GO:0006996	4	organelle organization and biogenesis	1388	0.2143	312	0.3529	5.084041E-22	E
<input type="radio"/> GO:0006396	6	RNA processing	491	0.0758	144	0.1629	1.790836E-18	E
<input type="radio"/> GO:0016072	6	rRNA metabolic process	256	0.0395	90	0.1018	4.221644E-16	E
<input type="radio"/> GO:0006364	6,7	rRNA processing	249	0.0384	86	0.0973	9.854380E-15	E
<input type="radio"/> GO:0008152	2	metabolic process	3516	0.5429	584	0.6606	8.889363E-12	E
<input type="radio"/> GO:0044237	3	cellular metabolic process	3403	0.5255	562	0.6357	4.137178E-10	E
<input type="radio"/> GO:0044238	3	primary metabolic process	3247	0.5014	541	0.6120	4.382476E-10	E
<input type="radio"/> GO:0022607	4	cellular component assembly	471	0.0727	118	0.1335	3.002171E-09	E
<input type="radio"/> GO:0042273	6,5	ribosomal large subunit biogenesis and assembly	64	0.0099	32	0.0362	3.374204E-09	E
<input type="radio"/> GO:0022618	6,5	protein-RNA complex assembly	144	0.0222	50	0.0566	7.263902E-08	E
<input type="radio"/> GO:0043283	4	biopolymer metabolic process	2230	0.3443	387	0.4378	1.786197E-07	E
<input type="radio"/> GO:0065003	5,4	macromolecular complex assembly	328	0.0506	85	0.0962	7.271062E-07	E
<input type="radio"/> GO:0000466	8,9	maturation of 5.8S rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	34	0.0053	20	0.0226	1.048215E-06	E
<input type="radio"/> GO:0006399	6	tRNA metabolic process	121	0.0187	42	0.0475	2.505895E-06	E
<input type="radio"/> GO:0000460	7,8	maturation of 5.8S rRNA	26	0.0056	20	0.0226	4.125864E-	E

<input type="radio"/>	GO:0000460	7,9	maturation of 5.8S rRNA	30	0.0030	20	0.0220	06		E
<input type="radio"/>	GO:0006360	8,7	transcription from RNA polymerase I promoter	34	0.0053	18	0.0204	6.892361E-05		E
<input type="radio"/>	GO:0043170	3	macromolecule metabolic process	2841	0.4387	458	0.5181	8.742682E-05		E
<input type="radio"/>	GO:0000470	7,8	maturation of LSU-rRNA	14	0.0022	11	0.0124	9.223964E-05		E
<input type="radio"/>	GO:0000463	8,9	maturation of LSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	14	0.0022	11	0.0124	9.223964E-05		E
<input type="radio"/>	GO:0042255	7,6	ribosome assembly	66	0.0102	26	0.0294	0.0001717		E
<input type="radio"/>	GO:0000027	9,7,8,6	ribosomal large subunit assembly and maintenance	41	0.0063	19	0.0215	0.0004328		E
<input type="radio"/>	GO:0051168	9,7,8	nuclear export	102	0.0158	32	0.0362	0.0024502		E
<input type="radio"/>	GO:0006351	7,6	transcription, DNA-dependent	522	0.0806	107	0.1210	0.0024553		E
<input type="radio"/>	GO:0032774	6	RNA biosynthetic process	524	0.0809	107	0.1210	0.0029325		E
<input type="radio"/>	GO:0006350	5	transcription	567	0.0876	113	0.1278	0.0049429		E
<input type="radio"/>	GO:0000054	10,11,6,8,9	ribosome export from nucleus	28	0.0043	14	0.0158	0.0050824		E
<input type="radio"/>	GO:0016071	6	mRNA metabolic process	210	0.0324	52	0.0588	0.0061275		E
<input type="radio"/>	GO:0000398	8,10	nuclear mRNA splicing, via spliceosome	102	0.0158	31	0.0351	0.0071490		E
<input type="radio"/>	GO:0000377	9	RNA splicing, via transesterification reactions with bulged adenosine as nucleophile	103	0.0159	31	0.0351	0.0088584		E
<input type="radio"/>	GO:0000462	8,9	maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	45	0.0069	18	0.0204	0.0109496		E
<input type="radio"/>	GO:0030490	7,8	maturation of SSU-rRNA	45	0.0069	18	0.0204	0.0109496		E
<input type="radio"/>	GO:0006913	8,6,7	nucleocytoplasmic transport	129	0.0199	36	0.0407	0.0109556		E
<input type="radio"/>	GO:0051169	7,5,6	nuclear transport	129	0.0199	36	0.0407	0.0109556		E
<input type="radio"/>	GO:0000375	8	RNA splicing, via transesterification reactions	110	0.0170	32	0.0362	0.0135761		E
<input type="radio"/>	GO:0042257	8,7	ribosomal subunit assembly	55	0.0085	20	0.0226	0.0183890		E
<input type="radio"/>	GO:0006611	9,10,7,8	protein export from nucleus	56	0.0086	20	0.0226	0.0247560		E
<input type="radio"/>	GO:0008033	7	tRNA processing	84	0.0130	26	0.0294	0.0272212		E
<input type="radio"/>	GO:0019752	5	carboxylic acid metabolic process	314	0.0485	68	0.0769	0.0286945		E
<input type="radio"/>	GO:0006082	4	organic acid metabolic process	314	0.0485	68	0.0769	0.0286945		E
<input type="radio"/>	GO:0043039	7,8	tRNA aminoacylation	32	0.0049	14	0.0158	0.0334441		E
<input type="radio"/>	GO:0006418	8,7,9,6	tRNA aminoacylation for protein translation	32	0.0049	14	0.0158	0.0334441		E
<input type="radio"/>	GO:0043038	6,7	amino acid activation	32	0.0049	14	0.0158	0.0334441		E
<input type="radio"/>	GO:0006397	7	mRNA processing	157	0.0242	40	0.0452	0.0350748		E
<input type="radio"/>	GO:0006519	4	amino acid and derivative metabolic process	202	0.0312	48	0.0543	0.0407683		E
<input type="radio"/>	GO:0006400	7,8	tRNA modification	52	0.0080	18	0.0204	0.0988868		E
<input type="radio"/>	GO:0006520	5,6	amino acid metabolic process	187	0.0289	44	0.0498	0.1040024		E
<input type="radio"/>	GO:0006355	8,7	regulation of transcription, DNA-dependent	359	0.0554	72	0.0814	0.1918938		E
<input type="radio"/>	GO:0022403	5,4	cell cycle phase	353	0.0545	71	0.0803	0.1941959		E
<input type="radio"/>	GO:0008380	7	RNA splicing	132	0.0204	33	0.0373	0.2297631		E
<input type="radio"/>	GO:0006725	4	aromatic compound metabolic process	60	0.0093	19	0.0215	0.2319544		E
<input type="radio"/>	GO:0007049	3	cell cycle	458	0.0707	87	0.0984	0.2840025		E
<input type="radio"/>	GO:0006997	5	nuclear organization and biogenesis	57	0.0088	18	0.0204	0.3485563		E
<input type="radio"/>	GO:0045449	7,6	regulation of transcription	386	0.0596	75	0.0848	0.3660900		E
<input type="radio"/>	GO:0019856	7,6	pyrimidine base biosynthetic process	15	0.0023	8	0.0090	0.3671507		E

<input type="radio"/>	GO:0000279	6,5	M phase	258	0.0398	54	0.0611	0.3994575	E
<input type="radio"/>	GO:0022402	4,3	cell cycle process	439	0.0678	83	0.0939	0.4372926	E
<input type="radio"/>	GO:0006413	7,6	translational initiation	49	0.0076	16	0.0181	0.4921324	E
<input type="radio"/>	GO:0044249	4	cellular biosynthetic process	366	0.0565	71	0.0803	0.5290709	E
<input type="radio"/>	GO:0009308	4	amine metabolic process	228	0.0352	48	0.0543	0.6947900	E
<input type="radio"/>	GO:0018193	7	peptidyl-amino acid modification	28	0.0043	11	0.0124	0.7117316	E
<input type="radio"/>	GO:0000479	8,9	endonucleolytic cleavage of tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	20	0.0031	9	0.0102	0.7257807	E
<input type="radio"/>	GO:0000447	9,10	endonucleolytic cleavage between SSU-rRNA and 5.8S rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	20	0.0031	9	0.0102	0.7257807	E
<input type="radio"/>	GO:0000478	7,8	endonucleolytic cleavages during rRNA processing	20	0.0031	9	0.0102	0.7257807	E
<input type="radio"/>	GO:0051327	7,5,6	M phase of meiotic cell cycle	148	0.0229	34	0.0385	0.8762258	E
<input type="radio"/>	GO:0051321	4	meiotic cell cycle	148	0.0229	34	0.0385	0.8762258	E
<input type="radio"/>	GO:0007126	8,6,7,5	meiosis	148	0.0229	34	0.0385	0.8762258	E
<input type="radio"/>	GO:0030476	8,6,7	spore wall assembly (sensu Fungi)	42	0.0065	14	0.0158	0.8783488	E
<input type="radio"/>	GO:0042244	5,6	spore wall assembly	42	0.0065	14	0.0158	0.8783488	E
<input type="radio"/>	GO:0022413	5,4	reproductive process in single-celled organism	149	0.0230	34	0.0385	0.9827884	E
<input type="radio"/>	GO:0048610	3,4	reproductive cellular process	149	0.0230	34	0.0385	0.9827884	E
<input type="radio"/>	GO:0007089	8,9,7,6	traversing start control point of mitotic cell cycle	6	0.0009	3	0.0034	1.0000000	E
<input type="radio"/>	GO:0046039	9	GTP metabolic process	2	0.0003	2	0.0023	1.0000000	E
<input type="radio"/>	GO:0006356	9,8	regulation of transcription from RNA polymerase I promoter	8	0.0012	3	0.0034	1.0000000	E
<input type="radio"/>	GO:0009176	8	pyrimidine deoxyribonucleoside monophosphate metabolic process	1	0.0002	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0007242	5	intracellular signaling cascade	137	0.0212	25	0.0283	1.0000000	E
<input type="radio"/>	GO:0016481	8,7	negative regulation of transcription	162	0.0250	31	0.0351	1.0000000	E
<input type="radio"/>	GO:0000726	7,6	non-recombinational repair	35	0.0054	5	0.0057	1.0000000	E
<input type="radio"/>	GO:0006376	8,7,10,12,3	mRNA splice site selection	6	0.0009	2	0.0023	1.0000000	E
<input type="radio"/>	GO:0018342	9,8,7	protein prenylation	5	0.0008	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0000747	4	conjugation with cellular fusion	118	0.0182	22	0.0249	1.0000000	E
<input type="radio"/>	GO:0000092	8,9,10,7	mitotic anaphase B	5	0.0008	2	0.0023	1.0000000	E
<input type="radio"/>	GO:0042723	6	thiamin and derivative metabolic process	22	0.0034	6	0.0068	1.0000000	E
<input type="radio"/>	GO:0045013	10,8,9,6	negative regulation of transcription by carbon catabolites	8	0.0012	2	0.0023	1.0000000	E
<input type="radio"/>	GO:0015766	5,6	disaccharide transport	2	0.0003	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0043414	6	biopolymer methylation	83	0.0128	13	0.0147	1.0000000	E
<input type="radio"/>	GO:0000411	11,9,10,7	positive regulation of transcription by galactose	5	0.0008	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0031326	6,5	regulation of cellular biosynthetic process	67	0.0103	11	0.0124	1.0000000	E
<input type="radio"/>	GO:0018202	8	peptidyl-histidine modification	5	0.0008	3	0.0034	1.0000000	E
<input type="radio"/>	GO:0016577	11,9,10	histone demethylation	4	0.0006	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0006560	7,8	proline metabolic process	7	0.0011	3	0.0034	1.0000000	E
<input type="radio"/>	GO:0031382	9,8,10,7	mating projection biogenesis	7	0.0011	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0043132	5,6	NAD transport	2	0.0003	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0031056	6,8,11,5,9,7	regulation of histone modification	2	0.0003	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0006286	8,7	base-excision repair, base-free sugar-phosphate removal	1	0.0002	1	0.0011	1.0000000	E

<input type="radio"/>	GO:0033108	8,7	mitochondrial respiratory chain complex assembly	2	0.0003	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0009302	8,7	snoRNA transcription	1	0.0002	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0007026	8,7,11,9,6	negative regulation of microtubule depolymerization	5	0.0008	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0000372	10	Group I intron splicing	7	0.0011	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0007004	9	telomere maintenance via telomerase	17	0.0026	3	0.0034	1.0000000	E
<input type="radio"/>	GO:0045016	8,6,7,9	mitochondrial magnesium ion transport	2	0.0003	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0043137	7,10,6,9	DNA replication, removal of RNA primer	5	0.0008	2	0.0023	1.0000000	E
<input type="radio"/>	GO:0051656	6,3,5,4	establishment of organelle localization	29	0.0045	8	0.0090	1.0000000	E
<input type="radio"/>	GO:0006403	4	RNA localization	90	0.0139	22	0.0249	1.0000000	E
<input type="radio"/>	GO:0030472	6,5,10	mitotic spindle organization and biogenesis in nucleus	22	0.0034	4	0.0045	1.0000000	E
<input type="radio"/>	GO:0045761	6,9,10	regulation of adenylate cyclase activity	2	0.0003	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0051439	7,5,4	regulation of ubiquitin ligase activity during mitotic cell cycle	5	0.0008	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0006975	9,8,5	DNA damage induced protein phosphorylation	2	0.0003	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0048878	5	chemical homeostasis	121	0.0187	20	0.0226	1.0000000	E
<input type="radio"/>	GO:0043174	5	nucleoside salvage	6	0.0009	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0006779	6,7	porphyrin biosynthetic process	13	0.0020	3	0.0034	1.0000000	E
<input type="radio"/>	GO:0040001	5,4,7,8,9,6	establishment of mitotic spindle localization	10	0.0015	2	0.0023	1.0000000	E
<input type="radio"/>	GO:0046113	6,5	nucleobase catabolic process	1	0.0002	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0006537	8,9	glutamate biosynthetic process	13	0.0020	2	0.0023	1.0000000	E
<input type="radio"/>	GO:0055074	9	calcium ion homeostasis	9	0.0014	2	0.0023	1.0000000	E
<input type="radio"/>	GO:0009081	6,7	branched chain family amino acid metabolic process	16	0.0025	5	0.0057	1.0000000	E
<input type="radio"/>	GO:0000337	9,8,5	regulation of DNA transposition	10	0.0015	2	0.0023	1.0000000	E
<input type="radio"/>	GO:0016180	7	snRNA processing	4	0.0006	2	0.0023	1.0000000	E
<input type="radio"/>	GO:0019541	7	propionate metabolic process	5	0.0008	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0046036	9	CTP metabolic process	2	0.0003	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0007584	6,4	response to nutrient	18	0.0028	4	0.0045	1.0000000	E
<input type="radio"/>	GO:0000316	7,8	sulfite transport	2	0.0003	2	0.0023	1.0000000	E
<input type="radio"/>	GO:0006549	7,8	isoleucine metabolic process	3	0.0005	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0050896	2	response to stimulus	763	0.1178	108	0.1222	1.0000000	E
<input type="radio"/>	GO:0032787	6	monocarboxylic acid metabolic process	126	0.0195	25	0.0283	1.0000000	E
<input type="radio"/>	GO:0016114	7,6,8,5	terpenoid biosynthetic process	2	0.0003	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0009451	6	RNA modification	139	0.0215	26	0.0294	1.0000000	E
<input type="radio"/>	GO:0009147	7	pyrimidine nucleoside triphosphate metabolic process	4	0.0006	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0030808	8,6,7,5	regulation of nucleotide biosynthetic process	2	0.0003	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0000717	8,7	nucleotide-excision repair, DNA duplex unwinding	6	0.0009	2	0.0023	1.0000000	E
<input type="radio"/>	GO:0031385	6,8,11,10,9,7,12	regulation of termination of mating projection growth	5	0.0008	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0032092	6	positive regulation of protein binding	1	0.0002	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0051568	12,10,11,9	histone H3-K4 methylation	1	0.0002	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0040031	7	snRNA modification	7	0.0011	3	0.0034	1.0000000	E
<input type="radio"/>	GO:0015677	9,10	copper ion import	8	0.0012	4	0.0045	1.0000000	E
<input type="radio"/>	GO:0006432	9,8,10,7	phenylalanyl-tRNA aminoacylation	3	0.0005	2	0.0023	1.0000000	E
<input type="radio"/>	GO:0009743	5,4	response to carbohydrate stimulus	6	0.0009	1	0.0011	1.0000000	E

<input type="checkbox"/>	GO:0031497	5,9	chromatin assembly	104	0.0161	22	0.0249	1.0000000	E
<input type="checkbox"/>	GO:0016573	11,9	histone acetylation	40	0.0062	8	0.0090	1.0000000	E
<input type="checkbox"/>	GO:0007021	7	tubulin folding	11	0.0017	4	0.0045	1.0000000	E
<input type="checkbox"/>	GO:0043666	6	regulation of phosphoprotein phosphatase activity	3	0.0005	1	0.0011	1.0000000	E
<input type="checkbox"/>	GO:0018283	9,7	iron incorporation into metallo-sulfur cluster	1	0.0002	1	0.0011	1.0000000	E
<input type="checkbox"/>	GO:0007264	6	small GTPase mediated signal transduction	61	0.0094	9	0.0102	1.0000000	E
<input type="checkbox"/>	GO:0051017	9	actin filament bundle formation	5	0.0008	1	0.0011	1.0000000	E
<input type="checkbox"/>	GO:0030259	6,7	lipid glycosylation	1	0.0002	1	0.0011	1.0000000	E
<input type="checkbox"/>	GO:0051231	5,4,9,7	spindle elongation	20	0.0031	3	0.0034	1.0000000	E
<input type="checkbox"/>	GO:0016077	7	snoRNA catabolic process	4	0.0006	2	0.0023	1.0000000	E
<input type="checkbox"/>	GO:0044272	5	sulfur compound biosynthetic process	22	0.0034	7	0.0079	1.0000000	E
<input type="checkbox"/>	GO:0017038	5,6,7	protein import	109	0.0168	16	0.0181	1.0000000	E
<input type="checkbox"/>	GO:0006555	7,8,6	methionine metabolic process	24	0.0037	9	0.0102	1.0000000	E
<input type="checkbox"/>	GO:0009260	6,7	ribonucleotide biosynthetic process	40	0.0062	8	0.0090	1.0000000	E
<input type="checkbox"/>	GO:0009209	8,9	pyrimidine ribonucleoside triphosphate biosynthetic process	2	0.0003	1	0.0011	1.0000000	E
<input type="checkbox"/>	GO:0045722	7,9,8,10,6,11	positive regulation of gluconeogenesis	4	0.0006	1	0.0011	1.0000000	E
<input type="checkbox"/>	GO:0006074	8,9	1,3-beta-glucan metabolic process	4	0.0006	1	0.0011	1.0000000	E
<input type="checkbox"/>	GO:0007064	10,8,5,6,9,7,4	mitotic sister chromatid cohesion	22	0.0034	7	0.0079	1.0000000	E
<input type="checkbox"/>	GO:0009117	5	nucleotide metabolic process	111	0.0171	24	0.0271	1.0000000	E
<input type="checkbox"/>	GO:0055066	8	di-, tri-valent inorganic cation homeostasis	64	0.0099	13	0.0147	1.0000000	E
<input type="checkbox"/>	GO:0006037	8,9,6,7,10	cell wall chitin metabolic process	14	0.0022	2	0.0023	1.0000000	E
<input type="checkbox"/>	GO:0015788	7,8	UDP-N-acetylglucosamine transport	1	0.0002	1	0.0011	1.0000000	E
<input type="checkbox"/>	GO:0006404	10,8,5,7,9,6	RNA import into nucleus	3	0.0005	1	0.0011	1.0000000	E
<input type="checkbox"/>	GO:0006206	6	pyrimidine base metabolic process	17	0.0026	8	0.0090	1.0000000	E
<input type="checkbox"/>	GO:0006783	7,6,8	heme biosynthetic process	13	0.0020	3	0.0034	1.0000000	E
<input type="checkbox"/>	GO:0045021	7,6	error-free DNA repair	4	0.0006	1	0.0011	1.0000000	E
<input type="checkbox"/>	GO:0009069	6,7	serine family amino acid metabolic process	24	0.0037	4	0.0045	1.0000000	E
<input type="checkbox"/>	GO:0000160	5	two-component signal transduction system (phosphorelay)	3	0.0005	1	0.0011	1.0000000	E
<input type="checkbox"/>	GO:0006301	7,6	postreplication repair	13	0.0020	2	0.0023	1.0000000	E
<input type="checkbox"/>	GO:0008054	7,6,11,10,12	cyclin catabolic process	12	0.0019	2	0.0023	1.0000000	E
<input type="checkbox"/>	GO:0009892	5,4	negative regulation of metabolic process	208	0.0321	38	0.0430	1.0000000	E
<input type="checkbox"/>	GO:0042559	6	pteridine and derivative biosynthetic process	2	0.0003	1	0.0011	1.0000000	E
<input type="checkbox"/>	GO:0015758	7,8	glucose transport	6	0.0009	2	0.0023	1.0000000	E
<input type="checkbox"/>	GO:0006826	7,8,9	iron ion transport	20	0.0031	4	0.0045	1.0000000	E
<input type="checkbox"/>	GO:0042819	7	vitamin B6 biosynthetic process	1	0.0002	1	0.0011	1.0000000	E
<input type="checkbox"/>	GO:0007029	5	endoplasmic reticulum organization and biogenesis	6	0.0009	1	0.0011	1.0000000	E
<input type="checkbox"/>	GO:0006426	9,8,10,7	glycyl-tRNA aminoacylation	2	0.0003	2	0.0023	1.0000000	E
<input type="checkbox"/>	GO:0007109	7,6,5,4	cytokinesis, completion of separation	11	0.0017	2	0.0023	1.0000000	E
<input type="checkbox"/>	GO:0006452	8,7,6	translational frameshifting	3	0.0005	1	0.0011	1.0000000	E
<input type="checkbox"/>	GO:0006429	9,8,10,7	leucyl-tRNA aminoacylation	2	0.0003	1	0.0011	1.0000000	E
<input type="checkbox"/>	GO:0006739	9,8	NADP metabolic process	17	0.0026	4	0.0045	1.0000000	E
<input type="checkbox"/>	GO:0051123	10,7,9,6	transcriptional preinitiation complex assembly	1	0.0002	1	0.0011	1.0000000	E

<input type="radio"/>	GO:0009890	6,5	negative regulation of biosynthetic process	8	0.0012	5	0.0057	1.0000000	E
<input type="radio"/>	GO:0000742	7,5	karyogamy during conjugation with cellular fusion	17	0.0026	6	0.0068	1.0000000	E
<input type="radio"/>	GO:0015723	7,8	bilirubin transport	2	0.0003	2	0.0023	1.0000000	E
<input type="radio"/>	GO:0019395	6,8,7	fatty acid oxidation	11	0.0017	5	0.0057	1.0000000	E
<input type="radio"/>	GO:0046148	5	pigment biosynthetic process	19	0.0029	3	0.0034	1.0000000	E
<input type="radio"/>	GO:0045990	9,7,8,5	regulation of transcription by carbon catabolites	14	0.0022	3	0.0034	1.0000000	E
<input type="radio"/>	GO:0000413	8	protein peptidyl-prolyl isomerization	1	0.0002	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0006140	7,6	regulation of nucleotide metabolic process	2	0.0003	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0017148	8,7,6	negative regulation of protein biosynthetic process	6	0.0009	4	0.0045	1.0000000	E
<input type="radio"/>	GO:0006865	5,6,7	amino acid transport	39	0.0060	10	0.0113	1.0000000	E
<input type="radio"/>	GO:0032264	7,8	IMP salvage	1	0.0002	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0005979	8,7,9,10,6	regulation of glycogen biosynthetic process	6	0.0009	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0007532	9,5,7,8,6	regulation of transcription, mating-type specific	8	0.0012	2	0.0023	1.0000000	E
<input type="radio"/>	GO:0005992	7,8	trehalose biosynthetic process	7	0.0011	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0006345	10,6,9	loss of chromatin silencing	9	0.0014	2	0.0023	1.0000000	E
<input type="radio"/>	GO:0000097	7,8,6	sulfur amino acid biosynthetic process	13	0.0020	6	0.0068	1.0000000	E
<input type="radio"/>	GO:0042558	5	pteridine and derivative metabolic process	2	0.0003	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0000749	5	response to pheromone during conjugation with cellular fusion	57	0.0088	9	0.0102	1.0000000	E
<input type="radio"/>	GO:0018195	8	peptidyl-arginine modification	2	0.0003	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0050794	4,3	regulation of cellular process	738	0.1140	119	0.1346	1.0000000	E
<input type="radio"/>	GO:0015031	4,5,6	protein transport	280	0.0432	48	0.0543	1.0000000	E
<input type="radio"/>	GO:0031565	8,7	cytokinesis checkpoint	4	0.0006	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0009075	6,7	histidine family amino acid metabolic process	14	0.0022	3	0.0034	1.0000000	E
<input type="radio"/>	GO:0006221	6,7	pyrimidine nucleotide biosynthetic process	5	0.0008	3	0.0034	1.0000000	E
<input type="radio"/>	GO:0046487	5,7	glyoxylate metabolic process	5	0.0008	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0051649	5,3,4	establishment of cellular localization	606	0.0936	99	0.1120	1.0000000	E
<input type="radio"/>	GO:0015680	7,5,9,6,10	intracellular copper ion transport	5	0.0008	2	0.0023	1.0000000	E
<input type="radio"/>	GO:0007535	6,8,4,7	donor selection	5	0.0008	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0046335	6,7,8,9	ethanolamine biosynthetic process	4	0.0006	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0008535	8,7	cytochrome c oxidase complex assembly	9	0.0014	2	0.0023	1.0000000	E
<input type="radio"/>	GO:0046083	7	adenine metabolic process	3	0.0005	2	0.0023	1.0000000	E
<input type="radio"/>	GO:0009452	7	RNA capping	4	0.0006	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0006498	9,10,8,7	N-terminal protein lipidation	5	0.0008	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0017182	9	peptidyl-diphthamide metabolic process	5	0.0008	3	0.0034	1.0000000	E
<input type="radio"/>	GO:0006431	9,8,10,7	methionyl-tRNA aminoacylation	3	0.0005	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0000147	5,9,8	actin cortical patch assembly	14	0.0022	3	0.0034	1.0000000	E
<input type="radio"/>	GO:0006417	7,6,5	regulation of translation	47	0.0073	9	0.0102	1.0000000	E
<input type="radio"/>	GO:0000122	10,9	negative regulation of transcription from RNA polymerase II promoter	63	0.0097	12	0.0136	1.0000000	E
<input type="radio"/>	GO:0042592	4	homeostatic process	134	0.0207	21	0.0238	1.0000000	E
<input type="radio"/>	GO:0006220	6	pyrimidine nucleotide metabolic process	7	0.0011	3	0.0034	1.0000000	E
<input type="radio"/>	GO:0006609	10,11,8,9,7	mRNA-binding (hnRNP) protein import into nucleus	25	0.0039	5	0.0057	1.0000000	E
<input type="radio"/>	GO:0000414	8,10,13,7,11,12,9	regulation of histone H3-K36 methylation	1	0.0002	1	0.0011	1.0000000	E

<input type="radio"/>	GO:0032505	4,3	reproduction of a single-celled organism	194	0.0300	38	0.0430	1.0000000	E
<input type="radio"/>	GO:0019388	8,9	galactose catabolic process	5	0.0008	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0043331	4	response to dsRNA	7	0.0011	4	0.0045	1.0000000	E
<input type="radio"/>	GO:0065004	6,5	protein-DNA complex assembly	74	0.0114	16	0.0181	1.0000000	E
<input type="radio"/>	GO:0009263	6,7	deoxyribonucleotide biosynthetic process	3	0.0005	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0030148	7,6,8	sphingolipid biosynthetic process	20	0.0031	5	0.0057	1.0000000	E
<input type="radio"/>	GO:0045815	5	positive regulation of gene expression, epigenetic	9	0.0014	2	0.0023	1.0000000	E
<input type="radio"/>	GO:0018319	10,9,8	protein amino acid myristoylation	5	0.0008	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0000184	8	mRNA catabolic process, nonsense-mediated decay	9	0.0014	2	0.0023	1.0000000	E
<input type="radio"/>	GO:0019933	8	cAMP-mediated signaling	9	0.0014	2	0.0023	1.0000000	E
<input type="radio"/>	GO:0051234	2,3	establishment of localization	1004	0.1550	163	0.1844	1.0000000	E
<input type="radio"/>	GO:0048017	8	inositol lipid-mediated signaling	16	0.0025	4	0.0045	1.0000000	E
<input type="radio"/>	GO:0000244	7,6,10,12	assembly of spliceosomal tri-snRNP	3	0.0005	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0006999	6	nuclear pore organization and biogenesis	29	0.0045	7	0.0079	1.0000000	E
<input type="radio"/>	GO:0006259	5	DNA metabolic process	523	0.0808	88	0.0995	1.0000000	E
<input type="radio"/>	GO:0016567	9	protein ubiquitination	66	0.0102	11	0.0124	1.0000000	E
<input type="radio"/>	GO:0016078	7	tRNA catabolic process	5	0.0008	2	0.0023	1.0000000	E
<input type="radio"/>	GO:0042439	6,7	ethanolamine and derivative metabolic process	4	0.0006	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0006886	7,5,6	intracellular protein transport	274	0.0423	48	0.0543	1.0000000	E
<input type="radio"/>	GO:0006348	11,7,8,12,10	chromatin silencing at telomere	60	0.0093	11	0.0124	1.0000000	E
<input type="radio"/>	GO:0006289	7,6	nucleotide-excision repair	44	0.0068	9	0.0102	1.0000000	E
<input type="radio"/>	GO:0006530	8,9	asparagine catabolic process	5	0.0008	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0046856	7,9,8,10	phosphoinositide dephosphorylation	7	0.0011	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0045011	10	actin cable formation	5	0.0008	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0051128	5,4	regulation of cellular component organization and biogenesis	30	0.0046	5	0.0057	1.0000000	E
<input type="radio"/>	GO:0030802	9,7,8,6	regulation of cyclic nucleotide biosynthetic process	2	0.0003	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0006646	7,8,9,6,10	phosphatidylethanolamine biosynthetic process	4	0.0006	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0045943	10,9	positive regulation of transcription from RNA polymerase I promoter	4	0.0006	3	0.0034	1.0000000	E
<input type="radio"/>	GO:0000819	7,4	sister chromatid segregation	62	0.0096	12	0.0136	1.0000000	E
<input type="radio"/>	GO:0000135	9,8	septin checkpoint	4	0.0006	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0000723	8	telomere maintenance	274	0.0423	40	0.0452	1.0000000	E
<input type="radio"/>	GO:0043634	8	polyadenylation-dependent ncRNA catabolic process	7	0.0011	3	0.0034	1.0000000	E
<input type="radio"/>	GO:0007187	7,8	G-protein signaling, coupled to cyclic nucleotide second messenger	5	0.0008	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0008104	4	protein localization	330	0.0510	51	0.0577	1.0000000	E
<input type="radio"/>	GO:0051436	8,6,5	negative regulation of ubiquitin ligase activity during mitotic cell cycle	3	0.0005	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0015693	7,8	magnesium ion transport	5	0.0008	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0045040	10,9,7,8	protein import into mitochondrial outer membrane	6	0.0009	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0007091	9,7,5,8,6,4	mitotic metaphase/anaphase transition	15	0.0023	3	0.0034	1.0000000	E
<input type="radio"/>	GO:0009228	7,8	thiamin biosynthetic process	19	0.0029	5	0.0057	1.0000000	E
<input type="radio"/>	GO:0009062	6,7,8	fatty acid catabolic process	2	0.0003	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0007018	8,7,6	microtubule-based movement	15	0.0023	5	0.0057	1.0000000	E
<input type="radio"/>	GO:0032988	6	protein-RNA complex disassembly	4	0.0006	1	0.0011	1.0000000	E

<input type="checkbox"/>	GO:0007068	10,8,6,9,7,5	negative regulation of transcription, mitotic	7	0.0011	2	0.0023	1.0000000	E
<input type="checkbox"/>	GO:0040007	2	growth	141	0.0218	22	0.0249	1.0000000	E
<input type="checkbox"/>	GO:0007059	3	chromosome segregation	119	0.0184	24	0.0271	1.0000000	E
<input type="checkbox"/>	GO:0031323	5,4	regulation of cellular metabolic process	507	0.0783	91	0.1029	1.0000000	E
<input type="checkbox"/>	GO:0032320	8,9,10	positive regulation of Ras GTPase activity	2	0.0003	1	0.0011	1.0000000	E
<input type="checkbox"/>	GO:0030001	6,7	metal ion transport	62	0.0096	14	0.0158	1.0000000	E
<input type="checkbox"/>	GO:0031929	6	TOR signaling pathway	13	0.0020	2	0.0023	1.0000000	E
<input type="checkbox"/>	GO:0015691	7,8,9	cadmium ion transport	2	0.0003	2	0.0023	1.0000000	E
<input type="checkbox"/>	GO:0006772	7	thiamin metabolic process	20	0.0031	5	0.0057	1.0000000	E
<input type="checkbox"/>	GO:0051325	6,5	interphase	112	0.0173	18	0.0204	1.0000000	E
<input type="checkbox"/>	GO:0000278	4	mitotic cell cycle	266	0.0411	47	0.0532	1.0000000	E
<input type="checkbox"/>	GO:0046483	4	heterocycle metabolic process	76	0.0117	20	0.0226	1.0000000	E
<input type="checkbox"/>	GO:0000056	11,12,7,9,10	ribosomal small subunit export from nucleus	7	0.0011	3	0.0034	1.0000000	E
<input type="checkbox"/>	GO:0018004	10,9	N-terminal protein formylation	1	0.0002	1	0.0011	1.0000000	E
<input type="checkbox"/>	GO:0009083	7,8	branched chain family amino acid catabolic process	4	0.0006	1	0.0011	1.0000000	E
<input type="checkbox"/>	GO:0040008	4,3	regulation of growth	13	0.0020	2	0.0023	1.0000000	E
<input type="checkbox"/>	GO:0018377	9,8,7	protein myristoylation	5	0.0008	1	0.0011	1.0000000	E
<input type="checkbox"/>	GO:0006643	5,6	membrane lipid metabolic process	125	0.0193	20	0.0226	1.0000000	E
<input type="checkbox"/>	GO:0009142	6,7	nucleoside triphosphate biosynthetic process	27	0.0042	4	0.0045	1.0000000	E
<input type="checkbox"/>	GO:0000165	7	MAPKKK cascade	20	0.0031	3	0.0034	1.0000000	E
<input type="checkbox"/>	GO:0043001	10,8,7,9	Golgi to plasma membrane protein transport	5	0.0008	1	0.0011	1.0000000	E
<input type="checkbox"/>	GO:0055065	8	metal ion homeostasis	19	0.0029	4	0.0045	1.0000000	E
<input type="checkbox"/>	GO:0008655	5	pyrimidine salvage	5	0.0008	1	0.0011	1.0000000	E
<input type="checkbox"/>	GO:0006482	9	protein amino acid demethylation	4	0.0006	1	0.0011	1.0000000	E
<input type="checkbox"/>	GO:0031578	9,11,10,8	mitotic cell cycle spindle orientation checkpoint	4	0.0006	1	0.0011	1.0000000	E
<input type="checkbox"/>	GO:0033353	7,6	S-adenosylmethionine cycle	1	0.0002	1	0.0011	1.0000000	E
<input type="checkbox"/>	GO:0046073	9	dTMP metabolic process	1	0.0002	1	0.0011	1.0000000	E
<input type="checkbox"/>	GO:0009187	6	cyclic nucleotide metabolic process	2	0.0003	1	0.0011	1.0000000	E
<input type="checkbox"/>	GO:0006972	5	hyperosmotic response	11	0.0017	3	0.0034	1.0000000	E
<input type="checkbox"/>	GO:0009201	7,8	ribonucleoside triphosphate biosynthetic process	24	0.0037	4	0.0045	1.0000000	E
<input type="checkbox"/>	GO:0000710	11,9,8,6,5,10,7,4	meiotic mismatch repair	7	0.0011	2	0.0023	1.0000000	E
<input type="checkbox"/>	GO:0009064	6,7	glutamine family amino acid metabolic process	43	0.0066	7	0.0079	1.0000000	E
<input type="checkbox"/>	GO:0009162	7	deoxyribonucleoside monophosphate metabolic process	1	0.0002	1	0.0011	1.0000000	E
<input type="checkbox"/>	GO:0006696	7,8,9	ergosterol biosynthetic process	26	0.0040	5	0.0057	1.0000000	E
<input type="checkbox"/>	GO:0016233	9	telomere capping	5	0.0008	2	0.0023	1.0000000	E
<input type="checkbox"/>	GO:0018346	10,9,8	protein amino acid prenylation	5	0.0008	1	0.0011	1.0000000	E
<input type="checkbox"/>	GO:0018065	8	protein-cofactor linkage	3	0.0005	1	0.0011	1.0000000	E
<input type="checkbox"/>	GO:0045934	7,6	negative regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	179	0.0276	34	0.0385	1.0000000	E
<input type="checkbox"/>	GO:0030036	7	actin cytoskeleton organization and biogenesis	107	0.0165	18	0.0204	1.0000000	E
<input type="checkbox"/>	GO:0006544	7,8	glycine metabolic process	6	0.0009	1	0.0011	1.0000000	E
<input type="checkbox"/>	GO:0007035	13,10,6,11	vacuolar acidification	24	0.0037	5	0.0057	1.0000000	E

<input type="radio"/>	GO:0046942	5,6	carboxylic acid transport	54	0.0083	12	0.0136	1.0000000	E
<input type="radio"/>	GO:0007008	6,7	outer mitochondrial membrane organization and biogenesis	7	0.0011	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0009310	5,6	amine catabolic process	32	0.0049	5	0.0057	1.0000000	E
<input type="radio"/>	GO:0006334	6,7,10	nucleosome assembly	13	0.0020	4	0.0045	1.0000000	E
<input type="radio"/>	GO:0009123	6	nucleoside monophosphate metabolic process	19	0.0029	6	0.0068	1.0000000	E
<input type="radio"/>	GO:0045047	9,8,7,6,5	protein targeting to ER	33	0.0051	5	0.0057	1.0000000	E
<input type="radio"/>	GO:0000083	10,9,6,5,7,8,4	G1/S-specific transcription in mitotic cell cycle	12	0.0019	5	0.0057	1.0000000	E
<input type="radio"/>	GO:0006479	9,7	protein amino acid methylation	23	0.0036	5	0.0057	1.0000000	E
<input type="radio"/>	GO:0019932	6	second-messenger-mediated signaling	32	0.0049	8	0.0090	1.0000000	E
<input type="radio"/>	GO:0046033	9	AMP metabolic process	1	0.0002	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0006241	9,10	CTP biosynthetic process	2	0.0003	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0048015	7	phosphoinositide-mediated signaling	16	0.0025	4	0.0045	1.0000000	E
<input type="radio"/>	GO:0006367	8,9,7	transcription initiation from RNA polymerase II promoter	44	0.0068	9	0.0102	1.0000000	E
<input type="radio"/>	GO:0006270	8,6	DNA replication initiation	33	0.0051	8	0.0090	1.0000000	E
<input type="radio"/>	GO:0016337	4	cell-cell adhesion	5	0.0008	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0015942	5,7	formate metabolic process	3	0.0005	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0009719	3	response to endogenous stimulus	243	0.0375	37	0.0419	1.0000000	E
<input type="radio"/>	GO:0018344	10,9,8	protein geranylgeranylation	4	0.0006	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0006302	7,6	double-strand break repair	57	0.0088	9	0.0102	1.0000000	E
<input type="radio"/>	GO:0051056	6,7,5	regulation of small GTPase mediated signal transduction	6	0.0009	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0031060	7,9,12,6,10,11,8	regulation of histone methylation	1	0.0002	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0000387	5,9,11	spliceosomal snRNP biogenesis	3	0.0005	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0006450	8,7,6	regulation of translational fidelity	13	0.0020	3	0.0034	1.0000000	E
<input type="radio"/>	GO:0030800	9,8	negative regulation of cyclic nucleotide metabolic process	2	0.0003	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0016053	5	organic acid biosynthetic process	17	0.0026	6	0.0068	1.0000000	E
<input type="radio"/>	GO:0009653	4,3	anatomical structure morphogenesis	248	0.0383	40	0.0452	1.0000000	E
<input type="radio"/>	GO:0008213	8	protein amino acid alkylation	23	0.0036	5	0.0057	1.0000000	E
<input type="radio"/>	GO:0018216	9,10,8	peptidyl-arginine methylation	1	0.0002	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0006623	9,8,7,6	protein targeting to vacuole	67	0.0103	10	0.0113	1.0000000	E
<input type="radio"/>	GO:0045141	9,7,5,8,6,4	telomere clustering	2	0.0003	2	0.0023	1.0000000	E
<input type="radio"/>	GO:0051653	6,5	spindle localization	10	0.0015	2	0.0023	1.0000000	E
<input type="radio"/>	GO:0030950	8,7	establishment and/or maintenance of actin cytoskeleton polarity	9	0.0014	2	0.0023	1.0000000	E
<input type="radio"/>	GO:0045896	9,7,5,8,6,4	regulation of transcription, mitotic	7	0.0011	2	0.0023	1.0000000	E
<input type="radio"/>	GO:0016569	9	covalent chromatin modification	91	0.0141	17	0.0192	1.0000000	E
<input type="radio"/>	GO:0030543	5	2-micrometer plasmid partitioning	3	0.0005	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0000753	7,8,6	cellular morphogenesis during conjugation with cellular fusion	18	0.0028	3	0.0034	1.0000000	E
<input type="radio"/>	GO:0043330	5,6	response to exogenous dsRNA	7	0.0011	4	0.0045	1.0000000	E
<input type="radio"/>	GO:0009636	4	response to toxin	28	0.0043	4	0.0045	1.0000000	E
<input type="radio"/>	GO:0006430	9,8,10,7	lysyl-tRNA aminoacylation	2	0.0003	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0065008	3	regulation of biological quality	260	0.0401	41	0.0464	1.0000000	E
<input type="radio"/>	GO:0030497	8,7,9,6	fatty acid elongation	4	0.0006	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0051098	4	regulation of binding	1	0.0002	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0006547	7,8	histidine metabolic process	14	0.0022	3	0.0034	1.0000000	E

<input type="checkbox"/>	GO:0051083	8	cotranslational protein folding	5	0.0008	1	0.0011	1.0000000	E
<input type="checkbox"/>	GO:0030435	5	sporulation	123	0.0190	27	0.0305	1.0000000	E
<input type="checkbox"/>	GO:0006605	8,6,7	protein targeting	258	0.0398	46	0.0520	1.0000000	E
<input type="checkbox"/>	GO:0046394	6	carboxylic acid biosynthetic process	17	0.0026	6	0.0068	1.0000000	E
<input type="checkbox"/>	GO:0000741	6	karyogamy	17	0.0026	6	0.0068	1.0000000	E
<input type="checkbox"/>	GO:0031032	8	actomyosin structure organization and biogenesis	3	0.0005	2	0.0023	1.0000000	E
<input type="checkbox"/>	GO:0006336	7,8,11	DNA replication-independent nucleosome assembly	5	0.0008	2	0.0023	1.0000000	E
<input type="checkbox"/>	GO:0009437	6,7	carnitine metabolic process	3	0.0005	1	0.0011	1.0000000	E
<input type="checkbox"/>	GO:0006358	10,9	regulation of global transcription from RNA polymerase II promoter	6	0.0009	1	0.0011	1.0000000	E
<input type="checkbox"/>	GO:0045893	9,8	positive regulation of transcription, DNA-dependent	95	0.0147	18	0.0204	1.0000000	E
<input type="checkbox"/>	GO:0042787	10,9,11	protein ubiquitination during ubiquitin-dependent protein catabolic process	14	0.0022	3	0.0034	1.0000000	E
<input type="checkbox"/>	GO:0000715	7,8	nucleotide-excision repair, DNA damage recognition	7	0.0011	2	0.0023	1.0000000	E
<input type="checkbox"/>	GO:0008645	6,7	hexose transport	26	0.0040	5	0.0057	1.0000000	E
<input type="checkbox"/>	GO:0055072	9	iron ion homeostasis	38	0.0059	8	0.0090	1.0000000	E
<input type="checkbox"/>	GO:0016074	6	snoRNA metabolic process	17	0.0026	7	0.0079	1.0000000	E
<input type="checkbox"/>	GO:0030071	8,10,6,9,7,5	regulation of mitotic metaphase/anaphase transition	4	0.0006	1	0.0011	1.0000000	E
<input type="checkbox"/>	GO:0051322	6,7,5	anaphase	6	0.0009	2	0.0023	1.0000000	E
<input type="checkbox"/>	GO:0006820	5,6	anion transport	17	0.0026	6	0.0068	1.0000000	E
<input type="checkbox"/>	GO:0007117	6,5,4	budding cell bud growth	35	0.0054	5	0.0057	1.0000000	E
<input type="checkbox"/>	GO:0006562	8,9	proline catabolic process	4	0.0006	2	0.0023	1.0000000	E
<input type="checkbox"/>	GO:0051352	6	negative regulation of ligase activity	3	0.0005	1	0.0011	1.0000000	E
<input type="checkbox"/>	GO:0006817	7,8	phosphate transport	10	0.0015	3	0.0034	1.0000000	E
<input type="checkbox"/>	GO:0030154	4	cell differentiation	173	0.0267	31	0.0351	1.0000000	E
<input type="checkbox"/>	GO:0006402	7	mRNA catabolic process	60	0.0093	15	0.0170	1.0000000	E
<input type="checkbox"/>	GO:0009435	8,7,10,9	NAD biosynthetic process	7	0.0011	2	0.0023	1.0000000	E
<input type="checkbox"/>	GO:0030865	6	cortical cytoskeleton organization and biogenesis	16	0.0025	4	0.0045	1.0000000	E
<input type="checkbox"/>	GO:0045821	7,11,12,6	positive regulation of glycolysis	3	0.0005	1	0.0011	1.0000000	E
<input type="checkbox"/>	GO:0009098	8,9	leucine biosynthetic process	5	0.0008	1	0.0011	1.0000000	E
<input type="checkbox"/>	GO:0006081	4	aldehyde metabolic process	21	0.0032	3	0.0034	1.0000000	E
<input type="checkbox"/>	GO:0008615	8	pyridoxine biosynthetic process	1	0.0002	1	0.0011	1.0000000	E
<input type="checkbox"/>	GO:0015749	5,6	monosaccharide transport	26	0.0040	5	0.0057	1.0000000	E
<input type="checkbox"/>	GO:0006038	9,10,7,8,11	cell wall chitin biosynthetic process	13	0.0020	2	0.0023	1.0000000	E
<input type="checkbox"/>	GO:0051382	8,7	kinetochore assembly	3	0.0005	1	0.0011	1.0000000	E
<input type="checkbox"/>	GO:0047484	4,5	regulation of response to osmotic stress	1	0.0002	1	0.0011	1.0000000	E
<input type="checkbox"/>	GO:0009219	7	pyrimidine deoxyribonucleotide metabolic process	3	0.0005	1	0.0011	1.0000000	E
<input type="checkbox"/>	GO:0001302	5	replicative cell aging	39	0.0060	6	0.0068	1.0000000	E
<input type="checkbox"/>	GO:0009991	4	response to extracellular stimulus	37	0.0057	6	0.0068	1.0000000	E
<input type="checkbox"/>	GO:0050684	8,7	regulation of mRNA processing	3	0.0005	1	0.0011	1.0000000	E
<input type="checkbox"/>	GO:0000915	7,6,10,5	cytokinesis, contractile ring formation	3	0.0005	2	0.0023	1.0000000	E
<input type="checkbox"/>	GO:0000335	10,9,6	negative regulation of DNA transposition	8	0.0012	2	0.0023	1.0000000	E
<input type="checkbox"/>	GO:0051641	4,3	cellular localization	642	0.0991	103	0.1165	1.0000000	E
<input type="checkbox"/>	GO:0031938	12,8,5,9,13,11	regulation of chromatin silencing at telomere	6	0.0009	1	0.0011	1.0000000	E

<input type="radio"/>	GO:0050667	7,8,6	homocysteine metabolic process	2	0.0003	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0051444	7	negative regulation of ubiquitin ligase activity	3	0.0005	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0018348	11,10,9	protein amino acid geranylgeranylation	4	0.0006	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0043096	7,6	purine base salvage	1	0.0002	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0009177	8,9	pyrimidine deoxyribonucleoside monophosphate biosynthetic process	1	0.0002	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0009110	5	vitamin biosynthetic process	46	0.0071	11	0.0124	1.0000000	E
<input type="radio"/>	GO:0009112	5	nucleobase metabolic process	31	0.0048	11	0.0124	1.0000000	E
<input type="radio"/>	GO:0031055	10	chromatin remodeling at centromere	2	0.0003	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0008053	6	mitochondrial fusion	4	0.0006	3	0.0034	1.0000000	E
<input type="radio"/>	GO:0043630	9,10	ncRNA polyadenylation during polyadenylation-dependent ncRNA catabolic process	5	0.0008	3	0.0034	1.0000000	E
<input type="radio"/>	GO:0046515	7,6	hypusine biosynthetic process	2	0.0003	2	0.0023	1.0000000	E
<input type="radio"/>	GO:0010043	6	response to zinc ion	2	0.0003	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0018027	10,11,9	peptidyl-lysine di-methylation	1	0.0002	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0006566	7,8	threonine metabolic process	8	0.0012	2	0.0023	1.0000000	E
<input type="radio"/>	GO:0051453	11,8,9	regulation of cellular pH	25	0.0039	5	0.0057	1.0000000	E
<input type="radio"/>	GO:0006467	7,8	protein thiol-disulfide exchange	2	0.0003	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0031365	8	N-terminal protein amino acid modification	15	0.0023	5	0.0057	1.0000000	E
<input type="radio"/>	GO:0009199	7	ribonucleoside triphosphate metabolic process	25	0.0039	4	0.0045	1.0000000	E
<input type="radio"/>	GO:0046656	7,8,9	folic acid biosynthetic process	2	0.0003	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0006353	8,7	transcription termination	20	0.0031	4	0.0045	1.0000000	E
<input type="radio"/>	GO:0006401	6	RNA catabolic process	74	0.0114	20	0.0226	1.0000000	E
<input type="radio"/>	GO:0000750	8,7,6	pheromone-dependent signal transduction during conjugation with cellular fusion	28	0.0043	4	0.0045	1.0000000	E
<input type="radio"/>	GO:0055075	9	potassium ion homeostasis	5	0.0008	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0008612	8,7,9	hypusine biosynthetic process from peptidyl-lysine	1	0.0002	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0043087	6	regulation of GTPase activity	5	0.0008	2	0.0023	1.0000000	E
<input type="radio"/>	GO:0051053	8,7	negative regulation of DNA metabolic process	20	0.0031	4	0.0045	1.0000000	E
<input type="radio"/>	GO:0009272	7	chitin- and beta-glucan-containing cell wall biogenesis	33	0.0051	5	0.0057	1.0000000	E
<input type="radio"/>	GO:0043461	8,7	F-type ATPase complex assembly	3	0.0005	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0019674	9,8	NAD metabolic process	21	0.0032	4	0.0045	1.0000000	E
<input type="radio"/>	GO:0015674	6,7	di-, tri-valent inorganic cation transport	34	0.0053	9	0.0102	1.0000000	E
<input type="radio"/>	GO:0033036	3	macromolecule localization	382	0.0590	65	0.0735	1.0000000	E
<input type="radio"/>	GO:0009127	7,8	purine nucleoside monophosphate biosynthetic process	16	0.0025	4	0.0045	1.0000000	E
<input type="radio"/>	GO:0043633	7	modification-dependent RNA catabolic process	7	0.0011	3	0.0034	1.0000000	E
<input type="radio"/>	GO:0051029	5,7,6,8	rRNA transport	26	0.0040	7	0.0079	1.0000000	E
<input type="radio"/>	GO:0009371	10,9,6	positive regulation of transcription by pheromones	5	0.0008	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0000920	6,4	cell separation during cytokinesis	13	0.0020	2	0.0023	1.0000000	E
<input type="radio"/>	GO:0030003	8,6	cellular cation homeostasis	102	0.0158	19	0.0215	1.0000000	E
<input type="radio"/>	GO:0043144	7	snoRNA processing	8	0.0012	3	0.0034	1.0000000	E
<input type="radio"/>	GO:0051383	6	kinetochore organization and biogenesis	3	0.0005	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0022414	3,2	reproductive process	183	0.0283	38	0.0430	1.0000000	E
<input type="radio"/>	GO:0048284	5	organelle fusion	22	0.0034	9	0.0102	1.0000000	E

<input type="radio"/>	GO:0006624	9	vacuolar protein processing	4	0.0006	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0051174	6,5	regulation of phosphorus metabolic process	7	0.0011	2	0.0023	1.0000000	E
<input type="radio"/>	GO:0031509	7,11	telomeric heterochromatin formation	60	0.0093	11	0.0124	1.0000000	E
<input type="radio"/>	GO:0000912	6,5,9,4	cytokinesis, formation of actomyosin apparatus	3	0.0005	2	0.0023	1.0000000	E
<input type="radio"/>	GO:0007023	8	post-chaperonin tubulin folding pathway	5	0.0008	2	0.0023	1.0000000	E
<input type="radio"/>	GO:0045143	10,8,7,5,9,6,4	homologous chromosome segregation	6	0.0009	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0009395	7,8	phospholipid catabolic process	3	0.0005	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0032220	7,6	plasma membrane fusion during cytogamy	1	0.0002	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0006338	9	chromatin remodeling	155	0.0239	25	0.0283	1.0000000	E
<input type="radio"/>	GO:0032200	7	telomere organization and biogenesis	274	0.0423	40	0.0452	1.0000000	E
<input type="radio"/>	GO:0006424	9,8,10,7	glutamyl-tRNA aminoacylation	2	0.0003	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0031327	7,6	negative regulation of cellular biosynthetic process	6	0.0009	4	0.0045	1.0000000	E
<input type="radio"/>	GO:0006730	4	one-carbon compound metabolic process	97	0.0150	16	0.0181	1.0000000	E
<input type="radio"/>	GO:0006974	4	response to DNA damage stimulus	234	0.0361	36	0.0407	1.0000000	E
<input type="radio"/>	GO:0015804	6,7,8	neutral amino acid transport	2	0.0003	2	0.0023	1.0000000	E
<input type="radio"/>	GO:0051438	6	regulation of ubiquitin ligase activity	6	0.0009	2	0.0023	1.0000000	E
<input type="radio"/>	GO:0007165	4	signal transduction	209	0.0323	36	0.0407	1.0000000	E
<input type="radio"/>	GO:0042946	5,6	glucoside transport	5	0.0008	2	0.0023	1.0000000	E
<input type="radio"/>	GO:0000101	6,7,8	sulfur amino acid transport	5	0.0008	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0000390	7,9,11	spliceosome disassembly	4	0.0006	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0006406	11,9,6,8,10,7	mRNA export from nucleus	66	0.0102	18	0.0204	1.0000000	E
<input type="radio"/>	GO:0048523	5,4	negative regulation of cellular process	239	0.0369	39	0.0441	1.0000000	E
<input type="radio"/>	GO:0046112	6,5	nucleobase biosynthetic process	21	0.0032	8	0.0090	1.0000000	E
<input type="radio"/>	GO:0042357	6,7	thiamin diphosphate metabolic process	1	0.0002	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0048311	7,6	mitochondrion distribution	26	0.0040	4	0.0045	1.0000000	E
<input type="radio"/>	GO:0015802	6,7,8	basic amino acid transport	9	0.0014	3	0.0034	1.0000000	E
<input type="radio"/>	GO:0009410	4	response to xenobiotic stimulus	7	0.0011	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0015840	5,6	urea transport	2	0.0003	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0048519	4	negative regulation of biological process	242	0.0374	39	0.0441	1.0000000	E
<input type="radio"/>	GO:0006810	3,4	transport	981	0.1515	159	0.1799	1.0000000	E
<input type="radio"/>	GO:0051666	5,4	actin cortical patch localization	2	0.0003	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0006575	5	amino acid derivative metabolic process	31	0.0048	7	0.0079	1.0000000	E
<input type="radio"/>	GO:0031204	9,11,10,7,8	posttranslational protein targeting to membrane, translocation	4	0.0006	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0032259	5	methylation	83	0.0128	13	0.0147	1.0000000	E
<input type="radio"/>	GO:0000209	10	protein polyubiquitination	20	0.0031	3	0.0034	1.0000000	E
<input type="radio"/>	GO:0000055	11,12,7,9,10	ribosomal large subunit export from nucleus	11	0.0017	5	0.0057	1.0000000	E
<input type="radio"/>	GO:0015780	5,6	nucleotide-sugar transport	4	0.0006	2	0.0023	1.0000000	E
<input type="radio"/>	GO:0009073	7,6,8	aromatic amino acid family biosynthetic process	16	0.0025	4	0.0045	1.0000000	E
<input type="radio"/>	GO:0007034	7,5,6	vacuolar transport	114	0.0176	16	0.0181	1.0000000	E
<input type="radio"/>	GO:0009309	5,6	amine biosynthetic process	114	0.0176	21	0.0238	1.0000000	E
<input type="radio"/>	GO:0046500	6,5	S-adenosylmethionine metabolic process	3	0.0005	2	0.0023	1.0000000	E
<input type="radio"/>	GO:0044270	5,4	nitrogen compound catabolic process	32	0.0049	5	0.0057	1.0000000	E
<input type="radio"/>	GO:0008299	6,5,7	isoprenoid biosynthetic process	6	0.0009	2	0.0023	1.0000000	E

<input type="checkbox"/>	GO:0040020	7,9,8,6	regulation of meiosis	22	0.0034	5	0.0057	1.0000000	E
<input type="checkbox"/>	GO:0006895	8,9,6,7	Golgi to endosome transport	13	0.0020	2	0.0023	1.0000000	E
<input type="checkbox"/>	GO:0006658	8,9	phosphatidylserine metabolic process	3	0.0005	1	0.0011	1.0000000	E
<input type="checkbox"/>	GO:0016568	8	chromatin modification	223	0.0344	38	0.0430	1.0000000	E
<input type="checkbox"/>	GO:0000266	6	mitochondrial fission	5	0.0008	1	0.0011	1.0000000	E
<input type="checkbox"/>	GO:0019222	4,3	regulation of metabolic process	538	0.0831	95	0.1075	1.0000000	E
<input type="checkbox"/>	GO:0006499	10,11,9,8	N-terminal protein myristoylation	5	0.0008	1	0.0011	1.0000000	E
<input type="checkbox"/>	GO:0006556	8,7,6,9,5	S-adenosylmethionine biosynthetic process	2	0.0003	1	0.0011	1.0000000	E
<input type="checkbox"/>	GO:0006629	4	lipid metabolic process	242	0.0374	44	0.0498	1.0000000	E
<input type="checkbox"/>	GO:0051336	5	regulation of hydrolase activity	10	0.0015	3	0.0034	1.0000000	E
<input type="checkbox"/>	GO:0019284	9,7,8,6,10	methionine biosynthetic process from S-adenosylmethionine	1	0.0002	1	0.0011	1.0000000	E
<input type="checkbox"/>	GO:0051129	6,5	negative regulation of cell organization and biogenesis	7	0.0011	1	0.0011	1.0000000	E
<input type="checkbox"/>	GO:0031383	5,7,10,9,8,6,11	regulation of mating projection biogenesis	6	0.0009	1	0.0011	1.0000000	E
<input type="checkbox"/>	GO:0000738	6,7	DNA catabolic process, exonucleolytic	5	0.0008	1	0.0011	1.0000000	E
<input type="checkbox"/>	GO:0006166	6,8	purine ribonucleoside salvage	6	0.0009	1	0.0011	1.0000000	E
<input type="checkbox"/>	GO:0006468	8,7	protein amino acid phosphorylation	101	0.0156	20	0.0226	1.0000000	E
<input type="checkbox"/>	GO:0000729	7,8,10,9	DNA double-strand break processing	5	0.0008	1	0.0011	1.0000000	E
<input type="checkbox"/>	GO:0018409	9	peptide or protein amino-terminal blocking	15	0.0023	5	0.0057	1.0000000	E
<input type="checkbox"/>	GO:0042183	6,8	formate catabolic process	3	0.0005	1	0.0011	1.0000000	E
<input type="checkbox"/>	GO:0006387	8	snRNA capping	1	0.0002	1	0.0011	1.0000000	E
<input type="checkbox"/>	GO:0006427	9,8,10,7	histidyl-tRNA aminoacylation	1	0.0002	1	0.0011	1.0000000	E
<input type="checkbox"/>	GO:0016458	5	gene silencing	95	0.0147	19	0.0215	1.0000000	E
<input type="checkbox"/>	GO:0009063	6,7	amino acid catabolic process	29	0.0045	5	0.0057	1.0000000	E
<input type="checkbox"/>	GO:0006734	9,8	NADH metabolic process	14	0.0022	2	0.0023	1.0000000	E
<input type="checkbox"/>	GO:0006769	8,7	nicotinamide metabolic process	42	0.0065	9	0.0102	1.0000000	E
<input type="checkbox"/>	GO:0046058	7	cAMP metabolic process	2	0.0003	1	0.0011	1.0000000	E
<input type="checkbox"/>	GO:0000743	9,10,8,7,6	nuclear migration during conjugation with cellular fusion	4	0.0006	2	0.0023	1.0000000	E
<input type="checkbox"/>	GO:0009130	7,8	pyrimidine nucleoside monophosphate biosynthetic process	1	0.0002	1	0.0011	1.0000000	E
<input type="checkbox"/>	GO:0006740	10,9	NADPH regeneration	14	0.0022	3	0.0034	1.0000000	E
<input type="checkbox"/>	GO:0006408	11,9,6,8,10,7	snRNA export from nucleus	23	0.0036	5	0.0057	1.0000000	E
<input type="checkbox"/>	GO:0008283	3	cell proliferation	5	0.0008	1	0.0011	1.0000000	E
<input type="checkbox"/>	GO:0006733	6	oxidoreduction coenzyme metabolic process	56	0.0086	9	0.0102	1.0000000	E
<input type="checkbox"/>	GO:0046351	6,7	disaccharide biosynthetic process	7	0.0011	1	0.0011	1.0000000	E
<input type="checkbox"/>	GO:0015718	6,7	monocarboxylic acid transport	10	0.0015	2	0.0023	1.0000000	E
<input type="checkbox"/>	GO:0007103	6,7,5,8	spindle pole body duplication in nuclear envelope	13	0.0020	2	0.0023	1.0000000	E
<input type="checkbox"/>	GO:0043687	7	post-translational protein modification	388	0.0599	63	0.0713	1.0000000	E
<input type="checkbox"/>	GO:0015700	7,8	arsenite transport	1	0.0002	1	0.0011	1.0000000	E
<input type="checkbox"/>	GO:0009259	6	ribonucleotide metabolic process	43	0.0066	9	0.0102	1.0000000	E
<input type="checkbox"/>	GO:0009161	7	ribonucleoside monophosphate metabolic process	17	0.0026	5	0.0057	1.0000000	E
<input type="checkbox"/>	GO:0045116	9	protein neddylation	6	0.0009	2	0.0023	1.0000000	E
<input type="checkbox"/>	GO:0032318	7,8,9	regulation of Ras GTPase activity	2	0.0003	1	0.0011	1.0000000	E
<input type="checkbox"/>	GO:0000731	7,6	DNA synthesis during DNA repair	4	0.0006	1	0.0011	1.0000000	E
<input type="checkbox"/>	GO:0007266	8	Rho protein signal transduction	17	0.0026	3	0.0034	1.0000000	E

<input type="checkbox"/>	GO:0051276	5	chromosome organization and biogenesis	572	0.0883	98	0.1109	1.0000000	E
<input type="checkbox"/>	GO:0031111	7,10,6	negative regulation of microtubule polymerization or depolymerization	5	0.0008	1	0.0011	1.0000000	E
<input type="checkbox"/>	GO:0016076	7	snRNA catabolic process	4	0.0006	2	0.0023	1.0000000	E
<input type="checkbox"/>	GO:0007001	6	chromosome organization and biogenesis (sensu Eukaryota)	567	0.0876	97	0.1097	1.0000000	E
<input type="checkbox"/>	GO:0016075	7	rRNA catabolic process	5	0.0008	3	0.0034	1.0000000	E
<input type="checkbox"/>	GO:0009152	7,8	purine ribonucleotide biosynthetic process	38	0.0059	7	0.0079	1.0000000	E
<input type="checkbox"/>	GO:0007047	5	cell wall organization and biogenesis	200	0.0309	34	0.0385	1.0000000	E
<input type="checkbox"/>	GO:0006379	8	mRNA cleavage	26	0.0040	5	0.0057	1.0000000	E
<input type="checkbox"/>	GO:0001403	6,4,8,9	invasive growth (sensu Saccharomyces)	42	0.0065	6	0.0068	1.0000000	E
<input type="checkbox"/>	GO:0033559	6,8,7	unsaturated fatty acid metabolic process	1	0.0002	1	0.0011	1.0000000	E
<input type="checkbox"/>	GO:0001718	8,7,11,10,9	conversion of met-tRNAf to fmet-tRNA	1	0.0002	1	0.0011	1.0000000	E
<input type="checkbox"/>	GO:0000183	11,7,8,12,10	chromatin silencing at rDNA	18	0.0028	7	0.0079	1.0000000	E
<input type="checkbox"/>	GO:0018205	8	peptidyl-lysine modification	4	0.0006	2	0.0023	1.0000000	E
<input type="checkbox"/>	GO:0009268	4	response to pH	5	0.0008	2	0.0023	1.0000000	E
<input type="checkbox"/>	GO:0006285	7,8	base-excision repair, AP site formation	3	0.0005	1	0.0011	1.0000000	E
<input type="checkbox"/>	GO:0006551	7,8	leucine metabolic process	7	0.0011	1	0.0011	1.0000000	E
<input type="checkbox"/>	GO:0006323	6	DNA packaging	253	0.0391	43	0.0486	1.0000000	E
<input type="checkbox"/>	GO:0007129	10,8,7,5,9,6,4	synapsis	10	0.0015	4	0.0045	1.0000000	E
<input type="checkbox"/>	GO:0000040	8,9,10	low affinity iron ion transport	1	0.0002	1	0.0011	1.0000000	E
<input type="checkbox"/>	GO:0000921	8,7	septin ring assembly	9	0.0014	2	0.0023	1.0000000	E
<input type="checkbox"/>	GO:0006778	5,6	porphyrin metabolic process	14	0.0022	3	0.0034	1.0000000	E
<input type="checkbox"/>	GO:0030952	6	establishment and/or maintenance of cytoskeleton polarity	9	0.0014	2	0.0023	1.0000000	E
<input type="checkbox"/>	GO:0043631	8	RNA polyadenylation	24	0.0037	5	0.0057	1.0000000	E
<input type="checkbox"/>	GO:0048025	10,9,12	negative regulation of nuclear mRNA splicing, via spliceosome	1	0.0002	1	0.0011	1.0000000	E
<input type="checkbox"/>	GO:0009150	7	purine ribonucleotide metabolic process	41	0.0063	8	0.0090	1.0000000	E
<input type="checkbox"/>	GO:0006831	9,10	low-affinity zinc ion transport	1	0.0002	1	0.0011	1.0000000	E
<input type="checkbox"/>	GO:0000226	7	microtubule cytoskeleton organization and biogenesis	81	0.0125	14	0.0158	1.0000000	E
<input type="checkbox"/>	GO:0007265	7	Ras protein signal transduction	39	0.0060	7	0.0079	1.0000000	E
<input type="checkbox"/>	GO:0000725	7,6	recombinational repair	29	0.0045	5	0.0057	1.0000000	E
<input type="checkbox"/>	GO:0006607	10,11,8,9,7	NLS-bearing substrate import into nucleus	23	0.0036	5	0.0057	1.0000000	E
<input type="checkbox"/>	GO:0016579	9	protein deubiquitination	20	0.0031	3	0.0034	1.0000000	E
<input type="checkbox"/>	GO:0006428	9,8,10,7	isoleucyl-tRNA aminoacylation	1	0.0002	1	0.0011	1.0000000	E
<input type="checkbox"/>	GO:0032185	6	septin cytoskeleton organization and biogenesis	9	0.0014	2	0.0023	1.0000000	E
<input type="checkbox"/>	GO:0000430	11,9,10,7	regulation of transcription from RNA polymerase II promoter by glucose	7	0.0011	2	0.0023	1.0000000	E
<input type="checkbox"/>	GO:0015819	7,8,9	lysine transport	1	0.0002	1	0.0011	1.0000000	E
<input type="checkbox"/>	GO:0015837	4,5	amine transport	50	0.0077	14	0.0158	1.0000000	E
<input type="checkbox"/>	GO:0042364	6	water-soluble vitamin biosynthetic process	46	0.0071	11	0.0124	1.0000000	E
<input type="checkbox"/>	GO:0045014	11,9,10,7	negative regulation of transcription by glucose	7	0.0011	2	0.0023	1.0000000	E
<input type="checkbox"/>	GO:0031384	6,8,11,10,9,7,12	regulation of initiation of mating projection growth	4	0.0006	1	0.0011	1.0000000	E
<input type="checkbox"/>	GO:0009889	5,4	regulation of biosynthetic process	69	0.0107	12	0.0136	1.0000000	E
<input type="checkbox"/>	GO:0045041	10,9,8,7	protein import into mitochondrial intermembrane space	6	0.0009	2	0.0023	1.0000000	E
<input type="checkbox"/>	GO:0051647	6,5	nucleus localization	20	0.0031	7	0.0079	1.0000000	E

<input type="radio"/>	GO:0030466	11,7,8,12,10	chromatin silencing at silent mating-type cassette	30	0.0046	8	0.0090	1.0000000	E
<input type="radio"/>	GO:0051180	4,5	vitamin transport	9	0.0014	2	0.0023	1.0000000	E
<input type="radio"/>	GO:0032974	8,6,7,9	amino acid export from vacuole	3	0.0005	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0030437	7,6	sporulation (sensu Fungi)	108	0.0167	26	0.0294	1.0000000	E
<input type="radio"/>	GO:0016572	11,9,8	histone phosphorylation	2	0.0003	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0007010	5	cytoskeleton organization and biogenesis	227	0.0351	45	0.0509	1.0000000	E
<input type="radio"/>	GO:0010133	9,8,10	proline catabolic process to glutamate	2	0.0003	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0030799	8,7	regulation of cyclic nucleotide metabolic process	2	0.0003	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0006825	8,9	copper ion transport	14	0.0022	5	0.0057	1.0000000	E
<input type="radio"/>	GO:0031684	7	heterotrimeric G-protein complex cycle	3	0.0005	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0000087	7,5,6	M phase of mitotic cell cycle	129	0.0199	23	0.0260	1.0000000	E
<input type="radio"/>	GO:0006796	5	phosphate metabolic process	212	0.0327	35	0.0396	1.0000000	E
<input type="radio"/>	GO:0019725	5,3	cellular homeostasis	128	0.0198	21	0.0238	1.0000000	E
<input type="radio"/>	GO:0006567	8,9	threonine catabolic process	3	0.0005	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0045935	7,6	positive regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	108	0.0167	19	0.0215	1.0000000	E
<input type="radio"/>	GO:0006390	8,7	transcription from mitochondrial promoter	3	0.0005	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0006144	6	purine base metabolic process	14	0.0022	3	0.0034	1.0000000	E
<input type="radio"/>	GO:0032446	8	protein modification by small protein conjugation	84	0.0130	14	0.0158	1.0000000	E
<input type="radio"/>	GO:0000459	7,8	exonucleolytic trimming during rRNA processing	1	0.0002	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0051170	9,7,8	nuclear import	50	0.0077	8	0.0090	1.0000000	E
<input type="radio"/>	GO:0045851	8	pH reduction	24	0.0037	5	0.0057	1.0000000	E
<input type="radio"/>	GO:0018282	8,6	metal incorporation into metallo-sulfur cluster	1	0.0002	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0000734	7,9,8	gene conversion at mating-type locus, DNA repair synthesis	1	0.0002	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0051099	5	positive regulation of binding	1	0.0002	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0016259	7,8,6	selenocysteine metabolic process	1	0.0002	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0016578	11,9,10	histone deubiquitination	1	0.0002	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0006342	10,6,7,11,9	chromatin silencing	95	0.0147	19	0.0215	1.0000000	E
<input type="radio"/>	GO:0019748	3	secondary metabolic process	23	0.0036	4	0.0045	1.0000000	E
<input type="radio"/>	GO:0016125	5,6,7	sterol metabolic process	42	0.0065	6	0.0068	1.0000000	E
<input type="radio"/>	GO:0006814	7,8	sodium ion transport	4	0.0006	2	0.0023	1.0000000	E
<input type="radio"/>	GO:0007024	8	alpha-tubulin folding	2	0.0003	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0008214	8	protein amino acid dealkylation	4	0.0006	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0042274	6,5	ribosomal small subunit biogenesis and assembly	26	0.0040	4	0.0045	1.0000000	E
<input type="radio"/>	GO:0007127	9,7,6,8,5	meiosis I	75	0.0116	14	0.0158	1.0000000	E
<input type="radio"/>	GO:0019988	7,8,9,6	charged-tRNA modification	2	0.0003	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0050658	4,6,5,7	RNA transport	80	0.0124	20	0.0226	1.0000000	E
<input type="radio"/>	GO:0006829	8,9	zinc ion transport	7	0.0011	2	0.0023	1.0000000	E
<input type="radio"/>	GO:0015805	7,8,9	S-adenosylmethionine transport	2	0.0003	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0042168	6,7,5	heme metabolic process	14	0.0022	3	0.0034	1.0000000	E
<input type="radio"/>	GO:0043543	7	protein amino acid acylation	62	0.0096	12	0.0136	1.0000000	E
<input type="radio"/>	GO:0043629	9	ncRNA polyadenylation	5	0.0008	3	0.0034	1.0000000	E
<input type="radio"/>	GO:0046498	6	S-adenosylhomocysteine metabolic process	1	0.0002	1	0.0011	1.0000000	E

<input type="radio"/>	GO:0030447	3	filamentous growth	94	0.0145	13	0.0147	1.0000000	E
<input type="radio"/>	GO:0007062	7,4	sister chromatid cohesion	31	0.0048	9	0.0102	1.0000000	E
<input type="radio"/>	GO:0009072	6,5,7	aromatic amino acid family metabolic process	21	0.0032	4	0.0045	1.0000000	E
<input type="radio"/>	GO:0042044	4,5	fluid transport	3	0.0005	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0043623	7,6	cellular protein complex assembly	69	0.0107	12	0.0136	1.0000000	E
<input type="radio"/>	GO:0006891	8,6,5,7	intra-Golgi vesicle-mediated transport	21	0.0032	5	0.0057	1.0000000	E
<input type="radio"/>	GO:0006145	7,6	purine base catabolic process	1	0.0002	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0051246	5,4	regulation of protein metabolic process	72	0.0111	12	0.0136	1.0000000	E
<input type="radio"/>	GO:0046098	7	guanine metabolic process	1	0.0002	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0006620	10,9,8,7,6	posttranslational protein targeting to membrane	8	0.0012	3	0.0034	1.0000000	E
<input type="radio"/>	GO:0009082	7,8	branched chain family amino acid biosynthetic process	13	0.0020	4	0.0045	1.0000000	E
<input type="radio"/>	GO:0051318	6,7,5	G1 phase	27	0.0042	7	0.0079	1.0000000	E
<input type="radio"/>	GO:0015931	4,5	nucleobase, nucleoside, nucleotide and nucleic acid transport	90	0.0139	20	0.0226	1.0000000	E
<input type="radio"/>	GO:0032005	7,6	signal transduction during conjugation with cellular fusion	28	0.0043	4	0.0045	1.0000000	E
<input type="radio"/>	GO:0006665	6,7	sphingolipid metabolic process	30	0.0046	8	0.0090	1.0000000	E
<input type="radio"/>	GO:0043102	6,5,7	amino acid salvage	3	0.0005	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0030846	10,9	transcription termination from Pol II promoter, RNA polymerase(A) coupled	10	0.0015	3	0.0034	1.0000000	E
<input type="radio"/>	GO:0000196	8,6	MAPKKK cascade during cell wall biogenesis	4	0.0006	2	0.0023	1.0000000	E
<input type="radio"/>	GO:0051443	7	positive regulation of ubiquitin ligase activity	3	0.0005	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0008204	6,7,8	ergosterol metabolic process	26	0.0040	5	0.0057	1.0000000	E
<input type="radio"/>	GO:0030815	10,9	negative regulation of cAMP metabolic process	2	0.0003	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0030968	7,5,6	unfolded protein response	9	0.0014	2	0.0023	1.0000000	E
<input type="radio"/>	GO:0006146	8,7	adenine catabolic process	1	0.0002	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0033014	6	tetrapyrrole biosynthetic process	13	0.0020	3	0.0034	1.0000000	E
<input type="radio"/>	GO:0006721	6,7,4	terpenoid metabolic process	2	0.0003	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0006813	7,8	potassium ion transport	5	0.0008	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0032263	7,8	GMP salvage	1	0.0002	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0006882	10,8	cellular zinc ion homeostasis	10	0.0015	3	0.0034	1.0000000	E
<input type="radio"/>	GO:0000059	8,10,11,7,9	protein import into nucleus, docking	4	0.0006	2	0.0023	1.0000000	E
<input type="radio"/>	GO:0006357	9,8	regulation of transcription from RNA polymerase II promoter	221	0.0341	46	0.0520	1.0000000	E
<input type="radio"/>	GO:0006284	7,6	base-excision repair	12	0.0019	3	0.0034	1.0000000	E
<input type="radio"/>	GO:0045026	6	plasma membrane fusion	3	0.0005	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0000114	10,8,9,5,7,4	G1-specific transcription in mitotic cell cycle	15	0.0023	4	0.0045	1.0000000	E
<input type="radio"/>	GO:0045980	8,7	negative regulation of nucleotide metabolic process	2	0.0003	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0000412	11,9	histone peptidyl-prolyl isomerization	1	0.0002	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0006545	8,9	glycine biosynthetic process	2	0.0003	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0015809	7,8,9	arginine transport	2	0.0003	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0033013	5	tetrapyrrole metabolic process	14	0.0022	3	0.0034	1.0000000	E
<input type="radio"/>	GO:0045892	9,8	negative regulation of transcription, DNA-dependent	156	0.0241	31	0.0351	1.0000000	E
<input type="radio"/>	GO:0009746	6,5	response to hexose stimulus	5	0.0008	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0051248	6,5	negative regulation of protein metabolic process	18	0.0028	5	0.0057	1.0000000	E

<input type="radio"/>	GO:0009303	8,7	rRNA transcription	3	0.0005	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0051646	6,5	mitochondrion localization	27	0.0042	4	0.0045	1.0000000	E
<input type="radio"/>	GO:0006839	7,5,6	mitochondrial transport	65	0.0100	10	0.0113	1.0000000	E
<input type="radio"/>	GO:0055067	8	monovalent inorganic cation homeostasis	34	0.0053	6	0.0068	1.0000000	E
<input type="radio"/>	GO:0000245	7,6,9,11	spliceosome assembly	19	0.0029	6	0.0068	1.0000000	E
<input type="radio"/>	GO:0031114	7,10,6,8	regulation of microtubule depolymerization	5	0.0008	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0007017	6	microtubule-based process	101	0.0156	21	0.0238	1.0000000	E
<input type="radio"/>	GO:0043254	6,7,5	regulation of protein complex assembly	6	0.0009	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0019413	7,8	acetate biosynthetic process	3	0.0005	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0030866	8,7	cortical actin cytoskeleton organization and biogenesis	16	0.0025	4	0.0045	1.0000000	E
<input type="radio"/>	GO:0006879	10,8	cellular iron ion homeostasis	38	0.0059	8	0.0090	1.0000000	E
<input type="radio"/>	GO:0006633	7,6,8,5	fatty acid biosynthetic process	13	0.0020	5	0.0057	1.0000000	E
<input type="radio"/>	GO:0031110	6,9,5	regulation of microtubule polymerization or depolymerization	15	0.0023	3	0.0034	1.0000000	E
<input type="radio"/>	GO:0048285	5	organelle fission	6	0.0009	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0050789	3	regulation of biological process	761	0.1175	122	0.1380	1.0000000	E
<input type="radio"/>	GO:0006310	6	DNA recombination	122	0.0188	22	0.0249	1.0000000	E
<input type="radio"/>	GO:0045039	10,9,7,8	protein import into mitochondrial inner membrane	8	0.0012	3	0.0034	1.0000000	E
<input type="radio"/>	GO:0009208	8	pyrimidine ribonucleoside triphosphate metabolic process	2	0.0003	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0000358	9,8,10,11,12,13	formation of catalytic U2-type spliceosome for second transesterification step	2	0.0003	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0048856	3	anatomical structure development	248	0.0383	40	0.0452	1.0000000	E
<input type="radio"/>	GO:0006608	10,11,8,9,7	snRNP protein import into nucleus	23	0.0036	5	0.0057	1.0000000	E
<input type="radio"/>	GO:0009168	8,9	purine ribonucleoside monophosphate biosynthetic process	15	0.0023	4	0.0045	1.0000000	E
<input type="radio"/>	GO:0051320	7,6,5	S phase	20	0.0031	3	0.0034	1.0000000	E
<input type="radio"/>	GO:0050790	4	regulation of catalytic activity	45	0.0069	7	0.0079	1.0000000	E
<input type="radio"/>	GO:0044271	5,4	nitrogen compound biosynthetic process	115	0.0178	21	0.0238	1.0000000	E
<input type="radio"/>	GO:0007163	6,3,7	establishment and/or maintenance of cell polarity	115	0.0178	18	0.0204	1.0000000	E
<input type="radio"/>	GO:0000022	6,5,10,8	mitotic spindle elongation	20	0.0031	3	0.0034	1.0000000	E
<input type="radio"/>	GO:0009229	7,8	thiamin diphosphate biosynthetic process	1	0.0002	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0006188	9,10	IMP biosynthetic process	14	0.0022	3	0.0034	1.0000000	E
<input type="radio"/>	GO:0016973	12,10,7,9,11,8	poly(A)+ mRNA export from nucleus	8	0.0012	2	0.0023	1.0000000	E
<input type="radio"/>	GO:0006824	7,8,9	cobalt ion transport	2	0.0003	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0065007	2	biological regulation	948	0.1464	157	0.1776	1.0000000	E
<input type="radio"/>	GO:0006627	10,9,8,7	mitochondrial protein processing	6	0.0009	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0043094	4	metabolic compound salvage	19	0.0029	5	0.0057	1.0000000	E
<input type="radio"/>	GO:0006767	5	water-soluble vitamin metabolic process	89	0.0137	19	0.0215	1.0000000	E
<input type="radio"/>	GO:0008610	5,4,6	lipid biosynthetic process	129	0.0199	23	0.0260	1.0000000	E
<input type="radio"/>	GO:0030474	5,6,4,7	spindle pole body duplication	14	0.0022	2	0.0023	1.0000000	E
<input type="radio"/>	GO:0007157	5	heterophilic cell adhesion	4	0.0006	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0009066	6,7	aspartate family amino acid metabolic process	46	0.0071	11	0.0124	1.0000000	E
<input type="radio"/>	GO:0000280	3	nuclear division	2	0.0003	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0000429	10,8,9,6	regulation of transcription from RNA polymerase II promoter by carbon catabolites	7	0.0011	2	0.0023	1.0000000	E

<input type="radio"/>	GO:0008614	7	pyridoxine metabolic process	8	0.0012	5	0.0057	1.0000000	E
<input type="radio"/>	GO:0000755	6,5	cytogamy	7	0.0011	3	0.0034	1.0000000	E
<input type="radio"/>	GO:0015849	4,5	organic acid transport	55	0.0085	13	0.0147	1.0000000	E
<input type="radio"/>	GO:0019438	5	aromatic compound biosynthetic process	18	0.0028	5	0.0057	1.0000000	E
<input type="radio"/>	GO:0007000	6	nucleolus organization and biogenesis	2	0.0003	2	0.0023	1.0000000	E
<input type="radio"/>	GO:0051704	2	multi-organism process	139	0.0215	25	0.0283	1.0000000	E
<input type="radio"/>	GO:0000132	6,5,8,9,10,7	establishment of mitotic spindle orientation	10	0.0015	2	0.0023	1.0000000	E
<input type="radio"/>	GO:0009061	6	anaerobic respiration	2	0.0003	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0006313	7,4	transposition, DNA-mediated	10	0.0015	2	0.0023	1.0000000	E
<input type="radio"/>	GO:0000391	8,10,12	U2-dependent spliceosome disassembly	4	0.0006	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0030818	11,9,10,8	negative regulation of cAMP biosynthetic process	2	0.0003	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0018206	8	peptidyl-methionine modification	3	0.0005	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0030007	10,8	cellular potassium ion homeostasis	5	0.0008	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0009314	4	response to radiation	2	0.0003	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0030814	9,8	regulation of cAMP metabolic process	2	0.0003	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0007006	5,6	mitochondrial membrane organization and biogenesis	24	0.0037	5	0.0057	1.0000000	E
<input type="radio"/>	GO:0051640	5,4	organelle localization	56	0.0086	12	0.0136	1.0000000	E
<input type="radio"/>	GO:0046907	6,4,5	intracellular transport	545	0.0842	90	0.1018	1.0000000	E
<input type="radio"/>	GO:0007070	11,9,6,7,10,8,5	negative regulation of transcription from RNA polymerase II promoter, mitotic	6	0.0009	2	0.0023	1.0000000	E
<input type="radio"/>	GO:0000910	4	cytokinesis	109	0.0168	16	0.0181	1.0000000	E
<input type="radio"/>	GO:0050657	5,6	nucleic acid transport	80	0.0124	20	0.0226	1.0000000	E
<input type="radio"/>	GO:0007329	11,10,7	positive regulation of transcription from RNA polymerase II promoter by pheromones	5	0.0008	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0051347	6	positive regulation of transferase activity	6	0.0009	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0043085	5	positive regulation of enzyme activity	11	0.0017	2	0.0023	1.0000000	E
<input type="radio"/>	GO:0008202	5,6	steroid metabolic process	43	0.0066	6	0.0068	1.0000000	E
<input type="radio"/>	GO:0009167	8	purine ribonucleoside monophosphate metabolic process	17	0.0026	5	0.0057	1.0000000	E
<input type="radio"/>	GO:0000752	7,5,6	agglutination during conjugation with cellular fusion	4	0.0006	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0006421	9,8,10,7	asparaginyl-tRNA aminoacylation	1	0.0002	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0006273	9,8	lagging strand elongation	18	0.0028	3	0.0034	1.0000000	E
<input type="radio"/>	GO:0055069	9	zinc ion homeostasis	10	0.0015	3	0.0034	1.0000000	E
<input type="radio"/>	GO:0000415	9,11,14,8,12,13,10	negative regulation of histone H3-K36 methylation	1	0.0002	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0042790	9,8	transcription of nuclear rRNA large RNA polymerase I transcript	1	0.0002	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0048518	4	positive regulation of biological process	124	0.0191	21	0.0238	1.0000000	E
<input type="radio"/>	GO:0045941	8,7	positive regulation of transcription	101	0.0156	19	0.0215	1.0000000	E
<input type="radio"/>	GO:0031106	7	septin ring organization	9	0.0014	2	0.0023	1.0000000	E
<input type="radio"/>	GO:0030100	6,7,5	regulation of endocytosis	3	0.0005	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0016036	8,7,6	cellular response to phosphate starvation	4	0.0006	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0006561	8,9	proline biosynthetic process	3	0.0005	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0051031	5,7,6,8	tRNA transport	30	0.0046	6	0.0068	1.0000000	E
<input type="radio"/>	GO:0046037	9	GMP metabolic process	2	0.0003	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0045913	6,5	positive regulation of carbohydrate metabolic process	7	0.0011	2	0.0023	1.0000000	E
<input type="radio"/>	GO:0000077	9,8,6	DNA damage checkpoint	14	0.0022	2	0.0023	1.0000000	E

<input type="checkbox"/>	GO:0000001	8,7,6	mitochondrion inheritance	26	0.0040	4	0.0045	1.0000000	E
<input type="checkbox"/>	GO:0006606	9,10,7,8,6	protein import into nucleus	50	0.0077	8	0.0090	1.0000000	E
<input type="checkbox"/>	GO:0042149	8,7,6	cellular response to glucose starvation	5	0.0008	1	0.0011	1.0000000	E
<input type="checkbox"/>	GO:0045816	11,10	negative regulation of global transcription from RNA polymerase II promoter	5	0.0008	1	0.0011	1.0000000	E
<input type="checkbox"/>	GO:0030817	10,8,9,7	regulation of cAMP biosynthetic process	2	0.0003	1	0.0011	1.0000000	E
<input type="checkbox"/>	GO:0015824	7,8,9	proline transport	2	0.0003	2	0.0023	1.0000000	E
<input type="checkbox"/>	GO:0000409	10,8,9,6	regulation of transcription by galactose	5	0.0008	1	0.0011	1.0000000	E
<input type="checkbox"/>	GO:0006473	8	protein amino acid acetylation	48	0.0074	10	0.0113	1.0000000	E
<input type="checkbox"/>	GO:0015781	6,7	pyrimidine nucleotide-sugar transport	2	0.0003	1	0.0011	1.0000000	E
<input type="checkbox"/>	GO:0040023	6,7,4,5	establishment of nucleus localization	20	0.0031	7	0.0079	1.0000000	E
<input type="checkbox"/>	GO:0031145	11,10,12	anaphase-promoting complex-dependent proteasomal ubiquitin-dependent protein catabolic process	15	0.0023	3	0.0034	1.0000000	E
<input type="checkbox"/>	GO:0008643	4,5	carbohydrate transport	38	0.0059	10	0.0113	1.0000000	E
<input type="checkbox"/>	GO:0009102	6,7,8	biotin biosynthetic process	7	0.0011	1	0.0011	1.0000000	E
<input type="checkbox"/>	GO:0006797	6	polyphosphate metabolic process	5	0.0008	2	0.0023	1.0000000	E
<input type="checkbox"/>	GO:0051340	5	regulation of ligase activity	6	0.0009	2	0.0023	1.0000000	E
<input type="checkbox"/>	GO:0006807	3	nitrogen compound metabolic process	251	0.0388	50	0.0566	1.0000000	E
<input type="checkbox"/>	GO:0006110	6,10,11,5	regulation of glycolysis	6	0.0009	1	0.0011	1.0000000	E
<input type="checkbox"/>	GO:0006164	6,7	purine nucleotide biosynthetic process	41	0.0063	7	0.0079	1.0000000	E
<input type="checkbox"/>	GO:0006283	8,7	transcription-coupled nucleotide-excision repair	9	0.0014	2	0.0023	1.0000000	E
<input type="checkbox"/>	GO:0001101	4	response to acid	11	0.0017	2	0.0023	1.0000000	E
<input type="checkbox"/>	GO:0032392	6	DNA geometric change	16	0.0025	3	0.0034	1.0000000	E
<input type="checkbox"/>	GO:0006333	8	chromatin assembly or disassembly	119	0.0184	22	0.0249	1.0000000	E
<input type="checkbox"/>	GO:0006660	9,10	phosphatidylserine catabolic process	1	0.0002	1	0.0011	1.0000000	E
<input type="checkbox"/>	GO:0006260	6	DNA replication	117	0.0181	19	0.0215	1.0000000	E
<input type="checkbox"/>	GO:0050801	6	ion homeostasis	119	0.0184	20	0.0226	1.0000000	E
<input type="checkbox"/>	GO:0051301	3	cell division	246	0.0380	48	0.0543	1.0000000	E
<input type="checkbox"/>	GO:0001308	11,7,10	loss of chromatin silencing during replicative cell aging	8	0.0012	2	0.0023	1.0000000	E
<input type="checkbox"/>	GO:0048622	6,5	reproductive sporulation	108	0.0167	26	0.0294	1.0000000	E
<input type="checkbox"/>	GO:0015698	6,7	inorganic anion transport	16	0.0025	6	0.0068	1.0000000	E
<input type="checkbox"/>	GO:0022411	4	cellular component disassembly	36	0.0056	5	0.0057	1.0000000	E
<input type="checkbox"/>	GO:0006636	8,7,9,6	unsaturated fatty acid biosynthetic process	1	0.0002	1	0.0011	1.0000000	E
<input type="checkbox"/>	GO:0006183	9,10	GTP biosynthetic process	2	0.0003	2	0.0023	1.0000000	E
<input type="checkbox"/>	GO:0000902	5,6	cell morphogenesis	248	0.0383	40	0.0452	1.0000000	E
<input type="checkbox"/>	GO:0031667	5	response to nutrient levels	37	0.0057	6	0.0068	1.0000000	E
<input type="checkbox"/>	GO:0000084	8,7,6	S phase of mitotic cell cycle	18	0.0028	3	0.0034	1.0000000	E
<input type="checkbox"/>	GO:0006984	6	ER-nuclear signaling pathway	9	0.0014	2	0.0023	1.0000000	E
<input type="checkbox"/>	GO:0006369	9,8	transcription termination from RNA polymerase II promoter	18	0.0028	3	0.0034	1.0000000	E
<input type="checkbox"/>	GO:0015887	5,6	pantothenate transport	1	0.0002	1	0.0011	1.0000000	E
<input type="checkbox"/>	GO:0051030	5,7,6,8	snRNA transport	23	0.0036	5	0.0057	1.0000000	E
<input type="checkbox"/>	GO:0051236	3,4,5	establishment of RNA localization	80	0.0124	20	0.0226	1.0000000	E
<input type="checkbox"/>	GO:0006409	11,9,6,8,10,7	tRNA export from nucleus	29	0.0045	6	0.0068	1.0000000	E
<input type="checkbox"/>	GO:0006621	7,6,5,4	protein retention in ER	7	0.0011	1	0.0011	1.0000000	E
<input type="checkbox"/>	GO:0045184	3,4,5	establishment of protein localization	296	0.0457	49	0.0554	1.0000000	E

<input type="radio"/>	GO:0007580	10,6	extrachromosomal circular DNA accumulation during cell aging	2	0.0003	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0030005	9,7	cellular di-, tri-valent inorganic cation homeostasis	64	0.0099	13	0.0147	1.0000000	E
<input type="radio"/>	GO:0006741	8,7,10,9	NADP biosynthetic process	3	0.0005	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0007007	6,7	inner mitochondrial membrane organization and biogenesis	12	0.0019	4	0.0045	1.0000000	E
<input type="radio"/>	GO:0042398	6,5	amino acid derivative biosynthetic process	20	0.0031	4	0.0045	1.0000000	E
<input type="radio"/>	GO:0015791	4,5	polyol transport	6	0.0009	2	0.0023	1.0000000	E
<input type="radio"/>	GO:0019219	6,5	regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	440	0.0679	81	0.0916	1.0000000	E
<input type="radio"/>	GO:0019362	7,6	pyridine nucleotide metabolic process	45	0.0069	9	0.0102	1.0000000	E
<input type="radio"/>	GO:0006800	4	oxygen and reactive oxygen species metabolic process	6	0.0009	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0006610	10,11,8,9,7	ribosomal protein import into nucleus	23	0.0036	5	0.0057	1.0000000	E
<input type="radio"/>	GO:0031507	6,10	heterochromatin formation	95	0.0147	19	0.0215	1.0000000	E
<input type="radio"/>	GO:0006163	6	purine nucleotide metabolic process	47	0.0073	9	0.0102	1.0000000	E
<input type="radio"/>	GO:0030384	8,9	phosphoinositide metabolic process	43	0.0066	7	0.0079	1.0000000	E
<input type="radio"/>	GO:0000433	12,10,11,8	negative regulation of transcription from RNA polymerase II promoter by glucose	7	0.0011	2	0.0023	1.0000000	E
<input type="radio"/>	GO:0031344	4,6,8,7,5,9	regulation of cell projection organization and biogenesis	6	0.0009	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0007188	8,9	G-protein signaling, coupled to cAMP nucleotide second messenger	5	0.0008	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0006298	7,9,6	mismatch repair	25	0.0039	4	0.0045	1.0000000	E
<input type="radio"/>	GO:0042770	5	DNA damage response, signal transduction	14	0.0022	2	0.0023	1.0000000	E
<input type="radio"/>	GO:0000090	7,8,9,6	mitotic anaphase	6	0.0009	2	0.0023	1.0000000	E
<input type="radio"/>	GO:0032502	2	developmental process	436	0.0673	73	0.0826	1.0000000	E
<input type="radio"/>	GO:0044242	5,6	cellular lipid catabolic process	8	0.0012	2	0.0023	1.0000000	E
<input type="radio"/>	GO:0048024	9,8,11	regulation of nuclear mRNA splicing, via spliceosome	3	0.0005	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0016054	5	organic acid catabolic process	6	0.0009	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0007130	11,9,8,6,5,10,7,4	synaptonemal complex assembly	6	0.0009	2	0.0023	1.0000000	E
<input type="radio"/>	GO:0000103	6	sulfate assimilation	10	0.0015	3	0.0034	1.0000000	E
<input type="radio"/>	GO:0045229	4	external encapsulating structure organization and biogenesis	200	0.0309	34	0.0385	1.0000000	E
<input type="radio"/>	GO:0006097	6,8	glyoxylate cycle	4	0.0006	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0009076	7,8	histidine family amino acid biosynthetic process	14	0.0022	3	0.0034	1.0000000	E
<input type="radio"/>	GO:0043173	5	nucleotide salvage	4	0.0006	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0009893	5,4	positive regulation of metabolic process	116	0.0179	21	0.0238	1.0000000	E
<input type="radio"/>	GO:0046578	7,8,6	regulation of Ras protein signal transduction	6	0.0009	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0019236	4	response to pheromone	94	0.0145	14	0.0158	1.0000000	E
<input type="radio"/>	GO:0042546	6	cell wall biogenesis	33	0.0051	5	0.0057	1.0000000	E
<input type="radio"/>	GO:0009065	7,8	glutamine family amino acid catabolic process	13	0.0020	3	0.0034	1.0000000	E
<input type="radio"/>	GO:0019509	7,8,6,9	methionine salvage	3	0.0005	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0030541	4	plasmid partitioning	3	0.0005	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0000080	7,8,6	G1 phase of mitotic cell cycle	27	0.0042	7	0.0079	1.0000000	E
<input type="radio"/>	GO:0030004	9,7	cellular monovalent inorganic cation homeostasis	34	0.0053	6	0.0068	1.0000000	E
<input type="radio"/>	GO:0046854	7,9,8,10	phosphoinositide phosphorylation	5	0.0008	2	0.0023	1.0000000	E
<input type="radio"/>	GO:0006766	4	vitamin metabolic process	89	0.0137	19	0.0215	1.0000000	E

<input type="radio"/>	GO:0046839	6,7	phospholipid dephosphorylation	7	0.0011	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0032447	9	protein urmylation	5	0.0008	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0006116	10,9	NADH oxidation	11	0.0017	2	0.0023	1.0000000	E
<input type="radio"/>	GO:0007186	6	G-protein coupled receptor protein signaling pathway	34	0.0053	5	0.0057	1.0000000	E
<input type="radio"/>	GO:0006109	5,4	regulation of carbohydrate metabolic process	29	0.0045	4	0.0045	1.0000000	E
<input type="radio"/>	GO:0046580	8,9,7	negative regulation of Ras protein signal transduction	6	0.0009	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0043241	6,5	protein complex disassembly	28	0.0043	4	0.0045	1.0000000	E
<input type="radio"/>	GO:0006434	9,8,10,7	seryl-tRNA aminoacylation	2	0.0003	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0009220	7,8	pyrimidine ribonucleotide biosynthetic process	2	0.0003	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0046015	10,8,9,6	regulation of transcription by glucose	8	0.0012	2	0.0023	1.0000000	E
<input type="radio"/>	GO:0000350	8,7,10,12	generation of catalytic spliceosome for second transesterification step	4	0.0006	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0007005	5	mitochondrion organization and biogenesis	110	0.0170	17	0.0192	1.0000000	E
<input type="radio"/>	GO:0051028	5,7,6,8	mRNA transport	66	0.0102	18	0.0204	1.0000000	E
<input type="radio"/>	GO:0030029	6	actin filament-based process	112	0.0173	18	0.0204	1.0000000	E
<input type="radio"/>	GO:0009615	4,5	response to virus	7	0.0011	4	0.0045	1.0000000	E
<input type="radio"/>	GO:0031324	6,5	negative regulation of cellular metabolic process	198	0.0306	37	0.0419	1.0000000	E
<input type="radio"/>	GO:0006231	9,10	dTMP biosynthetic process	1	0.0002	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0032973	6,7,8	amino acid export	3	0.0005	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0007234	7,6	osmosensory signaling pathway via two-component system	3	0.0005	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0006461	6,5	protein complex assembly	116	0.0179	20	0.0226	1.0000000	E
<input type="radio"/>	GO:0017183	10,4	peptidyl-diphthamide biosynthetic process from peptidyl-histidine	5	0.0008	3	0.0034	1.0000000	E
<input type="radio"/>	GO:0018256	8	protein amino acid formylation	1	0.0002	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0015771	6,7,8	trehalose transport	1	0.0002	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0000096	6,7,5	sulfur amino acid metabolic process	33	0.0051	11	0.0124	1.0000000	E
<input type="radio"/>	GO:0007097	7,8,5,6	nuclear migration	20	0.0031	7	0.0079	1.0000000	E
<input type="radio"/>	GO:0016570	10,8	histone modification	91	0.0141	17	0.0192	1.0000000	E
<input type="radio"/>	GO:0015918	5,6	sterol transport	15	0.0023	3	0.0034	1.0000000	E
<input type="radio"/>	GO:0006280	6	mutagenesis	9	0.0014	3	0.0034	1.0000000	E
<input type="radio"/>	GO:0006791	5	sulfur utilization	10	0.0015	3	0.0034	1.0000000	E
<input type="radio"/>	GO:0051452	12,9,10	cellular pH reduction	24	0.0037	5	0.0057	1.0000000	E
<input type="radio"/>	GO:0031279	5	regulation of cyclase activity	2	0.0003	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0006631	5,7,6	fatty acid metabolic process	47	0.0073	13	0.0147	1.0000000	E
<input type="radio"/>	GO:0016310	6	phosphorylation	155	0.0239	25	0.0283	1.0000000	E
<input type="radio"/>	GO:0000437	11,9,10,7	negative regulation of transcription from RNA polymerase II promoter by carbon catabolites	7	0.0011	2	0.0023	1.0000000	E
<input type="radio"/>	GO:0006694	6,5,7	steroid biosynthetic process	32	0.0049	6	0.0068	1.0000000	E
<input type="radio"/>	GO:0051351	6	positive regulation of ligase activity	3	0.0005	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0043393	5	regulation of protein binding	1	0.0002	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0016049	5,3,7,8	cell growth	102	0.0158	15	0.0170	1.0000000	E
<input type="radio"/>	GO:0006267	8,7	pre-replicative complex assembly	15	0.0023	3	0.0034	1.0000000	E
<input type="radio"/>	GO:0009126	7	purine nucleoside monophosphate metabolic process	18	0.0028	5	0.0057	1.0000000	E
<input type="radio"/>	GO:0030809	9,7,8,6	negative regulation of nucleotide biosynthetic process	2	0.0003	1	0.0011	1.0000000	E

<input type="radio"/>	GO:0031120	8	snRNA pseudouridine synthesis	7	0.0011	3	0.0034	1.0000000	E
<input type="radio"/>	GO:0009129	7	pyrimidine nucleoside monophosphate metabolic process	1	0.0002	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0006811	4,5	ion transport	115	0.0178	21	0.0238	1.0000000	E
<input type="radio"/>	GO:0000771	6,4	agglutination	4	0.0006	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0006513	10	protein monoubiquitination	22	0.0034	4	0.0045	1.0000000	E
<input type="radio"/>	GO:0006474	10,9	N-terminal protein amino acid acetylation	9	0.0014	3	0.0034	1.0000000	E
<input type="radio"/>	GO:0006580	5,7,8	ethanolamine metabolic process	4	0.0006	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0000746	3	conjugation	118	0.0182	22	0.0249	1.0000000	E
<input type="radio"/>	GO:0009221	7,8	pyrimidine deoxyribonucleotide biosynthetic process	2	0.0003	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0000070	9,7,5,8,6,4	mitotic sister chromatid segregation	59	0.0091	12	0.0136	1.0000000	E
<input type="radio"/>	GO:0048522	5,4	positive regulation of cellular process	124	0.0191	21	0.0238	1.0000000	E
<input type="radio"/>	GO:0045005	8,6	maintenance of fidelity during DNA-dependent DNA replication	25	0.0039	4	0.0045	1.0000000	E
<input type="radio"/>	GO:0046467	6,5,7	membrane lipid biosynthetic process	78	0.0120	12	0.0136	1.0000000	E
<input type="radio"/>	GO:0048590	3	non-developmental growth	35	0.0054	5	0.0057	1.0000000	E
<input type="radio"/>	GO:0009092	7,8	homoserine metabolic process	7	0.0011	2	0.0023	1.0000000	E
<input type="radio"/>	GO:0043681	6,7,8	protein import into mitochondrion	40	0.0062	6	0.0068	1.0000000	E
<input type="radio"/>	GO:0009156	7,8	ribonucleoside monophosphate biosynthetic process	15	0.0023	4	0.0045	1.0000000	E
<input type="radio"/>	GO:0042542	6	response to hydrogen peroxide	4	0.0006	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0007346	7,5,6	regulation of progression through mitotic cell cycle	13	0.0020	3	0.0034	1.0000000	E
<input type="radio"/>	GO:0046021	10,8,5,6,9,7,4	regulation of transcription from RNA polymerase II promoter, mitotic	6	0.0009	2	0.0023	1.0000000	E
<input type="radio"/>	GO:0007154	3	cell communication	240	0.0371	41	0.0464	1.0000000	E
<input type="radio"/>	GO:0051707	3,4	response to other organism	7	0.0011	4	0.0045	1.0000000	E
<input type="radio"/>	GO:0046516	6	hypusine metabolic process	2	0.0003	2	0.0023	1.0000000	E
<input type="radio"/>	GO:0050686	9,8	negative regulation of mRNA processing	1	0.0002	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0032218	5,6	riboflavin transport	1	0.0002	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0046834	6,7	lipid phosphorylation	5	0.0008	2	0.0023	1.0000000	E
<input type="radio"/>	GO:0030803	10,8,9,7	negative regulation of cyclic nucleotide biosynthetic process	2	0.0003	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0009166	5,6	nucleotide catabolic process	7	0.0011	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0006768	5,7,6	biotin metabolic process	7	0.0011	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0006171	7,8	cAMP biosynthetic process	2	0.0003	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0044255	4,5	cellular lipid metabolic process	229	0.0354	40	0.0452	1.0000000	E
<input type="radio"/>	GO:0019220	7,6	regulation of phosphate metabolic process	7	0.0011	2	0.0023	1.0000000	E
<input type="radio"/>	GO:0000767	6,7	cellular morphogenesis during conjugation	20	0.0031	3	0.0034	1.0000000	E
<input type="radio"/>	GO:0043624	7,6	cellular protein complex disassembly	28	0.0043	4	0.0045	1.0000000	E
<input type="radio"/>	GO:0019754	5	one-carbon compound catabolic process	3	0.0005	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0006812	5,6	cation transport	97	0.0150	15	0.0170	1.0000000	E
<input type="radio"/>	GO:0006384	8,9,7	transcription initiation from RNA polymerase III promoter	11	0.0017	2	0.0023	1.0000000	E
<input type="radio"/>	GO:0009749	7,6	response to glucose stimulus	5	0.0008	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0045991	10,8,9,6	positive regulation of transcription by carbon catabolites	5	0.0008	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0001301	9,5	progressive alteration of chromatin during cell aging	10	0.0015	3	0.0034	1.0000000	E
<input type="radio"/>	GO:0000003	2	reproduction	323	0.0499	59	0.0667	1.0000000	E
<input type="radio"/>	GO:0051339	5	regulation of lyase activity	2	0.0003	1	0.0011	1.0000000	E

<input type="radio"/>	GO:0007067	8,6,7,5	mitosis	127	0.0196	23	0.0260	1.0000000	E
<input type="radio"/>	GO:0000017	6,7	alpha-glucoside transport	5	0.0008	2	0.0023	1.0000000	E
<input type="radio"/>	GO:0006383	8,7	transcription from RNA polymerase III promoter	38	0.0059	12	0.0136	1.0000000	E
<input type="radio"/>	GO:0006875	9,7	cellular metal ion homeostasis	19	0.0029	4	0.0045	1.0000000	E
<input type="radio"/>	GO:0006885	7	regulation of pH	29	0.0045	5	0.0057	1.0000000	E
<input type="radio"/>	GO:0006816	7,8	calcium ion transport	5	0.0008	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0006998	5,6	nuclear membrane organization and biogenesis	7	0.0011	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0006405	10,8,5,7,9,6	RNA export from nucleus	79	0.0122	20	0.0226	1.0000000	E
<input type="radio"/>	GO:0006793	4	phosphorus metabolic process	212	0.0327	35	0.0396	1.0000000	E
<input type="radio"/>	GO:0016571	11,9,10,8	histone methylation	18	0.0028	4	0.0045	1.0000000	E
<input type="radio"/>	GO:0017196	11,9,10	N-terminal peptidyl-methionine acetylation	3	0.0005	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0018022	9,10,8	peptidyl-lysine methylation	3	0.0005	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0006083	7	acetate metabolic process	6	0.0009	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0001558	5,6,4,8,9	regulation of cell growth	11	0.0017	2	0.0023	1.0000000	E
<input type="radio"/>	GO:0031325	6,5	positive regulation of cellular metabolic process	116	0.0179	21	0.0238	1.0000000	E
<input type="radio"/>	GO:0006873	7,5	cellular ion homeostasis	115	0.0178	20	0.0226	1.0000000	E
<input type="radio"/>	GO:0030488	8,9	tRNA methylation	15	0.0023	6	0.0068	1.0000000	E
<input type="radio"/>	GO:0006612	9,7,8	protein targeting to membrane	39	0.0060	6	0.0068	1.0000000	E
<input type="radio"/>	GO:0006281	6,5	DNA repair	193	0.0298	33	0.0373	1.0000000	E
<input type="radio"/>	GO:0006874	10,8	cellular calcium ion homeostasis	9	0.0014	2	0.0023	1.0000000	E
<input type="radio"/>	GO:0006167	9,10	AMP biosynthetic process	1	0.0002	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0007243	6	protein kinase cascade	23	0.0036	5	0.0057	1.0000000	E
<input type="radio"/>	GO:0032261	6,7	purine nucleotide salvage	2	0.0003	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0009396	6,7,8	folic acid and derivative biosynthetic process	6	0.0009	2	0.0023	1.0000000	E
<input type="radio"/>	GO:0043101	5	purine salvage	9	0.0014	3	0.0034	1.0000000	E
<input type="radio"/>	GO:0006261	7	DNA-dependent DNA replication	97	0.0150	18	0.0204	1.0000000	E
<input type="radio"/>	GO:0006760	5,7	folic acid and derivative metabolic process	9	0.0014	3	0.0034	1.0000000	E
<input type="radio"/>	GO:0009068	7,8	aspartate family amino acid catabolic process	10	0.0015	2	0.0023	1.0000000	E
<input type="radio"/>	GO:0008298	5	intracellular mRNA localization	10	0.0015	2	0.0023	1.0000000	E
<input type="radio"/>	GO:0008156	9,8	negative regulation of DNA replication	8	0.0012	2	0.0023	1.0000000	E
<input type="radio"/>	GO:0006278	7	RNA-dependent DNA replication	4	0.0006	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0050000	6,5	chromosome localization	4	0.0006	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0006512	8	ubiquitin cycle	88	0.0136	14	0.0158	1.0000000	E
<input type="radio"/>	GO:0048228	6,9,8,5	actin cortical patch distribution	1	0.0002	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0051329	7,5,6	interphase of mitotic cell cycle	112	0.0173	18	0.0204	1.0000000	E
<input type="radio"/>	GO:0008361	4,6,7	regulation of cell size	129	0.0199	20	0.0226	1.0000000	E
<input type="radio"/>	GO:0007131	10,8,7,5,9,6,4	meiotic recombination	55	0.0085	11	0.0124	1.0000000	E
<input type="radio"/>	GO:0006118	4	electron transport	33	0.0051	5	0.0057	1.0000000	E
<input type="radio"/>	GO:0007232	7,6	osmosensory signaling pathway via Sho1 osmosensor	5	0.0008	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0048869	3	cellular developmental process	173	0.0267	31	0.0351	1.0000000	E
<input type="radio"/>	GO:0045898	11,4,8,10,7	regulation of transcriptional preinitiation complex assembly	1	0.0002	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0045132	9,7,8,6,4	meiotic chromosome segregation	17	0.0026	4	0.0045	1.0000000	E
<input type="radio"/>	GO:0042440	4	pigment metabolic process	20	0.0031	3	0.0034	1.0000000	E

<input type="checkbox"/>	GO:0030258	5,6	lipid modification	13	0.0020	4	0.0045	1.0000000	E
<input type="checkbox"/>	GO:0006720	5,6	isoprenoid metabolic process	6	0.0009	2	0.0023	1.0000000	E
<input type="checkbox"/>	GO:0009218	7	pyrimidine ribonucleotide metabolic process	2	0.0003	1	0.0011	1.0000000	E
<input type="checkbox"/>	GO:0033205	5,4	cytokinesis during cell cycle	7	0.0011	2	0.0023	1.0000000	E
<input type="checkbox"/>	GO:0042762	6,5	regulation of sulfur metabolic process	1	0.0002	1	0.0011	1.0000000	E
<input type="checkbox"/>	GO:0019354	8,7,9	siroheme biosynthetic process	2	0.0003	1	0.0011	1.0000000	E
<input type="checkbox"/>	GO:0006464	6	protein modification process	520	0.0803	84	0.0950	1.0000000	E
<input type="checkbox"/>	GO:0046655	6,8	folic acid metabolic process	2	0.0003	1	0.0011	1.0000000	E
<input type="checkbox"/>	GO:0042724	7	thiamin and derivative biosynthetic process	20	0.0031	6	0.0068	1.0000000	E
<input type="checkbox"/>	GO:0032984	5	macromolecular complex disassembly	32	0.0049	5	0.0057	1.0000000	E
<input type="checkbox"/>	GO:0001304	10,6	progressive alteration of chromatin during replicative cell aging	9	0.0014	2	0.0023	1.0000000	E
<input type="checkbox"/>	GO:0019722	7	calcium-mediated signaling	7	0.0011	2	0.0023	1.0000000	E
<input type="checkbox"/>	GO:0009190	6,7	cyclic nucleotide biosynthetic process	2	0.0003	1	0.0011	1.0000000	E
<input type="checkbox"/>	GO:0006098	9,10,11	pentose-phosphate shunt	11	0.0017	3	0.0034	1.0000000	E
<input type="checkbox"/>	GO:0046040	9	IMP metabolic process	14	0.0022	3	0.0034	1.0000000	E
<input type="checkbox"/>	GO:0000916	6,5,4	cytokinesis, contractile ring contraction	4	0.0006	1	0.0011	1.0000000	E
<input type="checkbox"/>	GO:0000349	8,7,10,12	generation of catalytic spliceosome for first transesterification step	4	0.0006	1	0.0011	1.0000000	E
<input type="checkbox"/>	GO:0031109	8	microtubule polymerization or depolymerization	16	0.0025	3	0.0034	1.0000000	E
<input type="checkbox"/>	GO:0006425	9,8,10,7	glutaminyl-tRNA aminoacylation	1	0.0002	1	0.0011	1.0000000	E
<input type="checkbox"/>	GO:0030641	10,8	cellular hydrogen ion homeostasis	25	0.0039	5	0.0057	1.0000000	E
<input type="checkbox"/>	GO:0006676	8,10,9,11	mannosyl diphosphorylinositol ceramide metabolic process	1	0.0002	1	0.0011	1.0000000	E
<input type="checkbox"/>	GO:0008652	6,7	amino acid biosynthetic process	106	0.0164	20	0.0226	1.0000000	E
<input type="checkbox"/>	GO:0045814	5	negative regulation of gene expression, epigenetic	95	0.0147	19	0.0215	1.0000000	E
<input type="checkbox"/>	GO:0006973	6,4	intracellular accumulation of glycerol	1	0.0002	1	0.0011	1.0000000	E
<input type="checkbox"/>	GO:0016126	6,7,8	sterol biosynthetic process	32	0.0049	6	0.0068	1.0000000	E
<input type="checkbox"/>	GO:0030969	8,6,7	UFP-specific transcription factor mRNA processing during unfolded protein response	2	0.0003	1	0.0011	1.0000000	E
<input type="checkbox"/>	GO:0055080	7	cation homeostasis	102	0.0158	19	0.0215	1.0000000	E
<input type="checkbox"/>	GO:0040029	4	regulation of gene expression, epigenetic	100	0.0154	19	0.0215	1.0000000	E
<input type="checkbox"/>	GO:0009165	5,6	nucleotide biosynthetic process	59	0.0091	14	0.0158	1.0000000	E
<input type="checkbox"/>	GO:0045910	9,8	negative regulation of DNA recombination	12	0.0019	2	0.0023	1.0000000	E
<input type="checkbox"/>	GO:0006352	7,8,6	transcription initiation	55	0.0085	11	0.0124	1.0000000	E
<input type="checkbox"/>	GO:0006168	8,7	adenine salvage	1	0.0002	1	0.0011	1.0000000	E
<input type="checkbox"/>	GO:0016042	4,5	lipid catabolic process	8	0.0012	2	0.0023	1.0000000	E
<input type="checkbox"/>	GO:0006325	7	establishment and/or maintenance of chromatin architecture	253	0.0391	43	0.0486	1.0000000	E
<input type="checkbox"/>	GO:0009067	7,8	aspartate family amino acid biosynthetic process	20	0.0031	3	0.0034	1.0000000	E
<input type="checkbox"/>	GO:0009605	3	response to external stimulus	37	0.0057	6	0.0068	1.0000000	E
<input type="checkbox"/>	GO:0000041	7,8	transition metal ion transport	46	0.0071	10	0.0113	1.0000000	E
<input type="checkbox"/>	GO:0030705	7,5,6	cytoskeleton-dependent intracellular transport	17	0.0026	5	0.0057	1.0000000	E
<input type="checkbox"/>	GO:0046395	6	carboxylic acid catabolic process	4	0.0006	1	0.0011	1.0000000	E
<input type="checkbox"/>	GO:0045860	7,8	positive regulation of protein kinase activity	6	0.0009	1	0.0011	1.0000000	E
<input type="checkbox"/>	GO:0006075	9,8,10	1,3-beta-glucan biosynthetic process	4	0.0006	1	0.0011	1.0000000	E

<input type="checkbox"/>	GO:0051293	6,7,8,4,5	establishment of spindle localization	10	0.0015	2	0.0023	1.0000000	E
<input type="checkbox"/>	GO:0032508	7	DNA duplex unwinding	16	0.0025	3	0.0034	1.0000000	E
<input type="checkbox"/>	GO:0009124	6,7	nucleoside monophosphate biosynthetic process	17	0.0026	5	0.0057	1.0000000	E
<input type="checkbox"/>	GO:0006303	8,7	double-strand break repair via nonhomologous end joining	23	0.0036	4	0.0045	1.0000000	E
<input type="checkbox"/>	GO:0009607	3	response to biotic stimulus	25	0.0039	6	0.0068	1.0000000	E
<input type="checkbox"/>	GO:0046475	8,9	glycerophospholipid catabolic process	3	0.0005	1	0.0011	1.0000000	E
<input type="checkbox"/>	GO:0055082	6,4	cellular chemical homeostasis	115	0.0178	20	0.0226	1.0000000	E
<input type="checkbox"/>	GO:0019953	3	sexual reproduction	118	0.0182	22	0.0249	1.0000000	E
<input type="checkbox"/>	GO:0019935	7	cyclic-nucleotide-mediated signaling	9	0.0014	2	0.0023	1.0000000	E
<input type="checkbox"/>	GO:0032258	10,9,8,7	CVT pathway	4	0.0006	1	0.0011	1.0000000	E
<input type="checkbox"/>	GO:0006541	7,8	glutamine metabolic process	2	0.0003	1	0.0011	1.0000000	E
<input type="checkbox"/>	GO:0042816	6	vitamin B6 metabolic process	8	0.0012	5	0.0057	1.0000000	E
<input type="checkbox"/>	GO:0000105	8,9	histidine biosynthetic process	14	0.0022	3	0.0034	1.0000000	E
<input type="checkbox"/>	GO:0051253	8,7	negative regulation of RNA metabolic process	1	0.0002	1	0.0011	1.0000000	E
<input type="checkbox"/>	GO:0065009	3	regulation of a molecular function	46	0.0071	8	0.0090	1.0000000	E
<input type="checkbox"/>	GO:0007019	9,7	microtubule depolymerization	6	0.0009	1	0.0011	1.0000000	E
<input type="checkbox"/>	GO:0051179	2	localization	1051	0.1623	169	0.1912	1.0000000	E
<input type="checkbox"/>	GO:0006438	9,8,10,7	valyl-tRNA aminoacylation	1	0.0002	1	0.0011	1.0000000	E
<input type="checkbox"/>	GO:0009157	7,8	deoxyribonucleoside monophosphate biosynthetic process	1	0.0002	1	0.0011	1.0000000	E
<input type="checkbox"/>	GO:0006366	8,7	transcription from RNA polymerase II promoter	343	0.0530	64	0.0724	1.0000000	E
<input type="checkbox"/>	GO:0000376	9	RNA splicing, via transesterification reactions with guanosine as nucleophile	7	0.0011	1	0.0011	1.0000000	E
<input type="checkbox"/>	GO:0015793	5,6	glycerol transport	4	0.0006	2	0.0023	1.0000000	E
<input type="checkbox"/>	GO:0030010	7,4,8	establishment of cell polarity	103	0.0159	17	0.0192	1.0000000	E
<input type="checkbox"/>	GO:0015757	7,8	galactose transport	2	0.0003	1	0.0011	1.0000000	E
<input type="checkbox"/>	GO:0009262	6	deoxyribonucleotide metabolic process	9	0.0014	3	0.0034	1.0000000	E
<input type="checkbox"/>	GO:0051058	7,8,6	negative regulation of small GTPase mediated signal transduction	6	0.0009	1	0.0011	1.0000000	E
<input type="checkbox"/>	GO:0046156	7,8,6	siroheme metabolic process	2	0.0003	1	0.0011	1.0000000	E
<input type="checkbox"/>	GO:0031935	11,7,4,8,12,10	regulation of chromatin silencing	6	0.0009	1	0.0011	1.0000000	E
<input type="checkbox"/>	GO:0046337	5,7,8	phosphatidylethanolamine metabolic process	4	0.0006	1	0.0011	1.0000000	E
<input type="checkbox"/>	GO:0009086	8,9,7	methionine biosynthetic process	7	0.0011	3	0.0034	1.0000000	E
<input type="checkbox"/>	GO:0019363	7,6,8	pyridine nucleotide biosynthetic process	10	0.0015	3	0.0034	1.0000000	E
<input type="checkbox"/>	GO:0009264	6,7	deoxyribonucleotide catabolic process	5	0.0008	1	0.0011	1.0000000	E
<input type="checkbox"/>	GO:0006833	5,6	water transport	3	0.0005	1	0.0011	1.0000000	E
<input type="checkbox"/>	GO:0045944	10,9	positive regulation of transcription from RNA polymerase II promoter	76	0.0117	12	0.0136	1.0000000	E
<input type="checkbox"/>	GO:0051294	7,8,9,5,6	establishment of spindle orientation	10	0.0015	2	0.0023	1.0000000	E
<input type="checkbox"/>	GO:0046466	6,7	membrane lipid catabolic process	4	0.0006	1	0.0011	1.0000000	E
<input type="checkbox"/>	GO:0006635	7,9,8	fatty acid beta-oxidation	9	0.0014	4	0.0045	1.0000000	E
<input type="checkbox"/>	GO:0042886	4,5	amide transport	2	0.0003	1	0.0011	1.0000000	E
<input type="checkbox"/>	GO:0006790	4	sulfur metabolic process	67	0.0103	14	0.0158	1.0000000	E
<input type="checkbox"/>	GO:0016560	8,11,10,7,9	protein import into peroxisome matrix, docking	5	0.0008	1	0.0011	1.0000000	E
<input type="checkbox"/>	GO:0015846	5,6	polyamine transport	12	0.0019	4	0.0045	1.0000000	E
<input type="checkbox"/>	GO:0016073	6	snRNA metabolic process	15	0.0023	7	0.0079	1.0000000	E

<input type="radio"/>	GO:0000393	7,6,9,11	spliceosomal conformational changes to generate catalytic conformation	9	0.0014	2	0.0023	1.0000000	E
<input type="radio"/>	GO:0006673	7,9,8,10	inositolphosphoceramide metabolic process	2	0.0003	1	0.0011	1.0000000	E
<input type="radio"/>	GO:0032989	4,5	cellular structure morphogenesis	248	0.0383	40	0.0452	1.0000000	E
<input type="radio"/>	GO:0042221	3	response to chemical stimulus	382	0.0590	55	0.0622	1.0000000	E
<input type="radio"/>	GO:0006407	11,9,6,8,10,7	rRNA export from nucleus	26	0.0040	7	0.0079	1.0000000	E
<input type="radio"/>	GO:0043412	5	biopolymer modification	664	0.1025	111	0.1256	1.0000000	E
<input type="radio"/>	GO:0030473	8,9,6,7	nuclear migration, microtubule-mediated	15	0.0023	5	0.0057	1.0000000	E
<input type="radio"/>	GO:0009145	7,8	purine nucleoside triphosphate biosynthetic process	22	0.0034	3	0.0034	1.0000000	D
<input type="radio"/>	GO:0046219	7,8,6	indolalkylamine biosynthetic process	10	0.0015	1	0.0011	1.0000000	D
<input type="radio"/>	GO:0043161	10,9,11	proteasomal ubiquitin-dependent protein catabolic process	63	0.0097	7	0.0079	1.0000000	D
<input type="radio"/>	GO:0006511	9,8,10	ubiquitin-dependent protein catabolic process	148	0.0229	14	0.0158	1.0000000	D
<input type="radio"/>	GO:0015980	4	energy derivation by oxidation of organic compounds	145	0.0224	13	0.0147	1.0000000	D
<input type="radio"/>	GO:0006753	7	nucleoside phosphate metabolic process	20	0.0031	1	0.0011	1.0000000	D
<input type="radio"/>	GO:0007531	4,6,5	mating type determination	35	0.0054	4	0.0045	1.0000000	D
<input type="radio"/>	GO:0009373	9,8,5	regulation of transcription by pheromones	10	0.0015	1	0.0011	1.0000000	D
<input type="radio"/>	GO:0001510	7	RNA methylation	60	0.0093	8	0.0090	1.0000000	D
<input type="radio"/>	GO:0043549	6	regulation of kinase activity	25	0.0039	2	0.0023	1.0000000	D
<input type="radio"/>	GO:0009056	3	catabolic process	438	0.0676	51	0.0577	1.0000000	D
<input type="radio"/>	GO:0031023	5	microtubule organizing center organization and biogenesis	16	0.0025	2	0.0023	1.0000000	D
<input type="radio"/>	GO:0019318	6,7	hexose metabolic process	85	0.0131	8	0.0090	1.0000000	D
<input type="radio"/>	GO:0010038	5	response to metal ion	18	0.0028	2	0.0023	1.0000000	D
<input type="radio"/>	GO:0006897	6,5	endocytosis	86	0.0133	11	0.0124	1.0000000	D
<input type="radio"/>	GO:0009070	7,8	serine family amino acid biosynthetic process	12	0.0019	1	0.0011	1.0000000	D
<input type="radio"/>	GO:0006271	8,7	DNA strand elongation during DNA replication	32	0.0049	4	0.0045	1.0000000	D
<input type="radio"/>	GO:0016051	5	carbohydrate biosynthetic process	77	0.0119	7	0.0079	1.0000000	D
<input type="radio"/>	GO:0044260	4	cellular macromolecule metabolic process	1552	0.2397	181	0.2048	1.0000000	D
<input type="radio"/>	GO:0006067	5	ethanol metabolic process	12	0.0019	1	0.0011	1.0000000	D
<input type="radio"/>	GO:0051049	5,4	regulation of transport	11	0.0017	1	0.0011	1.0000000	D
<input type="radio"/>	GO:0045859	7	regulation of protein kinase activity	25	0.0039	2	0.0023	1.0000000	D
<input type="radio"/>	GO:0046364	6,7	monosaccharide biosynthetic process	30	0.0046	2	0.0023	1.0000000	D
<input type="radio"/>	GO:0048278	4,5,6	vesicle docking	14	0.0022	1	0.0011	1.0000000	D
<input type="radio"/>	GO:0000086	8,5,6,7,4	G2/M transition of mitotic cell cycle	35	0.0054	2	0.0023	1.0000000	D
<input type="radio"/>	GO:0008150	1	biological process	6476	1.0000	884	1.0000	1.0000000	D
<input type="radio"/>	GO:0009651	5	response to salt stress	15	0.0023	2	0.0023	1.0000000	D
<input type="radio"/>	GO:0042435	7,5	indole derivative biosynthetic process	10	0.0015	1	0.0011	1.0000000	D
<input type="radio"/>	GO:0007533	5,7,6	mating type switching	29	0.0045	2	0.0023	1.0000000	D
<input type="radio"/>	GO:0022610	2	biological adhesion	9	0.0014	1	0.0011	1.0000000	D
<input type="radio"/>	GO:0016192	4,5	vesicle-mediated transport	328	0.0506	32	0.0362	1.0000000	D
<input type="radio"/>	GO:0016311	6	dephosphorylation	41	0.0063	4	0.0045	1.0000000	D
<input type="radio"/>	GO:0016197	7,5,6	endosome transport	49	0.0076	5	0.0057	1.0000000	D
<input type="radio"/>	GO:0043162	10,9,11	ubiquitin-dependent protein catabolic process via the multivesicular body pathway	16	0.0025	2	0.0023	1.0000000	D
<input type="radio"/>	GO:0051052	7,6	regulation of DNA metabolic process	41	0.0063	5	0.0057	1.0000000	D

<input type="radio"/>	GO:0006066	4	alcohol metabolic process	163	0.0252	17	0.0192	1.0000000	D
<input type="radio"/>	GO:0000288	10,8,9	mRNA catabolic process, deadenylation-dependent decay	24	0.0037	1	0.0011	1.0000000	D
<input type="radio"/>	GO:0000271	6,7	polysaccharide biosynthetic process	41	0.0063	4	0.0045	1.0000000	D
<input type="radio"/>	GO:0007568	3	aging	49	0.0076	6	0.0068	1.0000000	D
<input type="radio"/>	GO:0009108	6	coenzyme biosynthetic process	66	0.0102	7	0.0079	1.0000000	D
<input type="radio"/>	GO:0006042	7,8	glucosamine biosynthetic process	17	0.0026	2	0.0023	1.0000000	D
<input type="radio"/>	GO:0000154	7,8	rRNA modification	85	0.0131	7	0.0079	1.0000000	D
<input type="radio"/>	GO:0000082	8,5,6,7,4	G1/S transition of mitotic cell cycle	52	0.0080	7	0.0079	1.0000000	D
<input type="radio"/>	GO:0043086	5	negative regulation of enzyme activity	11	0.0017	1	0.0011	1.0000000	D
<input type="radio"/>	GO:0042278	6	purine nucleoside metabolic process	12	0.0019	1	0.0011	1.0000000	D
<input type="radio"/>	GO:0006090	7	pyruvate metabolic process	38	0.0059	3	0.0034	1.0000000	D
<input type="radio"/>	GO:0030847	10,9	transcription termination from Pol II promoter, RNA polymerase(A)-independent	9	0.0014	1	0.0011	1.0000000	D
<input type="radio"/>	GO:0006112	5	energy reserve metabolic process	39	0.0060	4	0.0045	1.0000000	D
<input type="radio"/>	GO:0007105	6,4	cytokinesis, site selection	66	0.0102	9	0.0102	1.0000000	D
<input type="radio"/>	GO:0006308	5,6	DNA catabolic process	20	0.0031	1	0.0011	1.0000000	D
<input type="radio"/>	GO:0051603	7,8	proteolysis involved in cellular protein catabolic process	151	0.0233	14	0.0158	1.0000000	D
<input type="radio"/>	GO:0022616	6	DNA strand elongation	32	0.0049	4	0.0045	1.0000000	D
<input type="radio"/>	GO:0046903	3,4	secretion	250	0.0386	27	0.0305	1.0000000	D
<input type="radio"/>	GO:0007020	8	microtubule nucleation	23	0.0036	2	0.0023	1.0000000	D
<input type="radio"/>	GO:0046128	7	purine ribonucleoside metabolic process	11	0.0017	1	0.0011	1.0000000	D
<input type="radio"/>	GO:0006906	6,5	vesicle fusion	28	0.0043	1	0.0011	1.0000000	D
<input type="radio"/>	GO:0051186	4	cofactor metabolic process	170	0.0263	20	0.0226	1.0000000	D
<input type="radio"/>	GO:0044257	6,7	cellular protein catabolic process	160	0.0247	14	0.0158	1.0000000	D
<input type="radio"/>	GO:0044275	6	cellular carbohydrate catabolic process	80	0.0124	5	0.0057	1.0000000	D
<input type="radio"/>	GO:0044248	4	cellular catabolic process	425	0.0656	50	0.0566	1.0000000	D
<input type="radio"/>	GO:0006644	6,7	phospholipid metabolic process	97	0.0150	13	0.0147	1.0000000	D
<input type="radio"/>	GO:0015985	6,8,7,9	energy coupled proton transport, down electrochemical gradient	20	0.0031	1	0.0011	1.0000000	D
<input type="radio"/>	GO:0044267	5	cellular protein metabolic process	1498	0.2313	175	0.1980	1.0000000	D
<input type="radio"/>	GO:0009058	3	biosynthetic process	1249	0.1929	155	0.1753	1.0000000	D
<input type="radio"/>	GO:0006487	9,8,7	protein amino acid N-linked glycosylation	48	0.0074	4	0.0045	1.0000000	D
<input type="radio"/>	GO:0006979	4	response to oxidative stress	71	0.0110	9	0.0102	1.0000000	D
<input type="radio"/>	GO:0051261	6	protein depolymerization	10	0.0015	1	0.0011	1.0000000	D
<input type="radio"/>	GO:0051235	3,2	maintenance of localization	33	0.0051	1	0.0011	1.0000000	D
<input type="radio"/>	GO:0008654	7,6,8	phospholipid biosynthetic process	58	0.0090	7	0.0079	1.0000000	D
<input type="radio"/>	GO:0006374	9,11	nuclear mRNA splicing via U2-type spliceosome	15	0.0023	2	0.0023	1.0000000	D
<input type="radio"/>	GO:0015893	4,5	drug transport	13	0.0020	1	0.0011	1.0000000	D
<input type="radio"/>	GO:0016237	4,6	microautophagy	11	0.0017	1	0.0011	1.0000000	D
<input type="radio"/>	GO:0043487	8,7	regulation of RNA stability	30	0.0046	3	0.0034	1.0000000	D
<input type="radio"/>	GO:0031118	8,9	rRNA pseudouridine synthesis	31	0.0048	1	0.0011	1.0000000	D
<input type="radio"/>	GO:0030468	8,5,9	establishment of cell polarity (sensu Fungi)	66	0.0102	9	0.0102	1.0000000	D
<input type="radio"/>	GO:0010035	4	response to inorganic substance	24	0.0037	2	0.0023	1.0000000	D
<input type="radio"/>	GO:0000079	8,7,6	regulation of cyclin-dependent protein kinase activity	15	0.0023	1	0.0011	1.0000000	D

<input type="checkbox"/>	GO:0006470	8,7	protein amino acid dephosphorylation	29	0.0045	2	0.0023	1.0000000	D
<input type="checkbox"/>	GO:0031570	8,7	DNA integrity checkpoint	18	0.0028	2	0.0023	1.0000000	D
<input type="checkbox"/>	GO:0006754	7,9,6,8,10	ATP biosynthetic process	20	0.0031	1	0.0011	1.0000000	D
<input type="checkbox"/>	GO:0045003	9,8	double-strand break repair via synthesis-dependent strand annealing	17	0.0026	1	0.0011	1.0000000	D
<input type="checkbox"/>	GO:0019740	4	nitrogen utilization	17	0.0026	2	0.0023	1.0000000	D
<input type="checkbox"/>	GO:0048468	3,5	cell development	52	0.0080	4	0.0045	1.0000000	D
<input type="checkbox"/>	GO:0006122	10,7,5	mitochondrial electron transport, ubiquinol to cytochrome c	9	0.0014	1	0.0011	1.0000000	D
<input type="checkbox"/>	GO:0046034	5,9	ATP metabolic process	21	0.0032	1	0.0011	1.0000000	D
<input type="checkbox"/>	GO:0031163	5	metallo-sulfur cluster assembly	11	0.0017	1	0.0011	1.0000000	D
<input type="checkbox"/>	GO:0006388	9,8	tRNA splicing	14	0.0022	1	0.0011	1.0000000	D
<input type="checkbox"/>	GO:0022406	3	membrane docking	14	0.0022	1	0.0011	1.0000000	D
<input type="checkbox"/>	GO:0009144	7	purine nucleoside triphosphate metabolic process	23	0.0036	3	0.0034	1.0000000	D
<input type="checkbox"/>	GO:0031669	6,5	cellular response to nutrient levels	19	0.0029	2	0.0023	1.0000000	D
<input type="checkbox"/>	GO:0006476	8	protein amino acid deacetylation	26	0.0040	3	0.0034	1.0000000	D
<input type="checkbox"/>	GO:0006818	4,5	hydrogen transport	24	0.0037	1	0.0011	1.0000000	D
<input type="checkbox"/>	GO:0042493	4	response to drug	121	0.0187	15	0.0170	1.0000000	D
<input type="checkbox"/>	GO:0030011	7,4,8	maintenance of cell polarity	8	0.0012	1	0.0011	1.0000000	D
<input type="checkbox"/>	GO:0009060	6	aerobic respiration	84	0.0130	5	0.0057	1.0000000	D
<input type="checkbox"/>	GO:0031137	6,5	regulation of conjugation with cellular fusion	30	0.0046	4	0.0045	1.0000000	D
<input type="checkbox"/>	GO:0045786	6,7,5	negative regulation of progression through cell cycle	13	0.0020	1	0.0011	1.0000000	D
<input type="checkbox"/>	GO:0043285	5	biopolymer catabolic process	277	0.0428	36	0.0407	1.0000000	D
<input type="checkbox"/>	GO:0044262	5	cellular carbohydrate metabolic process	213	0.0329	16	0.0181	1.0000000	D
<input type="checkbox"/>	GO:0000074	6,5	regulation of progression through cell cycle	167	0.0258	21	0.0238	1.0000000	D
<input type="checkbox"/>	GO:0006749	6,5	glutathione metabolic process	14	0.0022	1	0.0011	1.0000000	D
<input type="checkbox"/>	GO:0000394	8	RNA splicing, via endonucleolytic cleavage and ligation	14	0.0022	1	0.0011	1.0000000	D
<input type="checkbox"/>	GO:0032507	6,5,4	maintenance of cellular protein localization	29	0.0045	1	0.0011	1.0000000	D
<input type="checkbox"/>	GO:0007231	6,5	osmosensory signaling pathway	22	0.0034	2	0.0023	1.0000000	D
<input type="checkbox"/>	GO:0006040	5,6	amino sugar metabolic process	19	0.0029	2	0.0023	1.0000000	D
<input type="checkbox"/>	GO:0006855	5,6	multidrug transport	8	0.0012	1	0.0011	1.0000000	D
<input type="checkbox"/>	GO:0042773	8,5	ATP synthesis coupled electron transport	25	0.0039	2	0.0023	1.0000000	D
<input type="checkbox"/>	GO:0005978	8,7,9	glycogen biosynthetic process	15	0.0023	1	0.0011	1.0000000	D
<input type="checkbox"/>	GO:0006276	3	plasmid maintenance	11	0.0017	1	0.0011	1.0000000	D
<input type="checkbox"/>	GO:0006091	3	generation of precursor metabolites and energy	183	0.0283	19	0.0215	1.0000000	D
<input type="checkbox"/>	GO:0051651	5,4,3	maintenance of cellular localization	29	0.0045	1	0.0011	1.0000000	D
<input type="checkbox"/>	GO:0033554	4	cellular response to stress	21	0.0032	2	0.0023	1.0000000	D
<input type="checkbox"/>	GO:0006986	4,5	response to unfolded protein	18	0.0028	2	0.0023	1.0000000	D
<input type="checkbox"/>	GO:0006111	8,7,9,10,6	regulation of gluconeogenesis	13	0.0020	1	0.0011	1.0000000	D
<input type="checkbox"/>	GO:0046165	5	alcohol biosynthetic process	35	0.0054	2	0.0023	1.0000000	D
<input type="checkbox"/>	GO:0046365	6,7	monosaccharide catabolic process	44	0.0068	5	0.0057	1.0000000	D
<input type="checkbox"/>	GO:0007118	7,6,5	budding cell apical bud growth	14	0.0022	1	0.0011	1.0000000	D
<input type="checkbox"/>	GO:0007052	5,4,9	mitotic spindle organization and biogenesis	44	0.0068	6	0.0068	1.0000000	D
<input type="checkbox"/>	GO:0005984	6	disaccharide metabolic process	31	0.0048	1	0.0011	1.0000000	D

<input type="checkbox"/>	GO:0006888	8,6,5,7	ER to Golgi vesicle-mediated transport	81	0.0125	5	0.0057	1.0000000	D
<input type="checkbox"/>	GO:0009100	6	glycoprotein metabolic process	79	0.0122	7	0.0079	1.0000000	D
<input type="checkbox"/>	GO:0000903	6,4,8,7,9	cellular morphogenesis during vegetative growth	8	0.0012	1	0.0011	1.0000000	D
<input type="checkbox"/>	GO:0006950	3	response to stress	488	0.0754	64	0.0724	1.0000000	D
<input type="checkbox"/>	GO:0006119	7,4	oxidative phosphorylation	46	0.0071	3	0.0034	1.0000000	D
<input type="checkbox"/>	GO:0000302	5	response to reactive oxygen species	12	0.0019	1	0.0011	1.0000000	D
<input type="checkbox"/>	GO:0006486	8,7,6	protein amino acid glycosylation	73	0.0113	7	0.0079	1.0000000	D
<input type="checkbox"/>	GO:0046489	9,8,10	phosphoinositide biosynthetic process	28	0.0043	3	0.0034	1.0000000	D
<input type="checkbox"/>	GO:0009250	7,8	glucan biosynthetic process	25	0.0039	2	0.0023	1.0000000	D
<input type="checkbox"/>	GO:0006568	7,8,6	tryptophan metabolic process	10	0.0015	1	0.0011	1.0000000	D
<input type="checkbox"/>	GO:0006752	6	group transfer coenzyme metabolic process	44	0.0068	4	0.0045	1.0000000	D
<input type="checkbox"/>	GO:0015914	5,6	phospholipid transport	12	0.0019	1	0.0011	1.0000000	D
<input type="checkbox"/>	GO:0046349	6,7	amino sugar biosynthetic process	17	0.0026	2	0.0023	1.0000000	D
<input type="checkbox"/>	GO:0048858	6,7	cell projection morphogenesis	8	0.0012	1	0.0011	1.0000000	D
<input type="checkbox"/>	GO:0006613	10,9,8,7,6	cotranslational protein targeting to membrane	23	0.0036	2	0.0023	1.0000000	D
<input type="checkbox"/>	GO:0000002	6	mitochondrial genome maintenance	31	0.0048	2	0.0023	1.0000000	D
<input type="checkbox"/>	GO:0031668	5,4	cellular response to extracellular stimulus	19	0.0029	2	0.0023	1.0000000	D
<input type="checkbox"/>	GO:0006506	10,9,8,7,11	GPI anchor biosynthetic process	26	0.0040	3	0.0034	1.0000000	D
<input type="checkbox"/>	GO:0019538	4	protein metabolic process	1547	0.2389	182	0.2059	1.0000000	D
<input type="checkbox"/>	GO:0009206	8,9	purine ribonucleoside triphosphate biosynthetic process	22	0.0034	3	0.0034	1.0000000	D
<input type="checkbox"/>	GO:0051273	7,8	beta-glucan metabolic process	12	0.0019	1	0.0011	1.0000000	D
<input type="checkbox"/>	GO:0006272	9,8	leading strand elongation	14	0.0022	1	0.0011	1.0000000	D
<input type="checkbox"/>	GO:0007124	6,4,8,9	pseudohyphal growth	61	0.0094	8	0.0090	1.0000000	D
<input type="checkbox"/>	GO:0006123	10,7,5	mitochondrial electron transport, cytochrome c to oxygen	10	0.0015	1	0.0011	1.0000000	D
<input type="checkbox"/>	GO:0043413	6	biopolymer glycosylation	73	0.0113	7	0.0079	1.0000000	D
<input type="checkbox"/>	GO:0046019	10,9,6	regulation of transcription from RNA polymerase II promoter by pheromones	10	0.0015	1	0.0011	1.0000000	D
<input type="checkbox"/>	GO:0006041	6,7	glucosamine metabolic process	19	0.0029	2	0.0023	1.0000000	D
<input type="checkbox"/>	GO:0006031	9,7,8,10	chitin biosynthetic process	15	0.0023	2	0.0023	1.0000000	D
<input type="checkbox"/>	GO:0032940	6,4,5	secretion by cell	250	0.0386	27	0.0305	1.0000000	D
<input type="checkbox"/>	GO:0006576	5,6	biogenic amine metabolic process	24	0.0037	3	0.0034	1.0000000	D
<input type="checkbox"/>	GO:0031167	8,9	rRNA methylation	44	0.0068	1	0.0011	1.0000000	D
<input type="checkbox"/>	GO:0030150	10,9,8,7	protein import into mitochondrial matrix	22	0.0034	1	0.0011	1.0000000	D
<input type="checkbox"/>	GO:0048308	5	organelle inheritance	40	0.0062	4	0.0045	1.0000000	D
<input type="checkbox"/>	GO:0046519	7,8	sphingoid metabolic process	10	0.0015	1	0.0011	1.0000000	D
<input type="checkbox"/>	GO:0000282	7,9,5,6,10	cellular bud site selection	66	0.0102	9	0.0102	1.0000000	D
<input type="checkbox"/>	GO:0005996	5,6	monosaccharide metabolic process	92	0.0142	8	0.0090	1.0000000	D
<input type="checkbox"/>	GO:0006536	7,8	glutamate metabolic process	16	0.0025	2	0.0023	1.0000000	D
<input type="checkbox"/>	GO:0016050	5	vesicle organization and biogenesis	16	0.0025	1	0.0011	1.0000000	D
<input type="checkbox"/>	GO:0016575	11,9	histone deacetylation	24	0.0037	2	0.0023	1.0000000	D
<input type="checkbox"/>	GO:0006732	5	coenzyme metabolic process	136	0.0210	15	0.0170	1.0000000	D
<input type="checkbox"/>	GO:0016485	8	protein processing	38	0.0059	4	0.0045	1.0000000	D
<input type="checkbox"/>	GO:0043632	6	modification-dependent macromolecule catabolic process	155	0.0239	17	0.0192	1.0000000	D
<input type="checkbox"/>	GO:0048193	7,5,6	Golgi vesicle transport	166	0.0256	16	0.0181	1.0000000	D

<input type="checkbox"/>	GO:0030433	9,11,10,12	ER-associated protein catabolic process	35	0.0054	4	0.0045	1.0000000	D
<input type="checkbox"/>	GO:0001300	5	chronological cell aging	13	0.0020	1	0.0011	1.0000000	D
<input type="checkbox"/>	GO:0006446	8,7,6	regulation of translational initiation	10	0.0015	1	0.0011	1.0000000	D
<input type="checkbox"/>	GO:0043574	7,5,6	peroxisomal transport	20	0.0031	2	0.0023	1.0000000	D
<input type="checkbox"/>	GO:0051252	7,6	regulation of RNA metabolic process	36	0.0056	4	0.0045	1.0000000	D
<input type="checkbox"/>	GO:0045185	5,4,3	maintenance of protein localization	30	0.0046	1	0.0011	1.0000000	D
<input type="checkbox"/>	GO:0000075	7,6	cell cycle checkpoint	53	0.0082	7	0.0079	1.0000000	D
<input type="checkbox"/>	GO:0009628	3	response to abiotic stimulus	117	0.0181	14	0.0158	1.0000000	D
<input type="checkbox"/>	GO:0006887	8,6,5,7	exocytosis	44	0.0068	2	0.0023	1.0000000	D
<input type="checkbox"/>	GO:0006311	10,8,7,5,9,6,4	meiotic gene conversion	22	0.0034	2	0.0023	1.0000000	D
<input type="checkbox"/>	GO:0006893	9,7,6,8	Golgi to plasma membrane transport	30	0.0046	3	0.0034	1.0000000	D
<input type="checkbox"/>	GO:0045333	5	cellular respiration	89	0.0137	7	0.0079	1.0000000	D
<input type="checkbox"/>	GO:0006944	5	membrane fusion	59	0.0091	3	0.0034	1.0000000	D
<input type="checkbox"/>	GO:0007569	4	cell aging	49	0.0076	6	0.0068	1.0000000	D
<input type="checkbox"/>	GO:0006626	9,8,7,6	protein targeting to mitochondrion	52	0.0080	7	0.0079	1.0000000	D
<input type="checkbox"/>	GO:0007120	8,6,10,7,11,5	axial cellular bud site selection	22	0.0034	2	0.0023	1.0000000	D
<input type="checkbox"/>	GO:0051181	4,5	cofactor transport	10	0.0015	1	0.0011	1.0000000	D
<input type="checkbox"/>	GO:0009119	6	ribonucleoside metabolic process	13	0.0020	1	0.0011	1.0000000	D
<input type="checkbox"/>	GO:0005975	4	carbohydrate metabolic process	233	0.0360	17	0.0192	1.0000000	D
<input type="checkbox"/>	GO:0015672	6,7	monovalent inorganic cation transport	32	0.0049	3	0.0034	1.0000000	D
<input type="checkbox"/>	GO:0006073	6,7	glucan metabolic process	46	0.0071	4	0.0045	1.0000000	D
<input type="checkbox"/>	GO:0005977	7,6,8	glycogen metabolic process	32	0.0049	3	0.0034	1.0000000	D
<input type="checkbox"/>	GO:0043486	11	histone exchange	9	0.0014	1	0.0011	1.0000000	D
<input type="checkbox"/>	GO:0046164	5	alcohol catabolic process	47	0.0073	5	0.0057	1.0000000	D
<input type="checkbox"/>	GO:0006528	7,8	asparagine metabolic process	9	0.0014	1	0.0011	1.0000000	D
<input type="checkbox"/>	GO:0042157	6	lipoprotein metabolic process	48	0.0074	5	0.0057	1.0000000	D
<input type="checkbox"/>	GO:0009966	5,4	regulation of signal transduction	26	0.0040	1	0.0011	1.0000000	D
<input type="checkbox"/>	GO:0043488	9,8,7	regulation of mRNA stability	30	0.0046	3	0.0034	1.0000000	D
<input type="checkbox"/>	GO:0006045	8,9	N-acetylglucosamine biosynthetic process	17	0.0026	2	0.0023	1.0000000	D
<input type="checkbox"/>	GO:0007121	8,6,10,7,11,5	bipolar cellular bud site selection	32	0.0049	3	0.0034	1.0000000	D
<input type="checkbox"/>	GO:0051278	8,7	chitin- and beta-glucan-containing cell wall polysaccharide biosynthetic process	24	0.0037	3	0.0034	1.0000000	D
<input type="checkbox"/>	GO:0000162	9,8,7,10	tryptophan biosynthetic process	10	0.0015	1	0.0011	1.0000000	D
<input type="checkbox"/>	GO:0006012	7,8	galactose metabolic process	10	0.0015	1	0.0011	1.0000000	D
<input type="checkbox"/>	GO:0045002	8,7	double-strand break repair via single-strand annealing	14	0.0022	1	0.0011	1.0000000	D
<input type="checkbox"/>	GO:0019319	7,8	hexose biosynthetic process	30	0.0046	2	0.0023	1.0000000	D
<input type="checkbox"/>	GO:0019941	8,7,9	modification-dependent protein catabolic process	148	0.0229	14	0.0158	1.0000000	D
<input type="checkbox"/>	GO:0009101	7,5	glycoprotein biosynthetic process	78	0.0120	7	0.0079	1.0000000	D
<input type="checkbox"/>	GO:0000290	11,8,9,10	deadenylation-dependent decapping	9	0.0014	1	0.0011	1.0000000	D
<input type="checkbox"/>	GO:0065002	8,6,7	intracellular protein transport across a membrane	11	0.0017	1	0.0011	1.0000000	D
<input type="checkbox"/>	GO:0006354	8,6,7	RNA elongation	59	0.0091	7	0.0079	1.0000000	D
<input type="checkbox"/>	GO:0006007	8,9	glucose catabolic process	34	0.0053	4	0.0045	1.0000000	D
<input type="checkbox"/>	GO:0016226	6	iron-sulfur cluster assembly	11	0.0017	1	0.0011	1.0000000	D
<input type="checkbox"/>	GO:0007530	4,5	sex determination	35	0.0054	4	0.0045	1.0000000	D
<input type="checkbox"/>	GO:0032990	5,6	cell part morphogenesis	8	0.0012	1	0.0011	1.0000000	D
<input type="checkbox"/>	GO:0009966	8,7,9	aromatic amino acid family biosynthetic	10	0.0015	1	0.0011	1.0000000	D

<input type="radio"/>	GO:0009090	8,7,9	process, anthranilate pathway	10	0.0013	1	0.0011	1.0000000	<input type="checkbox"/>
<input type="radio"/>	GO:0006497	8,7,6	protein amino acid lipidation	48	0.0074	5	0.0057	1.0000000	<input type="checkbox"/>
<input type="radio"/>	GO:0009084	7,8	glutamine family amino acid biosynthetic process	27	0.0042	3	0.0034	1.0000000	<input type="checkbox"/>
<input type="radio"/>	GO:0010382	6,4	cell wall metabolic process	26	0.0040	2	0.0023	1.0000000	<input type="checkbox"/>
<input type="radio"/>	GO:0006268	8	DNA unwinding during replication	10	0.0015	1	0.0011	1.0000000	<input type="checkbox"/>
<input type="radio"/>	GO:0042147	8,6,7	retrograde transport, endosome to Golgi	17	0.0026	1	0.0011	1.0000000	<input type="checkbox"/>
<input type="radio"/>	GO:0006508	6	proteolysis	178	0.0275	14	0.0158	1.0000000	<input type="checkbox"/>
<input type="radio"/>	GO:0007155	3	cell adhesion	9	0.0014	1	0.0011	1.0000000	<input type="checkbox"/>
<input type="radio"/>	GO:0009306	7,5,4,6	protein secretion	8	0.0012	1	0.0011	1.0000000	<input type="checkbox"/>
<input type="radio"/>	GO:0006525	7,8,5,4	arginine metabolic process	15	0.0023	1	0.0011	1.0000000	<input type="checkbox"/>
<input type="radio"/>	GO:0051338	5	regulation of transferase activity	26	0.0040	2	0.0023	1.0000000	<input type="checkbox"/>
<input type="radio"/>	GO:0009116	5	nucleoside metabolic process	18	0.0028	1	0.0011	1.0000000	<input type="checkbox"/>
<input type="radio"/>	GO:0006094	8,9	gluconeogenesis	28	0.0043	2	0.0023	1.0000000	<input type="checkbox"/>
<input type="radio"/>	GO:0006890	8,6,5,7	retrograde vesicle-mediated transport, Golgi to ER	24	0.0037	3	0.0034	1.0000000	<input type="checkbox"/>
<input type="radio"/>	GO:0009267	7,6,5	cellular response to starvation	19	0.0029	2	0.0023	1.0000000	<input type="checkbox"/>
<input type="radio"/>	GO:0009266	4	response to temperature stimulus	28	0.0043	1	0.0011	1.0000000	<input type="checkbox"/>
<input type="radio"/>	GO:0006030	8,6,7,9	chitin metabolic process	17	0.0026	2	0.0023	1.0000000	<input type="checkbox"/>
<input type="radio"/>	GO:0019320	7,8	hexose catabolic process	39	0.0060	5	0.0057	1.0000000	<input type="checkbox"/>
<input type="radio"/>	GO:0030030	7,6,8	cell projection organization and biogenesis	8	0.0012	1	0.0011	1.0000000	<input type="checkbox"/>
<input type="radio"/>	GO:0006625	9,8,6,7	protein targeting to peroxisome	20	0.0031	2	0.0023	1.0000000	<input type="checkbox"/>
<input type="radio"/>	GO:0006096	9,10	glycolysis	24	0.0037	1	0.0011	1.0000000	<input type="checkbox"/>
<input type="radio"/>	GO:0015891	4,5	siderophore transport	9	0.0014	1	0.0011	1.0000000	<input type="checkbox"/>
<input type="radio"/>	GO:0006368	9,7,8	RNA elongation from RNA polymerase II promoter	53	0.0082	7	0.0079	1.0000000	<input type="checkbox"/>
<input type="radio"/>	GO:0006808	6,5	regulation of nitrogen utilization	8	0.0012	1	0.0011	1.0000000	<input type="checkbox"/>
<input type="radio"/>	GO:0006970	4	response to osmotic stress	89	0.0137	11	0.0124	1.0000000	<input type="checkbox"/>
<input type="radio"/>	GO:0000051	4,3	urea cycle intermediate metabolic process	15	0.0023	1	0.0011	1.0000000	<input type="checkbox"/>
<input type="radio"/>	GO:0006616	9,12,11,7,10,8	SRP-dependent cotranslational protein targeting to membrane, translocation	10	0.0015	1	0.0011	1.0000000	<input type="checkbox"/>
<input type="radio"/>	GO:0000028	9,7,8,6	ribosomal small subunit assembly and maintenance	14	0.0022	1	0.0011	1.0000000	<input type="checkbox"/>
<input type="radio"/>	GO:0031577	8,7	spindle checkpoint	24	0.0037	3	0.0034	1.0000000	<input type="checkbox"/>
<input type="radio"/>	GO:0006586	6,7	indolalkylamine metabolic process	10	0.0015	1	0.0011	1.0000000	<input type="checkbox"/>
<input type="radio"/>	GO:0005991	6,7	trehalose metabolic process	10	0.0015	1	0.0011	1.0000000	<input type="checkbox"/>
<input type="radio"/>	GO:0009141	6	nucleoside triphosphate metabolic process	30	0.0046	4	0.0045	1.0000000	<input type="checkbox"/>
<input type="radio"/>	GO:0019954	3	asexual reproduction	85	0.0131	9	0.0102	1.0000000	<input type="checkbox"/>
<input type="radio"/>	GO:0007323	9	peptide pheromone maturation	8	0.0012	1	0.0011	1.0000000	<input type="checkbox"/>
<input type="radio"/>	GO:0015992	5,7,6,8	proton transport	24	0.0037	1	0.0011	1.0000000	<input type="checkbox"/>
<input type="radio"/>	GO:0031505	6	chitin- and beta-glucan-containing cell wall organization and biogenesis	44	0.0068	5	0.0057	1.0000000	<input type="checkbox"/>
<input type="radio"/>	GO:0043044	10	ATP-dependent chromatin remodeling	23	0.0036	2	0.0023	1.0000000	<input type="checkbox"/>
<input type="radio"/>	GO:0043255	7,6,5	regulation of carbohydrate biosynthetic process	19	0.0029	2	0.0023	1.0000000	<input type="checkbox"/>
<input type="radio"/>	GO:0006505	9,10	GPI anchor metabolic process	27	0.0042	3	0.0034	1.0000000	<input type="checkbox"/>
<input type="radio"/>	GO:0007031	5	peroxisome organization and biogenesis	40	0.0062	3	0.0034	1.0000000	<input type="checkbox"/>
<input type="radio"/>	GO:0030467	7,4,8	establishment and/or maintenance of cell polarity (sensu Fungi)	66	0.0102	9	0.0102	1.0000000	<input type="checkbox"/>
<input type="radio"/>	GO:0006275	8,7	regulation of DNA replication	19	0.0029	2	0.0023	1.0000000	<input type="checkbox"/>
<input type="radio"/>	GO:0042430	5	indole and derivative metabolic process	10	0.0015	1	0.0011	1.0000000	<input type="checkbox"/>

<input type="checkbox"/>	GO:0005976	5	polysaccharide metabolic process	65	0.0100	6	0.0068	1.0000000	D
<input type="checkbox"/>	GO:0007050	7,8,6	cell cycle arrest	11	0.0017	1	0.0011	1.0000000	D
<input type="checkbox"/>	GO:0051274	8,9	beta-glucan biosynthetic process	11	0.0017	1	0.0011	1.0000000	D
<input type="checkbox"/>	GO:0007096	8,10,9,7	regulation of exit from mitosis	24	0.0037	3	0.0034	1.0000000	D
<input type="checkbox"/>	GO:0006113	5	fermentation	17	0.0026	2	0.0023	1.0000000	D
<input type="checkbox"/>	GO:0006378	9	mRNA polyadenylation	18	0.0028	2	0.0023	1.0000000	D
<input type="checkbox"/>	GO:0051300	5,4,6	spindle pole body organization and biogenesis	16	0.0025	2	0.0023	1.0000000	D
<input type="checkbox"/>	GO:0007534	6,8,7	gene conversion at mating-type locus	23	0.0036	1	0.0011	1.0000000	D
<input type="checkbox"/>	GO:0007051	8	spindle organization and biogenesis	47	0.0073	6	0.0068	1.0000000	D
<input type="checkbox"/>	GO:0006457	6	protein folding	84	0.0130	11	0.0124	1.0000000	D
<input type="checkbox"/>	GO:0030163	6,5	protein catabolic process	173	0.0267	15	0.0170	1.0000000	D
<input type="checkbox"/>	GO:0006515	8,9	misfolded or incompletely synthesized protein catabolic process	38	0.0059	4	0.0045	1.0000000	D
<input type="checkbox"/>	GO:0000751	8,9,7,6	cell cycle arrest in response to pheromone	8	0.0012	1	0.0011	1.0000000	D
<input type="checkbox"/>	GO:0051171	5,4	regulation of nitrogen metabolic process	8	0.0012	1	0.0011	1.0000000	D
<input type="checkbox"/>	GO:0010324	5	membrane invagination	96	0.0148	12	0.0136	1.0000000	D
<input type="checkbox"/>	GO:0042401	6,7	biogenic amine biosynthetic process	18	0.0028	2	0.0023	1.0000000	D
<input type="checkbox"/>	GO:0051726	5,4	regulation of cell cycle	167	0.0258	21	0.0238	1.0000000	D
<input type="checkbox"/>	GO:0045324	8,6,7	late endosome to vacuole transport	21	0.0032	2	0.0023	1.0000000	D
<input type="checkbox"/>	GO:0007033	5	vacuole organization and biogenesis	67	0.0103	9	0.0102	1.0000000	D
<input type="checkbox"/>	GO:0010383	7,5,6	cell wall polysaccharide metabolic process	16	0.0025	2	0.0023	1.0000000	D
<input type="checkbox"/>	GO:0042775	9,6	organelle ATP synthesis coupled electron transport	25	0.0039	2	0.0023	1.0000000	D
<input type="checkbox"/>	GO:0030031	8,7,9	cell projection biogenesis	8	0.0012	1	0.0011	1.0000000	D
<input type="checkbox"/>	GO:0007015	8	actin filament organization	61	0.0094	8	0.0090	1.0000000	D
<input type="checkbox"/>	GO:0015986	8,10,7,9,11,5	ATP synthesis coupled proton transport	20	0.0031	1	0.0011	1.0000000	D
<input type="checkbox"/>	GO:0042144	6	vacuole fusion, non-autophagic	28	0.0043	1	0.0011	1.0000000	D
<input type="checkbox"/>	GO:0007093	8,10,9,7	mitotic cell cycle checkpoint	27	0.0042	3	0.0034	1.0000000	D
<input type="checkbox"/>	GO:0016044	4	membrane organization and biogenesis	188	0.0290	20	0.0226	1.0000000	D
<input type="checkbox"/>	GO:0045045	7,5,4,6	secretory pathway	243	0.0375	26	0.0294	1.0000000	D
<input type="checkbox"/>	GO:0046474	8,7,9	glycerophospholipid biosynthetic process	39	0.0060	3	0.0034	1.0000000	D
<input type="checkbox"/>	GO:0007088	7,9,8,6	regulation of mitosis	55	0.0085	6	0.0068	1.0000000	D
<input type="checkbox"/>	GO:0001522	7	pseudouridine synthesis	39	0.0060	3	0.0034	1.0000000	D
<input type="checkbox"/>	GO:0007094	9,11,10,8	mitotic cell cycle spindle assembly checkpoint	20	0.0031	2	0.0023	1.0000000	D
<input type="checkbox"/>	GO:0006006	7,8	glucose metabolic process	65	0.0100	7	0.0079	1.0000000	D
<input type="checkbox"/>	GO:0016052	5	carbohydrate catabolic process	80	0.0124	5	0.0057	1.0000000	D
<input type="checkbox"/>	GO:0006892	8,6,5,7	post-Golgi vesicle-mediated transport	69	0.0107	7	0.0079	1.0000000	D
<input type="checkbox"/>	GO:0006650	7,8	glycerophospholipid metabolic process	60	0.0093	8	0.0090	1.0000000	D
<input type="checkbox"/>	GO:0009894	5,4	regulation of catabolic process	15	0.0023	1	0.0011	1.0000000	D
<input type="checkbox"/>	GO:0042594	6,4	response to starvation	19	0.0029	2	0.0023	1.0000000	D
<input type="checkbox"/>	GO:0042434	6	indole derivative metabolic process	10	0.0015	1	0.0011	1.0000000	D
<input type="checkbox"/>	GO:0007166	5	cell surface receptor linked signal transduction	52	0.0080	7	0.0079	1.0000000	D
<input type="checkbox"/>	GO:0010033	4	response to organic substance	10	0.0015	1	0.0011	1.0000000	D
<input type="checkbox"/>	GO:0046999	5,4	regulation of conjugation	30	0.0046	4	0.0045	1.0000000	D
<input type="checkbox"/>	GO:0006493	9,8,7	protein amino acid O-linked glycosylation	16	0.0025	2	0.0023	1.0000000	D
<input type="checkbox"/>	GO:0044264	5,6	cellular polysaccharide metabolic process	65	0.0100	6	0.0068	1.0000000	D

<input type="radio"/>	GO:0009205	8	purine ribonucleoside triphosphate metabolic process	23	0.0036	3	0.0034	1.0000000	D
<input type="radio"/>	GO:0051789	4	response to protein stimulus	18	0.0028	2	0.0023	1.0000000	D
<input type="radio"/>	GO:0016558	10,9,7,8,6	protein import into peroxisome matrix	17	0.0026	2	0.0023	1.0000000	D
<input type="radio"/>	GO:0000724	8,7	double-strand break repair via homologous recombination	25	0.0039	3	0.0034	1.0000000	D
<input type="radio"/>	GO:0006672	8,9	ceramide metabolic process	8	0.0012	1	0.0011	1.0000000	D
<input type="radio"/>	GO:0003006	3,4	reproductive developmental process	35	0.0054	4	0.0045	1.0000000	D
<input type="radio"/>	GO:0042158	7,5	lipoprotein biosynthetic process	48	0.0074	5	0.0057	1.0000000	D
<input type="radio"/>	GO:0007114	5,4	cell budding	85	0.0131	9	0.0102	1.0000000	D
<input type="radio"/>	GO:0051716	3	cellular response to stimulus	21	0.0032	2	0.0023	1.0000000	D
<input type="radio"/>	GO:0009057	4	macromolecule catabolic process	345	0.0533	41	0.0464	1.0000000	D
<input type="radio"/>	GO:0006896	9,8,7,6	Golgi to vacuole transport	24	0.0037	1	0.0011	1.0000000	D
<input type="radio"/>	GO:0009408	5,4	response to heat	23	0.0036	1	0.0011	1.0000000	D
<input type="radio"/>	GO:0006312	7	mitotic recombination	45	0.0069	1	0.0011	1.0000000	D
<input type="radio"/>	GO:0006914	3	autophagy	45	0.0069	6	0.0068	1.0000000	D
<input type="radio"/>	GO:0006614	11,10,9,8,7	SRP-dependent cotranslational protein targeting to membrane	20	0.0031	1	0.0011	1.0000000	D
<input type="radio"/>	GO:0032506	5,3	cytokinetic process	88	0.0136	12	0.0136	1.0000000	D
<input type="radio"/>	GO:0051188	5	cofactor biosynthetic process	79	0.0122	10	0.0113	1.0000000	D
<input type="radio"/>	GO:0006044	7,8	N-acetylglucosamine metabolic process	19	0.0029	2	0.0023	1.0000000	D
<input type="radio"/>	GO:0006488	10,9,8	dolichol-linked oligosaccharide biosynthetic process	11	0.0017	1	0.0011	1.0000000	D
<input type="radio"/>	GO:0000018	8,7	regulation of DNA recombination	18	0.0028	2	0.0023	1.0000000	D
<input type="radio"/>	GO:0044265	5	cellular macromolecule catabolic process	314	0.0485	39	0.0441	1.0000000	D
<input type="radio"/>	GO:0006869	4,5	lipid transport	34	0.0053	4	0.0045	1.0000000	D
<input type="radio"/>	GO:0006412	6,5	translation	688	0.1062	63	0.0713	0.0527140	D
<input type="radio"/>	GO:0032196	3	transposition	105	0.0162	2	0.0023	0.0338188	D
<input type="radio"/>	GO:0009059	4	macromolecule biosynthetic process	886	0.1368	82	0.0928	0.0067192	D
<input type="radio"/>	GO:0043284	5	biopolymer biosynthetic process	354	0.0547	6	0.0068	4.456820E-13	D
<input type="radio"/>	GO:0006414	7,6	translational elongation	313	0.0483	2	0.0023	6.005590E-15	D