

# GO-Stats Results

Your dataset contains **269** annotated gene products.

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

Color codes			
<b>E</b>	The term is enriched in your gene set.	<b>D</b>	The term is depleted in your gene set.
	P-value < 0.01		0.01 < P-value < 0.05
<b>RO</b>	Number of genes annotated for this term in the reference set.	<b>RF</b>	Frequency of genes annotated for this term in the reference set.
<b>DO</b>	Number of genes annotated for this term in your gene set.	<b>DF</b>	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:0006082	4	<a href="#">organic acid metabolic process</a>	314	0.0485	35	0.1301	3.792548E-05	E
<input type="radio"/> GO:0019752	5	<a href="#">carboxylic acid metabolic process</a>	314	0.0485	35	0.1301	3.792548E-05	E
<input type="radio"/> GO:0006807	3	<a href="#">nitrogen compound metabolic process</a>	251	0.0388	30	0.1115	8.031062E-05	E
<input type="radio"/> GO:0044249	4	<a href="#">cellular biosynthetic process</a>	366	0.0565	37	0.1375	0.0001853	E
<input type="radio"/> GO:0009308	4	<a href="#">amine metabolic process</a>	228	0.0352	26	0.0967	0.0014217	E
<input type="radio"/> GO:0006519	4	<a href="#">amino acid and derivative metabolic process</a>	202	0.0312	21	0.0781	0.0531651	E
<input type="radio"/> GO:0006520	5,6	<a href="#">amino acid metabolic process</a>	187	0.0289	20	0.0743	0.0536708	E
<input type="radio"/> GO:0008652	6,7	<a href="#">amino acid biosynthetic process</a>	106	0.0164	14	0.0520	0.0756323	E
<input type="radio"/> GO:0006100	6	<a href="#">tricarboxylic acid cycle intermediate metabolic process</a>	20	0.0031	6	0.0223	0.0961831	E
<input type="radio"/> GO:0009309	5,6	<a href="#">amine biosynthetic process</a>	114	0.0176	14	0.0520	0.1612858	E
<input type="radio"/> GO:0044271	5,4	<a href="#">nitrogen compound biosynthetic process</a>	115	0.0178	14	0.0520	0.1762816	E
<input type="radio"/> GO:0006950	3	<a href="#">response to stress</a>	488	0.0754	36	0.1338	0.2158807	E
<input type="radio"/> GO:0006546	8,9	<a href="#">glycine catabolic process</a>	4	0.0006	3	0.0112	0.2480333	E
<input type="radio"/> GO:0046470	8,9	<a href="#">phosphatidylcholine metabolic process</a>	9	0.0014	4	0.0149	0.2716489	E
<input type="radio"/> GO:0009987	2	<a href="#">cellular process</a>	4654	0.7187	216	0.8030	0.2865393	E
<input type="radio"/> GO:0005975	4	<a href="#">carbohydrate metabolic process</a>	233	0.0360	21	0.0781	0.3528353	E
<input type="radio"/> GO:0046165	5	<a href="#">alcohol biosynthetic process</a>	35	0.0054	7	0.0260	0.3803443	E
<input type="radio"/> GO:0032787	6	<a href="#">monocarboxylic acid metabolic process</a>	126	0.0195	14	0.0520	0.4349791	E
<input type="radio"/> GO:0009084	7,8	<a href="#">glutamine family amino acid biosynthetic process</a>	27	0.0042	6	0.0223	0.5489394	E
<input type="radio"/> GO:0015980	4	<a href="#">energy derivation by oxidation of organic compounds</a>	145	0.0224	15	0.0558	0.5778838	E
<input type="radio"/> GO:0006102	6,7	<a href="#">isocitrate metabolic process</a>	5	0.0008	3	0.0112	0.5945978	E
<input type="radio"/> GO:0009071	7,8	<a href="#">serine family amino acid catabolic process</a>	5	0.0008	3	0.0112	0.5945978	E
<input type="radio"/> GO:0051234	2,3	<a href="#">establishment of localization</a>	1004	0.1550	60	0.2230	0.6130285	E
<input type="radio"/> GO:0006090	7	<a href="#">pyruvate metabolic process</a>	38	0.0059	7	0.0260	0.6301876	E
<input type="radio"/> GO:0030503	5,7,4	<a href="#">regulation of cell redox homeostasis</a>	11	0.0017	4	0.0149	0.6543442	E
<input type="radio"/> GO:0045454	6,4	<a href="#">cell redox homeostasis</a>	11	0.0017	4	0.0149	0.6543442	E

<input type="checkbox"/>	GO:0006094	8,9	<a href="#">gluconeogenesis</a>	28	0.0043	6	0.0223	0.6701581	E
<input type="checkbox"/>	GO:0051179	2	<a href="#">localization</a>	1051	0.1623	62	0.2305	0.6826370	E
<input type="checkbox"/>	GO:0044262	5	<a href="#">cellular carbohydrate metabolic process</a>	213	0.0329	19	0.0706	0.7170021	E
<input type="checkbox"/>	GO:0016051	5	<a href="#">carbohydrate biosynthetic process</a>	77	0.0119	10	0.0372	0.8286957	E
<input type="checkbox"/>	GO:0006732	5	<a href="#">coenzyme metabolic process</a>	136	0.0210	14	0.0520	0.8901844	E
<input type="checkbox"/>	GO:0009109	6	<a href="#">coenzyme catabolic process</a>	20	0.0031	5	0.0186	0.9025183	E
<input type="checkbox"/>	GO:0006810	3,4	<a href="#">transport</a>	981	0.1515	58	0.2156	0.9370491	E
<input type="checkbox"/>	GO:0019319	7,8	<a href="#">hexose biosynthetic process</a>	30	0.0046	6	0.0223	0.9718157	E
<input type="checkbox"/>	GO:0046364	6,7	<a href="#">monosaccharide biosynthetic process</a>	30	0.0046	6	0.0223	0.9718157	E
<input type="checkbox"/>	GO:0030476	8,6,7	<a href="#">spore wall assembly (sensu Fungi)</a>	42	0.0065	4	0.0149	1.0000000	E
<input type="checkbox"/>	GO:0006827	8,9,10	<a href="#">high affinity iron ion transport</a>	4	0.0006	1	0.0037	1.0000000	E
<input type="checkbox"/>	GO:0000147	5,9,8	<a href="#">actin cortical patch assembly</a>	14	0.0022	3	0.0112	1.0000000	E
<input type="checkbox"/>	GO:0006030	8,6,7,9	<a href="#">chitin metabolic process</a>	17	0.0026	2	0.0074	1.0000000	E
<input type="checkbox"/>	GO:0003006	3,4	<a href="#">reproductive developmental process</a>	35	0.0054	3	0.0112	1.0000000	E
<input type="checkbox"/>	GO:0007096	8,10,9,7	<a href="#">regulation of exit from mitosis</a>	24	0.0037	1	0.0037	1.0000000	E
<input type="checkbox"/>	GO:0032502	2	<a href="#">developmental process</a>	436	0.0673	24	0.0892	1.0000000	E
<input type="checkbox"/>	GO:0001101	4	<a href="#">response to acid</a>	11	0.0017	3	0.0112	1.0000000	E
<input type="checkbox"/>	GO:0016311	6	<a href="#">dephosphorylation</a>	41	0.0063	2	0.0074	1.0000000	E
<input type="checkbox"/>	GO:0046463	6,7,8	<a href="#">acylglycerol biosynthetic process</a>	2	0.0003	2	0.0074	1.0000000	E
<input type="checkbox"/>	GO:0040020	7,9,8,6	<a href="#">regulation of meiosis</a>	22	0.0034	1	0.0037	1.0000000	E
<input type="checkbox"/>	GO:0033037	4	<a href="#">polysaccharide localization</a>	1	0.0002	1	0.0037	1.0000000	E
<input type="checkbox"/>	GO:0006343	11,7,8,12,10	<a href="#">establishment of chromatin silencing</a>	2	0.0003	1	0.0037	1.0000000	E
<input type="checkbox"/>	GO:0030437	7,6	<a href="#">sporulation (sensu Fungi)</a>	108	0.0167	8	0.0297	1.0000000	E
<input type="checkbox"/>	GO:0007018	8,7,6	<a href="#">microtubule-based movement</a>	15	0.0023	1	0.0037	1.0000000	E
<input type="checkbox"/>	GO:0007163	6,3,7	<a href="#">establishment and/or maintenance of cell polarity</a>	115	0.0178	7	0.0260	1.0000000	E
<input type="checkbox"/>	GO:0046700	5	<a href="#">heterocycle catabolic process</a>	7	0.0011	1	0.0037	1.0000000	E
<input type="checkbox"/>	GO:0006986	4,5	<a href="#">response to unfolded protein</a>	18	0.0028	3	0.0112	1.0000000	E
<input type="checkbox"/>	GO:0007119	7,6,5	<a href="#">budding cell isotropic bud growth</a>	8	0.0012	1	0.0037	1.0000000	E
<input type="checkbox"/>	GO:0007097	7,8,5,6	<a href="#">nuclear migration</a>	20	0.0031	1	0.0037	1.0000000	E
<input type="checkbox"/>	GO:0019627	5	<a href="#">urea metabolic process</a>	2	0.0003	1	0.0037	1.0000000	E
<input type="checkbox"/>	GO:0030433	9,11,10,12	<a href="#">ER-associated protein catabolic process</a>	35	0.0054	2	0.0074	1.0000000	E
<input type="checkbox"/>	GO:0031570	8,7	<a href="#">DNA integrity checkpoint</a>	18	0.0028	2	0.0074	1.0000000	E
<input type="checkbox"/>	GO:0042158	7,5	<a href="#">lipoprotein biosynthetic process</a>	48	0.0074	3	0.0112	1.0000000	E
<input type="checkbox"/>	GO:0046148	5	<a href="#">pigment biosynthetic process</a>	19	0.0029	1	0.0037	1.0000000	E
<input type="checkbox"/>	GO:0051293	6,7,8,4,5	<a href="#">establishment of spindle localization</a>	10	0.0015	3	0.0112	1.0000000	E
<input type="checkbox"/>	GO:0018022	9,10,8	<a href="#">peptidyl-lysine methylation</a>	3	0.0005	1	0.0037	1.0000000	E
<input type="checkbox"/>	GO:0051093	5,4	<a href="#">negative regulation of developmental process</a>	2	0.0003	2	0.0074	1.0000000	E
<input type="checkbox"/>	GO:0042592	4	<a href="#">homeostatic process</a>	134	0.0207	9	0.0335	1.0000000	E
<input type="checkbox"/>	GO:0017157	6,9,5,7,8	<a href="#">regulation of exocytosis</a>	3	0.0005	1	0.0037	1.0000000	E
<input type="checkbox"/>	GO:0030474	5,6,4,7	<a href="#">spindle pole body duplication</a>	14	0.0022	1	0.0037	1.0000000	E
<input type="checkbox"/>	GO:0000086	8,5,6,7,4	<a href="#">G2/M transition of mitotic cell cycle</a>	35	0.0054	2	0.0074	1.0000000	E
<input type="checkbox"/>	GO:0000767	6,7	<a href="#">cellular morphogenesis during conjugation</a>	20	0.0031	3	0.0112	1.0000000	E
<input type="checkbox"/>	GO:0000501	4	<a href="#">flocculation via cell wall protein-carbohydrate interaction</a>	9	0.0014	1	0.0037	1.0000000	E
<input type="checkbox"/>	GO:0006116	10,9	<a href="#">NADH oxidation</a>	11	0.0017	1	0.0037	1.0000000	E
<input type="checkbox"/>	GO:0065008	3	<a href="#">regulation of biological quality</a>	260	0.0401	15	0.0558	1.0000000	E

<input type="radio"/>	GO:0032990	5,6	<a href="#">cell part morphogenesis</a>	8	0.0012	1	0.0037	1.0000000	E
<input type="radio"/>	GO:0016485	8	<a href="#">protein processing</a>	38	0.0059	3	0.0112	1.0000000	E
<input type="radio"/>	GO:0009168	8,9	<a href="#">purine ribonucleoside monophosphate biosynthetic process</a>	15	0.0023	1	0.0037	1.0000000	E
<input type="radio"/>	GO:0046942	5,6	<a href="#">carboxylic acid transport</a>	54	0.0083	5	0.0186	1.0000000	E
<input type="radio"/>	GO:0050793	4,3	<a href="#">regulation of developmental process</a>	7	0.0011	2	0.0074	1.0000000	E
<input type="radio"/>	GO:0046092	8	<a href="#">deoxycytidine metabolic process</a>	1	0.0002	1	0.0037	1.0000000	E
<input type="radio"/>	GO:0009123	6	<a href="#">nucleoside monophosphate metabolic process</a>	19	0.0029	1	0.0037	1.0000000	E
<input type="radio"/>	GO:0030174	9,7,8	<a href="#">regulation of DNA replication initiation</a>	10	0.0015	1	0.0037	1.0000000	E
<input type="radio"/>	GO:0007005	5	<a href="#">mitochondrion organization and biogenesis</a>	110	0.0170	9	0.0335	1.0000000	E
<input type="radio"/>	GO:0030952	6	<a href="#">establishment and/or maintenance of cytoskeleton polarity</a>	9	0.0014	1	0.0037	1.0000000	E
<input type="radio"/>	GO:0006106	7	<a href="#">fumarate metabolic process</a>	1	0.0002	1	0.0037	1.0000000	E
<input type="radio"/>	GO:0006497	8,7,6	<a href="#">protein amino acid lipidation</a>	48	0.0074	3	0.0112	1.0000000	E
<input type="radio"/>	GO:0033261	7,8,6	<a href="#">regulation of progression through S phase</a>	5	0.0008	1	0.0037	1.0000000	E
<input type="radio"/>	GO:0042594	6,4	<a href="#">response to starvation</a>	19	0.0029	1	0.0037	1.0000000	E
<input type="radio"/>	GO:0006639	6,5,7	<a href="#">acylglycerol metabolic process</a>	5	0.0008	2	0.0074	1.0000000	E
<input type="radio"/>	GO:0015976	3	<a href="#">carbon utilization</a>	1	0.0002	1	0.0037	1.0000000	E
<input type="radio"/>	GO:0006984	6	<a href="#">ER-nuclear signaling pathway</a>	9	0.0014	1	0.0037	1.0000000	E
<input type="radio"/>	GO:0007117	6,5,4	<a href="#">budding cell bud growth</a>	35	0.0054	3	0.0112	1.0000000	E
<input type="radio"/>	GO:0006644	6,7	<a href="#">phospholipid metabolic process</a>	97	0.0150	9	0.0335	1.0000000	E
<input type="radio"/>	GO:0009228	7,8	<a href="#">thiamin biosynthetic process</a>	19	0.0029	3	0.0112	1.0000000	E
<input type="radio"/>	GO:0007047	5	<a href="#">cell wall organization and biogenesis</a>	200	0.0309	15	0.0558	1.0000000	E
<input type="radio"/>	GO:0030029	6	<a href="#">actin filament-based process</a>	112	0.0173	10	0.0372	1.0000000	E
<input type="radio"/>	GO:0000077	9,8,6	<a href="#">DNA damage checkpoint</a>	14	0.0022	1	0.0037	1.0000000	E
<input type="radio"/>	GO:0006281	6,5	<a href="#">DNA repair</a>	193	0.0298	10	0.0372	1.0000000	E
<input type="radio"/>	GO:0019954	3	<a href="#">asexual reproduction</a>	85	0.0131	6	0.0223	1.0000000	E
<input type="radio"/>	GO:0005996	5,6	<a href="#">monosaccharide metabolic process</a>	92	0.0142	7	0.0260	1.0000000	E
<input type="radio"/>	GO:0006555	7,8,6	<a href="#">methionine metabolic process</a>	24	0.0037	1	0.0037	1.0000000	E
<input type="radio"/>	GO:0016237	4,6	<a href="#">microautophagy</a>	11	0.0017	1	0.0037	1.0000000	E
<input type="radio"/>	GO:0051278	8,7	<a href="#">chitin- and beta-glucan-containing cell wall polysaccharide biosynthetic process</a>	24	0.0037	1	0.0037	1.0000000	E
<input type="radio"/>	GO:0009264	6,7	<a href="#">deoxyribonucleotide catabolic process</a>	5	0.0008	1	0.0037	1.0000000	E
<input type="radio"/>	GO:0046160	7,8,6	<a href="#">heme a metabolic process</a>	3	0.0005	1	0.0037	1.0000000	E
<input type="radio"/>	GO:0051656	6,3,5,4	<a href="#">establishment of organelle localization</a>	29	0.0045	3	0.0112	1.0000000	E
<input type="radio"/>	GO:0006273	9,8	<a href="#">lagging strand elongation</a>	18	0.0028	1	0.0037	1.0000000	E
<input type="radio"/>	GO:0015798	5,6	<a href="#">myo-inositol transport</a>	2	0.0003	1	0.0037	1.0000000	E
<input type="radio"/>	GO:0030397	5	<a href="#">membrane disassembly</a>	1	0.0002	1	0.0037	1.0000000	E
<input type="radio"/>	GO:0043162	10,9,11	<a href="#">ubiquitin-dependent protein catabolic process via the multivesicular body pathway</a>	16	0.0025	2	0.0074	1.0000000	E
<input type="radio"/>	GO:0042440	4	<a href="#">pigment metabolic process</a>	20	0.0031	1	0.0037	1.0000000	E
<input type="radio"/>	GO:0000041	7,8	<a href="#">transition metal ion transport</a>	46	0.0071	4	0.0149	1.0000000	E
<input type="radio"/>	GO:0007531	4,6,5	<a href="#">mating type determination</a>	35	0.0054	3	0.0112	1.0000000	E
<input type="radio"/>	GO:0016125	5,6,7	<a href="#">sterol metabolic process</a>	42	0.0065	2	0.0074	1.0000000	E
<input type="radio"/>	GO:0009075	6,7	<a href="#">histidine family amino acid metabolic process</a>	14	0.0022	2	0.0074	1.0000000	E
<input type="radio"/>	GO:0010383	7,5,6	<a href="#">cell wall polysaccharide metabolic process</a>	16	0.0025	1	0.0037	1.0000000	E
<input type="radio"/>	GO:0006436	9,8,10,7	<a href="#">tryptophanyl-tRNA aminoacylation</a>	2	0.0003	1	0.0037	1.0000000	E
<input type="radio"/>	GO:0030435	5	<a href="#">sporulation</a>	123	0.0190	10	0.0372	1.0000000	E

<input type="radio"/>	GO:0006113	5	<a href="#">fermentation</a>	17	0.0026	3	0.0112	1.0000000	E
<input type="radio"/>	GO:0045851	8	<a href="#">pH reduction</a>	24	0.0037	1	0.0037	1.0000000	E
<input type="radio"/>	GO:0006631	5,7,6	<a href="#">fatty acid metabolic process</a>	47	0.0073	3	0.0112	1.0000000	E
<input type="radio"/>	GO:0017156	9,7,6,8	<a href="#">calcium ion-dependent exocytosis</a>	1	0.0002	1	0.0037	1.0000000	E
<input type="radio"/>	GO:0051716	3	<a href="#">cellular response to stimulus</a>	21	0.0032	1	0.0037	1.0000000	E
<input type="radio"/>	GO:0045002	8,7	<a href="#">double-strand break repair via single-strand annealing</a>	14	0.0022	2	0.0074	1.0000000	E
<input type="radio"/>	GO:0006047	8,6,9	<a href="#">UDP-N-acetylglucosamine metabolic process</a>	2	0.0003	1	0.0037	1.0000000	E
<input type="radio"/>	GO:0000921	8,7	<a href="#">septin ring assembly</a>	9	0.0014	1	0.0037	1.0000000	E
<input type="radio"/>	GO:0007089	8,9,7,6	<a href="#">traversing start control point of mitotic cell cycle</a>	6	0.0009	1	0.0037	1.0000000	E
<input type="radio"/>	GO:0040023	6,7,4,5	<a href="#">establishment of nucleus localization</a>	20	0.0031	1	0.0037	1.0000000	E
<input type="radio"/>	GO:0006873	7,5	<a href="#">cellular ion homeostasis</a>	115	0.0178	5	0.0186	1.0000000	E
<input type="radio"/>	GO:0007039	7,8	<a href="#">vacuolar protein catabolic process</a>	11	0.0017	3	0.0112	1.0000000	E
<input type="radio"/>	GO:0006744	8,7	<a href="#">ubiquinone biosynthetic process</a>	9	0.0014	1	0.0037	1.0000000	E
<input type="radio"/>	GO:0015833	4,5	<a href="#">peptide transport</a>	7	0.0011	1	0.0037	1.0000000	E
<input type="radio"/>	GO:0006980	5	<a href="#">redox signal response</a>	1	0.0002	1	0.0037	1.0000000	E
<input type="radio"/>	GO:0042938	5,6	<a href="#">dipeptide transport</a>	2	0.0003	1	0.0037	1.0000000	E
<input type="radio"/>	GO:0006071	6	<a href="#">glycerol metabolic process</a>	9	0.0014	2	0.0074	1.0000000	E
<input type="radio"/>	GO:0022413	5,4	<a href="#">reproductive process in single-celled organism</a>	149	0.0230	12	0.0446	1.0000000	E
<input type="radio"/>	GO:0055067	8	<a href="#">monovalent inorganic cation homeostasis</a>	34	0.0053	2	0.0074	1.0000000	E
<input type="radio"/>	GO:0030154	4	<a href="#">cell differentiation</a>	173	0.0267	13	0.0483	1.0000000	E
<input type="radio"/>	GO:0009066	6,7	<a href="#">aspartate family amino acid metabolic process</a>	46	0.0071	2	0.0074	1.0000000	E
<input type="radio"/>	GO:0030036	7	<a href="#">actin cytoskeleton organization and biogenesis</a>	107	0.0165	10	0.0372	1.0000000	E
<input type="radio"/>	GO:0000045	5	<a href="#">autophagic vacuole formation</a>	4	0.0006	1	0.0037	1.0000000	E
<input type="radio"/>	GO:0006518	4	<a href="#">peptide metabolic process</a>	11	0.0017	3	0.0112	1.0000000	E
<input type="radio"/>	GO:0006048	9,7,10	<a href="#">UDP-N-acetylglucosamine biosynthetic process</a>	2	0.0003	1	0.0037	1.0000000	E
<input type="radio"/>	GO:0006506	10,9,8,7,11	<a href="#">GPI anchor biosynthetic process</a>	26	0.0040	2	0.0074	1.0000000	E
<input type="radio"/>	GO:0017158	7,10,6,8,9	<a href="#">regulation of calcium ion-dependent exocytosis</a>	1	0.0002	1	0.0037	1.0000000	E
<input type="radio"/>	GO:0000076	11,9,8,10	<a href="#">DNA replication checkpoint</a>	5	0.0008	1	0.0037	1.0000000	E
<input type="radio"/>	GO:0051231	5,4,9,7	<a href="#">spindle elongation</a>	20	0.0031	1	0.0037	1.0000000	E
<input type="radio"/>	GO:0000709	11,9,8,5,6,10,7,4	<a href="#">meiotic joint molecule formation</a>	2	0.0003	1	0.0037	1.0000000	E
<input type="radio"/>	GO:0051053	8,7	<a href="#">negative regulation of DNA metabolic process</a>	20	0.0031	1	0.0037	1.0000000	E
<input type="radio"/>	GO:0046121	6,7	<a href="#">deoxyribonucleoside catabolic process</a>	1	0.0002	1	0.0037	1.0000000	E
<input type="radio"/>	GO:0015719	7,8	<a href="#">allantoate transport</a>	1	0.0002	1	0.0037	1.0000000	E
<input type="radio"/>	GO:0006662	4	<a href="#">glycerol ether metabolic process</a>	5	0.0008	2	0.0074	1.0000000	E
<input type="radio"/>	GO:0006811	4,5	<a href="#">ion transport</a>	115	0.0178	7	0.0260	1.0000000	E
<input type="radio"/>	GO:0009110	5	<a href="#">vitamin biosynthetic process</a>	46	0.0071	5	0.0186	1.0000000	E
<input type="radio"/>	GO:0045920	7,10,6,8,9	<a href="#">negative regulation of exocytosis</a>	1	0.0002	1	0.0037	1.0000000	E
<input type="radio"/>	GO:0051030	5,7,6,8	<a href="#">snRNA transport</a>	23	0.0036	1	0.0037	1.0000000	E
<input type="radio"/>	GO:0030148	7,6,8	<a href="#">sphingolipid biosynthetic process</a>	20	0.0031	1	0.0037	1.0000000	E
<input type="radio"/>	GO:0015802	6,7,8	<a href="#">basic amino acid transport</a>	9	0.0014	1	0.0037	1.0000000	E
<input type="radio"/>	GO:0046937	5	<a href="#">phytochelatin metabolic process</a>	2	0.0003	1	0.0037	1.0000000	E
<input type="radio"/>	GO:0019563	7	<a href="#">glycerol catabolic process</a>	3	0.0005	1	0.0037	1.0000000	E
<input type="radio"/>	GO:0009311	5	<a href="#">oligosaccharide metabolic process</a>	7	0.0011	1	0.0037	1.0000000	E

<input type="radio"/>	GO:0031577	8,7	<a href="#">spindle checkpoint</a>	24	0.0037	1	0.0037	1.0000000	E
<input type="radio"/>	GO:0051171	5,4	<a href="#">regulation of nitrogen metabolic process</a>	8	0.0012	1	0.0037	1.0000000	E
<input type="radio"/>	GO:0007052	5,4,9	<a href="#">mitotic spindle organization and biogenesis</a>	44	0.0068	2	0.0074	1.0000000	E
<input type="radio"/>	GO:0045017	6,5,7	<a href="#">glycerolipid biosynthetic process</a>	2	0.0003	2	0.0074	1.0000000	E
<input type="radio"/>	GO:0006312	7	<a href="#">mitotic recombination</a>	45	0.0069	3	0.0112	1.0000000	E
<input type="radio"/>	GO:0009719	3	<a href="#">response to endogenous stimulus</a>	243	0.0375	12	0.0446	1.0000000	E
<input type="radio"/>	GO:0033262	8,9,7	<a href="#">regulation of DNA replication during S phase</a>	2	0.0003	1	0.0037	1.0000000	E
<input type="radio"/>	GO:0006501	9,8,7	<a href="#">C-terminal protein lipidation</a>	4	0.0006	1	0.0037	1.0000000	E
<input type="radio"/>	GO:0044264	5,6	<a href="#">cellular polysaccharide metabolic process</a>	65	0.0100	4	0.0149	1.0000000	E
<input type="radio"/>	GO:0006790	4	<a href="#">sulfur metabolic process</a>	67	0.0103	7	0.0260	1.0000000	E
<input type="radio"/>	GO:0006656	9,8,10	<a href="#">phosphatidylcholine biosynthetic process</a>	7	0.0011	3	0.0112	1.0000000	E
<input type="radio"/>	GO:0006865	5,6,7	<a href="#">amino acid transport</a>	39	0.0060	3	0.0112	1.0000000	E
<input type="radio"/>	GO:0055066	8	<a href="#">di-, tri-valent inorganic cation homeostasis</a>	64	0.0099	3	0.0112	1.0000000	E
<input type="radio"/>	GO:0051791	6,8,7	<a href="#">medium-chain fatty acid metabolic process</a>	3	0.0005	1	0.0037	1.0000000	E
<input type="radio"/>	GO:0006638	5,6	<a href="#">neutral lipid metabolic process</a>	5	0.0008	2	0.0074	1.0000000	E
<input type="radio"/>	GO:0006624	9	<a href="#">vacuolar protein processing</a>	4	0.0006	2	0.0074	1.0000000	E
<input type="radio"/>	GO:0009266	4	<a href="#">response to temperature stimulus</a>	28	0.0043	4	0.0149	1.0000000	E
<input type="radio"/>	GO:0009272	7	<a href="#">chitin- and beta-glucan-containing cell wall biogenesis</a>	33	0.0051	2	0.0074	1.0000000	E
<input type="radio"/>	GO:0006972	5	<a href="#">hyperosmotic response</a>	11	0.0017	1	0.0037	1.0000000	E
<input type="radio"/>	GO:0051775	4	<a href="#">response to redox state</a>	1	0.0002	1	0.0037	1.0000000	E
<input type="radio"/>	GO:0046356	7	<a href="#">acetyl-CoA catabolic process</a>	15	0.0023	4	0.0149	1.0000000	E
<input type="radio"/>	GO:0000902	5,6	<a href="#">cell morphogenesis</a>	248	0.0383	12	0.0446	1.0000000	E
<input type="radio"/>	GO:0044237	3	<a href="#">cellular metabolic process</a>	3403	0.5255	150	0.5576	1.0000000	E
<input type="radio"/>	GO:0015793	5,6	<a href="#">glycerol transport</a>	4	0.0006	1	0.0037	1.0000000	E
<input type="radio"/>	GO:0045333	5	<a href="#">cellular respiration</a>	89	0.0137	10	0.0372	1.0000000	E
<input type="radio"/>	GO:0031106	7	<a href="#">septin ring organization</a>	9	0.0014	1	0.0037	1.0000000	E
<input type="radio"/>	GO:0030865	6	<a href="#">cortical cytoskeleton organization and biogenesis</a>	16	0.0025	3	0.0112	1.0000000	E
<input type="radio"/>	GO:0009164	5,6	<a href="#">nucleoside catabolic process</a>	4	0.0006	1	0.0037	1.0000000	E
<input type="radio"/>	GO:0007035	13,10,6,11	<a href="#">vacuolar acidification</a>	24	0.0037	1	0.0037	1.0000000	E
<input type="radio"/>	GO:0016044	4	<a href="#">membrane organization and biogenesis</a>	188	0.0290	15	0.0558	1.0000000	E
<input type="radio"/>	GO:0006108	7	<a href="#">malate metabolic process</a>	3	0.0005	1	0.0037	1.0000000	E
<input type="radio"/>	GO:0008104	4	<a href="#">protein localization</a>	330	0.0510	15	0.0558	1.0000000	E
<input type="radio"/>	GO:0006515	8,9	<a href="#">misfolded or incompletely synthesized protein catabolic process</a>	38	0.0059	2	0.0074	1.0000000	E
<input type="radio"/>	GO:0008152	2	<a href="#">metabolic process</a>	3516	0.5429	161	0.5985	1.0000000	E
<input type="radio"/>	GO:0016197	7,5,6	<a href="#">endosome transport</a>	49	0.0076	3	0.0112	1.0000000	E
<input type="radio"/>	GO:0009220	7,8	<a href="#">pyrimidine ribonucleotide biosynthetic process</a>	2	0.0003	1	0.0037	1.0000000	E
<input type="radio"/>	GO:0033260	8,7,6	<a href="#">DNA replication during S phase</a>	2	0.0003	1	0.0037	1.0000000	E
<input type="radio"/>	GO:0009119	6	<a href="#">ribonucleoside metabolic process</a>	13	0.0020	1	0.0037	1.0000000	E
<input type="radio"/>	GO:0000080	7,8,6	<a href="#">G1 phase of mitotic cell cycle</a>	27	0.0042	2	0.0074	1.0000000	E
<input type="radio"/>	GO:0051187	5	<a href="#">cofactor catabolic process</a>	21	0.0032	5	0.0186	1.0000000	E
<input type="radio"/>	GO:0006285	7,8	<a href="#">base-excision repair, AP site formation</a>	3	0.0005	1	0.0037	1.0000000	E
<input type="radio"/>	GO:0006592	8,9,6,5	<a href="#">ornithine biosynthetic process</a>	4	0.0006	1	0.0037	1.0000000	E
<input type="radio"/>	GO:0009086	8,9,7	<a href="#">methionine biosynthetic process</a>	7	0.0011	1	0.0037	1.0000000	E
<input type="radio"/>	GO:0046467	6,5,7	<a href="#">membrane lipid biosynthetic process</a>	78	0.0120	7	0.0260	1.0000000	E

<input type="checkbox"/>	GO:0006040	5,6	<a href="#">amino sugar metabolic process</a>	19	0.0029	3	0.0112	1.0000000	E
<input type="checkbox"/>	GO:0019432	7,8,9	<a href="#">triacylglycerol biosynthetic process</a>	2	0.0003	2	0.0074	1.0000000	E
<input type="checkbox"/>	GO:0006470	8,7	<a href="#">protein amino acid dephosphorylation</a>	29	0.0045	2	0.0074	1.0000000	E
<input type="checkbox"/>	GO:0042454	6,7	<a href="#">ribonucleoside catabolic process</a>	1	0.0002	1	0.0037	1.0000000	E
<input type="checkbox"/>	GO:0043254	6,7,5	<a href="#">regulation of protein complex assembly</a>	6	0.0009	1	0.0037	1.0000000	E
<input type="checkbox"/>	GO:0030163	6,5	<a href="#">protein catabolic process</a>	173	0.0267	10	0.0372	1.0000000	E
<input type="checkbox"/>	GO:0006216	8,9	<a href="#">cytidine catabolic process</a>	1	0.0002	1	0.0037	1.0000000	E
<input type="checkbox"/>	GO:0007007	6,7	<a href="#">inner mitochondrial membrane organization and biogenesis</a>	12	0.0019	1	0.0037	1.0000000	E
<input type="checkbox"/>	GO:0042157	6	<a href="#">lipoprotein metabolic process</a>	48	0.0074	3	0.0112	1.0000000	E
<input type="checkbox"/>	GO:0006839	7,5,6	<a href="#">mitochondrial transport</a>	65	0.0100	6	0.0223	1.0000000	E
<input type="checkbox"/>	GO:0006465	9,5	<a href="#">signal peptide processing</a>	7	0.0011	1	0.0037	1.0000000	E
<input type="checkbox"/>	GO:0006974	4	<a href="#">response to DNA damage stimulus</a>	234	0.0361	12	0.0446	1.0000000	E
<input type="checkbox"/>	GO:0045185	5,4,3	<a href="#">maintenance of protein localization</a>	30	0.0046	2	0.0074	1.0000000	E
<input type="checkbox"/>	GO:0031382	9,8,10,7	<a href="#">mating projection biogenesis</a>	7	0.0011	1	0.0037	1.0000000	E
<input type="checkbox"/>	GO:0018410	8	<a href="#">peptide or protein carboxyl-terminal blocking</a>	5	0.0008	1	0.0037	1.0000000	E
<input type="checkbox"/>	GO:0015893	4,5	<a href="#">drug transport</a>	13	0.0020	2	0.0074	1.0000000	E
<input type="checkbox"/>	GO:0045324	8,6,7	<a href="#">late endosome to vacuole transport</a>	21	0.0032	2	0.0074	1.0000000	E
<input type="checkbox"/>	GO:0051188	5	<a href="#">cofactor biosynthetic process</a>	79	0.0122	4	0.0149	1.0000000	E
<input type="checkbox"/>	GO:0006096	9,10	<a href="#">glycolysis</a>	24	0.0037	1	0.0037	1.0000000	E
<input type="checkbox"/>	GO:0015840	5,6	<a href="#">urea transport</a>	2	0.0003	1	0.0037	1.0000000	E
<input type="checkbox"/>	GO:0048468	3,5	<a href="#">cell development</a>	52	0.0080	3	0.0112	1.0000000	E
<input type="checkbox"/>	GO:0046489	9,8,10	<a href="#">phosphoinositide biosynthetic process</a>	28	0.0043	2	0.0074	1.0000000	E
<input type="checkbox"/>	GO:0015849	4,5	<a href="#">organic acid transport</a>	55	0.0085	5	0.0186	1.0000000	E
<input type="checkbox"/>	GO:0005991	6,7	<a href="#">trehalose metabolic process</a>	10	0.0015	1	0.0037	1.0000000	E
<input type="checkbox"/>	GO:0019740	4	<a href="#">nitrogen utilization</a>	17	0.0026	2	0.0074	1.0000000	E
<input type="checkbox"/>	GO:0006605	8,6,7	<a href="#">protein targeting</a>	258	0.0398	13	0.0483	1.0000000	E
<input type="checkbox"/>	GO:0045184	3,4,5	<a href="#">establishment of protein localization</a>	296	0.0457	14	0.0520	1.0000000	E
<input type="checkbox"/>	GO:0009056	3	<a href="#">catabolic process</a>	438	0.0676	28	0.1041	1.0000000	E
<input type="checkbox"/>	GO:0019794	6,7	<a href="#">nonprotein amino acid metabolic process</a>	9	0.0014	2	0.0074	1.0000000	E
<input type="checkbox"/>	GO:0031023	5	<a href="#">microtubule organizing center organization and biogenesis</a>	16	0.0025	1	0.0037	1.0000000	E
<input type="checkbox"/>	GO:0006778	5,6	<a href="#">porphyrin metabolic process</a>	14	0.0022	1	0.0037	1.0000000	E
<input type="checkbox"/>	GO:0009435	8,7,10,9	<a href="#">NAD biosynthetic process</a>	7	0.0011	2	0.0074	1.0000000	E
<input type="checkbox"/>	GO:0051789	4	<a href="#">response to protein stimulus</a>	18	0.0028	3	0.0112	1.0000000	E
<input type="checkbox"/>	GO:0006650	7,8	<a href="#">glycerophospholipid metabolic process</a>	60	0.0093	7	0.0260	1.0000000	E
<input type="checkbox"/>	GO:0009437	6,7	<a href="#">carnitine metabolic process</a>	3	0.0005	1	0.0037	1.0000000	E
<input type="checkbox"/>	GO:0008361	4,6,7	<a href="#">regulation of cell size</a>	129	0.0199	6	0.0223	1.0000000	E
<input type="checkbox"/>	GO:0019362	7,6	<a href="#">pyridine nucleotide metabolic process</a>	45	0.0069	5	0.0186	1.0000000	E
<input type="checkbox"/>	GO:0051647	6,5	<a href="#">nucleus localization</a>	20	0.0031	1	0.0037	1.0000000	E
<input type="checkbox"/>	GO:0006914	3	<a href="#">autophagy</a>	45	0.0069	6	0.0223	1.0000000	E
<input type="checkbox"/>	GO:0045003	9,8	<a href="#">double-strand break repair via synthesis-dependent strand annealing</a>	17	0.0026	2	0.0074	1.0000000	E
<input type="checkbox"/>	GO:0007346	7,5,6	<a href="#">regulation of progression through mitotic cell cycle</a>	13	0.0020	1	0.0037	1.0000000	E
<input type="checkbox"/>	GO:0046349	6,7	<a href="#">amino sugar biosynthetic process</a>	17	0.0026	3	0.0112	1.0000000	E
<input type="checkbox"/>	GO:0030866	8,7	<a href="#">cortical actin cytoskeleton organization and biogenesis</a>	16	0.0025	3	0.0112	1.0000000	E
<input type="checkbox"/>	GO:0006743	7,6	<a href="#">ubiquinone metabolic process</a>	9	0.0014	1	0.0037	1.0000000	E

<input type="checkbox"/>	GO:0030491	7,9,10,6,8	<a href="#">heteroduplex formation</a>	9	0.0014	2	0.0074	1.0000000	E
<input type="checkbox"/>	GO:0046135	6,7	<a href="#">pyrimidine nucleoside catabolic process</a>	2	0.0003	1	0.0037	1.0000000	E
<input type="checkbox"/>	GO:0007094	9,11,10,8	<a href="#">mitotic cell cycle spindle assembly checkpoint</a>	20	0.0031	1	0.0037	1.0000000	E
<input type="checkbox"/>	GO:0032505	4,3	<a href="#">reproduction of a single-celled organism</a>	194	0.0300	15	0.0558	1.0000000	E
<input type="checkbox"/>	GO:0006526	8,9,6,5	<a href="#">arginine biosynthetic process</a>	10	0.0015	3	0.0112	1.0000000	E
<input type="checkbox"/>	GO:0006544	7,8	<a href="#">glycine metabolic process</a>	6	0.0009	3	0.0112	1.0000000	E
<input type="checkbox"/>	GO:0000726	7,6	<a href="#">non-recombinational repair</a>	35	0.0054	3	0.0112	1.0000000	E
<input type="checkbox"/>	GO:0009166	5,6	<a href="#">nucleotide catabolic process</a>	7	0.0011	1	0.0037	1.0000000	E
<input type="checkbox"/>	GO:0009126	7	<a href="#">purine nucleoside monophosphate metabolic process</a>	18	0.0028	1	0.0037	1.0000000	E
<input type="checkbox"/>	GO:0006626	9,8,7,6	<a href="#">protein targeting to mitochondrion</a>	52	0.0080	4	0.0149	1.0000000	E
<input type="checkbox"/>	GO:0016575	11,9	<a href="#">histone deacetylation</a>	24	0.0037	1	0.0037	1.0000000	E
<input type="checkbox"/>	GO:0019856	7,6	<a href="#">pyrimidine base biosynthetic process</a>	15	0.0023	1	0.0037	1.0000000	E
<input type="checkbox"/>	GO:0006037	8,9,6,7,10	<a href="#">cell wall chitin metabolic process</a>	14	0.0022	1	0.0037	1.0000000	E
<input type="checkbox"/>	GO:0008655	5	<a href="#">pyrimidine salvage</a>	5	0.0008	1	0.0037	1.0000000	E
<input type="checkbox"/>	GO:0032210	7,10,6	<a href="#">regulation of telomere maintenance via telomerase</a>	2	0.0003	1	0.0037	1.0000000	E
<input type="checkbox"/>	GO:0048590	3	<a href="#">non-developmental growth</a>	35	0.0054	3	0.0112	1.0000000	E
<input type="checkbox"/>	GO:0009201	7,8	<a href="#">ribonucleoside triphosphate biosynthetic process</a>	24	0.0037	1	0.0037	1.0000000	E
<input type="checkbox"/>	GO:0000103	6	<a href="#">sulfate assimilation</a>	10	0.0015	2	0.0074	1.0000000	E
<input type="checkbox"/>	GO:0000128	3	<a href="#">flocculation</a>	9	0.0014	1	0.0037	1.0000000	E
<input type="checkbox"/>	GO:0006835	6,7	<a href="#">dicarboxylic acid transport</a>	3	0.0005	1	0.0037	1.0000000	E
<input type="checkbox"/>	GO:0000084	8,7,6	<a href="#">S phase of mitotic cell cycle</a>	18	0.0028	1	0.0037	1.0000000	E
<input type="checkbox"/>	GO:0030466	11,7,8,12,10	<a href="#">chromatin silencing at silent mating-type cassette</a>	30	0.0046	2	0.0074	1.0000000	E
<input type="checkbox"/>	GO:0006031	9,7,8,10	<a href="#">chitin biosynthetic process</a>	15	0.0023	2	0.0074	1.0000000	E
<input type="checkbox"/>	GO:0006591	7,8,5,4	<a href="#">ornithine metabolic process</a>	6	0.0009	2	0.0074	1.0000000	E
<input type="checkbox"/>	GO:0022610	2	<a href="#">biological adhesion</a>	9	0.0014	1	0.0037	1.0000000	E
<input type="checkbox"/>	GO:0030011	7,4,8	<a href="#">maintenance of cell polarity</a>	8	0.0012	1	0.0037	1.0000000	E
<input type="checkbox"/>	GO:0006576	5,6	<a href="#">biogenic amine metabolic process</a>	24	0.0037	1	0.0037	1.0000000	E
<input type="checkbox"/>	GO:0043648	6	<a href="#">dicarboxylic acid metabolic process</a>	9	0.0014	2	0.0074	1.0000000	E
<input type="checkbox"/>	GO:0006241	9,10	<a href="#">CTP biosynthetic process</a>	2	0.0003	1	0.0037	1.0000000	E
<input type="checkbox"/>	GO:0019236	4	<a href="#">response to pheromone</a>	94	0.0145	4	0.0149	1.0000000	E
<input type="checkbox"/>	GO:0007033	5	<a href="#">vacuole organization and biogenesis</a>	67	0.0103	3	0.0112	1.0000000	E
<input type="checkbox"/>	GO:0045021	7,6	<a href="#">error-free DNA repair</a>	4	0.0006	1	0.0037	1.0000000	E
<input type="checkbox"/>	GO:0015791	4,5	<a href="#">polyol transport</a>	6	0.0009	2	0.0074	1.0000000	E
<input type="checkbox"/>	GO:0030472	6,5,10	<a href="#">mitotic spindle organization and biogenesis in nucleus</a>	22	0.0034	1	0.0037	1.0000000	E
<input type="checkbox"/>	GO:0019650	7	<a href="#">glucose catabolic process to butanediol</a>	1	0.0002	1	0.0037	1.0000000	E
<input type="checkbox"/>	GO:0042724	7	<a href="#">thiamin and derivative biosynthetic process</a>	20	0.0031	3	0.0112	1.0000000	E
<input type="checkbox"/>	GO:0006749	6,5	<a href="#">glutathione metabolic process</a>	14	0.0022	3	0.0112	1.0000000	E
<input type="checkbox"/>	GO:0046164	5	<a href="#">alcohol catabolic process</a>	47	0.0073	2	0.0074	1.0000000	E
<input type="checkbox"/>	GO:0006536	7,8	<a href="#">glutamate metabolic process</a>	16	0.0025	3	0.0112	1.0000000	E
<input type="checkbox"/>	GO:0030641	10,8	<a href="#">cellular hydrogen ion homeostasis</a>	25	0.0039	2	0.0074	1.0000000	E
<input type="checkbox"/>	GO:0006641	7,6,8	<a href="#">triacylglycerol metabolic process</a>	5	0.0008	2	0.0074	1.0000000	E
<input type="checkbox"/>	GO:0045332	5,7,6,8	<a href="#">phospholipid translocation</a>	7	0.0011	1	0.0037	1.0000000	E
<input type="checkbox"/>	GO:0048308	5	<a href="#">organelle inheritance</a>	40	0.0062	2	0.0074	1.0000000	E
<input type="checkbox"/>	GO:0007105	6,4	<a href="#">cytokinesis, site selection</a>	66	0.0102	4	0.0149	1.0000000	E

<input type="checkbox"/>	GO:0006551	7,8	<a href="#">leucine metabolic process</a>	7	0.0011	2	0.0074	1.0000000	E
<input type="checkbox"/>	GO:0006041	6,7	<a href="#">glucosamine metabolic process</a>	19	0.0029	3	0.0112	1.0000000	E
<input type="checkbox"/>	GO:0033013	5	<a href="#">tetrapyrrole metabolic process</a>	14	0.0022	1	0.0037	1.0000000	E
<input type="checkbox"/>	GO:0030010	7,4,8	<a href="#">establishment of cell polarity</a>	103	0.0159	6	0.0223	1.0000000	E
<input type="checkbox"/>	GO:0051049	5,4	<a href="#">regulation of transport</a>	11	0.0017	1	0.0037	1.0000000	E
<input type="checkbox"/>	GO:0044273	5	<a href="#">sulfur compound catabolic process</a>	5	0.0008	1	0.0037	1.0000000	E
<input type="checkbox"/>	GO:0006607	10,11,8,9,7	<a href="#">NLS-bearing substrate import into nucleus</a>	23	0.0036	1	0.0037	1.0000000	E
<input type="checkbox"/>	GO:0006461	6,5	<a href="#">protein complex assembly</a>	116	0.0179	5	0.0186	1.0000000	E
<input type="checkbox"/>	GO:0015846	5,6	<a href="#">polyamine transport</a>	12	0.0019	1	0.0037	1.0000000	E
<input type="checkbox"/>	GO:0015809	7,8,9	<a href="#">arginine transport</a>	2	0.0003	1	0.0037	1.0000000	E
<input type="checkbox"/>	GO:0000003	2	<a href="#">reproduction</a>	323	0.0499	18	0.0669	1.0000000	E
<input type="checkbox"/>	GO:0032204	6,9,5	<a href="#">regulation of telomere maintenance</a>	2	0.0003	1	0.0037	1.0000000	E
<input type="checkbox"/>	GO:0009607	3	<a href="#">response to biotic stimulus</a>	25	0.0039	3	0.0112	1.0000000	E
<input type="checkbox"/>	GO:0009141	6	<a href="#">nucleoside triphosphate metabolic process</a>	30	0.0046	2	0.0074	1.0000000	E
<input type="checkbox"/>	GO:0006537	8,9	<a href="#">glutamate biosynthetic process</a>	13	0.0020	3	0.0112	1.0000000	E
<input type="checkbox"/>	GO:0009313	6	<a href="#">oligosaccharide catabolic process</a>	1	0.0002	1	0.0037	1.0000000	E
<input type="checkbox"/>	GO:0009063	6,7	<a href="#">amino acid catabolic process</a>	29	0.0045	5	0.0186	1.0000000	E
<input type="checkbox"/>	GO:0009161	7	<a href="#">ribonucleoside monophosphate metabolic process</a>	17	0.0026	1	0.0037	1.0000000	E
<input type="checkbox"/>	GO:0009891	6,5	<a href="#">positive regulation of biosynthetic process</a>	4	0.0006	1	0.0037	1.0000000	E
<input type="checkbox"/>	GO:0006388	9,8	<a href="#">tRNA splicing</a>	14	0.0022	1	0.0037	1.0000000	E
<input type="checkbox"/>	GO:0006301	7,6	<a href="#">postreplication repair</a>	13	0.0020	1	0.0037	1.0000000	E
<input type="checkbox"/>	GO:0048610	3,4	<a href="#">reproductive cellular process</a>	149	0.0230	12	0.0446	1.0000000	E
<input type="checkbox"/>	GO:0051453	11,8,9	<a href="#">regulation of cellular pH</a>	25	0.0039	2	0.0074	1.0000000	E
<input type="checkbox"/>	GO:0042723	6	<a href="#">thiamin and derivative metabolic process</a>	22	0.0034	3	0.0112	1.0000000	E
<input type="checkbox"/>	GO:0006000	7,8	<a href="#">fructose metabolic process</a>	6	0.0009	1	0.0037	1.0000000	E
<input type="checkbox"/>	GO:0030950	8,7	<a href="#">establishment and/or maintenance of actin cytoskeleton polarity</a>	9	0.0014	1	0.0037	1.0000000	E
<input type="checkbox"/>	GO:0051083	8	<a href="#">cotranslational protein folding</a>	5	0.0008	1	0.0037	1.0000000	E
<input type="checkbox"/>	GO:0046173	6	<a href="#">polyol biosynthetic process</a>	3	0.0005	1	0.0037	1.0000000	E
<input type="checkbox"/>	GO:0009081	6,7	<a href="#">branched chain family amino acid metabolic process</a>	16	0.0025	3	0.0112	1.0000000	E
<input type="checkbox"/>	GO:0032297	10,8,9	<a href="#">negative regulation of DNA replication initiation</a>	6	0.0009	1	0.0037	1.0000000	E
<input type="checkbox"/>	GO:0006188	9,10	<a href="#">IMP biosynthetic process</a>	14	0.0022	1	0.0037	1.0000000	E
<input type="checkbox"/>	GO:0000750	8,7,6	<a href="#">pheromone-dependent signal transduction during conjugation with cellular fusion</a>	28	0.0043	3	0.0112	1.0000000	E
<input type="checkbox"/>	GO:0007124	6,4,8,9	<a href="#">pseudohyphal growth</a>	61	0.0094	5	0.0186	1.0000000	E
<input type="checkbox"/>	GO:0045596	6,5	<a href="#">negative regulation of cell differentiation</a>	2	0.0003	2	0.0074	1.0000000	E
<input type="checkbox"/>	GO:0006808	6,5	<a href="#">regulation of nitrogen utilization</a>	8	0.0012	1	0.0037	1.0000000	E
<input type="checkbox"/>	GO:0007006	5,6	<a href="#">mitochondrial membrane organization and biogenesis</a>	24	0.0037	1	0.0037	1.0000000	E
<input type="checkbox"/>	GO:0009438	5	<a href="#">methylglyoxal metabolic process</a>	3	0.0005	1	0.0037	1.0000000	E
<input type="checkbox"/>	GO:0006885	7	<a href="#">regulation of pH</a>	29	0.0045	2	0.0074	1.0000000	E
<input type="checkbox"/>	GO:0030242	4,6	<a href="#">peroxisome degradation</a>	3	0.0005	2	0.0074	1.0000000	E
<input type="checkbox"/>	GO:0042174	7,6	<a href="#">negative regulation of sporulation</a>	2	0.0003	2	0.0074	1.0000000	E
<input type="checkbox"/>	GO:0000051	4,3	<a href="#">urea cycle intermediate metabolic process</a>	15	0.0023	4	0.0149	1.0000000	E
<input type="checkbox"/>	GO:0007114	5,4	<a href="#">cell budding</a>	85	0.0131	6	0.0223	1.0000000	E
<input type="checkbox"/>	GO:0006629	4	<a href="#">lipid metabolic process</a>	242	0.0374	17	0.0632	1.0000000	E



<input type="radio"/>	GO:0030968	7,5,6	<a href="#">unfolded protein response</a>	9	0.0014	1	0.0037	1.0000000	E
<input type="radio"/>	GO:0031505	6	<a href="#">chitin- and beta-glucan-containing cell wall organization and biogenesis</a>	44	0.0068	2	0.0074	1.0000000	E
<input type="radio"/>	GO:0030031	8,7,9	<a href="#">cell projection biogenesis</a>	8	0.0012	1	0.0037	1.0000000	E
<input type="radio"/>	GO:0016567	9	<a href="#">protein ubiquitination</a>	66	0.0102	4	0.0149	1.0000000	E
<input type="radio"/>	GO:0051641	4,3	<a href="#">cellular localization</a>	642	0.0991	29	0.1078	1.0000000	E
<input type="radio"/>	GO:0006623	9,8,7,6	<a href="#">protein targeting to vacuole</a>	67	0.0103	6	0.0223	1.0000000	E
<input type="radio"/>	GO:0042148	7,9,10,6,8	<a href="#">strand invasion</a>	1	0.0002	1	0.0037	1.0000000	E
<input type="radio"/>	GO:0000725	7,6	<a href="#">recombinational repair</a>	29	0.0045	3	0.0112	1.0000000	E
<input type="radio"/>	GO:0046125	7	<a href="#">pyrimidine deoxyribonucleoside metabolic process</a>	3	0.0005	1	0.0037	1.0000000	E
<input type="radio"/>	GO:0006084	6	<a href="#">acetyl-CoA metabolic process</a>	20	0.0031	4	0.0149	1.0000000	E
<input type="radio"/>	GO:0006766	4	<a href="#">vitamin metabolic process</a>	89	0.0137	9	0.0335	1.0000000	E
<input type="radio"/>	GO:0046127	7,8	<a href="#">pyrimidine deoxyribonucleoside catabolic process</a>	1	0.0002	1	0.0037	1.0000000	E
<input type="radio"/>	GO:0006828	8,9	<a href="#">manganese ion transport</a>	8	0.0012	1	0.0037	1.0000000	E
<input type="radio"/>	GO:0006217	8,9	<a href="#">deoxycytidine catabolic process</a>	1	0.0002	1	0.0037	1.0000000	E
<input type="radio"/>	GO:0030150	10,9,8,7	<a href="#">protein import into mitochondrial matrix</a>	22	0.0034	1	0.0037	1.0000000	E
<input type="radio"/>	GO:0006307	7,6	<a href="#">DNA dealkylation</a>	3	0.0005	1	0.0037	1.0000000	E
<input type="radio"/>	GO:0006616	9,12,11,7,10,8	<a href="#">SRP-dependent cotranslational protein targeting to membrane, translocation</a>	10	0.0015	1	0.0037	1.0000000	E
<input type="radio"/>	GO:0000011	6	<a href="#">vacuole inheritance</a>	14	0.0022	1	0.0037	1.0000000	E
<input type="radio"/>	GO:0016236	4	<a href="#">macroautophagy</a>	6	0.0009	1	0.0037	1.0000000	E
<input type="radio"/>	GO:0006272	9,8	<a href="#">leading strand elongation</a>	14	0.0022	1	0.0037	1.0000000	E
<input type="radio"/>	GO:0016192	4,5	<a href="#">vesicle-mediated transport</a>	328	0.0506	22	0.0818	1.0000000	E
<input type="radio"/>	GO:0045053	7,6,5,4	<a href="#">protein retention in Golgi</a>	20	0.0031	1	0.0037	1.0000000	E
<input type="radio"/>	GO:0046939	6,7	<a href="#">nucleotide phosphorylation</a>	1	0.0002	1	0.0037	1.0000000	E
<input type="radio"/>	GO:0000002	6	<a href="#">mitochondrial genome maintenance</a>	31	0.0048	4	0.0149	1.0000000	E
<input type="radio"/>	GO:0008202	5,6	<a href="#">steroid metabolic process</a>	43	0.0066	2	0.0074	1.0000000	E
<input type="radio"/>	GO:0015918	5,6	<a href="#">sterol transport</a>	15	0.0023	1	0.0037	1.0000000	E
<input type="radio"/>	GO:0019243	7,8,6	<a href="#">methylglyoxal catabolic process to D-lactate</a>	3	0.0005	1	0.0037	1.0000000	E
<input type="radio"/>	GO:0006826	7,8,9	<a href="#">iron ion transport</a>	20	0.0031	1	0.0037	1.0000000	E
<input type="radio"/>	GO:0007088	7,9,8,6	<a href="#">regulation of mitosis</a>	55	0.0085	3	0.0112	1.0000000	E
<input type="radio"/>	GO:0042770	5	<a href="#">DNA damage response, signal transduction</a>	14	0.0022	1	0.0037	1.0000000	E
<input type="radio"/>	GO:0000749	5	<a href="#">response to pheromone during conjugation with cellular fusion</a>	57	0.0088	3	0.0112	1.0000000	E
<input type="radio"/>	GO:0046999	5,4	<a href="#">regulation of conjugation</a>	30	0.0046	3	0.0112	1.0000000	E
<input type="radio"/>	GO:0030001	6,7	<a href="#">metal ion transport</a>	62	0.0096	5	0.0186	1.0000000	E
<input type="radio"/>	GO:0006163	6	<a href="#">purine nucleotide metabolic process</a>	47	0.0073	2	0.0074	1.0000000	E
<input type="radio"/>	GO:0015698	6,7	<a href="#">inorganic anion transport</a>	16	0.0025	1	0.0037	1.0000000	E
<input type="radio"/>	GO:0046907	6,4,5	<a href="#">intracellular transport</a>	545	0.0842	25	0.0929	1.0000000	E
<input type="radio"/>	GO:0015674	6,7	<a href="#">di-, tri-valent inorganic cation transport</a>	34	0.0053	2	0.0074	1.0000000	E
<input type="radio"/>	GO:0005976	5	<a href="#">polysaccharide metabolic process</a>	65	0.0100	4	0.0149	1.0000000	E
<input type="radio"/>	GO:0046938	6	<a href="#">phytochelatin biosynthetic process</a>	2	0.0003	1	0.0037	1.0000000	E
<input type="radio"/>	GO:0007534	6,8,7	<a href="#">gene conversion at mating-type locus</a>	23	0.0036	3	0.0112	1.0000000	E
<input type="radio"/>	GO:0009410	4	<a href="#">response to xenobiotic stimulus</a>	7	0.0011	1	0.0037	1.0000000	E
<input type="radio"/>	GO:0006384	8,9,7	<a href="#">transcription initiation from RNA polymerase III promoter</a>	11	0.0017	1	0.0037	1.0000000	E
<input type="radio"/>	GO:0007186	6	<a href="#">G-protein coupled receptor protein signaling pathway</a>	34	0.0053	3	0.0112	1.0000000	E

<input type="checkbox"/>	GO:0006970	4	<a href="#">response to osmotic stress</a>	89	0.0137	9	0.0335	1.0000000	E
<input type="checkbox"/>	GO:0000394	8	<a href="#">RNA splicing, via endonucleolytic cleavage and ligation</a>	14	0.0022	1	0.0037	1.0000000	E
<input type="checkbox"/>	GO:0019725	5,3	<a href="#">cellular homeostasis</a>	128	0.0198	9	0.0335	1.0000000	E
<input type="checkbox"/>	GO:0019363	7,6,8	<a href="#">pyridine nucleotide biosynthetic process</a>	10	0.0015	2	0.0074	1.0000000	E
<input type="checkbox"/>	GO:0006303	8,7	<a href="#">double-strand break repair via nonhomologous end joining</a>	23	0.0036	1	0.0037	1.0000000	E
<input type="checkbox"/>	GO:0006734	9,8	<a href="#">NADH metabolic process</a>	14	0.0022	1	0.0037	1.0000000	E
<input type="checkbox"/>	GO:0030447	3	<a href="#">filamentous growth</a>	94	0.0145	6	0.0223	1.0000000	E
<input type="checkbox"/>	GO:0051051	6,5	<a href="#">negative regulation of transport</a>	4	0.0006	1	0.0037	1.0000000	E
<input type="checkbox"/>	GO:0006042	7,8	<a href="#">glucosamine biosynthetic process</a>	17	0.0026	3	0.0112	1.0000000	E
<input type="checkbox"/>	GO:0006038	9,10,7,8,11	<a href="#">cell wall chitin biosynthetic process</a>	13	0.0020	1	0.0037	1.0000000	E
<input type="checkbox"/>	GO:0009132	6	<a href="#">nucleoside diphosphate metabolic process</a>	3	0.0005	1	0.0037	1.0000000	E
<input type="checkbox"/>	GO:0009209	8,9	<a href="#">pyrimidine ribonucleoside triphosphate biosynthetic process</a>	2	0.0003	1	0.0037	1.0000000	E
<input type="checkbox"/>	GO:0009991	4	<a href="#">response to extracellular stimulus</a>	37	0.0057	2	0.0074	1.0000000	E
<input type="checkbox"/>	GO:0007010	5	<a href="#">cytoskeleton organization and biogenesis</a>	227	0.0351	14	0.0520	1.0000000	E
<input type="checkbox"/>	GO:0007120	8,6,10,7,11,5	<a href="#">axial cellular bud site selection</a>	22	0.0034	1	0.0037	1.0000000	E
<input type="checkbox"/>	GO:0042375	5	<a href="#">quinone cofactor metabolic process</a>	9	0.0014	1	0.0037	1.0000000	E
<input type="checkbox"/>	GO:0046504	5	<a href="#">glycerol ether biosynthetic process</a>	2	0.0003	2	0.0074	1.0000000	E
<input type="checkbox"/>	GO:0015914	5,6	<a href="#">phospholipid transport</a>	12	0.0019	1	0.0037	1.0000000	E
<input type="checkbox"/>	GO:0006751	7,6	<a href="#">glutathione catabolic process</a>	4	0.0006	1	0.0037	1.0000000	E
<input type="checkbox"/>	GO:0006487	9,8,7	<a href="#">protein amino acid N-linked glycosylation</a>	48	0.0074	2	0.0074	1.0000000	E
<input type="checkbox"/>	GO:0009142	6,7	<a href="#">nucleoside triphosphate biosynthetic process</a>	27	0.0042	2	0.0074	1.0000000	E
<input type="checkbox"/>	GO:0006089	7	<a href="#">lactate metabolic process</a>	5	0.0008	1	0.0037	1.0000000	E
<input type="checkbox"/>	GO:0006165	7,8	<a href="#">nucleoside diphosphate phosphorylation</a>	1	0.0002	1	0.0037	1.0000000	E
<input type="checkbox"/>	GO:0009636	4	<a href="#">response to toxin</a>	28	0.0043	3	0.0112	1.0000000	E
<input type="checkbox"/>	GO:0006547	7,8	<a href="#">histidine metabolic process</a>	14	0.0022	2	0.0074	1.0000000	E
<input type="checkbox"/>	GO:0000288	10,8,9	<a href="#">mRNA catabolic process, deadenylation-dependent decay</a>	24	0.0037	1	0.0037	1.0000000	E
<input type="checkbox"/>	GO:0007034	7,5,6	<a href="#">vacuolar transport</a>	114	0.0176	8	0.0297	1.0000000	E
<input type="checkbox"/>	GO:0000097	7,8,6	<a href="#">sulfur amino acid biosynthetic process</a>	13	0.0020	1	0.0037	1.0000000	E
<input type="checkbox"/>	GO:0008213	8	<a href="#">protein amino acid alkylation</a>	23	0.0036	2	0.0074	1.0000000	E
<input type="checkbox"/>	GO:0022401	7,6	<a href="#">adaptation of signaling pathway</a>	15	0.0023	1	0.0037	1.0000000	E
<input type="checkbox"/>	GO:0006508	6	<a href="#">proteolysis</a>	178	0.0275	10	0.0372	1.0000000	E
<input type="checkbox"/>	GO:0046087	8	<a href="#">cytidine metabolic process</a>	2	0.0003	1	0.0037	1.0000000	E
<input type="checkbox"/>	GO:0006610	10,11,8,9,7	<a href="#">ribosomal protein import into nucleus</a>	23	0.0036	1	0.0037	1.0000000	E
<input type="checkbox"/>	GO:0051651	5,4,3	<a href="#">maintenance of cellular localization</a>	29	0.0045	2	0.0074	1.0000000	E
<input type="checkbox"/>	GO:0022607	4	<a href="#">cellular component assembly</a>	471	0.0727	20	0.0743	1.0000000	E
<input type="checkbox"/>	GO:0007264	6	<a href="#">small GTPase mediated signal transduction</a>	61	0.0094	4	0.0149	1.0000000	E
<input type="checkbox"/>	GO:0046352	7	<a href="#">disaccharide catabolic process</a>	24	0.0037	1	0.0037	1.0000000	E
<input type="checkbox"/>	GO:0006879	10,8	<a href="#">cellular iron ion homeostasis</a>	38	0.0059	2	0.0074	1.0000000	E
<input type="checkbox"/>	GO:0007266	8	<a href="#">Rho protein signal transduction</a>	17	0.0026	2	0.0074	1.0000000	E
<input type="checkbox"/>	GO:0043044	10	<a href="#">ATP-dependent chromatin remodeling</a>	23	0.0036	1	0.0037	1.0000000	E
<input type="checkbox"/>	GO:0065002	8,6,7	<a href="#">intracellular protein transport across a membrane</a>	11	0.0017	1	0.0037	1.0000000	E
<input type="checkbox"/>	GO:0030026	10,8	<a href="#">cellular manganese ion homeostasis</a>	5	0.0008	1	0.0037	1.0000000	E
<input type="checkbox"/>	GO:0050794	4,3	<a href="#">regulation of cellular process</a>	738	0.1140	31	0.1152	1.0000000	E
<input type="checkbox"/>	GO:0042244	5,6	<a href="#">spore wall assembly</a>	42	0.0065	4	0.0149	1.0000000	E

<input type="radio"/>	GO:0046112	6,5	<a href="#">nucleobase biosynthetic process</a>	21	0.0032	1	0.0037	1.0000000	E
<input type="radio"/>	GO:0006643	5,6	<a href="#">membrane lipid metabolic process</a>	125	0.0193	10	0.0372	1.0000000	E
<input type="radio"/>	GO:0007166	5	<a href="#">cell surface receptor linked signal transduction</a>	52	0.0080	4	0.0149	1.0000000	E
<input type="radio"/>	GO:0031532	8	<a href="#">actin cytoskeleton reorganization</a>	4	0.0006	1	0.0037	1.0000000	E
<input type="radio"/>	GO:0030037	5,4,9	<a href="#">actin filament reorganization during cell cycle</a>	4	0.0006	1	0.0037	1.0000000	E
<input type="radio"/>	GO:0032185	6	<a href="#">septin cytoskeleton organization and biogenesis</a>	9	0.0014	1	0.0037	1.0000000	E
<input type="radio"/>	GO:0043419	6	<a href="#">urea catabolic process</a>	2	0.0003	1	0.0037	1.0000000	E
<input type="radio"/>	GO:0006779	6,7	<a href="#">porphyrin biosynthetic process</a>	13	0.0020	1	0.0037	1.0000000	E
<input type="radio"/>	GO:0022414	3,2	<a href="#">reproductive process</a>	183	0.0283	14	0.0520	1.0000000	E
<input type="radio"/>	GO:0031119	8,9	<a href="#">tRNA pseudouridine synthesis</a>	4	0.0006	1	0.0037	1.0000000	E
<input type="radio"/>	GO:0008643	4,5	<a href="#">carbohydrate transport</a>	38	0.0059	2	0.0074	1.0000000	E
<input type="radio"/>	GO:0006769	8,7	<a href="#">nicotinamide metabolic process</a>	42	0.0065	5	0.0186	1.0000000	E
<input type="radio"/>	GO:0006006	7,8	<a href="#">glucose metabolic process</a>	65	0.0100	6	0.0223	1.0000000	E
<input type="radio"/>	GO:0006733	6	<a href="#">oxidoreduction coenzyme metabolic process</a>	56	0.0086	6	0.0223	1.0000000	E
<input type="radio"/>	GO:0055072	9	<a href="#">iron ion homeostasis</a>	38	0.0059	2	0.0074	1.0000000	E
<input type="radio"/>	GO:0032507	6,5,4	<a href="#">maintenance of cellular protein localization</a>	29	0.0045	2	0.0074	1.0000000	E
<input type="radio"/>	GO:0016053	5	<a href="#">organic acid biosynthetic process</a>	17	0.0026	2	0.0074	1.0000000	E
<input type="radio"/>	GO:0046486	5,6	<a href="#">glycerolipid metabolic process</a>	5	0.0008	2	0.0074	1.0000000	E
<input type="radio"/>	GO:0009127	7,8	<a href="#">purine nucleoside monophosphate biosynthetic process</a>	16	0.0025	1	0.0037	1.0000000	E
<input type="radio"/>	GO:0006553	7,8	<a href="#">lysine metabolic process</a>	9	0.0014	1	0.0037	1.0000000	E
<input type="radio"/>	GO:0007533	5,7,6	<a href="#">mating type switching</a>	29	0.0045	3	0.0112	1.0000000	E
<input type="radio"/>	GO:0010035	4	<a href="#">response to inorganic substance</a>	24	0.0037	1	0.0037	1.0000000	E
<input type="radio"/>	GO:0015978	4	<a href="#">carbon utilization by utilization of organic compounds</a>	1	0.0002	1	0.0037	1.0000000	E
<input type="radio"/>	GO:0031669	6,5	<a href="#">cellular response to nutrient levels</a>	19	0.0029	1	0.0037	1.0000000	E
<input type="radio"/>	GO:0051294	7,8,9,5,6	<a href="#">establishment of spindle orientation</a>	10	0.0015	3	0.0112	1.0000000	E
<input type="radio"/>	GO:0044238	3	<a href="#">primary metabolic process</a>	3247	0.5014	136	0.5056	1.0000000	E
<input type="radio"/>	GO:0018205	8	<a href="#">peptidyl-lysine modification</a>	4	0.0006	1	0.0037	1.0000000	E
<input type="radio"/>	GO:0009653	4,3	<a href="#">anatomical structure morphogenesis</a>	248	0.0383	12	0.0446	1.0000000	E
<input type="radio"/>	GO:0019795	7,8	<a href="#">nonprotein amino acid biosynthetic process</a>	6	0.0009	1	0.0037	1.0000000	E
<input type="radio"/>	GO:0051726	5,4	<a href="#">regulation of cell cycle</a>	167	0.0258	10	0.0372	1.0000000	E
<input type="radio"/>	GO:0007231	6,5	<a href="#">osmosensory signaling pathway</a>	22	0.0034	1	0.0037	1.0000000	E
<input type="radio"/>	GO:0046482	5,6,8	<a href="#">para-aminobenzoic acid metabolic process</a>	1	0.0002	1	0.0037	1.0000000	E
<input type="radio"/>	GO:0006614	11,10,9,8,7	<a href="#">SRP-dependent cotranslational protein targeting to membrane</a>	20	0.0031	1	0.0037	1.0000000	E
<input type="radio"/>	GO:0000730	7,9,10,8,6	<a href="#">DNA recombinase assembly</a>	5	0.0008	1	0.0037	1.0000000	E
<input type="radio"/>	GO:0006013	7,8	<a href="#">mannose metabolic process</a>	6	0.0009	1	0.0037	1.0000000	E
<input type="radio"/>	GO:0006784	8,7,9	<a href="#">heme a biosynthetic process</a>	3	0.0005	1	0.0037	1.0000000	E
<input type="radio"/>	GO:0051320	7,6,5	<a href="#">S phase</a>	20	0.0031	2	0.0074	1.0000000	E
<input type="radio"/>	GO:0055080	7	<a href="#">cation homeostasis</a>	102	0.0158	5	0.0186	1.0000000	E
<input type="radio"/>	GO:0015749	5,6	<a href="#">monosaccharide transport</a>	26	0.0040	2	0.0074	1.0000000	E
<input type="radio"/>	GO:0045041	10,9,8,7	<a href="#">protein import into mitochondrial intermembrane space</a>	6	0.0009	2	0.0074	1.0000000	E
<input type="radio"/>	GO:0006164	6,7	<a href="#">purine nucleotide biosynthetic process</a>	41	0.0063	2	0.0074	1.0000000	E
<input type="radio"/>	GO:0048858	6,7	<a href="#">cell projection morphogenesis</a>	8	0.0012	1	0.0037	1.0000000	E
<input type="radio"/>	GO:0009120	6	<a href="#">deoxyribonucleoside metabolic process</a>	3	0.0005	1	0.0037	1.0000000	E

<input type="checkbox"/>	GO:0031929	6	<a href="#">TOR signaling pathway</a>	13	0.0020	1	0.0037	1.0000000	E
<input type="checkbox"/>	GO:0006512	8	<a href="#">ubiquitin cycle</a>	88	0.0136	7	0.0260	1.0000000	E
<input type="checkbox"/>	GO:0043412	5	<a href="#">biopolymer modification</a>	664	0.1025	28	0.1041	1.0000000	E
<input type="checkbox"/>	GO:0045595	5,4	<a href="#">regulation of cell differentiation</a>	4	0.0006	2	0.0074	1.0000000	E
<input type="checkbox"/>	GO:0055082	6,4	<a href="#">cellular chemical homeostasis</a>	115	0.0178	5	0.0186	1.0000000	E
<input type="checkbox"/>	GO:0007004	9	<a href="#">telomere maintenance via telomerase</a>	17	0.0026	1	0.0037	1.0000000	E
<input type="checkbox"/>	GO:0006740	10,9	<a href="#">NADPH regeneration</a>	14	0.0022	2	0.0074	1.0000000	E
<input type="checkbox"/>	GO:0043094	4	<a href="#">metabolic compound salvage</a>	19	0.0029	1	0.0037	1.0000000	E
<input type="checkbox"/>	GO:0009108	6	<a href="#">coenzyme biosynthetic process</a>	66	0.0102	3	0.0112	1.0000000	E
<input type="checkbox"/>	GO:0009605	3	<a href="#">response to external stimulus</a>	37	0.0057	2	0.0074	1.0000000	E
<input type="checkbox"/>	GO:0051452	12,9,10	<a href="#">cellular pH reduction</a>	24	0.0037	1	0.0037	1.0000000	E
<input type="checkbox"/>	GO:0000209	10	<a href="#">protein polyubiquitination</a>	20	0.0031	3	0.0112	1.0000000	E
<input type="checkbox"/>	GO:0032506	5,3	<a href="#">cytokinetic process</a>	88	0.0136	4	0.0149	1.0000000	E
<input type="checkbox"/>	GO:0009082	7,8	<a href="#">branched chain family amino acid biosynthetic process</a>	13	0.0020	3	0.0112	1.0000000	E
<input type="checkbox"/>	GO:0045727	8,7,6	<a href="#">positive regulation of protein biosynthetic process</a>	4	0.0006	1	0.0037	1.0000000	E
<input type="checkbox"/>	GO:0046483	4	<a href="#">heterocycle metabolic process</a>	76	0.0117	4	0.0149	1.0000000	E
<input type="checkbox"/>	GO:0008053	6	<a href="#">mitochondrial fusion</a>	4	0.0006	1	0.0037	1.0000000	E
<input type="checkbox"/>	GO:0044255	4,5	<a href="#">cellular lipid metabolic process</a>	229	0.0354	17	0.0632	1.0000000	E
<input type="checkbox"/>	GO:0009069	6,7	<a href="#">serine family amino acid metabolic process</a>	24	0.0037	3	0.0112	1.0000000	E
<input type="checkbox"/>	GO:0051052	7,6	<a href="#">regulation of DNA metabolic process</a>	41	0.0063	2	0.0074	1.0000000	E
<input type="checkbox"/>	GO:0048856	3	<a href="#">anatomical structure development</a>	248	0.0383	12	0.0446	1.0000000	E
<input type="checkbox"/>	GO:0009083	7,8	<a href="#">branched chain family amino acid catabolic process</a>	4	0.0006	1	0.0037	1.0000000	E
<input type="checkbox"/>	GO:0030003	8,6	<a href="#">cellular cation homeostasis</a>	102	0.0158	5	0.0186	1.0000000	E
<input type="checkbox"/>	GO:0009124	6,7	<a href="#">nucleoside monophosphate biosynthetic process</a>	17	0.0026	1	0.0037	1.0000000	E
<input type="checkbox"/>	GO:0006612	9,7,8	<a href="#">protein targeting to membrane</a>	39	0.0060	2	0.0074	1.0000000	E
<input type="checkbox"/>	GO:0051640	5,4	<a href="#">organelle localization</a>	56	0.0086	4	0.0149	1.0000000	E
<input type="checkbox"/>	GO:0000226	7	<a href="#">microtubule cytoskeleton organization and biogenesis</a>	81	0.0125	4	0.0149	1.0000000	E
<input type="checkbox"/>	GO:0006275	8,7	<a href="#">regulation of DNA replication</a>	19	0.0029	2	0.0074	1.0000000	E
<input type="checkbox"/>	GO:0006213	6	<a href="#">pyrimidine nucleoside metabolic process</a>	5	0.0008	1	0.0037	1.0000000	E
<input type="checkbox"/>	GO:0031383	5,7,10,9,8,6,11	<a href="#">regulation of mating projection biogenesis</a>	6	0.0009	1	0.0037	1.0000000	E
<input type="checkbox"/>	GO:0051318	6,7,5	<a href="#">G1 phase</a>	27	0.0042	2	0.0074	1.0000000	E
<input type="checkbox"/>	GO:0000755	6,5	<a href="#">cytogamy</a>	7	0.0011	1	0.0037	1.0000000	E
<input type="checkbox"/>	GO:0009651	5	<a href="#">response to salt stress</a>	15	0.0023	1	0.0037	1.0000000	E
<input type="checkbox"/>	GO:0046185	5	<a href="#">aldehyde catabolic process</a>	6	0.0009	1	0.0037	1.0000000	E
<input type="checkbox"/>	GO:0019318	6,7	<a href="#">hexose metabolic process</a>	85	0.0131	7	0.0260	1.0000000	E
<input type="checkbox"/>	GO:0006825	8,9	<a href="#">copper ion transport</a>	14	0.0022	2	0.0074	1.0000000	E
<input type="checkbox"/>	GO:0009225	5	<a href="#">nucleotide-sugar metabolic process</a>	7	0.0011	1	0.0037	1.0000000	E
<input type="checkbox"/>	GO:0043605	5	<a href="#">amide catabolic process</a>	2	0.0003	1	0.0037	1.0000000	E
<input type="checkbox"/>	GO:0006791	5	<a href="#">sulfur utilization</a>	10	0.0015	2	0.0074	1.0000000	E
<input type="checkbox"/>	GO:0033014	6	<a href="#">tetrapyrrole biosynthetic process</a>	13	0.0020	1	0.0037	1.0000000	E
<input type="checkbox"/>	GO:0009218	7	<a href="#">pyrimidine ribonucleotide metabolic process</a>	2	0.0003	1	0.0037	1.0000000	E
<input type="checkbox"/>	GO:0006206	6	<a href="#">pyrimidine base metabolic process</a>	17	0.0026	1	0.0037	1.0000000	E
<input type="checkbox"/>	GO:0050801	6	<a href="#">ion homeostasis</a>	119	0.0184	5	0.0186	1.0000000	E
<input type="checkbox"/>	GO:0000271	6,7	<a href="#">polysaccharide biosynthetic process</a>	41	0.0063	3	0.0112	1.0000000	E

<input type="checkbox"/>	GO:0007051	8	<a href="#">spindle organization and biogenesis</a>	47	0.0073	2	0.0074	1.0000000	E
<input type="checkbox"/>	GO:0007154	3	<a href="#">cell communication</a>	240	0.0371	10	0.0372	1.0000000	E
<input type="checkbox"/>	GO:0031384	6,8,11,10,9,7,12	<a href="#">regulation of initiation of mating projection growth</a>	4	0.0006	1	0.0037	1.0000000	E
<input type="checkbox"/>	GO:0006783	7,6,8	<a href="#">heme biosynthetic process</a>	13	0.0020	1	0.0037	1.0000000	E
<input type="checkbox"/>	GO:0008654	7,6,8	<a href="#">phospholipid biosynthetic process</a>	58	0.0090	6	0.0223	1.0000000	E
<input type="checkbox"/>	GO:0019751	5	<a href="#">polyol metabolic process</a>	9	0.0014	2	0.0074	1.0000000	E
<input type="checkbox"/>	GO:0010324	5	<a href="#">membrane invagination</a>	96	0.0148	11	0.0409	1.0000000	E
<input type="checkbox"/>	GO:0044257	6,7	<a href="#">cellular protein catabolic process</a>	160	0.0247	9	0.0335	1.0000000	E
<input type="checkbox"/>	GO:0016233	9	<a href="#">telomere capping</a>	5	0.0008	1	0.0037	1.0000000	E
<input type="checkbox"/>	GO:0015718	6,7	<a href="#">monocarboxylic acid transport</a>	10	0.0015	1	0.0037	1.0000000	E
<input type="checkbox"/>	GO:0009259	6	<a href="#">ribonucleotide metabolic process</a>	43	0.0066	2	0.0074	1.0000000	E
<input type="checkbox"/>	GO:0044270	5,4	<a href="#">nitrogen compound catabolic process</a>	32	0.0049	5	0.0186	1.0000000	E
<input type="checkbox"/>	GO:0006220	6	<a href="#">pyrimidine nucleotide metabolic process</a>	7	0.0011	1	0.0037	1.0000000	E
<input type="checkbox"/>	GO:0006505	9,10	<a href="#">GPI anchor metabolic process</a>	27	0.0042	2	0.0074	1.0000000	E
<input type="checkbox"/>	GO:0006730	4	<a href="#">one-carbon compound metabolic process</a>	97	0.0150	7	0.0260	1.0000000	E
<input type="checkbox"/>	GO:0016579	9	<a href="#">protein deubiquitination</a>	20	0.0031	3	0.0112	1.0000000	E
<input type="checkbox"/>	GO:0051649	5,3,4	<a href="#">establishment of cellular localization</a>	606	0.0936	28	0.1041	1.0000000	E
<input type="checkbox"/>	GO:0006621	7,6,5,4	<a href="#">protein retention in ER</a>	7	0.0011	1	0.0037	1.0000000	E
<input type="checkbox"/>	GO:0044272	5	<a href="#">sulfur compound biosynthetic process</a>	22	0.0034	1	0.0037	1.0000000	E
<input type="checkbox"/>	GO:0032989	4,5	<a href="#">cellular structure morphogenesis</a>	248	0.0383	12	0.0446	1.0000000	E
<input type="checkbox"/>	GO:0007121	8,6,10,7,11,5	<a href="#">bipolar cellular bud site selection</a>	32	0.0049	4	0.0149	1.0000000	E
<input type="checkbox"/>	GO:0043603	4	<a href="#">amide metabolic process</a>	2	0.0003	1	0.0037	1.0000000	E
<input type="checkbox"/>	GO:0009064	6,7	<a href="#">glutamine family amino acid metabolic process</a>	43	0.0066	7	0.0260	1.0000000	E
<input type="checkbox"/>	GO:0006097	6,8	<a href="#">glyoxylate cycle</a>	4	0.0006	1	0.0037	1.0000000	E
<input type="checkbox"/>	GO:0000707	11,9,8,5,6,10,7,4	<a href="#">meiotic DNA recombinase assembly</a>	5	0.0008	1	0.0037	1.0000000	E
<input type="checkbox"/>	GO:0030384	8,9	<a href="#">phosphoinositide metabolic process</a>	43	0.0066	2	0.0074	1.0000000	E
<input type="checkbox"/>	GO:0009156	7,8	<a href="#">ribonucleoside monophosphate biosynthetic process</a>	15	0.0023	1	0.0037	1.0000000	E
<input type="checkbox"/>	GO:0007265	7	<a href="#">Ras protein signal transduction</a>	39	0.0060	3	0.0112	1.0000000	E
<input type="checkbox"/>	GO:0005993	8,7	<a href="#">trehalose catabolic process</a>	3	0.0005	1	0.0037	1.0000000	E
<input type="checkbox"/>	GO:0030004	9,7	<a href="#">cellular monovalent inorganic cation homeostasis</a>	34	0.0053	2	0.0074	1.0000000	E
<input type="checkbox"/>	GO:0050789	3	<a href="#">regulation of biological process</a>	761	0.1175	32	0.1190	1.0000000	E
<input type="checkbox"/>	GO:0006613	10,9,8,7,6	<a href="#">cotranslational protein targeting to membrane</a>	23	0.0036	1	0.0037	1.0000000	E
<input type="checkbox"/>	GO:0000075	7,6	<a href="#">cell cycle checkpoint</a>	53	0.0082	3	0.0112	1.0000000	E
<input type="checkbox"/>	GO:0006045	8,9	<a href="#">N-acetylglucosamine biosynthetic process</a>	17	0.0026	3	0.0112	1.0000000	E
<input type="checkbox"/>	GO:0046131	7	<a href="#">pyrimidine ribonucleoside metabolic process</a>	2	0.0003	1	0.0037	1.0000000	E
<input type="checkbox"/>	GO:0006772	7	<a href="#">thiamin metabolic process</a>	20	0.0031	3	0.0112	1.0000000	E
<input type="checkbox"/>	GO:0046133	7,8	<a href="#">pyrimidine ribonucleoside catabolic process</a>	1	0.0002	1	0.0037	1.0000000	E
<input type="checkbox"/>	GO:0032446	8	<a href="#">protein modification by small protein conjugation</a>	84	0.0130	4	0.0149	1.0000000	E
<input type="checkbox"/>	GO:0006302	7,6	<a href="#">double-strand break repair</a>	57	0.0088	3	0.0112	1.0000000	E
<input type="checkbox"/>	GO:0046036	9	<a href="#">CTP metabolic process</a>	2	0.0003	1	0.0037	1.0000000	E
<input type="checkbox"/>	GO:0006767	5	<a href="#">water-soluble vitamin metabolic process</a>	89	0.0137	9	0.0335	1.0000000	E
<input type="checkbox"/>	GO:0042168	6,7,5	<a href="#">heme metabolic process</a>	14	0.0022	1	0.0037	1.0000000	E
<input type="checkbox"/>	GO:0030705	7,5,6	<a href="#">cytoskeleton-dependent intracellular transport</a>	17	0.0026	1	0.0037	1.0000000	E

<input type="radio"/>	GO:0006114	7,6	<a href="#">glycerol biosynthetic process</a>	3	0.0005	1	0.0037	1.0000000	E
<input type="radio"/>	GO:0006112	5	<a href="#">energy reserve metabolic process</a>	39	0.0060	2	0.0074	1.0000000	E
<input type="radio"/>	GO:0006408	11,9,6,8,10,7	<a href="#">snRNA export from nucleus</a>	23	0.0036	1	0.0037	1.0000000	E
<input type="radio"/>	GO:0030473	8,9,6,7	<a href="#">nuclear migration, microtubule-mediated</a>	15	0.0023	1	0.0037	1.0000000	E
<input type="radio"/>	GO:0009208	8	<a href="#">pyrimidine ribonucleoside triphosphate metabolic process</a>	2	0.0003	1	0.0037	1.0000000	E
<input type="radio"/>	GO:0046474	8,7,9	<a href="#">glycerophospholipid biosynthetic process</a>	39	0.0060	5	0.0186	1.0000000	E
<input type="radio"/>	GO:0042886	4,5	<a href="#">amide transport</a>	2	0.0003	1	0.0037	1.0000000	E
<input type="radio"/>	GO:0048284	5	<a href="#">organelle fusion</a>	22	0.0034	1	0.0037	1.0000000	E
<input type="radio"/>	GO:0006311	10,8,7,5,9,6,4	<a href="#">meiotic gene conversion</a>	22	0.0034	1	0.0037	1.0000000	E
<input type="radio"/>	GO:0009262	6	<a href="#">deoxyribonucleotide metabolic process</a>	9	0.0014	1	0.0037	1.0000000	E
<input type="radio"/>	GO:0030030	7,6,8	<a href="#">cell projection organization and biogenesis</a>	8	0.0012	1	0.0037	1.0000000	E
<input type="radio"/>	GO:0006897	6,5	<a href="#">endocytosis</a>	86	0.0133	10	0.0372	1.0000000	E
<input type="radio"/>	GO:0019660	6	<a href="#">glycolytic fermentation</a>	8	0.0012	1	0.0037	1.0000000	E
<input type="radio"/>	GO:0009147	7	<a href="#">pyrimidine nucleoside triphosphate metabolic process</a>	4	0.0006	1	0.0037	1.0000000	E
<input type="radio"/>	GO:0000282	7,9,5,6,10	<a href="#">cellular bud site selection</a>	66	0.0102	4	0.0149	1.0000000	E
<input type="radio"/>	GO:0031137	6,5	<a href="#">regulation of conjugation with cellular fusion</a>	30	0.0046	3	0.0112	1.0000000	E
<input type="radio"/>	GO:0031328	7,6	<a href="#">positive regulation of cellular biosynthetic process</a>	4	0.0006	1	0.0037	1.0000000	E
<input type="radio"/>	GO:0007155	3	<a href="#">cell adhesion</a>	9	0.0014	1	0.0037	1.0000000	E
<input type="radio"/>	GO:0007118	7,6,5	<a href="#">budding cell apical bud growth</a>	14	0.0022	2	0.0074	1.0000000	E
<input type="radio"/>	GO:0009085	8,9	<a href="#">lysine biosynthetic process</a>	9	0.0014	1	0.0037	1.0000000	E
<input type="radio"/>	GO:0016049	5,3,7,8	<a href="#">cell growth</a>	102	0.0158	6	0.0223	1.0000000	E
<input type="radio"/>	GO:0001558	5,6,4,8,9	<a href="#">regulation of cell growth</a>	11	0.0017	1	0.0037	1.0000000	E
<input type="radio"/>	GO:0000753	7,8,6	<a href="#">cellular morphogenesis during conjugation with cellular fusion</a>	18	0.0028	2	0.0074	1.0000000	E
<input type="radio"/>	GO:0044248	4	<a href="#">cellular catabolic process</a>	425	0.0656	27	0.1004	1.0000000	E
<input type="radio"/>	GO:0009167	8	<a href="#">purine ribonucleoside monophosphate metabolic process</a>	17	0.0026	1	0.0037	1.0000000	E
<input type="radio"/>	GO:0043687	7	<a href="#">post-translational protein modification</a>	388	0.0599	21	0.0781	1.0000000	E
<input type="radio"/>	GO:0030468	8,5,9	<a href="#">establishment of cell polarity (sensu Fungi)</a>	66	0.0102	4	0.0149	1.0000000	E
<input type="radio"/>	GO:0000028	9,7,8,6	<a href="#">ribosomal small subunit assembly and maintenance</a>	14	0.0022	1	0.0037	1.0000000	E
<input type="radio"/>	GO:0045010	8	<a href="#">actin nucleation</a>	3	0.0005	1	0.0037	1.0000000	E
<input type="radio"/>	GO:0032973	6,7,8	<a href="#">amino acid export</a>	3	0.0005	1	0.0037	1.0000000	E
<input type="radio"/>	GO:0015847	6,7	<a href="#">putrescine transport</a>	3	0.0005	1	0.0037	1.0000000	E
<input type="radio"/>	GO:0046487	5,7	<a href="#">glyoxylate metabolic process</a>	5	0.0008	1	0.0037	1.0000000	E
<input type="radio"/>	GO:0007015	8	<a href="#">actin filament organization</a>	61	0.0094	7	0.0260	1.0000000	E
<input type="radio"/>	GO:0046040	9	<a href="#">IMP metabolic process</a>	14	0.0022	1	0.0037	1.0000000	E
<input type="radio"/>	GO:0046174	6	<a href="#">polyol catabolic process</a>	3	0.0005	1	0.0037	1.0000000	E
<input type="radio"/>	GO:0015031	4,5,6	<a href="#">protein transport</a>	280	0.0432	14	0.0520	1.0000000	E
<input type="radio"/>	GO:0045955	8,11,7,9,10	<a href="#">negative regulation of calcium ion-dependent exocytosis</a>	1	0.0002	1	0.0037	1.0000000	E
<input type="radio"/>	GO:0042173	6,5	<a href="#">regulation of sporulation</a>	4	0.0006	2	0.0074	1.0000000	E
<input type="radio"/>	GO:0006284	7,6	<a href="#">base-excision repair</a>	12	0.0019	2	0.0074	1.0000000	E
<input type="radio"/>	GO:0006066	4	<a href="#">alcohol metabolic process</a>	163	0.0252	13	0.0483	1.0000000	E
<input type="radio"/>	GO:0015848	6,7	<a href="#">spermidine transport</a>	2	0.0003	1	0.0037	1.0000000	E
<input type="radio"/>	GO:0006633	7,6,8,5	<a href="#">fatty acid biosynthetic process</a>	13	0.0020	2	0.0074	1.0000000	E
<input type="radio"/>	GO:0015680	7,5,9,6,10	<a href="#">intracellular copper ion transport</a>	5	0.0008	1	0.0037	1.0000000	E

<input type="radio"/>	GO:0009310	5,6	<a href="#">amine catabolic process</a>	32	0.0049	5	0.0186	1.0000000	E
<input type="radio"/>	GO:0000724	8,7	<a href="#">double-strand break repair via homologous recombination</a>	25	0.0039	2	0.0074	1.0000000	E
<input type="radio"/>	GO:0045426	7,6	<a href="#">quinone cofactor biosynthetic process</a>	9	0.0014	1	0.0037	1.0000000	E
<input type="radio"/>	GO:0006739	9,8	<a href="#">NADP metabolic process</a>	17	0.0026	2	0.0074	1.0000000	E
<input type="radio"/>	GO:0032005	7,6	<a href="#">signal transduction during conjugation with cellular fusion</a>	28	0.0043	3	0.0112	1.0000000	E
<input type="radio"/>	GO:0006221	6,7	<a href="#">pyrimidine nucleotide biosynthetic process</a>	5	0.0008	1	0.0037	1.0000000	E
<input type="radio"/>	GO:0007584	6,4	<a href="#">response to nutrient</a>	18	0.0028	1	0.0037	1.0000000	E
<input type="radio"/>	GO:0033036	3	<a href="#">macromolecule localization</a>	382	0.0590	17	0.0632	1.0000000	E
<input type="radio"/>	GO:0031668	5,4	<a href="#">cellular response to extracellular stimulus</a>	19	0.0029	1	0.0037	1.0000000	E
<input type="radio"/>	GO:0000722	9,8	<a href="#">telomere maintenance via recombination</a>	19	0.0029	1	0.0037	1.0000000	E
<input type="radio"/>	GO:0051596	6	<a href="#">methylglyoxal catabolic process</a>	3	0.0005	1	0.0037	1.0000000	E
<input type="radio"/>	GO:0009058	3	<a href="#">biosynthetic process</a>	1249	0.1929	62	0.2305	1.0000000	E
<input type="radio"/>	GO:0009628	3	<a href="#">response to abiotic stimulus</a>	117	0.0181	12	0.0446	1.0000000	E
<input type="radio"/>	GO:0046460	6,5,7	<a href="#">neutral lipid biosynthetic process</a>	2	0.0003	2	0.0074	1.0000000	E
<input type="radio"/>	GO:0006464	6	<a href="#">protein modification process</a>	520	0.0803	26	0.0967	1.0000000	E
<input type="radio"/>	GO:0006513	10	<a href="#">protein monoubiquitination</a>	22	0.0034	1	0.0037	1.0000000	E
<input type="radio"/>	GO:0006869	4,5	<a href="#">lipid transport</a>	34	0.0053	2	0.0074	1.0000000	E
<input type="radio"/>	GO:0032974	8,6,7,9	<a href="#">amino acid export from vacuole</a>	3	0.0005	1	0.0037	1.0000000	E
<input type="radio"/>	GO:0006886	7,5,6	<a href="#">intracellular protein transport</a>	274	0.0423	14	0.0520	1.0000000	E
<input type="radio"/>	GO:0009267	7,6,5	<a href="#">cellular response to starvation</a>	19	0.0029	1	0.0037	1.0000000	E
<input type="radio"/>	GO:0008610	5,4,6	<a href="#">lipid biosynthetic process</a>	129	0.0199	11	0.0409	1.0000000	E
<input type="radio"/>	GO:0006033	5	<a href="#">chitin localization</a>	1	0.0002	1	0.0037	1.0000000	E
<input type="radio"/>	GO:0006044	7,8	<a href="#">N-acetylglucosamine metabolic process</a>	19	0.0029	3	0.0112	1.0000000	E
<input type="radio"/>	GO:0009165	5,6	<a href="#">nucleotide biosynthetic process</a>	59	0.0091	5	0.0186	1.0000000	E
<input type="radio"/>	GO:0006760	5,7	<a href="#">folic acid and derivative metabolic process</a>	9	0.0014	1	0.0037	1.0000000	E
<input type="radio"/>	GO:0010038	5	<a href="#">response to metal ion</a>	18	0.0028	1	0.0037	1.0000000	E
<input type="radio"/>	GO:0006890	8,6,5,7	<a href="#">retrograde vesicle-mediated transport, Golgi to ER</a>	24	0.0037	3	0.0112	1.0000000	E
<input type="radio"/>	GO:0008156	9,8	<a href="#">negative regulation of DNA replication</a>	8	0.0012	1	0.0037	1.0000000	E
<input type="radio"/>	GO:0007530	4,5	<a href="#">sex determination</a>	35	0.0054	3	0.0112	1.0000000	E
<input type="radio"/>	GO:0006479	9,7	<a href="#">protein amino acid methylation</a>	23	0.0036	2	0.0074	1.0000000	E
<input type="radio"/>	GO:0000255	5	<a href="#">allantoin metabolic process</a>	7	0.0011	1	0.0037	1.0000000	E
<input type="radio"/>	GO:0015837	4,5	<a href="#">amine transport</a>	50	0.0077	4	0.0149	1.0000000	E
<input type="radio"/>	GO:0051595	5	<a href="#">response to methylglyoxal</a>	3	0.0005	1	0.0037	1.0000000	E
<input type="radio"/>	GO:0030005	9,7	<a href="#">cellular di-, tri-valent inorganic cation homeostasis</a>	64	0.0099	3	0.0112	1.0000000	E
<input type="radio"/>	GO:0030467	7,4,8	<a href="#">establishment and/or maintenance of cell polarity (sensu Fungi)</a>	66	0.0102	4	0.0149	1.0000000	E
<input type="radio"/>	GO:0019878	9,10	<a href="#">lysine biosynthetic process via aminoadipic acid</a>	8	0.0012	1	0.0037	1.0000000	E
<input type="radio"/>	GO:0042221	3	<a href="#">response to chemical stimulus</a>	382	0.0590	26	0.0967	1.0000000	E
<input type="radio"/>	GO:0046394	6	<a href="#">carboxylic acid biosynthetic process</a>	17	0.0026	2	0.0074	1.0000000	E
<input type="radio"/>	GO:0009260	6,7	<a href="#">ribonucleotide biosynthetic process</a>	40	0.0062	2	0.0074	1.0000000	E
<input type="radio"/>	GO:0008645	6,7	<a href="#">hexose transport</a>	26	0.0040	2	0.0074	1.0000000	E
<input type="radio"/>	GO:0051653	6,5	<a href="#">spindle localization</a>	10	0.0015	3	0.0112	1.0000000	E
<input type="radio"/>	GO:0009067	7,8	<a href="#">aspartate family amino acid biosynthetic process</a>	20	0.0031	2	0.0074	1.0000000	E
<input type="radio"/>	GO:0042546	6	<a href="#">cell wall biogenesis</a>	33	0.0051	2	0.0074	1.0000000	E

<input type="checkbox"/>	GO:0043043	5	<a href="#">peptide biosynthetic process</a>	2	0.0003	1	0.0037	1.0000000	E
<input type="checkbox"/>	GO:0031667	5	<a href="#">response to nutrient levels</a>	37	0.0057	2	0.0074	1.0000000	E
<input type="checkbox"/>	GO:0006608	10,11,8,9,7	<a href="#">snRNP protein import into nucleus</a>	23	0.0036	1	0.0037	1.0000000	E
<input type="checkbox"/>	GO:0048869	3	<a href="#">cellular developmental process</a>	173	0.0267	13	0.0483	1.0000000	E
<input type="checkbox"/>	GO:0006887	8,6,5,7	<a href="#">exocytosis</a>	44	0.0068	2	0.0074	1.0000000	E
<input type="checkbox"/>	GO:0006091	3	<a href="#">generation of precursor metabolites and energy</a>	183	0.0283	15	0.0558	1.0000000	E
<input type="checkbox"/>	GO:0019748	3	<a href="#">secondary metabolic process</a>	23	0.0036	1	0.0037	1.0000000	E
<input type="checkbox"/>	GO:0006081	4	<a href="#">aldehyde metabolic process</a>	21	0.0032	3	0.0112	1.0000000	E
<input type="checkbox"/>	GO:0000754	8,7,5	<a href="#">adaptation to pheromone during conjugation with cellular fusion</a>	15	0.0023	1	0.0037	1.0000000	E
<input type="checkbox"/>	GO:0051301	3	<a href="#">cell division</a>	246	0.0380	15	0.0558	1.0000000	E
<input type="checkbox"/>	GO:0019915	5	<a href="#">sequestering of lipid</a>	2	0.0003	2	0.0074	1.0000000	E
<input type="checkbox"/>	GO:0000338	8	<a href="#">protein deneddylation</a>	5	0.0008	2	0.0074	1.0000000	E
<input type="checkbox"/>	GO:0007031	5	<a href="#">peroxisome organization and biogenesis</a>	40	0.0062	3	0.0112	1.0000000	E
<input type="checkbox"/>	GO:0050896	2	<a href="#">response to stimulus</a>	763	0.1178	47	0.1747	1.0000000	E
<input type="checkbox"/>	GO:0000289	11,9,10	<a href="#">poly(A) tail shortening</a>	7	0.0011	1	0.0037	1.0000000	E
<input type="checkbox"/>	GO:0031385	6,8,11,10,9,7,12	<a href="#">regulation of termination of mating projection growth</a>	5	0.0008	1	0.0037	1.0000000	E
<input type="checkbox"/>	GO:0006816	7,8	<a href="#">calcium ion transport</a>	5	0.0008	1	0.0037	1.0000000	E
<input type="checkbox"/>	GO:0000022	6,5,10,8	<a href="#">mitotic spindle elongation</a>	20	0.0031	1	0.0037	1.0000000	E
<input type="checkbox"/>	GO:0016571	11,9,10,8	<a href="#">histone methylation</a>	18	0.0028	1	0.0037	1.0000000	E
<input type="checkbox"/>	GO:0051186	4	<a href="#">cofactor metabolic process</a>	170	0.0263	15	0.0558	1.0000000	E
<input type="checkbox"/>	GO:0000256	6	<a href="#">allantoin catabolic process</a>	7	0.0011	1	0.0037	1.0000000	E
<input type="checkbox"/>	GO:0000105	8,9	<a href="#">histidine biosynthetic process</a>	14	0.0022	2	0.0074	1.0000000	E
<input type="checkbox"/>	GO:0006820	5,6	<a href="#">anion transport</a>	17	0.0026	1	0.0037	1.0000000	E
<input type="checkbox"/>	GO:0006493	9,8,7	<a href="#">protein amino acid O-linked glycosylation</a>	16	0.0025	1	0.0037	1.0000000	E
<input type="checkbox"/>	GO:0000074	6,5	<a href="#">regulation of progression through cell cycle</a>	167	0.0258	10	0.0372	1.0000000	E
<input type="checkbox"/>	GO:0008298	5	<a href="#">intracellular mRNA localization</a>	10	0.0015	1	0.0037	1.0000000	E
<input type="checkbox"/>	GO:0031344	4,6,8,7,5,9	<a href="#">regulation of cell projection organization and biogenesis</a>	6	0.0009	1	0.0037	1.0000000	E
<input type="checkbox"/>	GO:0042364	6	<a href="#">water-soluble vitamin biosynthetic process</a>	46	0.0071	5	0.0186	1.0000000	E
<input type="checkbox"/>	GO:0006812	5,6	<a href="#">cation transport</a>	97	0.0150	5	0.0186	1.0000000	E
<input type="checkbox"/>	GO:0043681	6,7,8	<a href="#">protein import into mitochondrion</a>	40	0.0062	3	0.0112	1.0000000	E
<input type="checkbox"/>	GO:0006525	7,8,5,4	<a href="#">arginine metabolic process</a>	15	0.0023	4	0.0149	1.0000000	E
<input type="checkbox"/>	GO:0019674	9,8	<a href="#">NAD metabolic process</a>	21	0.0032	3	0.0112	1.0000000	E
<input type="checkbox"/>	GO:0006104	6,7	<a href="#">succinyl-CoA metabolic process</a>	2	0.0003	1	0.0037	1.0000000	E
<input type="checkbox"/>	GO:0009968	6,5	<a href="#">negative regulation of signal transduction</a>	17	0.0026	1	0.0037	1.0000000	E
<input type="checkbox"/>	GO:0055071	9	<a href="#">manganese ion homeostasis</a>	5	0.0008	1	0.0037	1.0000000	E
<input type="checkbox"/>	GO:0009117	5	<a href="#">nucleotide metabolic process</a>	111	0.0171	9	0.0335	1.0000000	E
<input type="checkbox"/>	GO:0009116	5	<a href="#">nucleoside metabolic process</a>	18	0.0028	1	0.0037	1.0000000	E
<input type="checkbox"/>	GO:0051300	5,4,6	<a href="#">spindle pole body organization and biogenesis</a>	16	0.0025	1	0.0037	1.0000000	E
<input type="checkbox"/>	GO:0000132	6,5,8,9,10,7	<a href="#">establishment of mitotic spindle orientation</a>	10	0.0015	3	0.0112	1.0000000	E
<input type="checkbox"/>	GO:0033554	4	<a href="#">cellular response to stress</a>	21	0.0032	1	0.0037	1.0000000	E
<input type="checkbox"/>	GO:0040007	2	<a href="#">growth</a>	141	0.0218	8	0.0297	1.0000000	E
<input type="checkbox"/>	GO:0008272	7,8	<a href="#">sulfate transport</a>	3	0.0005	1	0.0037	1.0000000	E
<input type="checkbox"/>	GO:0006099	8,7,6	<a href="#">tricarboxylic acid cycle</a>	15	0.0023	4	0.0149	1.0000000	E
<input type="checkbox"/>	GO:0045022	8,6,7	<a href="#">early endosome to late endosome transport</a>	1	0.0002	1	0.0037	1.0000000	E



<input type="radio"/>	GO:0040001	5,4,7,8,9,6	<a href="#">establishment of mitotic spindle localization</a>	10	0.0015	3	0.0112	1.0000000	E
<input type="radio"/>	GO:0051235	3,2	<a href="#">maintenance of localization</a>	33	0.0051	2	0.0074	1.0000000	E
<input type="radio"/>	GO:0048622	6,5	<a href="#">reproductive sporulation</a>	108	0.0167	8	0.0297	1.0000000	E
<input type="radio"/>	GO:0009098	8,9	<a href="#">leucine biosynthetic process</a>	5	0.0008	2	0.0074	1.0000000	E
<input type="radio"/>	GO:0009060	6	<a href="#">aerobic respiration</a>	84	0.0130	10	0.0372	1.0000000	E
<input type="radio"/>	GO:0040008	4,3	<a href="#">regulation of growth</a>	13	0.0020	1	0.0037	1.0000000	E
<input type="radio"/>	GO:0045229	4	<a href="#">external encapsulating structure organization and biogenesis</a>	200	0.0309	15	0.0558	1.0000000	E
<input type="radio"/>	GO:0032258	10,9,8,7	<a href="#">CVT pathway</a>	4	0.0006	2	0.0074	1.0000000	E
<input type="radio"/>	GO:0051128	5,4	<a href="#">regulation of cellular component organization and biogenesis</a>	30	0.0046	2	0.0074	1.0000000	E
<input type="radio"/>	GO:0006979	4	<a href="#">response to oxidative stress</a>	71	0.0110	7	0.0260	1.0000000	E
<input type="radio"/>	GO:0009076	7,8	<a href="#">histidine family amino acid biosynthetic process</a>	14	0.0022	2	0.0074	1.0000000	E
<input type="radio"/>	GO:0009408	5,4	<a href="#">response to heat</a>	23	0.0036	4	0.0149	1.0000000	E
<input type="radio"/>	GO:0051247	6,5	<a href="#">positive regulation of protein metabolic process</a>	5	0.0008	1	0.0037	1.0000000	E
<input type="radio"/>	GO:0016570	10,8	<a href="#">histone modification</a>	91	0.0141	2	0.0074	1.0000000	D
<input type="radio"/>	GO:0051028	5,7,6,8	<a href="#">mRNA transport</a>	66	0.0102	1	0.0037	1.0000000	D
<input type="radio"/>	GO:0006892	8,6,5,7	<a href="#">post-Golgi vesicle-mediated transport</a>	69	0.0107	1	0.0037	1.0000000	D
<input type="radio"/>	GO:0008033	7	<a href="#">tRNA processing</a>	84	0.0130	2	0.0074	1.0000000	D
<input type="radio"/>	GO:0045449	7,6	<a href="#">regulation of transcription</a>	386	0.0596	11	0.0409	1.0000000	D
<input type="radio"/>	GO:0007131	10,8,7,5,9,6,4	<a href="#">meiotic recombination</a>	55	0.0085	2	0.0074	1.0000000	D
<input type="radio"/>	GO:0048518	4	<a href="#">positive regulation of biological process</a>	124	0.0191	3	0.0112	1.0000000	D
<input type="radio"/>	GO:0006486	8,7,6	<a href="#">protein amino acid glycosylation</a>	73	0.0113	3	0.0112	1.0000000	D
<input type="radio"/>	GO:0006418	8,7,9,6	<a href="#">tRNA aminoacylation for protein translation</a>	32	0.0049	1	0.0037	1.0000000	D
<input type="radio"/>	GO:0006796	5	<a href="#">phosphate metabolic process</a>	212	0.0327	6	0.0223	1.0000000	D
<input type="radio"/>	GO:0042273	6,5	<a href="#">ribosomal large subunit biogenesis and assembly</a>	64	0.0099	1	0.0037	1.0000000	D
<input type="radio"/>	GO:0006401	6	<a href="#">RNA catabolic process</a>	74	0.0114	1	0.0037	1.0000000	D
<input type="radio"/>	GO:0006261	7	<a href="#">DNA-dependent DNA replication</a>	97	0.0150	3	0.0112	1.0000000	D
<input type="radio"/>	GO:0016569	9	<a href="#">covalent chromatin modification</a>	91	0.0141	2	0.0074	1.0000000	D
<input type="radio"/>	GO:0007049	3	<a href="#">cell cycle</a>	458	0.0707	18	0.0669	1.0000000	D
<input type="radio"/>	GO:0051031	5,7,6,8	<a href="#">tRNA transport</a>	30	0.0046	1	0.0037	1.0000000	D
<input type="radio"/>	GO:0006351	7,6	<a href="#">transcription, DNA-dependent</a>	522	0.0806	12	0.0446	1.0000000	D
<input type="radio"/>	GO:0016458	5	<a href="#">gene silencing</a>	95	0.0147	3	0.0112	1.0000000	D
<input type="radio"/>	GO:0045893	9,8	<a href="#">positive regulation of transcription, DNA-dependent</a>	95	0.0147	1	0.0037	1.0000000	D
<input type="radio"/>	GO:0006271	8,7	<a href="#">DNA strand elongation during DNA replication</a>	32	0.0049	1	0.0037	1.0000000	D
<input type="radio"/>	GO:0043038	6,7	<a href="#">amino acid activation</a>	32	0.0049	1	0.0037	1.0000000	D
<input type="radio"/>	GO:0009892	5,4	<a href="#">negative regulation of metabolic process</a>	208	0.0321	5	0.0186	1.0000000	D
<input type="radio"/>	GO:0045935	7,6	<a href="#">positive regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process</a>	108	0.0167	2	0.0074	1.0000000	D
<input type="radio"/>	GO:0044265	5	<a href="#">cellular macromolecule catabolic process</a>	314	0.0485	12	0.0446	1.0000000	D
<input type="radio"/>	GO:0050658	4,6,5,7	<a href="#">RNA transport</a>	80	0.0124	1	0.0037	1.0000000	D
<input type="radio"/>	GO:0006665	6,7	<a href="#">sphingolipid metabolic process</a>	30	0.0046	1	0.0037	1.0000000	D
<input type="radio"/>	GO:0006397	7	<a href="#">mRNA processing</a>	157	0.0242	1	0.0037	1.0000000	D
<input type="radio"/>	GO:0051325	6,5	<a href="#">interphase</a>	112	0.0173	4	0.0149	1.0000000	D
<input type="radio"/>	GO:0006888	8,6,5,7	<a href="#">ER to Golgi vesicle-mediated transport</a>	81	0.0125	3	0.0112	1.0000000	D

<input type="checkbox"/>	GO:0007017	6	<a href="#">microtubule-based process</a>	101	0.0156	4	0.0149	1.0000000	D
<input type="checkbox"/>	GO:0006405	10,8,5,7,9,6	<a href="#">RNA export from nucleus</a>	79	0.0122	1	0.0037	1.0000000	D
<input type="checkbox"/>	GO:0019953	3	<a href="#">sexual reproduction</a>	118	0.0182	4	0.0149	1.0000000	D
<input type="checkbox"/>	GO:0006260	6	<a href="#">DNA replication</a>	117	0.0181	4	0.0149	1.0000000	D
<input type="checkbox"/>	GO:0017038	5,6,7	<a href="#">protein import</a>	109	0.0168	4	0.0149	1.0000000	D
<input type="checkbox"/>	GO:0009150	7	<a href="#">purine ribonucleotide metabolic process</a>	41	0.0063	1	0.0037	1.0000000	D
<input type="checkbox"/>	GO:0043413	6	<a href="#">biopolymer glycosylation</a>	73	0.0113	3	0.0112	1.0000000	D
<input type="checkbox"/>	GO:0046365	6,7	<a href="#">monosaccharide catabolic process</a>	44	0.0068	1	0.0037	1.0000000	D
<input type="checkbox"/>	GO:0051329	7,5,6	<a href="#">interphase of mitotic cell cycle</a>	112	0.0173	4	0.0149	1.0000000	D
<input type="checkbox"/>	GO:0000746	3	<a href="#">conjugation</a>	118	0.0182	4	0.0149	1.0000000	D
<input type="checkbox"/>	GO:0046903	3,4	<a href="#">secretion</a>	250	0.0386	8	0.0297	1.0000000	D
<input type="checkbox"/>	GO:0000747	4	<a href="#">conjugation with cellular fusion</a>	118	0.0182	4	0.0149	1.0000000	D
<input type="checkbox"/>	GO:0006997	5	<a href="#">nuclear organization and biogenesis</a>	57	0.0088	2	0.0074	1.0000000	D
<input type="checkbox"/>	GO:0006406	11,9,6,8,10,7	<a href="#">mRNA export from nucleus</a>	66	0.0102	1	0.0037	1.0000000	D
<input type="checkbox"/>	GO:0031323	5,4	<a href="#">regulation of cellular metabolic process</a>	507	0.0783	13	0.0483	1.0000000	D
<input type="checkbox"/>	GO:0006350	5	<a href="#">transcription</a>	567	0.0876	14	0.0520	1.0000000	D
<input type="checkbox"/>	GO:0016481	8,7	<a href="#">negative regulation of transcription</a>	162	0.0250	4	0.0149	1.0000000	D
<input type="checkbox"/>	GO:0019222	4,3	<a href="#">regulation of metabolic process</a>	538	0.0831	14	0.0520	1.0000000	D
<input type="checkbox"/>	GO:0006468	8,7	<a href="#">protein amino acid phosphorylation</a>	101	0.0156	3	0.0112	1.0000000	D
<input type="checkbox"/>	GO:0000910	4	<a href="#">cytokinesis</a>	109	0.0168	4	0.0149	1.0000000	D
<input type="checkbox"/>	GO:0040029	4	<a href="#">regulation of gene expression, epigenetic</a>	100	0.0154	3	0.0112	1.0000000	D
<input type="checkbox"/>	GO:0051704	2	<a href="#">multi-organism process</a>	139	0.0215	5	0.0186	1.0000000	D
<input type="checkbox"/>	GO:0043039	7,8	<a href="#">tRNA aminoacylation</a>	32	0.0049	1	0.0037	1.0000000	D
<input type="checkbox"/>	GO:0045944	10,9	<a href="#">positive regulation of transcription from RNA polymerase II promoter</a>	76	0.0117	1	0.0037	1.0000000	D
<input type="checkbox"/>	GO:0022402	4,3	<a href="#">cell cycle process</a>	439	0.0678	18	0.0669	1.0000000	D
<input type="checkbox"/>	GO:0065003	5,4	<a href="#">macromolecular complex assembly</a>	328	0.0506	10	0.0372	1.0000000	D
<input type="checkbox"/>	GO:0016052	5	<a href="#">carbohydrate catabolic process</a>	80	0.0124	2	0.0074	1.0000000	D
<input type="checkbox"/>	GO:0006259	5	<a href="#">DNA metabolic process</a>	523	0.0808	19	0.0706	1.0000000	D
<input type="checkbox"/>	GO:0006073	6,7	<a href="#">glucan metabolic process</a>	46	0.0071	1	0.0037	1.0000000	D
<input type="checkbox"/>	GO:0048311	7,6	<a href="#">mitochondrion distribution</a>	26	0.0040	1	0.0037	1.0000000	D
<input type="checkbox"/>	GO:0006606	9,10,7,8,6	<a href="#">protein import into nucleus</a>	50	0.0077	1	0.0037	1.0000000	D
<input type="checkbox"/>	GO:0051246	5,4	<a href="#">regulation of protein metabolic process</a>	72	0.0111	2	0.0074	1.0000000	D
<input type="checkbox"/>	GO:0008150	1	<a href="#">biological process</a>	6476	1.0000	269	1.0000	1.0000000	D
<input type="checkbox"/>	GO:0051170	9,7,8	<a href="#">nuclear import</a>	50	0.0077	1	0.0037	1.0000000	D
<input type="checkbox"/>	GO:0009451	6	<a href="#">RNA modification</a>	139	0.0215	2	0.0074	1.0000000	D
<input type="checkbox"/>	GO:0043487	8,7	<a href="#">regulation of RNA stability</a>	30	0.0046	1	0.0037	1.0000000	D
<input type="checkbox"/>	GO:0042257	8,7	<a href="#">ribosomal subunit assembly</a>	55	0.0085	2	0.0074	1.0000000	D
<input type="checkbox"/>	GO:0000070	9,7,5,8,6,4	<a href="#">mitotic sister chromatid segregation</a>	59	0.0091	2	0.0074	1.0000000	D
<input type="checkbox"/>	GO:0006725	4	<a href="#">aromatic compound metabolic process</a>	60	0.0093	2	0.0074	1.0000000	D
<input type="checkbox"/>	GO:0006399	6	<a href="#">tRNA metabolic process</a>	121	0.0187	3	0.0112	1.0000000	D
<input type="checkbox"/>	GO:0016043	3	<a href="#">cellular component organization and biogenesis</a>	2264	0.3496	91	0.3383	1.0000000	D
<input type="checkbox"/>	GO:0007067	8,6,7,5	<a href="#">mitosis</a>	127	0.0196	5	0.0186	1.0000000	D
<input type="checkbox"/>	GO:0051168	9,7,8	<a href="#">nuclear export</a>	102	0.0158	2	0.0074	1.0000000	D
<input type="checkbox"/>	GO:0043623	7,6	<a href="#">cellular protein complex assembly</a>	69	0.0107	1	0.0037	1.0000000	D
<input type="checkbox"/>	GO:0006999	6	<a href="#">nuclear pore organization and biogenesis</a>	29	0.0045	1	0.0037	1.0000000	D

<input type="checkbox"/>	GO:0007127	9,7,6,8,5	<a href="#">meiosis I</a>	75	0.0116	2	0.0074	1.0000000	D
<input type="checkbox"/>	GO:0000279	6,5	<a href="#">M phase</a>	258	0.0398	9	0.0335	1.0000000	D
<input type="checkbox"/>	GO:0042255	7,6	<a href="#">ribosome assembly</a>	66	0.0102	2	0.0074	1.0000000	D
<input type="checkbox"/>	GO:0065004	6,5	<a href="#">protein-DNA complex assembly</a>	74	0.0114	3	0.0112	1.0000000	D
<input type="checkbox"/>	GO:0006323	6	<a href="#">DNA packaging</a>	253	0.0391	5	0.0186	1.0000000	D
<input type="checkbox"/>	GO:0042493	4	<a href="#">response to drug</a>	121	0.0187	4	0.0149	1.0000000	D
<input type="checkbox"/>	GO:0006342	10,6,7,11,9	<a href="#">chromatin silencing</a>	95	0.0147	3	0.0112	1.0000000	D
<input type="checkbox"/>	GO:0032259	5	<a href="#">methylation</a>	83	0.0128	3	0.0112	1.0000000	D
<input type="checkbox"/>	GO:0000154	7,8	<a href="#">rRNA modification</a>	85	0.0131	1	0.0037	1.0000000	D
<input type="checkbox"/>	GO:0006944	5	<a href="#">membrane fusion</a>	59	0.0091	2	0.0074	1.0000000	D
<input type="checkbox"/>	GO:0051236	3,4,5	<a href="#">establishment of RNA localization</a>	80	0.0124	1	0.0037	1.0000000	D
<input type="checkbox"/>	GO:0006511	9,8,10	<a href="#">ubiquitin-dependent protein catabolic process</a>	148	0.0229	6	0.0223	1.0000000	D
<input type="checkbox"/>	GO:0051169	7,5,6	<a href="#">nuclear transport</a>	129	0.0199	2	0.0074	1.0000000	D
<input type="checkbox"/>	GO:0015931	4,5	<a href="#">nucleobase, nucleoside, nucleotide and nucleic acid transport</a>	90	0.0139	1	0.0037	1.0000000	D
<input type="checkbox"/>	GO:0042274	6,5	<a href="#">ribosomal small subunit biogenesis and assembly</a>	26	0.0040	1	0.0037	1.0000000	D
<input type="checkbox"/>	GO:0051029	5,7,6,8	<a href="#">rRNA transport</a>	26	0.0040	1	0.0037	1.0000000	D
<input type="checkbox"/>	GO:0006289	7,6	<a href="#">nucleotide-excision repair</a>	44	0.0068	1	0.0037	1.0000000	D
<input type="checkbox"/>	GO:0009057	4	<a href="#">macromolecule catabolic process</a>	345	0.0533	13	0.0483	1.0000000	D
<input type="checkbox"/>	GO:0006457	6	<a href="#">protein folding</a>	84	0.0130	3	0.0112	1.0000000	D
<input type="checkbox"/>	GO:0006298	7,9,6	<a href="#">mismatch repair</a>	25	0.0039	1	0.0037	1.0000000	D
<input type="checkbox"/>	GO:0006348	11,7,8,12,10	<a href="#">chromatin silencing at telomere</a>	60	0.0093	2	0.0074	1.0000000	D
<input type="checkbox"/>	GO:0006109	5,4	<a href="#">regulation of carbohydrate metabolic process</a>	29	0.0045	1	0.0037	1.0000000	D
<input type="checkbox"/>	GO:0018193	7	<a href="#">peptidyl-amino acid modification</a>	28	0.0043	1	0.0037	1.0000000	D
<input type="checkbox"/>	GO:0006793	4	<a href="#">phosphorus metabolic process</a>	212	0.0327	6	0.0223	1.0000000	D
<input type="checkbox"/>	GO:0006913	8,6,7	<a href="#">nucleocytoplasmic transport</a>	129	0.0199	2	0.0074	1.0000000	D
<input type="checkbox"/>	GO:0006407	11,9,6,8,10,7	<a href="#">rRNA export from nucleus</a>	26	0.0040	1	0.0037	1.0000000	D
<input type="checkbox"/>	GO:0005977	7,6,8	<a href="#">glycogen metabolic process</a>	32	0.0049	1	0.0037	1.0000000	D
<input type="checkbox"/>	GO:0031325	6,5	<a href="#">positive regulation of cellular metabolic process</a>	116	0.0179	3	0.0112	1.0000000	D
<input type="checkbox"/>	GO:0000819	7,4	<a href="#">sister chromatid segregation</a>	62	0.0096	2	0.0074	1.0000000	D
<input type="checkbox"/>	GO:0006355	8,7	<a href="#">regulation of transcription, DNA-dependent</a>	359	0.0554	9	0.0335	1.0000000	D
<input type="checkbox"/>	GO:0007126	8,6,7,5	<a href="#">meiosis</a>	148	0.0229	4	0.0149	1.0000000	D
<input type="checkbox"/>	GO:0000096	6,7,5	<a href="#">sulfur amino acid metabolic process</a>	33	0.0051	1	0.0037	1.0000000	D
<input type="checkbox"/>	GO:0051646	6,5	<a href="#">mitochondrion localization</a>	27	0.0042	1	0.0037	1.0000000	D
<input type="checkbox"/>	GO:0032774	6	<a href="#">RNA biosynthetic process</a>	524	0.0809	12	0.0446	1.0000000	D
<input type="checkbox"/>	GO:0007093	8,10,9,7	<a href="#">mitotic cell cycle checkpoint</a>	27	0.0042	1	0.0037	1.0000000	D
<input type="checkbox"/>	GO:0007242	5	<a href="#">intracellular signaling cascade</a>	137	0.0212	5	0.0186	1.0000000	D
<input type="checkbox"/>	GO:0050657	5,6	<a href="#">nucleic acid transport</a>	80	0.0124	1	0.0037	1.0000000	D
<input type="checkbox"/>	GO:0009101	7,5	<a href="#">glycoprotein biosynthetic process</a>	78	0.0120	3	0.0112	1.0000000	D
<input type="checkbox"/>	GO:0006354	8,6,7	<a href="#">RNA elongation</a>	59	0.0091	2	0.0074	1.0000000	D
<input type="checkbox"/>	GO:0007059	3	<a href="#">chromosome segregation</a>	119	0.0184	2	0.0074	1.0000000	D
<input type="checkbox"/>	GO:0006476	8	<a href="#">protein amino acid deacetylation</a>	26	0.0040	1	0.0037	1.0000000	D
<input type="checkbox"/>	GO:0032200	7	<a href="#">telomere organization and biogenesis</a>	274	0.0423	11	0.0409	1.0000000	D
<input type="checkbox"/>	GO:0006007	8,9	<a href="#">glucose catabolic process</a>	34	0.0053	1	0.0037	1.0000000	D
<input type="checkbox"/>	GO:0022411	4	<a href="#">cellular component disassembly</a>	36	0.0056	1	0.0037	1.0000000	D

<input type="checkbox"/>	GO:0009100	6	<a href="#">glycoprotein metabolic process</a>	79	0.0122	3	0.0112	1.0000000	D
<input type="checkbox"/>	GO:0001522	7	<a href="#">pseudouridine synthesis</a>	39	0.0060	1	0.0037	1.0000000	D
<input type="checkbox"/>	GO:0006270	8,6	<a href="#">DNA replication initiation</a>	33	0.0051	1	0.0037	1.0000000	D
<input type="checkbox"/>	GO:0045045	7,5,4,6	<a href="#">secretory pathway</a>	243	0.0375	8	0.0297	1.0000000	D
<input type="checkbox"/>	GO:0042144	6	<a href="#">vacuole fusion, non-autophagic</a>	28	0.0043	1	0.0037	1.0000000	D
<input type="checkbox"/>	GO:0009059	4	<a href="#">macromolecule biosynthetic process</a>	886	0.1368	28	0.1041	1.0000000	D
<input type="checkbox"/>	GO:0032940	6,4,5	<a href="#">secretion by cell</a>	250	0.0386	8	0.0297	1.0000000	D
<input type="checkbox"/>	GO:0019219	6,5	<a href="#">regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process</a>	440	0.0679	12	0.0446	1.0000000	D
<input type="checkbox"/>	GO:0000027	9,7,8,6	<a href="#">ribosomal large subunit assembly and maintenance</a>	41	0.0063	1	0.0037	1.0000000	D
<input type="checkbox"/>	GO:0043632	6	<a href="#">modification-dependent macromolecule catabolic process</a>	155	0.0239	6	0.0223	1.0000000	D
<input type="checkbox"/>	GO:0006368	9,7,8	<a href="#">RNA elongation from RNA polymerase II promoter</a>	53	0.0082	2	0.0074	1.0000000	D
<input type="checkbox"/>	GO:0006338	9	<a href="#">chromatin remodeling</a>	155	0.0239	4	0.0149	1.0000000	D
<input type="checkbox"/>	GO:0019538	4	<a href="#">protein metabolic process</a>	1547	0.2389	56	0.2082	1.0000000	D
<input type="checkbox"/>	GO:0000723	8	<a href="#">telomere maintenance</a>	274	0.0423	11	0.0409	1.0000000	D
<input type="checkbox"/>	GO:0000087	7,5,6	<a href="#">M phase of mitotic cell cycle</a>	129	0.0199	5	0.0186	1.0000000	D
<input type="checkbox"/>	GO:0006366	8,7	<a href="#">transcription from RNA polymerase II promoter</a>	343	0.0530	7	0.0260	1.0000000	D
<input type="checkbox"/>	GO:0006413	7,6	<a href="#">translational initiation</a>	49	0.0076	1	0.0037	1.0000000	D
<input type="checkbox"/>	GO:0006575	5	<a href="#">amino acid derivative metabolic process</a>	31	0.0048	1	0.0037	1.0000000	D
<input type="checkbox"/>	GO:0048519	4	<a href="#">negative regulation of biological process</a>	242	0.0374	9	0.0335	1.0000000	D
<input type="checkbox"/>	GO:0045941	8,7	<a href="#">positive regulation of transcription</a>	101	0.0156	2	0.0074	1.0000000	D
<input type="checkbox"/>	GO:0048522	5,4	<a href="#">positive regulation of cellular process</a>	124	0.0191	3	0.0112	1.0000000	D
<input type="checkbox"/>	GO:0043285	5	<a href="#">biopolymer catabolic process</a>	277	0.0428	11	0.0409	1.0000000	D
<input type="checkbox"/>	GO:0045047	9,8,7,6,5	<a href="#">protein targeting to ER</a>	33	0.0051	1	0.0037	1.0000000	D
<input type="checkbox"/>	GO:0006403	4	<a href="#">RNA localization</a>	90	0.0139	2	0.0074	1.0000000	D
<input type="checkbox"/>	GO:0031324	6,5	<a href="#">negative regulation of cellular metabolic process</a>	198	0.0306	5	0.0186	1.0000000	D
<input type="checkbox"/>	GO:0006352	7,8,6	<a href="#">transcription initiation</a>	55	0.0085	2	0.0074	1.0000000	D
<input type="checkbox"/>	GO:0048878	5	<a href="#">chemical homeostasis</a>	121	0.0187	5	0.0186	1.0000000	D
<input type="checkbox"/>	GO:0006752	6	<a href="#">group transfer coenzyme metabolic process</a>	44	0.0068	1	0.0037	1.0000000	D
<input type="checkbox"/>	GO:0051321	4	<a href="#">meiotic cell cycle</a>	148	0.0229	4	0.0149	1.0000000	D
<input type="checkbox"/>	GO:0008380	7	<a href="#">RNA splicing</a>	132	0.0204	1	0.0037	1.0000000	D
<input type="checkbox"/>	GO:0009152	7,8	<a href="#">purine ribonucleotide biosynthetic process</a>	38	0.0059	1	0.0037	1.0000000	D
<input type="checkbox"/>	GO:0016310	6	<a href="#">phosphorylation</a>	155	0.0239	4	0.0149	1.0000000	D
<input type="checkbox"/>	GO:0006402	7	<a href="#">mRNA catabolic process</a>	60	0.0093	1	0.0037	1.0000000	D
<input type="checkbox"/>	GO:0043161	10,9,11	<a href="#">proteasomal ubiquitin-dependent protein catabolic process</a>	63	0.0097	2	0.0074	1.0000000	D
<input type="checkbox"/>	GO:0044275	6	<a href="#">cellular carbohydrate catabolic process</a>	80	0.0124	2	0.0074	1.0000000	D
<input type="checkbox"/>	GO:0031497	5,9	<a href="#">chromatin assembly</a>	104	0.0161	3	0.0112	1.0000000	D
<input type="checkbox"/>	GO:0045934	7,6	<a href="#">negative regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process</a>	179	0.0276	5	0.0186	1.0000000	D
<input type="checkbox"/>	GO:0009889	5,4	<a href="#">regulation of biosynthetic process</a>	69	0.0107	1	0.0037	1.0000000	D
<input type="checkbox"/>	GO:0043170	3	<a href="#">macromolecule metabolic process</a>	2841	0.4387	101	0.3755	1.0000000	D
<input type="checkbox"/>	GO:0009112	5	<a href="#">nucleobase metabolic process</a>	31	0.0048	1	0.0037	1.0000000	D
<input type="checkbox"/>	GO:0045005	8,6	<a href="#">maintenance of fidelity during DNA-dependent DNA replication</a>	25	0.0039	1	0.0037	1.0000000	D

<input type="radio"/>	GO:0045814	5	<a href="#">negative regulation of gene expression, epigenetic</a>	95	0.0147	3	0.0112	1.0000000	D
<input type="radio"/>	GO:0009893	5,4	<a href="#">positive regulation of metabolic process</a>	116	0.0179	3	0.0112	1.0000000	D
<input type="radio"/>	GO:0007165	4	<a href="#">signal transduction</a>	209	0.0323	8	0.0297	1.0000000	D
<input type="radio"/>	GO:0019941	8,7,9	<a href="#">modification-dependent protein catabolic process</a>	148	0.0229	6	0.0223	1.0000000	D
<input type="radio"/>	GO:0000278	4	<a href="#">mitotic cell cycle</a>	266	0.0411	11	0.0409	1.0000000	D
<input type="radio"/>	GO:0031326	6,5	<a href="#">regulation of cellular biosynthetic process</a>	67	0.0103	1	0.0037	1.0000000	D
<input type="radio"/>	GO:0031167	8,9	<a href="#">rRNA methylation</a>	44	0.0068	1	0.0037	1.0000000	D
<input type="radio"/>	GO:0048193	7,5,6	<a href="#">Golgi vesicle transport</a>	166	0.0256	5	0.0186	1.0000000	D
<input type="radio"/>	GO:0051252	7,6	<a href="#">regulation of RNA metabolic process</a>	36	0.0056	1	0.0037	1.0000000	D
<input type="radio"/>	GO:0044267	5	<a href="#">cellular protein metabolic process</a>	1498	0.2313	52	0.1933	1.0000000	D
<input type="radio"/>	GO:0043488	9,8,7	<a href="#">regulation of mRNA stability</a>	30	0.0046	1	0.0037	1.0000000	D
<input type="radio"/>	GO:0006417	7,6,5	<a href="#">regulation of translation</a>	47	0.0073	1	0.0037	1.0000000	D
<input type="radio"/>	GO:0019320	7,8	<a href="#">hexose catabolic process</a>	39	0.0060	1	0.0037	1.0000000	D
<input type="radio"/>	GO:0006310	6	<a href="#">DNA recombination</a>	122	0.0188	4	0.0149	1.0000000	D
<input type="radio"/>	GO:0044260	4	<a href="#">cellular macromolecule metabolic process</a>	1552	0.2397	54	0.2007	1.0000000	D
<input type="radio"/>	GO:0031509	7,11	<a href="#">telomeric heterochromatin formation</a>	60	0.0093	2	0.0074	1.0000000	D
<input type="radio"/>	GO:0006400	7,8	<a href="#">tRNA modification</a>	52	0.0080	1	0.0037	1.0000000	D
<input type="radio"/>	GO:0009199	7	<a href="#">ribonucleoside triphosphate metabolic process</a>	25	0.0039	1	0.0037	1.0000000	D
<input type="radio"/>	GO:0051276	5	<a href="#">chromosome organization and biogenesis</a>	572	0.0883	17	0.0632	1.0000000	D
<input type="radio"/>	GO:0005984	6	<a href="#">disaccharide metabolic process</a>	31	0.0048	1	0.0037	1.0000000	D
<input type="radio"/>	GO:0006383	8,7	<a href="#">transcription from RNA polymerase III promoter</a>	38	0.0059	1	0.0037	1.0000000	D
<input type="radio"/>	GO:0045892	9,8	<a href="#">negative regulation of transcription, DNA-dependent</a>	156	0.0241	4	0.0149	1.0000000	D
<input type="radio"/>	GO:0048523	5,4	<a href="#">negative regulation of cellular process</a>	239	0.0369	9	0.0335	1.0000000	D
<input type="radio"/>	GO:0006367	8,9,7	<a href="#">transcription initiation from RNA polymerase II promoter</a>	44	0.0068	1	0.0037	1.0000000	D
<input type="radio"/>	GO:0006357	9,8	<a href="#">regulation of transcription from RNA polymerase II promoter</a>	221	0.0341	4	0.0149	1.0000000	D
<input type="radio"/>	GO:0006996	4	<a href="#">organelle organization and biogenesis</a>	1388	0.2143	49	0.1822	1.0000000	D
<input type="radio"/>	GO:0016568	8	<a href="#">chromatin modification</a>	223	0.0344	5	0.0186	1.0000000	D
<input type="radio"/>	GO:0006333	8	<a href="#">chromatin assembly or disassembly</a>	119	0.0184	3	0.0112	1.0000000	D
<input type="radio"/>	GO:0000001	8,7,6	<a href="#">mitochondrion inheritance</a>	26	0.0040	1	0.0037	1.0000000	D
<input type="radio"/>	GO:0007001	6	<a href="#">chromosome organization and biogenesis (sensu Eukaryota)</a>	567	0.0876	17	0.0632	1.0000000	D
<input type="radio"/>	GO:0022616	6	<a href="#">DNA strand elongation</a>	32	0.0049	1	0.0037	1.0000000	D
<input type="radio"/>	GO:0006609	10,11,8,9,7	<a href="#">mRNA-binding (hnRNP) protein import into nucleus</a>	25	0.0039	1	0.0037	1.0000000	D
<input type="radio"/>	GO:0006325	7	<a href="#">establishment and/or maintenance of chromatin architecture</a>	253	0.0391	5	0.0186	1.0000000	D
<input type="radio"/>	GO:0022403	5,4	<a href="#">cell cycle phase</a>	353	0.0545	12	0.0446	1.0000000	D
<input type="radio"/>	GO:0001403	6,4,8,9	<a href="#">invasive growth (sensu Saccharomyces)</a>	42	0.0065	1	0.0037	1.0000000	D
<input type="radio"/>	GO:0051603	7,8	<a href="#">proteolysis involved in cellular protein catabolic process</a>	151	0.0233	6	0.0223	1.0000000	D
<input type="radio"/>	GO:0000082	8,5,6,7,4	<a href="#">G1/S transition of mitotic cell cycle</a>	52	0.0080	2	0.0074	1.0000000	D
<input type="radio"/>	GO:0009966	5,4	<a href="#">regulation of signal transduction</a>	26	0.0040	1	0.0037	1.0000000	D
<input type="radio"/>	GO:0043414	6	<a href="#">biopolymer methylation</a>	83	0.0128	3	0.0112	1.0000000	D
<input type="radio"/>	GO:0031507	6,10	<a href="#">heterochromatin formation</a>	95	0.0147	3	0.0112	1.0000000	D
<input type="radio"/>	GO:0065007	2	<a href="#">biological regulation</a>	948	0.1464	39	0.1450	1.0000000	D
<input type="radio"/>	GO:0001510	7	<a href="#">RNA methylation</a>	60	0.0093	1	0.0037	1.0000000	D

<input type="checkbox"/>	GO:0006409	11,9,6,8,10,7	<a href="#">tRNA export from nucleus</a>	29	0.0045	1	0.0037	1.0000000	D
<input type="checkbox"/>	GO:0006611	9,10,7,8	<a href="#">protein export from nucleus</a>	56	0.0086	2	0.0074	1.0000000	D
<input type="checkbox"/>	GO:0051327	7,5,6	<a href="#">M phase of meiotic cell cycle</a>	148	0.0229	4	0.0149	1.0000000	D
<input type="checkbox"/>	GO:0022618	6,5	<a href="#">protein-RNA complex assembly</a>	144	0.0222	3	0.0112	1.0000000	D
<input type="checkbox"/>	GO:0010382	6,4	<a href="#">cell wall metabolic process</a>	26	0.0040	1	0.0037	1.0000000	D
<input type="checkbox"/>	GO:0000122	10,9	<a href="#">negative regulation of transcription from RNA polymerase II promoter</a>	63	0.0097	1	0.0037	1.0000000	D
<input type="checkbox"/>	GO:0016071	6	<a href="#">mRNA metabolic process</a>	210	0.0324	1	0.0037	0.9987783	D
<input type="checkbox"/>	GO:0043284	5	<a href="#">biopolymer biosynthetic process</a>	354	0.0547	4	0.0149	0.4969504	D
<input type="checkbox"/>	GO:0006139	4	<a href="#">nucleobase, nucleoside, nucleotide and nucleic acid metabolic process</a>	1532	0.2366	42	0.1561	0.2547262	D
<input type="checkbox"/>	GO:0006412	6,5	<a href="#">translation</a>	688	0.1062	13	0.0483	0.2482740	D
<input type="checkbox"/>	GO:0006364	6,7	<a href="#">rRNA processing</a>	249	0.0384	1	0.0037	0.2141763	D
<input type="checkbox"/>	GO:0016072	6	<a href="#">rRNA metabolic process</a>	256	0.0395	1	0.0037	0.1618109	D
<input type="checkbox"/>	GO:0042254	5	<a href="#">ribosome biogenesis and assembly</a>	410	0.0633	4	0.0149	0.0743464	D
<input type="checkbox"/>	GO:0043283	4	<a href="#">biopolymer metabolic process</a>	2230	0.3443	64	0.2379	0.0303034	D
<input type="checkbox"/>	GO:0022613	4	<a href="#">ribonucleoprotein complex biogenesis and assembly</a>	483	0.0746	5	0.0186	0.0239100	D
<input type="checkbox"/>	GO:0006414	7,6	<a href="#">translational elongation</a>	313	0.0483	1	0.0037	0.0158854	D
<input type="checkbox"/>	GO:0006396	6	<a href="#">RNA processing</a>	491	0.0758	4	0.0149	0.0040128	D
<input type="checkbox"/>	GO:0016070	5	<a href="#">RNA metabolic process</a>	1058	0.1634	17	0.0632	0.0002587	D