

# GO-Stats Results

Your dataset contains **318** 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:0050896	2	<a href="#">response to stimulus</a>	763	0.1178	77	0.2421	1.021150E-10	E
<input type="radio"/> GO:0019222	4,3	<a href="#">regulation of metabolic process</a>	538	0.0831	53	0.1667	2.769143E-07	E
<input type="radio"/> GO:0007154	3	<a href="#">cell communication</a>	240	0.0371	31	0.0975	3.864128E-07	E
<input type="radio"/> GO:0050789	3	<a href="#">regulation of biological process</a>	761	0.1175	66	0.2075	8.923076E-07	E
<input type="radio"/> GO:0006950	3	<a href="#">response to stress</a>	488	0.0754	48	0.1509	1.091756E-06	E
<input type="radio"/> GO:0065007	2	<a href="#">biological regulation</a>	948	0.1464	77	0.2421	1.241291E-06	E
<input type="radio"/> GO:0005975	4	<a href="#">carbohydrate metabolic process</a>	233	0.0360	29	0.0912	1.927048E-06	E
<input type="radio"/> GO:0042221	3	<a href="#">response to chemical stimulus</a>	382	0.0590	40	0.1258	1.968446E-06	E
<input type="radio"/> GO:0043687	7	<a href="#">post-translational protein modification</a>	388	0.0599	40	0.1258	2.869911E-06	E
<input type="radio"/> GO:0031323	5,4	<a href="#">regulation of cellular metabolic process</a>	507	0.0783	47	0.1478	6.832323E-06	E
<input type="radio"/> GO:0050794	4,3	<a href="#">regulation of cellular process</a>	738	0.1140	61	0.1918	1.062877E-05	E
<input type="radio"/> GO:0000751	8,9,7,6	<a href="#">cell cycle arrest in response to pheromone</a>	8	0.0012	5	0.0157	1.337005E-05	E
<input type="radio"/> GO:0009056	3	<a href="#">catabolic process</a>	438	0.0676	40	0.1258	4.476875E-05	E
<input type="radio"/> GO:0009987	2	<a href="#">cellular process</a>	4654	0.7187	257	0.8082	4.623139E-05	E
<input type="radio"/> GO:0006109	5,4	<a href="#">regulation of carbohydrate metabolic process</a>	29	0.0045	8	0.0252	4.745947E-05	E
<input type="radio"/> GO:0007165	4	<a href="#">signal transduction</a>	209	0.0323	24	0.0755	5.133724E-05	E
<input type="radio"/> GO:0048523	5,4	<a href="#">negative regulation of cellular process</a>	239	0.0369	26	0.0818	6.242739E-05	E
<input type="radio"/> GO:0006112	5	<a href="#">energy reserve metabolic process</a>	39	0.0060	9	0.0283	7.239101E-05	E
<input type="radio"/> GO:0048519	4	<a href="#">negative regulation of biological process</a>	242	0.0374	26	0.0818	7.614316E-05	E
<input type="radio"/> GO:0007050	7,8,6	<a href="#">cell cycle arrest</a>	11	0.0017	5	0.0157	9.504970E-05	E
<input type="radio"/> GO:0044248	4	<a href="#">cellular catabolic process</a>	425	0.0656	38	0.1195	0.0001040	E

<input type="radio"/>	GO:0043285	5	<a href="#">biopolymer catabolic process</a>	277	0.0428	28	0.0881	0.0001148	E
<input type="radio"/>	GO:0015980	4	<a href="#">energy derivation by oxidation of organic compounds</a>	145	0.0224	18	0.0566	0.0001613	E
<input type="radio"/>	GO:0044262	5	<a href="#">cellular carbohydrate metabolic process</a>	213	0.0329	23	0.0723	0.0001753	E
<input type="radio"/>	GO:0009057	4	<a href="#">macromolecule catabolic process</a>	345	0.0533	32	0.1006	0.0001840	E
<input type="radio"/>	GO:0006350	5	<a href="#">transcription</a>	567	0.0876	46	0.1447	0.0001890	E
<input type="radio"/>	GO:0019219	6,5	<a href="#">regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process</a>	440	0.0679	38	0.1195	0.0002025	E
<input type="radio"/>	GO:0006464	6	<a href="#">protein modification process</a>	520	0.0803	43	0.1352	0.0002028	E
<input type="radio"/>	GO:0045786	6,7,5	<a href="#">negative regulation of progression through cell cycle</a>	13	0.0020	5	0.0157	0.0002398	E
<input type="radio"/>	GO:0009991	4	<a href="#">response to extracellular stimulus</a>	37	0.0057	8	0.0252	0.0002878	E
<input type="radio"/>	GO:0009605	3	<a href="#">response to external stimulus</a>	37	0.0057	8	0.0252	0.0002878	E
<input type="radio"/>	GO:0031667	5	<a href="#">response to nutrient levels</a>	37	0.0057	8	0.0252	0.0002878	E
<input type="radio"/>	GO:0007034	7,5,6	<a href="#">vacuolar transport</a>	114	0.0176	15	0.0472	0.0002923	E
<input type="radio"/>	GO:0006091	3	<a href="#">generation of precursor metabolites and energy</a>	183	0.0283	20	0.0629	0.0003768	E
<input type="radio"/>	GO:0030163	6,5	<a href="#">protein catabolic process</a>	173	0.0267	19	0.0597	0.0004861	E
<input type="radio"/>	GO:0045721	7,9,8,10,6,11	<a href="#">negative regulation of gluconeogenesis</a>	9	0.0014	4	0.0126	0.0005610	E
<input type="radio"/>	GO:0045912	6,5	<a href="#">negative regulation of carbohydrate metabolic process</a>	9	0.0014	4	0.0126	0.0005610	E
<input type="radio"/>	GO:0045449	7,6	<a href="#">regulation of transcription</a>	386	0.0596	33	0.1038	0.0005826	E
<input type="radio"/>	GO:0044238	3	<a href="#">primary metabolic process</a>	3247	0.5014	185	0.5818	0.0006061	E
<input type="radio"/>	GO:0008152	2	<a href="#">metabolic process</a>	3516	0.5429	198	0.6226	0.0006176	E
<input type="radio"/>	GO:0005977	7,6,8	<a href="#">glycogen metabolic process</a>	32	0.0049	7	0.0220	0.0006332	E
<input type="radio"/>	GO:0006357	9,8	<a href="#">regulation of transcription from RNA polymerase II promoter</a>	221	0.0341	22	0.0692	0.0006779	E
<input type="radio"/>	GO:0006366	8,7	<a href="#">transcription from RNA polymerase II promoter</a>	343	0.0530	30	0.0943	0.0006998	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	5	0.0157	0.0007011	E
<input type="radio"/>	GO:0044265	5	<a href="#">cellular macromolecule catabolic process</a>	314	0.0485	28	0.0881	0.0007708	E
<input type="radio"/>	GO:0010033	4	<a href="#">response to organic substance</a>	10	0.0015	4	0.0126	0.0008897	E
<input type="radio"/>	GO:0016051	5	<a href="#">carbohydrate biosynthetic process</a>	77	0.0119	11	0.0346	0.0008979	E
<input type="radio"/>	GO:0044237	3	<a href="#">cellular metabolic process</a>	3403	0.5255	191	0.6006	0.0010263	E
<input type="radio"/>	GO:0042149	8,7,6	<a href="#">cellular response to glucose starvation</a>	5	0.0008	3	0.0094	0.0010620	E
<input type="radio"/>	GO:0006623	9,8,7,6	<a href="#">protein targeting to vacuole</a>	67	0.0103	10	0.0314	0.0010790	E
<input type="radio"/>	GO:0044257	6,7	<a href="#">cellular protein catabolic process</a>	160	0.0247	17	0.0535	0.0012821	E
<input type="radio"/>	GO:0006810	3,4	<a href="#">transport</a>	981	0.1515	66	0.2075	0.0013281	E
<input type="radio"/>	GO:0009889	5,4	<a href="#">regulation of biosynthetic process</a>	69	0.0107	10	0.0314	0.0013407	E
<input type="radio"/>	GO:0031669	6,5	<a href="#">cellular response to nutrient levels</a>	19	0.0029	5	0.0157	0.0016081	E
<input type="radio"/>	GO:0031668	5,4	<a href="#">cellular response to extracellular stimulus</a>	19	0.0029	5	0.0157	0.0016081	E
<input type="radio"/>	GO:0043255	7,6,5	<a href="#">regulation of carbohydrate biosynthetic process</a>	19	0.0029	5	0.0157	0.0016081	E
<input type="radio"/>	GO:0009267	7,6,5	<a href="#">cellular response to starvation</a>	19	0.0029	5	0.0157	0.0016081	E
<input type="radio"/>	GO:0042594	6,4	<a href="#">response to starvation</a>	19	0.0029	5	0.0157	0.0016081	E
<input type="radio"/>	GO:0009266	4	<a href="#">response to temperature stimulus</a>	28	0.0043	6	0.0189	0.0016989	E
<input type="radio"/>	GO:0051179	2	<a href="#">localization</a>	1051	0.1623	69	0.2170	0.0018509	E
<input type="radio"/>	GO:0051704	2	<a href="#">multi-organism process</a>	139	0.0215	15	0.0472	0.0020167	E
<input type="radio"/>	GO:0032787	6	<a href="#">monocarboxylic acid metabolic process</a>	126	0.0195	14	0.0440	0.0021393	E

<input type="checkbox"/>	GO:0051234	2,3	<a href="#">establishment of localization</a>	1004	0.1550	66	0.2075	0.0021896	E
<input type="checkbox"/>	GO:0007031	5	<a href="#">peroxisome organization and biogenesis</a>	40	0.0062	7	0.0220	0.0023604	E
<input type="checkbox"/>	GO:0051599	5,4	<a href="#">response to hydrostatic pressure</a>	2	0.0003	2	0.0063	0.0024040	E
<input type="checkbox"/>	GO:0050826	6,5	<a href="#">response to freezing</a>	2	0.0003	2	0.0063	0.0024040	E
<input type="checkbox"/>	GO:0009415	4	<a href="#">response to water</a>	2	0.0003	2	0.0063	0.0024040	E
<input type="checkbox"/>	GO:0010286	6,5	<a href="#">heat acclimation</a>	2	0.0003	2	0.0063	0.0024040	E
<input type="checkbox"/>	GO:0006355	8,7	<a href="#">regulation of transcription, DNA-dependent</a>	359	0.0554	29	0.0912	0.0024755	E
<input type="checkbox"/>	GO:0006468	8,7	<a href="#">protein amino acid phosphorylation</a>	101	0.0156	12	0.0377	0.0024845	E
<input type="checkbox"/>	GO:0046907	6,4,5	<a href="#">intracellular transport</a>	545	0.0842	40	0.1258	0.0025015	E
<input type="checkbox"/>	GO:0051716	3	<a href="#">cellular response to stimulus</a>	21	0.0032	5	0.0157	0.0025479	E
<input type="checkbox"/>	GO:0033554	4	<a href="#">cellular response to stress</a>	21	0.0032	5	0.0157	0.0025479	E
<input type="checkbox"/>	GO:0001300	5	<a href="#">chronological cell aging</a>	13	0.0020	4	0.0126	0.0026089	E
<input type="checkbox"/>	GO:0006111	8,7,9,10,6	<a href="#">regulation of gluconeogenesis</a>	13	0.0020	4	0.0126	0.0026089	E
<input type="checkbox"/>	GO:0043170	3	<a href="#">macromolecule metabolic process</a>	2841	0.4387	160	0.5031	0.0027915	E
<input type="checkbox"/>	GO:0044264	5,6	<a href="#">cellular polysaccharide metabolic process</a>	65	0.0100	9	0.0283	0.0030313	E
<input type="checkbox"/>	GO:0005976	5	<a href="#">polysaccharide metabolic process</a>	65	0.0100	9	0.0283	0.0030313	E
<input type="checkbox"/>	GO:0051649	5,3,4	<a href="#">establishment of cellular localization</a>	606	0.0936	43	0.1352	0.0031574	E
<input type="checkbox"/>	GO:0009409	5,4	<a href="#">response to cold</a>	7	0.0011	3	0.0094	0.0033639	E
<input type="checkbox"/>	GO:0045014	11,9,10,7	<a href="#">negative regulation of transcription by glucose</a>	7	0.0011	3	0.0094	0.0033639	E
<input type="checkbox"/>	GO:0000437	11,9,10,7	<a href="#">negative regulation of transcription from RNA polymerase II promoter by carbon catabolites</a>	7	0.0011	3	0.0094	0.0033639	E
<input type="checkbox"/>	GO:0000433	12,10,11,8	<a href="#">negative regulation of transcription from RNA polymerase II promoter by glucose</a>	7	0.0011	3	0.0094	0.0033639	E
<input type="checkbox"/>	GO:0000430	11,9,10,7	<a href="#">regulation of transcription from RNA polymerase II promoter by glucose</a>	7	0.0011	3	0.0094	0.0033639	E
<input type="checkbox"/>	GO:0000429	10,8,9,6	<a href="#">regulation of transcription from RNA polymerase II promoter by carbon catabolites</a>	7	0.0011	3	0.0094	0.0033639	E
<input type="checkbox"/>	GO:0009892	5,4	<a href="#">negative regulation of metabolic process</a>	208	0.0321	19	0.0597	0.0034965	E
<input type="checkbox"/>	GO:0043412	5	<a href="#">biopolymer modification</a>	664	0.1025	46	0.1447	0.0035601	E
<input type="checkbox"/>	GO:0006508	6	<a href="#">proteolysis</a>	178	0.0275	17	0.0535	0.0035707	E
<input type="checkbox"/>	GO:0031326	6,5	<a href="#">regulation of cellular biosynthetic process</a>	67	0.0103	9	0.0283	0.0036731	E
<input type="checkbox"/>	GO:0009408	5,4	<a href="#">response to heat</a>	23	0.0036	5	0.0157	0.0038144	E
<input type="checkbox"/>	GO:0051603	7,8	<a href="#">proteolysis involved in cellular protein catabolic process</a>	151	0.0233	15	0.0472	0.0041348	E
<input type="checkbox"/>	GO:0031324	6,5	<a href="#">negative regulation of cellular metabolic process</a>	198	0.0306	18	0.0566	0.0044970	E
<input type="checkbox"/>	GO:0005978	8,7,9	<a href="#">glycogen biosynthetic process</a>	15	0.0023	4	0.0126	0.0045083	E
<input type="checkbox"/>	GO:0006896	9,8,7,6	<a href="#">Golgi to vacuole transport</a>	24	0.0037	5	0.0157	0.0045845	E
<input type="checkbox"/>	GO:0051641	4,3	<a href="#">cellular localization</a>	642	0.0991	44	0.1384	0.0049068	E
<input type="checkbox"/>	GO:0006073	6,7	<a href="#">glucan metabolic process</a>	46	0.0071	7	0.0220	0.0050339	E
<input type="checkbox"/>	GO:0045013	10,8,9,6	<a href="#">negative regulation of transcription by carbon catabolites</a>	8	0.0012	3	0.0094	0.0051201	E
<input type="checkbox"/>	GO:0046015	10,8,9,6	<a href="#">regulation of transcription by glucose</a>	8	0.0012	3	0.0094	0.0051201	E
<input type="checkbox"/>	GO:0006351	7,6	<a href="#">transcription, DNA-dependent</a>	522	0.0806	37	0.1164	0.0054661	E
<input type="checkbox"/>	GO:0032774	6	<a href="#">RNA biosynthetic process</a>	524	0.0809	37	0.1164	0.0057458	E
<input type="checkbox"/>	GO:0008645	6,7	<a href="#">hexose transport</a>	26	0.0040	5	0.0157	0.0064233	E
<input type="checkbox"/>	GO:0015749	5,6	<a href="#">monosaccharide transport</a>	26	0.0040	5	0.0157	0.0064233	E
<input type="checkbox"/>	GO:0006512	8	<a href="#">ubiquitin cycle</a>	88	0.0136	10	0.0314	0.0069697	E
<input type="checkbox"/>	GO:0016558	10,9,7,8,6	<a href="#">protein import into peroxisome matrix</a>	17	0.0026	4	0.0126	0.0071152	E

<input type="radio"/>	GO:0006886	7,5,6	<a href="#">intracellular protein transport</a>	274	0.0423	22	0.0692	0.0072070	E
<input type="radio"/>	GO:0009628	3	<a href="#">response to abiotic stimulus</a>	117	0.0181	12	0.0377	0.0072641	E
<input type="radio"/>	GO:0042026	7	<a href="#">protein refolding</a>	9	0.0014	3	0.0094	0.0073061	E
<input type="radio"/>	GO:0006605	8,6,7	<a href="#">protein targeting</a>	258	0.0398	21	0.0660	0.0073382	E
<input type="radio"/>	GO:0000747	4	<a href="#">conjugation with cellular fusion</a>	118	0.0182	12	0.0377	0.0076973	E
<input type="radio"/>	GO:0019953	3	<a href="#">sexual reproduction</a>	118	0.0182	12	0.0377	0.0076973	E
<input type="radio"/>	GO:0000746	3	<a href="#">conjugation</a>	118	0.0182	12	0.0377	0.0076973	E
<input type="radio"/>	GO:0015031	4,5,6	<a href="#">protein transport</a>	280	0.0432	22	0.0692	0.0088209	E
<input type="radio"/>	GO:0007242	5	<a href="#">intracellular signaling cascade</a>	137	0.0212	13	0.0409	0.0095666	E
<input type="radio"/>	GO:0044260	4	<a href="#">cellular macromolecule metabolic process</a>	1552	0.2397	90	0.2830	0.0096625	E
<input type="radio"/>	GO:0030435	5	<a href="#">sporulation</a>	123	0.0190	12	0.0377	0.0101398	E
<input type="radio"/>	GO:0019236	4	<a href="#">response to pheromone</a>	94	0.0145	10	0.0314	0.0103775	E
<input type="radio"/>	GO:0043283	4	<a href="#">biopolymer metabolic process</a>	2230	0.3443	124	0.3899	0.0103819	E
<input type="radio"/>	GO:0016310	6	<a href="#">phosphorylation</a>	155	0.0239	14	0.0440	0.0107956	E
<input type="radio"/>	GO:0048869	3	<a href="#">cellular developmental process</a>	173	0.0267	15	0.0472	0.0118448	E
<input type="radio"/>	GO:0030154	4	<a href="#">cell differentiation</a>	173	0.0267	15	0.0472	0.0118448	E
<input type="radio"/>	GO:0006625	9,8,6,7	<a href="#">protein targeting to peroxisome</a>	20	0.0031	4	0.0126	0.0124727	E
<input type="radio"/>	GO:0043574	7,5,6	<a href="#">peroxisomal transport</a>	20	0.0031	4	0.0126	0.0124727	E
<input type="radio"/>	GO:0006892	8,6,5,7	<a href="#">post-Golgi vesicle-mediated transport</a>	69	0.0107	8	0.0252	0.0127998	E
<input type="radio"/>	GO:0043623	7,6	<a href="#">cellular protein complex assembly</a>	69	0.0107	8	0.0252	0.0127998	E
<input type="radio"/>	GO:0007039	7,8	<a href="#">vacuolar protein catabolic process</a>	11	0.0017	3	0.0094	0.0129872	E
<input type="radio"/>	GO:0008608	7,4	<a href="#">attachment of spindle microtubules to kinetochore</a>	4	0.0006	2	0.0063	0.0130503	E
<input type="radio"/>	GO:0043618	9,10,8,6	<a href="#">regulation of transcription from RNA polymerase II promoter in response to stress</a>	4	0.0006	2	0.0063	0.0130503	E
<input type="radio"/>	GO:0043620	8,7,5	<a href="#">regulation of transcription in response to stress</a>	4	0.0006	2	0.0063	0.0130503	E
<input type="radio"/>	GO:0006085	7	<a href="#">acetyl-CoA biosynthetic process</a>	4	0.0006	2	0.0063	0.0130503	E
<input type="radio"/>	GO:0016192	4,5	<a href="#">vesicle-mediated transport</a>	328	0.0506	24	0.0755	0.0132510	E
<input type="radio"/>	GO:0006457	6	<a href="#">protein folding</a>	84	0.0130	9	0.0283	0.0136375	E
<input type="radio"/>	GO:0032446	8	<a href="#">protein modification by small protein conjugation</a>	84	0.0130	9	0.0283	0.0136375	E
<input type="radio"/>	GO:0008104	4	<a href="#">protein localization</a>	330	0.0510	24	0.0755	0.0139757	E
<input type="radio"/>	GO:0045184	3,4,5	<a href="#">establishment of protein localization</a>	296	0.0457	22	0.0692	0.0143308	E
<input type="radio"/>	GO:0019932	6	<a href="#">second-messenger-mediated signaling</a>	32	0.0049	5	0.0157	0.0145882	E
<input type="radio"/>	GO:0006793	4	<a href="#">phosphorus metabolic process</a>	212	0.0327	17	0.0535	0.0149515	E
<input type="radio"/>	GO:0006796	5	<a href="#">phosphate metabolic process</a>	212	0.0327	17	0.0535	0.0149515	E
<input type="radio"/>	GO:0006461	6,5	<a href="#">protein complex assembly</a>	116	0.0179	11	0.0346	0.0154347	E
<input type="radio"/>	GO:0045941	8,7	<a href="#">positive regulation of transcription</a>	101	0.0156	10	0.0314	0.0155956	E
<input type="radio"/>	GO:0006914	3	<a href="#">autophagy</a>	45	0.0069	6	0.0189	0.0157895	E
<input type="radio"/>	GO:0051321	4	<a href="#">meiotic cell cycle</a>	148	0.0229	13	0.0409	0.0158695	E
<input type="radio"/>	GO:0007126	8,6,7,5	<a href="#">meiosis</a>	148	0.0229	13	0.0409	0.0158695	E
<input type="radio"/>	GO:0006511	9,8,10	<a href="#">ubiquitin-dependent protein catabolic process</a>	148	0.0229	13	0.0409	0.0158695	E
<input type="radio"/>	GO:0051327	7,5,6	<a href="#">M phase of meiotic cell cycle</a>	148	0.0229	13	0.0409	0.0158695	E
<input type="radio"/>	GO:0019941	8,7,9	<a href="#">modification-dependent protein catabolic process</a>	148	0.0229	13	0.0409	0.0158695	E
<input type="radio"/>	GO:0044247	7,6	<a href="#">cellular polysaccharide catabolic process</a>	12	0.0019	3	0.0094	0.0164725	E
<input type="radio"/>	GO:0000272	6	<a href="#">polysaccharide catabolic process</a>	12	0.0019	3	0.0094	0.0164725	E

<input type="radio"/>	GO:0000074	6,5	<a href="#">regulation of progression through cell cycle</a>	167	0.0258	14	0.0440	0.0177400	E
<input type="radio"/>	GO:0051726	5,4	<a href="#">regulation of cell cycle</a>	167	0.0258	14	0.0440	0.0177400	E
<input type="radio"/>	GO:0000003	2	<a href="#">reproduction</a>	323	0.0499	23	0.0723	0.0183500	E
<input type="radio"/>	GO:0007127	9,7,6,8,5	<a href="#">meiosis I</a>	75	0.0116	8	0.0252	0.0191770	E
<input type="radio"/>	GO:0051186	4	<a href="#">cofactor metabolic process</a>	170	0.0263	14	0.0440	0.0198275	E
<input type="radio"/>	GO:0046165	5	<a href="#">alcohol biosynthetic process</a>	35	0.0054	5	0.0157	0.0202536	E
<input type="radio"/>	GO:0033036	3	<a href="#">macromolecule localization</a>	382	0.0590	26	0.0818	0.0205284	E
<input type="radio"/>	GO:0007188	8,9	<a href="#">G-protein signaling, coupled to cAMP nucleotide second messenger</a>	5	0.0008	2	0.0063	0.0206886	E
<input type="radio"/>	GO:0043087	6	<a href="#">regulation of GTPase activity</a>	5	0.0008	2	0.0063	0.0206886	E
<input type="radio"/>	GO:0018410	8	<a href="#">peptide or protein carboxyl-terminal blocking</a>	5	0.0008	2	0.0063	0.0206886	E
<input type="radio"/>	GO:0007187	7,8	<a href="#">G-protein signaling, coupled to cyclic nucleotide second messenger</a>	5	0.0008	2	0.0063	0.0206886	E
<input type="radio"/>	GO:0042710	3	<a href="#">biofilm formation</a>	5	0.0008	2	0.0063	0.0206886	E
<input type="radio"/>	GO:0009749	7,6	<a href="#">response to glucose stimulus</a>	5	0.0008	2	0.0063	0.0206886	E
<input type="radio"/>	GO:0015693	7,8	<a href="#">magnesium ion transport</a>	5	0.0008	2	0.0063	0.0206886	E
<input type="radio"/>	GO:0042219	6,5	<a href="#">amino acid derivative catabolic process</a>	5	0.0008	2	0.0063	0.0206886	E
<input type="radio"/>	GO:0009746	6,5	<a href="#">response to hexose stimulus</a>	5	0.0008	2	0.0063	0.0206886	E
<input type="radio"/>	GO:0043632	6	<a href="#">modification-dependent macromolecule catabolic process</a>	155	0.0239	13	0.0409	0.0209975	E
<input type="radio"/>	GO:0022402	4,3	<a href="#">cell cycle process</a>	439	0.0678	29	0.0912	0.0213160	E
<input type="radio"/>	GO:0005996	5,6	<a href="#">monosaccharide metabolic process</a>	92	0.0142	9	0.0283	0.0216458	E
<input type="radio"/>	GO:0007568	3	<a href="#">aging</a>	49	0.0076	6	0.0189	0.0222170	E
<input type="radio"/>	GO:0007569	4	<a href="#">cell aging</a>	49	0.0076	6	0.0189	0.0222170	E
<input type="radio"/>	GO:0045935	7,6	<a href="#">positive regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process</a>	108	0.0167	10	0.0314	0.0222212	E
<input type="radio"/>	GO:0030437	7,6	<a href="#">sporulation (sensu Fungi)</a>	108	0.0167	10	0.0314	0.0222212	E
<input type="radio"/>	GO:0048622	6,5	<a href="#">reproductive sporulation</a>	108	0.0167	10	0.0314	0.0222212	E
<input type="radio"/>	GO:0048522	5,4	<a href="#">positive regulation of cellular process</a>	124	0.0191	11	0.0346	0.0223473	E
<input type="radio"/>	GO:0048518	4	<a href="#">positive regulation of biological process</a>	124	0.0191	11	0.0346	0.0223473	E
<input type="radio"/>	GO:0045045	7,5,4,6	<a href="#">secretory pathway</a>	243	0.0375	18	0.0566	0.0228640	E
<input type="radio"/>	GO:0045990	9,7,8,5	<a href="#">regulation of transcription by carbon catabolites</a>	14	0.0022	3	0.0094	0.0246627	E
<input type="radio"/>	GO:0009250	7,8	<a href="#">glucan biosynthetic process</a>	25	0.0039	4	0.0126	0.0253778	E
<input type="radio"/>	GO:0055072	9	<a href="#">iron ion homeostasis</a>	38	0.0059	5	0.0157	0.0269681	E
<input type="radio"/>	GO:0008643	4,5	<a href="#">carbohydrate transport</a>	38	0.0059	5	0.0157	0.0269681	E
<input type="radio"/>	GO:0006879	10,8	<a href="#">cellular iron ion homeostasis</a>	38	0.0059	5	0.0157	0.0269681	E
<input type="radio"/>	GO:0006090	7	<a href="#">pyruvate metabolic process</a>	38	0.0059	5	0.0157	0.0269681	E
<input type="radio"/>	GO:0016567	9	<a href="#">protein ubiquitination</a>	66	0.0102	7	0.0220	0.0271335	E
<input type="radio"/>	GO:0032940	6,4,5	<a href="#">secretion by cell</a>	250	0.0386	18	0.0566	0.0274894	E
<input type="radio"/>	GO:0046903	3,4	<a href="#">secretion</a>	250	0.0386	18	0.0566	0.0274894	E
<input type="radio"/>	GO:0044267	5	<a href="#">cellular protein metabolic process</a>	1498	0.2313	82	0.2579	0.0274895	E
<input type="radio"/>	GO:0006066	4	<a href="#">alcohol metabolic process</a>	163	0.0252	13	0.0409	0.0279060	E
<input type="radio"/>	GO:0019538	4	<a href="#">protein metabolic process</a>	1547	0.2389	84	0.2642	0.0293186	E
<input type="radio"/>	GO:0009651	5	<a href="#">response to salt stress</a>	15	0.0023	3	0.0094	0.0293257	E
<input type="radio"/>	GO:0007265	7	<a href="#">Ras protein signal transduction</a>	39	0.0060	5	0.0157	0.0294300	E
<input type="radio"/>	GO:0001323	4,5,6	<a href="#">age-dependent general metabolic decline during chronological cell aging</a>	6	0.0009	2	0.0063	0.0295174	E

<input type="radio"/>	GO:0009743	5,4	<a href="#">response to carbohydrate stimulus</a>	6	0.0009	2	0.0063	0.0295174	E
<input type="radio"/>	GO:0001324	5,6,7	<a href="#">age-dependent response to oxidative stress during chronological cell aging</a>	6	0.0009	2	0.0063	0.0295174	E
<input type="radio"/>	GO:0006083	7	<a href="#">acetate metabolic process</a>	6	0.0009	2	0.0063	0.0295174	E
<input type="radio"/>	GO:0043254	6,7,5	<a href="#">regulation of protein complex assembly</a>	6	0.0009	2	0.0063	0.0295174	E
<input type="radio"/>	GO:0001306	4,5	<a href="#">age-dependent response to oxidative stress</a>	6	0.0009	2	0.0063	0.0295174	E
<input type="radio"/>	GO:0007049	3	<a href="#">cell cycle</a>	458	0.0707	29	0.0912	0.0298080	E
<input type="radio"/>	GO:0048193	7,5,6	<a href="#">Golgi vesicle transport</a>	166	0.0256	13	0.0409	0.0307676	E
<input type="radio"/>	GO:0031325	6,5	<a href="#">positive regulation of cellular metabolic process</a>	116	0.0179	10	0.0314	0.0314778	E
<input type="radio"/>	GO:0009893	5,4	<a href="#">positive regulation of metabolic process</a>	116	0.0179	10	0.0314	0.0314778	E
<input type="radio"/>	GO:0007017	6	<a href="#">microtubule-based process</a>	101	0.0156	9	0.0283	0.0332835	E
<input type="radio"/>	GO:0019318	6,7	<a href="#">hexose metabolic process</a>	85	0.0131	8	0.0252	0.0332856	E
<input type="radio"/>	GO:0007131	10,8,7,5,9,6,4	<a href="#">meiotic recombination</a>	55	0.0085	6	0.0189	0.0341650	E
<input type="radio"/>	GO:0000271	6,7	<a href="#">polysaccharide biosynthetic process</a>	41	0.0063	5	0.0157	0.0346708	E
<input type="radio"/>	GO:0006094	8,9	<a href="#">gluconeogenesis</a>	28	0.0043	4	0.0126	0.0353643	E
<input type="radio"/>	GO:0006732	5	<a href="#">coenzyme metabolic process</a>	136	0.0210	11	0.0346	0.0354885	E
<input type="radio"/>	GO:0009719	3	<a href="#">response to endogenous stimulus</a>	243	0.0375	17	0.0535	0.0358942	E
<input type="radio"/>	GO:0006979	4	<a href="#">response to oxidative stress</a>	71	0.0110	7	0.0220	0.0361302	E
<input type="radio"/>	GO:0042244	5,6	<a href="#">spore wall assembly</a>	42	0.0065	5	0.0157	0.0374418	E
<input type="radio"/>	GO:0030476	8,6,7	<a href="#">spore wall assembly (sensu Fungi)</a>	42	0.0065	5	0.0157	0.0374418	E
<input type="radio"/>	GO:0001403	6,4,8,9	<a href="#">invasive growth (sensu Saccharomyces)</a>	42	0.0065	5	0.0157	0.0374418	E
<input type="radio"/>	GO:0032502	2	<a href="#">developmental process</a>	436	0.0673	27	0.0849	0.0383386	E
<input type="radio"/>	GO:0000749	5	<a href="#">response to pheromone during conjugation with cellular fusion</a>	57	0.0088	6	0.0189	0.0387111	E
<input type="radio"/>	GO:0006139	4	<a href="#">nucleobase, nucleoside, nucleotide and nucleic acid metabolic process</a>	1532	0.2366	81	0.2547	0.0390120	E
<input type="radio"/>	GO:0006595	6,7	<a href="#">polyamine metabolic process</a>	7	0.0011	2	0.0063	0.0393061	E
<input type="radio"/>	GO:0005980	9,8,7	<a href="#">glycogen catabolic process</a>	7	0.0011	2	0.0063	0.0393061	E
<input type="radio"/>	GO:0007571	3,4	<a href="#">age-dependent general metabolic decline</a>	7	0.0011	2	0.0063	0.0393061	E
<input type="radio"/>	GO:0005992	7,8	<a href="#">trehalose biosynthetic process</a>	7	0.0011	2	0.0063	0.0393061	E
<input type="radio"/>	GO:0046351	6,7	<a href="#">disaccharide biosynthetic process</a>	7	0.0011	2	0.0063	0.0393061	E
<input type="radio"/>	GO:0009410	4	<a href="#">response to xenobiotic stimulus</a>	7	0.0011	2	0.0063	0.0393061	E
<input type="radio"/>	GO:0019722	7	<a href="#">calcium-mediated signaling</a>	7	0.0011	2	0.0063	0.0393061	E
<input type="radio"/>	GO:0042147	8,6,7	<a href="#">retrograde transport, endosome to Golgi</a>	17	0.0026	3	0.0094	0.0396577	E
<input type="radio"/>	GO:0019740	4	<a href="#">nitrogen utilization</a>	17	0.0026	3	0.0094	0.0396577	E
<input type="radio"/>	GO:0019319	7,8	<a href="#">hexose biosynthetic process</a>	30	0.0046	4	0.0126	0.0428356	E
<input type="radio"/>	GO:0046364	6,7	<a href="#">monosaccharide biosynthetic process</a>	30	0.0046	4	0.0126	0.0428356	E
<input type="radio"/>	GO:0045934	7,6	<a href="#">negative regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process</a>	179	0.0276	13	0.0409	0.0446038	E
<input type="radio"/>	GO:0007584	6,4	<a href="#">response to nutrient</a>	18	0.0028	3	0.0094	0.0452683	E
<input type="radio"/>	GO:0006378	9	<a href="#">mRNA polyadenylation</a>	18	0.0028	3	0.0094	0.0452683	E
<input type="radio"/>	GO:0045944	10,9	<a href="#">positive regulation of transcription from RNA polymerase II promoter</a>	76	0.0117	7	0.0220	0.0463046	E
<input type="radio"/>	GO:0016043	3	<a href="#">cellular component organization and biogenesis</a>	2264	0.3496	113	0.3553	0.0467539	E
<input type="radio"/>	GO:0006082	4	<a href="#">organic acid metabolic process</a>	314	0.0485	20	0.0629	0.0473737	E
<input type="radio"/>	GO:0019752	5	<a href="#">carboxylic acid metabolic process</a>	314	0.0485	20	0.0629	0.0473737	E
<input type="radio"/>	GO:0007264	6	<a href="#">small GTPase mediated signal transduction</a>	61	0.0094	6	0.0189	0.0485269	E

<input type="radio"/>	GO:0000279	6,5	<a href="#">M phase</a>	258	0.0398	17	0.0535	0.0488907	E
<input type="radio"/>	GO:0006120	10,7,5	<a href="#">mitochondrial electron transport, NADH to ubiquinone</a>	1	0.0002	1	0.0031	0.0491044	E
<input type="radio"/>	GO:0019654	8,6	<a href="#">acetate fermentation</a>	1	0.0002	1	0.0031	0.0491044	E
<input type="radio"/>	GO:0032443	9,8,7,10	<a href="#">regulation of ergosterol biosynthetic process</a>	1	0.0002	1	0.0031	0.0491044	E
<input type="radio"/>	GO:0006517	8	<a href="#">protein deglycosylation</a>	1	0.0002	1	0.0031	0.0491044	E
<input type="radio"/>	GO:0001578	8	<a href="#">microtubule bundle formation</a>	1	0.0002	1	0.0031	0.0491044	E
<input type="radio"/>	GO:0019218	6,5,7	<a href="#">regulation of steroid metabolic process</a>	1	0.0002	1	0.0031	0.0491044	E
<input type="radio"/>	GO:0015880	6,7	<a href="#">coenzyme A transport</a>	1	0.0002	1	0.0031	0.0491044	E
<input type="radio"/>	GO:0006481	9,10,8	<a href="#">C-terminal protein amino acid methylation</a>	1	0.0002	1	0.0031	0.0491044	E
<input type="radio"/>	GO:0045471	5	<a href="#">response to ethanol</a>	1	0.0002	1	0.0031	0.0491044	E
<input type="radio"/>	GO:0051084	7	<a href="#">posttranslational protein folding</a>	1	0.0002	1	0.0031	0.0491044	E
<input type="radio"/>	GO:0051085	8	<a href="#">chaperone cofactor-dependent protein folding</a>	1	0.0002	1	0.0031	0.0491044	E
<input type="radio"/>	GO:0000719	8,7	<a href="#">photoreactive repair</a>	1	0.0002	1	0.0031	0.0491044	E
<input type="radio"/>	GO:0019547	9,8,10,7,6,5	<a href="#">arginine catabolic process to ornithine</a>	1	0.0002	1	0.0031	0.0491044	E
<input type="radio"/>	GO:0051182	5,6	<a href="#">coenzyme transport</a>	1	0.0002	1	0.0031	0.0491044	E
<input type="radio"/>	GO:0000066	8,6,7,9	<a href="#">mitochondrial ornithine transport</a>	1	0.0002	1	0.0031	0.0491044	E
<input type="radio"/>	GO:0015822	6,7,8	<a href="#">ornithine transport</a>	1	0.0002	1	0.0031	0.0491044	E
<input type="radio"/>	GO:0006516	7	<a href="#">glycoprotein catabolic process</a>	1	0.0002	1	0.0031	0.0491044	E
<input type="radio"/>	GO:0006039	9,10,7,6,11,8	<a href="#">cell wall chitin catabolic process</a>	1	0.0002	1	0.0031	0.0491044	E
<input type="radio"/>	GO:0046890	7,6,5	<a href="#">regulation of lipid biosynthetic process</a>	1	0.0002	1	0.0031	0.0491044	E
<input type="radio"/>	GO:0006290	7,6	<a href="#">pyrimidine dimer repair</a>	1	0.0002	1	0.0031	0.0491044	E
<input type="radio"/>	GO:0016998	5	<a href="#">cell wall catabolic process</a>	1	0.0002	1	0.0031	0.0491044	E
<input type="radio"/>	GO:0050810	8,7,6	<a href="#">regulation of steroid biosynthetic process</a>	1	0.0002	1	0.0031	0.0491044	E
<input type="radio"/>	GO:0022414	3,2	<a href="#">reproductive process</a>	183	0.0283	13	0.0409	0.0492283	E
<input type="radio"/>	GO:0009890	6,5	<a href="#">negative regulation of biosynthetic process</a>	8	0.0012	2	0.0063	0.0498480	E
<input type="radio"/>	GO:0006808	6,5	<a href="#">regulation of nitrogen utilization</a>	8	0.0012	2	0.0063	0.0498480	E
<input type="radio"/>	GO:0051171	5,4	<a href="#">regulation of nitrogen metabolic process</a>	8	0.0012	2	0.0063	0.0498480	E
<input type="radio"/>	GO:0015940	7,8	<a href="#">pantothenate biosynthetic process</a>	8	0.0012	2	0.0063	0.0498480	E
<input type="radio"/>	GO:0015939	7	<a href="#">pantothenate metabolic process</a>	8	0.0012	2	0.0063	0.0498480	E
<input type="radio"/>	GO:0043543	7	<a href="#">protein amino acid acylation</a>	62	0.0096	6	0.0189	0.0511131	E
<input type="radio"/>	GO:0045893	9,8	<a href="#">positive regulation of transcription, DNA-dependent</a>	95	0.0147	8	0.0252	0.0511157	E
<input type="radio"/>	GO:0006275	8,7	<a href="#">regulation of DNA replication</a>	19	0.0029	3	0.0094	0.0511341	E
<input type="radio"/>	GO:0007051	8	<a href="#">spindle organization and biogenesis</a>	47	0.0073	5	0.0157	0.0526110	E
<input type="radio"/>	GO:0022413	5,4	<a href="#">reproductive process in single-celled organism</a>	149	0.0230	11	0.0346	0.0527026	E
<input type="radio"/>	GO:0048610	3,4	<a href="#">reproductive cellular process</a>	149	0.0230	11	0.0346	0.0527026	E
<input type="radio"/>	GO:0000122	10,9	<a href="#">negative regulation of transcription from RNA polymerase II promoter</a>	63	0.0097	6	0.0189	0.0537454	E
<input type="radio"/>	GO:0044275	6	<a href="#">cellular carbohydrate catabolic process</a>	80	0.0124	7	0.0220	0.0551262	E
<input type="radio"/>	GO:0016052	5	<a href="#">carbohydrate catabolic process</a>	80	0.0124	7	0.0220	0.0551262	E
<input type="radio"/>	GO:0006473	8	<a href="#">protein amino acid acetylation</a>	48	0.0074	5	0.0157	0.0558693	E
<input type="radio"/>	GO:0055066	8	<a href="#">di-, tri-valent inorganic cation homeostasis</a>	64	0.0099	6	0.0189	0.0564200	E
<input type="radio"/>	GO:0030005	9,7	<a href="#">cellular di-, tri-valent inorganic cation homeostasis</a>	64	0.0099	6	0.0189	0.0564200	E
<input type="radio"/>	GO:0044249	4	<a href="#">cellular biosynthetic process</a>	366	0.0565	22	0.0692	0.0564333	E
<input type="radio"/>	GO:0016579	9	<a href="#">protein deubiquitination</a>	20	0.0031	3	0.0094	0.0572230	E

<input type="radio"/>	GO:000022	6,5,10,8	<a href="#">mitotic spindle elongation</a>	20	0.0031	3	0.0094	0.0572230	E
<input type="radio"/>	GO:0051231	5,4,9,7	<a href="#">spindle elongation</a>	20	0.0031	3	0.0094	0.0572230	E
<input type="radio"/>	GO:0006084	6	<a href="#">acetyl-CoA metabolic process</a>	20	0.0031	3	0.0094	0.0572230	E
<input type="radio"/>	GO:0000226	7	<a href="#">microtubule cytoskeleton organization and biogenesis</a>	81	0.0125	7	0.0220	0.0574068	E
<input type="radio"/>	GO:0022607	4	<a href="#">cellular component assembly</a>	471	0.0727	27	0.0849	0.0579923	E
<input type="radio"/>	GO:0006006	7,8	<a href="#">glucose metabolic process</a>	65	0.0100	6	0.0189	0.0591331	E
<input type="radio"/>	GO:0015674	6,7	<a href="#">di-, tri-valent inorganic cation transport</a>	34	0.0053	4	0.0126	0.0593601	E
<input type="radio"/>	GO:0019935	7	<a href="#">cyclic-nucleotide-mediated signaling</a>	9	0.0014	2	0.0063	0.0609591	E
<input type="radio"/>	GO:0019933	8	<a href="#">cAMP-mediated signaling</a>	9	0.0014	2	0.0063	0.0609591	E
<input type="radio"/>	GO:0009251	8,7	<a href="#">glucan catabolic process</a>	9	0.0014	2	0.0063	0.0609591	E
<input type="radio"/>	GO:0022403	5,4	<a href="#">cell cycle phase</a>	353	0.0545	21	0.0660	0.0615863	E
<input type="radio"/>	GO:0000723	8	<a href="#">telomere maintenance</a>	274	0.0423	17	0.0535	0.0634141	E
<input type="radio"/>	GO:0032200	7	<a href="#">telomere organization and biogenesis</a>	274	0.0423	17	0.0535	0.0634141	E
<input type="radio"/>	GO:0009060	6	<a href="#">aerobic respiration</a>	84	0.0130	7	0.0220	0.0643879	E
<input type="radio"/>	GO:0055080	7	<a href="#">cation homeostasis</a>	102	0.0158	8	0.0252	0.0650658	E
<input type="radio"/>	GO:0030003	8,6	<a href="#">cellular cation homeostasis</a>	102	0.0158	8	0.0252	0.0650658	E
<input type="radio"/>	GO:0007166	5	<a href="#">cell surface receptor linked signal transduction</a>	52	0.0080	5	0.0157	0.0694470	E
<input type="radio"/>	GO:0045229	4	<a href="#">external encapsulating structure organization and biogenesis</a>	200	0.0309	13	0.0409	0.0696509	E
<input type="radio"/>	GO:0007047	5	<a href="#">cell wall organization and biogenesis</a>	200	0.0309	13	0.0409	0.0696509	E
<input type="radio"/>	GO:0007001	6	<a href="#">chromosome organization and biogenesis (sensu Eukaryota)</a>	567	0.0876	30	0.0943	0.0713517	E
<input type="radio"/>	GO:0016481	8,7	<a href="#">negative regulation of transcription</a>	162	0.0250	11	0.0346	0.0714221	E
<input type="radio"/>	GO:0030174	9,7,8	<a href="#">regulation of DNA replication initiation</a>	10	0.0015	2	0.0063	0.0724756	E
<input type="radio"/>	GO:0005991	6,7	<a href="#">trehalose metabolic process</a>	10	0.0015	2	0.0063	0.0724756	E
<input type="radio"/>	GO:0051336	5	<a href="#">regulation of hydrolase activity</a>	10	0.0015	2	0.0063	0.0724756	E
<input type="radio"/>	GO:0051276	5	<a href="#">chromosome organization and biogenesis</a>	572	0.0883	30	0.0943	0.0728233	E
<input type="radio"/>	GO:0000075	7,6	<a href="#">cell cycle checkpoint</a>	53	0.0082	5	0.0157	0.0729449	E
<input type="radio"/>	GO:0051301	3	<a href="#">cell division</a>	246	0.0380	15	0.0472	0.0754900	E
<input type="radio"/>	GO:0006766	4	<a href="#">vitamin metabolic process</a>	89	0.0137	7	0.0220	0.0763237	E
<input type="radio"/>	GO:0006970	4	<a href="#">response to osmotic stress</a>	89	0.0137	7	0.0220	0.0763237	E
<input type="radio"/>	GO:0006767	5	<a href="#">water-soluble vitamin metabolic process</a>	89	0.0137	7	0.0220	0.0763237	E
<input type="radio"/>	GO:0045333	5	<a href="#">cellular respiration</a>	89	0.0137	7	0.0220	0.0763237	E
<input type="radio"/>	GO:0016485	8	<a href="#">protein processing</a>	38	0.0059	4	0.0126	0.0773602	E
<input type="radio"/>	GO:0051246	5,4	<a href="#">regulation of protein metabolic process</a>	72	0.0111	6	0.0189	0.0788684	E
<input type="radio"/>	GO:0006807	3	<a href="#">nitrogen compound metabolic process</a>	251	0.0388	15	0.0472	0.0802621	E
<input type="radio"/>	GO:0001302	5	<a href="#">replicative cell aging</a>	39	0.0060	4	0.0126	0.0819970	E
<input type="radio"/>	GO:0043631	8	<a href="#">RNA polyadenylation</a>	24	0.0037	3	0.0094	0.0831683	E
<input type="radio"/>	GO:0031577	8,7	<a href="#">spindle checkpoint</a>	24	0.0037	3	0.0094	0.0831683	E
<input type="radio"/>	GO:0010035	4	<a href="#">response to inorganic substance</a>	24	0.0037	3	0.0094	0.0831683	E
<input type="radio"/>	GO:0006259	5	<a href="#">DNA metabolic process</a>	523	0.0808	26	0.0818	0.0832958	E
<input type="radio"/>	GO:0006733	6	<a href="#">oxidoreduction coenzyme metabolic process</a>	56	0.0086	5	0.0157	0.0835800	E
<input type="radio"/>	GO:0019321	6,7	<a href="#">pentose metabolic process</a>	11	0.0017	2	0.0063	0.0842522	E
<input type="radio"/>	GO:0006116	10,9	<a href="#">NADH oxidation</a>	11	0.0017	2	0.0063	0.0842522	E
<input type="radio"/>	GO:0006974	4	<a href="#">response to DNA damage stimulus</a>	234	0.0361	14	0.0440	0.0843843	E
<input type="radio"/>	GO:0016573	11,9	<a href="#">histone acetylation</a>	40	0.0062	4	0.0126	0.0866635	E



<input type="checkbox"/>	GO:0065008	3	<a href="#">regulation of biological quality</a>	260	0.0401	15	0.0472	0.0881810	E
<input type="checkbox"/>	GO:0006873	7,5	<a href="#">cellular ion homeostasis</a>	115	0.0178	8	0.0252	0.0917295	E
<input type="checkbox"/>	GO:0055082	6,4	<a href="#">cellular chemical homeostasis</a>	115	0.0178	8	0.0252	0.0917295	E
<input type="checkbox"/>	GO:0045892	9,8	<a href="#">negative regulation of transcription, DNA-dependent</a>	156	0.0241	10	0.0314	0.0922556	E
<input type="checkbox"/>	GO:0010324	5	<a href="#">membrane invagination</a>	96	0.0148	7	0.0220	0.0930771	E
<input type="checkbox"/>	GO:0000736	7,8,9	<a href="#">double-strand break repair via single-strand annealing, removal of nonhomologous ends</a>	2	0.0003	1	0.0031	0.0934007	E
<input type="checkbox"/>	GO:0030802	9,7,8,6	<a href="#">regulation of cyclic nucleotide biosynthetic process</a>	2	0.0003	1	0.0031	0.0934007	E
<input type="checkbox"/>	GO:0030815	10,9	<a href="#">negative regulation of cAMP metabolic process</a>	2	0.0003	1	0.0031	0.0934007	E
<input type="checkbox"/>	GO:0006451	8,7,6	<a href="#">translational readthrough</a>	2	0.0003	1	0.0031	0.0934007	E
<input type="checkbox"/>	GO:0019216	5,4	<a href="#">regulation of lipid metabolic process</a>	2	0.0003	1	0.0031	0.0934007	E
<input type="checkbox"/>	GO:0030803	10,8,9,7	<a href="#">negative regulation of cyclic nucleotide biosynthetic process</a>	2	0.0003	1	0.0031	0.0934007	E
<input type="checkbox"/>	GO:0006975	9,8,5	<a href="#">DNA damage induced protein phosphorylation</a>	2	0.0003	1	0.0031	0.0934007	E
<input type="checkbox"/>	GO:0006467	7,8	<a href="#">protein thiol-disulfide exchange</a>	2	0.0003	1	0.0031	0.0934007	E
<input type="checkbox"/>	GO:0006527	8,9,6,5	<a href="#">arginine catabolic process</a>	2	0.0003	1	0.0031	0.0934007	E
<input type="checkbox"/>	GO:0010133	9,8,10	<a href="#">proline catabolic process to glutamate</a>	2	0.0003	1	0.0031	0.0934007	E
<input type="checkbox"/>	GO:0006115	6	<a href="#">ethanol biosynthetic process</a>	2	0.0003	1	0.0031	0.0934007	E
<input type="checkbox"/>	GO:0009187	6	<a href="#">cyclic nucleotide metabolic process</a>	2	0.0003	1	0.0031	0.0934007	E
<input type="checkbox"/>	GO:0030817	10,8,9,7	<a href="#">regulation of cAMP biosynthetic process</a>	2	0.0003	1	0.0031	0.0934007	E
<input type="checkbox"/>	GO:0043148	10,9,6,5,4,13,11,8	<a href="#">mitotic spindle stabilization</a>	2	0.0003	1	0.0031	0.0934007	E
<input type="checkbox"/>	GO:0016926	8	<a href="#">protein desumoylation</a>	2	0.0003	1	0.0031	0.0934007	E
<input type="checkbox"/>	GO:0016540	9	<a href="#">protein autoprocessing</a>	2	0.0003	1	0.0031	0.0934007	E
<input type="checkbox"/>	GO:0006086	8	<a href="#">acetyl-CoA biosynthetic process from pyruvate</a>	2	0.0003	1	0.0031	0.0934007	E
<input type="checkbox"/>	GO:0048250	8,6,9,7,10	<a href="#">mitochondrial iron ion transport</a>	2	0.0003	1	0.0031	0.0934007	E
<input type="checkbox"/>	GO:0046461	6,7	<a href="#">neutral lipid catabolic process</a>	2	0.0003	1	0.0031	0.0934007	E
<input type="checkbox"/>	GO:0008295	8,9	<a href="#">spermidine biosynthetic process</a>	2	0.0003	1	0.0031	0.0934007	E
<input type="checkbox"/>	GO:0019365	8,6,7	<a href="#">pyridine nucleotide salvage</a>	2	0.0003	1	0.0031	0.0934007	E
<input type="checkbox"/>	GO:0006140	7,6	<a href="#">regulation of nucleotide metabolic process</a>	2	0.0003	1	0.0031	0.0934007	E
<input type="checkbox"/>	GO:0016572	11,9,8	<a href="#">histone phosphorylation</a>	2	0.0003	1	0.0031	0.0934007	E
<input type="checkbox"/>	GO:0030799	8,7	<a href="#">regulation of cyclic nucleotide metabolic process</a>	2	0.0003	1	0.0031	0.0934007	E
<input type="checkbox"/>	GO:0032320	8,9,10	<a href="#">positive regulation of Ras GTPase activity</a>	2	0.0003	1	0.0031	0.0934007	E
<input type="checkbox"/>	GO:0006043	7,8	<a href="#">glucosamine catabolic process</a>	2	0.0003	1	0.0031	0.0934007	E
<input type="checkbox"/>	GO:0046058	7	<a href="#">cAMP metabolic process</a>	2	0.0003	1	0.0031	0.0934007	E
<input type="checkbox"/>	GO:0044269	5	<a href="#">glycerol ether catabolic process</a>	2	0.0003	1	0.0031	0.0934007	E
<input type="checkbox"/>	GO:0006171	7,8	<a href="#">cAMP biosynthetic process</a>	2	0.0003	1	0.0031	0.0934007	E
<input type="checkbox"/>	GO:0046348	6,7	<a href="#">amino sugar catabolic process</a>	2	0.0003	1	0.0031	0.0934007	E
<input type="checkbox"/>	GO:0009190	6,7	<a href="#">cyclic nucleotide biosynthetic process</a>	2	0.0003	1	0.0031	0.0934007	E
<input type="checkbox"/>	GO:0030809	9,7,8,6	<a href="#">negative regulation of nucleotide biosynthetic process</a>	2	0.0003	1	0.0031	0.0934007	E
<input type="checkbox"/>	GO:0030818	11,9,10,8	<a href="#">negative regulation of cAMP biosynthetic process</a>	2	0.0003	1	0.0031	0.0934007	E
<input type="checkbox"/>	GO:0032318	7,8,9	<a href="#">regulation of Ras GTPase activity</a>	2	0.0003	1	0.0031	0.0934007	E
<input type="checkbox"/>	GO:0019433	8,7,9	<a href="#">triacylglycerol catabolic process</a>	2	0.0003	1	0.0031	0.0934007	E
<input type="checkbox"/>	GO:0030808	8,6,7,5	<a href="#">regulation of nucleotide biosynthetic process</a>	2	0.0003	1	0.0031	0.0934007	E

<input type="radio"/>	GO:0030814	9,8	<a href="#">regulation of cAMP metabolic process</a>	2	0.0003	1	0.0031	0.0934007	E
<input type="radio"/>	GO:0045980	8,7	<a href="#">negative regulation of nucleotide metabolic process</a>	2	0.0003	1	0.0031	0.0934007	E
<input type="radio"/>	GO:0030800	9,8	<a href="#">negative regulation of cyclic nucleotide metabolic process</a>	2	0.0003	1	0.0031	0.0934007	E
<input type="radio"/>	GO:0043146	9,8,12,10,7	<a href="#">spindle stabilization</a>	2	0.0003	1	0.0031	0.0934007	E
<input type="radio"/>	GO:0006032	9,10,8,7	<a href="#">chitin catabolic process</a>	2	0.0003	1	0.0031	0.0934007	E
<input type="radio"/>	GO:0046503	6,7	<a href="#">glycerolipid catabolic process</a>	2	0.0003	1	0.0031	0.0934007	E
<input type="radio"/>	GO:0046777	9,10,8	<a href="#">protein amino acid autophosphorylation</a>	2	0.0003	1	0.0031	0.0934007	E
<input type="radio"/>	GO:0008216	7,8	<a href="#">spermidine metabolic process</a>	2	0.0003	1	0.0031	0.0934007	E
<input type="radio"/>	GO:0046497	8,7	<a href="#">nicotinate nucleotide metabolic process</a>	2	0.0003	1	0.0031	0.0934007	E
<input type="radio"/>	GO:0006046	8,9	<a href="#">N-acetylglucosamine catabolic process</a>	2	0.0003	1	0.0031	0.0934007	E
<input type="radio"/>	GO:0006642	8,7,9	<a href="#">triacylglycerol mobilization</a>	2	0.0003	1	0.0031	0.0934007	E
<input type="radio"/>	GO:0043458	7,8	<a href="#">ethanol biosynthetic process during fermentation</a>	2	0.0003	1	0.0031	0.0934007	E
<input type="radio"/>	GO:0046464	7,6,8	<a href="#">acylglycerol catabolic process</a>	2	0.0003	1	0.0031	0.0934007	E
<input type="radio"/>	GO:0019358	9,7,8	<a href="#">nicotinate nucleotide salvage</a>	2	0.0003	1	0.0031	0.0934007	E
<input type="radio"/>	GO:0016568	8	<a href="#">chromatin modification</a>	223	0.0344	13	0.0409	0.0948791	E
<input type="radio"/>	GO:0009966	5,4	<a href="#">regulation of signal transduction</a>	26	0.0040	3	0.0094	0.0966587	E
<input type="radio"/>	GO:0006379	8	<a href="#">mRNA cleavage</a>	26	0.0040	3	0.0094	0.0966587	E
<input type="radio"/>	GO:0007010	5	<a href="#">cytoskeleton organization and biogenesis</a>	227	0.0351	13	0.0409	0.0984991	E
<input type="radio"/>	GO:0050801	6	<a href="#">ion homeostasis</a>	119	0.0184	8	0.0252	0.0995868	E
<input type="radio"/>	GO:0009064	6,7	<a href="#">glutamine family amino acid metabolic process</a>	43	0.0066	4	0.0126	0.1007186	E
<input type="radio"/>	GO:0048878	5	<a href="#">chemical homeostasis</a>	121	0.0187	8	0.0252	0.1033818	E
<input type="radio"/>	GO:0009084	7,8	<a href="#">glutamine family amino acid biosynthetic process</a>	27	0.0042	3	0.0094	0.1034304	E
<input type="radio"/>	GO:0007093	8,10,9,7	<a href="#">mitotic cell cycle checkpoint</a>	27	0.0042	3	0.0094	0.1034304	E
<input type="radio"/>	GO:0030001	6,7	<a href="#">metal ion transport</a>	62	0.0096	5	0.0157	0.1048907	E
<input type="radio"/>	GO:0006310	6	<a href="#">DNA recombination</a>	122	0.0188	8	0.0252	0.1052398	E
<input type="radio"/>	GO:0007052	5,4,9	<a href="#">mitotic spindle organization and biogenesis</a>	44	0.0068	4	0.0126	0.1053826	E
<input type="radio"/>	GO:0016049	5,3,7,8	<a href="#">cell growth</a>	102	0.0158	7	0.0220	0.1068360	E
<input type="radio"/>	GO:0009065	7,8	<a href="#">glutamine family amino acid catabolic process</a>	13	0.0020	2	0.0063	0.1080891	E
<input type="radio"/>	GO:0006537	8,9	<a href="#">glutamate biosynthetic process</a>	13	0.0020	2	0.0063	0.1080891	E
<input type="radio"/>	GO:0019362	7,6	<a href="#">pyridine nucleotide metabolic process</a>	45	0.0069	4	0.0126	0.1100174	E
<input type="radio"/>	GO:0009636	4	<a href="#">response to toxin</a>	28	0.0043	3	0.0094	0.1101838	E
<input type="radio"/>	GO:0032505	4,3	<a href="#">reproduction of a single-celled organism</a>	194	0.0300	11	0.0346	0.1111387	E
<input type="radio"/>	GO:0006325	7	<a href="#">establishment and/or maintenance of chromatin architecture</a>	253	0.0391	13	0.0409	0.1135972	E
<input type="radio"/>	GO:0006323	6	<a href="#">DNA packaging</a>	253	0.0391	13	0.0409	0.1135972	E
<input type="radio"/>	GO:0006839	7,5,6	<a href="#">mitochondrial transport</a>	65	0.0100	5	0.0157	0.1152246	E
<input type="radio"/>	GO:0019725	5,3	<a href="#">cellular homeostasis</a>	128	0.0198	8	0.0252	0.1157337	E
<input type="radio"/>	GO:0009308	4	<a href="#">amine metabolic process</a>	228	0.0352	12	0.0377	0.1161371	E
<input type="radio"/>	GO:0044255	4,5	<a href="#">cellular lipid metabolic process</a>	229	0.0354	12	0.0377	0.1165570	E
<input type="radio"/>	GO:0006470	8,7	<a href="#">protein amino acid dephosphorylation</a>	29	0.0045	3	0.0094	0.1168935	E
<input type="radio"/>	GO:0006897	6,5	<a href="#">endocytosis</a>	86	0.0133	6	0.0189	0.1178579	E
<input type="radio"/>	GO:0006631	5,7,6	<a href="#">fatty acid metabolic process</a>	47	0.0073	4	0.0126	0.1191559	E
<input type="radio"/>	GO:0006629	4	<a href="#">lipid metabolic process</a>	242	0.0374	12	0.0377	0.1195124	E
<input type="radio"/>	GO:0000077	9,8,6	<a href="#">DNA damage checkpoint</a>	14	0.0022	2	0.0063	0.1199382	E

<input type="radio"/>	GO:0006037	8,9,6,7,10	<a href="#">cell wall chitin metabolic process</a>	14	0.0022	2	0.0063	0.1199382	E
<input type="radio"/>	GO:0042770	5	<a href="#">DNA damage response, signal transduction</a>	14	0.0022	2	0.0063	0.1199382	E
<input type="radio"/>	GO:0006734	9,8	<a href="#">NADH metabolic process</a>	14	0.0022	2	0.0063	0.1199382	E
<input type="radio"/>	GO:0042787	10,9,11	<a href="#">protein ubiquitination during ubiquitin-dependent protein catabolic process</a>	14	0.0022	2	0.0063	0.1199382	E
<input type="radio"/>	GO:0017038	5,6,7	<a href="#">protein import</a>	109	0.0168	7	0.0220	0.1214358	E
<input type="radio"/>	GO:0006893	9,7,6,8	<a href="#">Golgi to plasma membrane transport</a>	30	0.0046	3	0.0094	0.1235356	E
<input type="radio"/>	GO:0042592	4	<a href="#">homeostatic process</a>	134	0.0207	8	0.0252	0.1248896	E
<input type="radio"/>	GO:0016044	4	<a href="#">membrane organization and biogenesis</a>	188	0.0290	10	0.0314	0.1262944	E
<input type="radio"/>	GO:0016197	7,5,6	<a href="#">endosome transport</a>	49	0.0076	4	0.0126	0.1280532	E
<input type="radio"/>	GO:0016569	9	<a href="#">covalent chromatin modification</a>	91	0.0141	6	0.0189	0.1300839	E
<input type="radio"/>	GO:0016570	10,8	<a href="#">histone modification</a>	91	0.0141	6	0.0189	0.1300839	E
<input type="radio"/>	GO:0006575	5	<a href="#">amino acid derivative metabolic process</a>	31	0.0048	3	0.0094	0.1300879	E
<input type="radio"/>	GO:0005984	6	<a href="#">disaccharide metabolic process</a>	31	0.0048	3	0.0094	0.1300879	E
<input type="radio"/>	GO:0006519	4	<a href="#">amino acid and derivative metabolic process</a>	202	0.0312	10	0.0314	0.1303420	E
<input type="radio"/>	GO:0022401	7,6	<a href="#">adaptation of signaling pathway</a>	15	0.0023	2	0.0063	0.1316228	E
<input type="radio"/>	GO:0006267	8,7	<a href="#">pre-replicative complex assembly</a>	15	0.0023	2	0.0063	0.1316228	E
<input type="radio"/>	GO:0000737	6,7	<a href="#">DNA catabolic process, endonucleolytic</a>	15	0.0023	2	0.0063	0.1316228	E
<input type="radio"/>	GO:0006525	7,8,5,4	<a href="#">arginine metabolic process</a>	15	0.0023	2	0.0063	0.1316228	E
<input type="radio"/>	GO:0000051	4,3	<a href="#">urea cycle intermediate metabolic process</a>	15	0.0023	2	0.0063	0.1316228	E
<input type="radio"/>	GO:0000754	8,7,5	<a href="#">adaptation to pheromone during conjugation with cellular fusion</a>	15	0.0023	2	0.0063	0.1316228	E
<input type="radio"/>	GO:0016584	6,10	<a href="#">nucleosome positioning</a>	3	0.0005	1	0.0031	0.1332410	E
<input type="radio"/>	GO:0043068	6,7,9,5	<a href="#">positive regulation of programmed cell death</a>	3	0.0005	1	0.0031	0.1332410	E
<input type="radio"/>	GO:0042402	6,7	<a href="#">biogenic amine catabolic process</a>	3	0.0005	1	0.0031	0.1332410	E
<input type="radio"/>	GO:0043328	10,9,11,8,7,12	<a href="#">protein targeting to vacuole during ubiquitin-dependent protein catabolic process via the MVB pathway</a>	3	0.0005	1	0.0031	0.1332410	E
<input type="radio"/>	GO:0006883	10,8	<a href="#">cellular sodium ion homeostasis</a>	3	0.0005	1	0.0031	0.1332410	E
<input type="radio"/>	GO:0055078	9	<a href="#">sodium ion homeostasis</a>	3	0.0005	1	0.0031	0.1332410	E
<input type="radio"/>	GO:0006598	7,8	<a href="#">polyamine catabolic process</a>	3	0.0005	1	0.0031	0.1332410	E
<input type="radio"/>	GO:0006880	11,9,5,4	<a href="#">intracellular sequestering of iron ion</a>	3	0.0005	1	0.0031	0.1332410	E
<input type="radio"/>	GO:0051596	6	<a href="#">methylglyoxal catabolic process</a>	3	0.0005	1	0.0031	0.1332410	E
<input type="radio"/>	GO:0051791	6,8,7	<a href="#">medium-chain fatty acid metabolic process</a>	3	0.0005	1	0.0031	0.1332410	E
<input type="radio"/>	GO:0009438	5	<a href="#">methylglyoxal metabolic process</a>	3	0.0005	1	0.0031	0.1332410	E
<input type="radio"/>	GO:0050821	7	<a href="#">protein stabilization</a>	3	0.0005	1	0.0031	0.1332410	E
<input type="radio"/>	GO:0006390	8,7	<a href="#">transcription from mitochondrial promoter</a>	3	0.0005	1	0.0031	0.1332410	E
<input type="radio"/>	GO:0043065	7,8,10,6	<a href="#">positive regulation of apoptosis</a>	3	0.0005	1	0.0031	0.1332410	E
<input type="radio"/>	GO:0006449	8,7,9,6	<a href="#">regulation of translational termination</a>	3	0.0005	1	0.0031	0.1332410	E
<input type="radio"/>	GO:0051238	4,3	<a href="#">sequestering of metal ion</a>	3	0.0005	1	0.0031	0.1332410	E
<input type="radio"/>	GO:0019243	7,8,6	<a href="#">methylglyoxal catabolic process to D-lactate</a>	3	0.0005	1	0.0031	0.1332410	E
<input type="radio"/>	GO:0051225	5,9	<a href="#">spindle assembly</a>	3	0.0005	1	0.0031	0.1332410	E
<input type="radio"/>	GO:0031647	6	<a href="#">regulation of protein stability</a>	3	0.0005	1	0.0031	0.1332410	E
<input type="radio"/>	GO:0000320	7,6	<a href="#">re-entry into mitotic cell cycle</a>	3	0.0005	1	0.0031	0.1332410	E
<input type="radio"/>	GO:0051595	5	<a href="#">response to methylglyoxal</a>	3	0.0005	1	0.0031	0.1332410	E
<input type="radio"/>	GO:0043200	5,4	<a href="#">response to amino acid stimulus</a>	3	0.0005	1	0.0031	0.1332410	E
<input type="radio"/>	GO:0000321	9,8,7,6	<a href="#">re-entry into mitotic cell cycle after pheromone arrest</a>	3	0.0005	1	0.0031	0.1332410	E

<input type="checkbox"/>	GO:0031684	7	<a href="#">heterotrimeric G-protein complex cycle</a>	3	0.0005	1	0.0031	0.1332410	E
<input type="checkbox"/>	GO:0040007	2	<a href="#">growth</a>	141	0.0218	8	0.0252	0.1335638	E
<input type="checkbox"/>	GO:0044270	5,4	<a href="#">nitrogen compound catabolic process</a>	32	0.0049	3	0.0094	0.1365295	E
<input type="checkbox"/>	GO:0009310	5,6	<a href="#">amine catabolic process</a>	32	0.0049	3	0.0094	0.1365295	E
<input type="checkbox"/>	GO:0030447	3	<a href="#">filamentous growth</a>	94	0.0145	6	0.0189	0.1367220	E
<input type="checkbox"/>	GO:0048468	3,5	<a href="#">cell development</a>	52	0.0080	4	0.0126	0.1407877	E
<input type="checkbox"/>	GO:0006270	8,6	<a href="#">DNA replication initiation</a>	33	0.0051	3	0.0094	0.1428411	E
<input type="checkbox"/>	GO:0051235	3,2	<a href="#">maintenance of localization</a>	33	0.0051	3	0.0094	0.1428411	E
<input type="checkbox"/>	GO:0006118	4	<a href="#">electron transport</a>	33	0.0051	3	0.0094	0.1428411	E
<input type="checkbox"/>	GO:0045047	9,8,7,6,5	<a href="#">protein targeting to ER</a>	33	0.0051	3	0.0094	0.1428411	E
<input type="checkbox"/>	GO:0010383	7,5,6	<a href="#">cell wall polysaccharide metabolic process</a>	16	0.0025	2	0.0063	0.1430689	E
<input type="checkbox"/>	GO:0006536	7,8	<a href="#">glutamate metabolic process</a>	16	0.0025	2	0.0063	0.1430689	E
<input type="checkbox"/>	GO:0006338	9	<a href="#">chromatin remodeling</a>	155	0.0239	8	0.0252	0.1436408	E
<input type="checkbox"/>	GO:0007186	6	<a href="#">G-protein coupled receptor protein signaling pathway</a>	34	0.0053	3	0.0094	0.1490051	E
<input type="checkbox"/>	GO:0008361	4,6,7	<a href="#">regulation of cell size</a>	129	0.0199	7	0.0220	0.1493865	E
<input type="checkbox"/>	GO:0009968	6,5	<a href="#">negative regulation of signal transduction</a>	17	0.0026	2	0.0063	0.1542132	E
<input type="checkbox"/>	GO:0006113	5	<a href="#">fermentation</a>	17	0.0026	2	0.0063	0.1542132	E
<input type="checkbox"/>	GO:0006030	8,6,7,9	<a href="#">chitin metabolic process</a>	17	0.0026	2	0.0063	0.1542132	E
<input type="checkbox"/>	GO:0000910	4	<a href="#">cytokinesis</a>	109	0.0168	6	0.0189	0.1601913	E
<input type="checkbox"/>	GO:0009117	5	<a href="#">nucleotide metabolic process</a>	111	0.0171	6	0.0189	0.1619896	E
<input type="checkbox"/>	GO:0006811	4,5	<a href="#">ion transport</a>	115	0.0178	6	0.0189	0.1646320	E
<input type="checkbox"/>	GO:0031570	8,7	<a href="#">DNA integrity checkpoint</a>	18	0.0028	2	0.0063	0.1650020	E
<input type="checkbox"/>	GO:0010038	5	<a href="#">response to metal ion</a>	18	0.0028	2	0.0063	0.1650020	E
<input type="checkbox"/>	GO:0051248	6,5	<a href="#">negative regulation of protein metabolic process</a>	18	0.0028	2	0.0063	0.1650020	E
<input type="checkbox"/>	GO:0042493	4	<a href="#">response to drug</a>	121	0.0187	6	0.0189	0.1662782	E
<input type="checkbox"/>	GO:0006814	7,8	<a href="#">sodium ion transport</a>	4	0.0006	1	0.0031	0.1689545	E
<input type="checkbox"/>	GO:0005981	6,10,9,5,8	<a href="#">regulation of glycogen catabolic process</a>	4	0.0006	1	0.0031	0.1689545	E
<input type="checkbox"/>	GO:0019568	8,9	<a href="#">arabinose catabolic process</a>	4	0.0006	1	0.0031	0.1689545	E
<input type="checkbox"/>	GO:0045021	7,6	<a href="#">error-free DNA repair</a>	4	0.0006	1	0.0031	0.1689545	E
<input type="checkbox"/>	GO:0006596	7,8	<a href="#">polyamine biosynthetic process</a>	4	0.0006	1	0.0031	0.1689545	E
<input type="checkbox"/>	GO:0032258	10,9,8,7	<a href="#">CVT pathway</a>	4	0.0006	1	0.0031	0.1689545	E
<input type="checkbox"/>	GO:0050000	6,5	<a href="#">chromosome localization</a>	4	0.0006	1	0.0031	0.1689545	E
<input type="checkbox"/>	GO:0043067	5,6,8,4	<a href="#">regulation of programmed cell death</a>	4	0.0006	1	0.0031	0.1689545	E
<input type="checkbox"/>	GO:0000196	8,6	<a href="#">MAPKKK cascade during cell wall biogenesis</a>	4	0.0006	1	0.0031	0.1689545	E
<input type="checkbox"/>	GO:0031578	9,11,10,8	<a href="#">mitotic cell cycle spindle orientation checkpoint</a>	4	0.0006	1	0.0031	0.1689545	E
<input type="checkbox"/>	GO:0006898	7,6	<a href="#">receptor-mediated endocytosis</a>	4	0.0006	1	0.0031	0.1689545	E
<input type="checkbox"/>	GO:0000735	7,9,8	<a href="#">removal of nonhomologous ends</a>	4	0.0006	1	0.0031	0.1689545	E
<input type="checkbox"/>	GO:0006501	9,8,7	<a href="#">C-terminal protein lipidation</a>	4	0.0006	1	0.0031	0.1689545	E
<input type="checkbox"/>	GO:0016036	8,7,6	<a href="#">cellular response to phosphate starvation</a>	4	0.0006	1	0.0031	0.1689545	E
<input type="checkbox"/>	GO:0000916	6,5,4	<a href="#">cytokinesis, contractile ring contraction</a>	4	0.0006	1	0.0031	0.1689545	E
<input type="checkbox"/>	GO:0042843	8,9	<a href="#">D-xylose catabolic process</a>	4	0.0006	1	0.0031	0.1689545	E
<input type="checkbox"/>	GO:0043173	5	<a href="#">nucleotide salvage</a>	4	0.0006	1	0.0031	0.1689545	E
<input type="checkbox"/>	GO:0006097	6,8	<a href="#">glyoxylate cycle</a>	4	0.0006	1	0.0031	0.1689545	E
<input type="checkbox"/>	GO:0015908	5,6	<a href="#">fatty acid transport</a>	4	0.0006	1	0.0031	0.1689545	E

<input type="checkbox"/>	GO:0042981	6,7,9,5	<a href="#">regulation of apoptosis</a>	4	0.0006	1	0.0031	0.1689545	E
<input type="checkbox"/>	GO:0031321	4,8,6,7	<a href="#">prospore formation</a>	4	0.0006	1	0.0031	0.1689545	E
<input type="checkbox"/>	GO:0042732	7,8	<a href="#">D-xylose metabolic process</a>	4	0.0006	1	0.0031	0.1689545	E
<input type="checkbox"/>	GO:0046686	6	<a href="#">response to cadmium ion</a>	4	0.0006	1	0.0031	0.1689545	E
<input type="checkbox"/>	GO:0000059	8,10,11,7,9	<a href="#">protein import into nucleus, docking</a>	4	0.0006	1	0.0031	0.1689545	E
<input type="checkbox"/>	GO:0006101	6,7	<a href="#">citrate metabolic process</a>	4	0.0006	1	0.0031	0.1689545	E
<input type="checkbox"/>	GO:0006562	8,9	<a href="#">proline catabolic process</a>	4	0.0006	1	0.0031	0.1689545	E
<input type="checkbox"/>	GO:0019566	7,8	<a href="#">arabinose metabolic process</a>	4	0.0006	1	0.0031	0.1689545	E
<input type="checkbox"/>	GO:0006121	10,7,5	<a href="#">mitochondrial electron transport, succinate to ubiquinone</a>	4	0.0006	1	0.0031	0.1689545	E
<input type="checkbox"/>	GO:0006402	7	<a href="#">mRNA catabolic process</a>	60	0.0093	4	0.0126	0.1697928	E
<input type="checkbox"/>	GO:0006515	8,9	<a href="#">misfolded or incompletely synthesized protein catabolic process</a>	38	0.0059	3	0.0094	0.1718834	E
<input type="checkbox"/>	GO:0032506	5,3	<a href="#">cytokinetic process</a>	88	0.0136	5	0.0157	0.1724743	E
<input type="checkbox"/>	GO:0007124	6,4,8,9	<a href="#">pseudohyphal growth</a>	61	0.0094	4	0.0126	0.1728153	E
<input type="checkbox"/>	GO:0046148	5	<a href="#">pigment biosynthetic process</a>	19	0.0029	2	0.0063	0.1753904	E
<input type="checkbox"/>	GO:0006041	6,7	<a href="#">glucosamine metabolic process</a>	19	0.0029	2	0.0063	0.1753904	E
<input type="checkbox"/>	GO:0009228	7,8	<a href="#">thiamin biosynthetic process</a>	19	0.0029	2	0.0063	0.1753904	E
<input type="checkbox"/>	GO:0006040	5,6	<a href="#">amino sugar metabolic process</a>	19	0.0029	2	0.0063	0.1753904	E
<input type="checkbox"/>	GO:0006044	7,8	<a href="#">N-acetylglucosamine metabolic process</a>	19	0.0029	2	0.0063	0.1753904	E
<input type="checkbox"/>	GO:0006612	9,7,8	<a href="#">protein targeting to membrane</a>	39	0.0060	3	0.0094	0.1770962	E
<input type="checkbox"/>	GO:0043161	10,9,11	<a href="#">proteasomal ubiquitin-dependent protein catabolic process</a>	63	0.0097	4	0.0126	0.1784184	E
<input type="checkbox"/>	GO:0006261	7	<a href="#">DNA-dependent DNA replication</a>	97	0.0150	5	0.0157	0.1804718	E
<input type="checkbox"/>	GO:0006812	5,6	<a href="#">cation transport</a>	97	0.0150	5	0.0157	0.1804718	E
<input type="checkbox"/>	GO:0006772	7	<a href="#">thiamin metabolic process</a>	20	0.0031	2	0.0063	0.1853410	E
<input type="checkbox"/>	GO:0000209	10	<a href="#">protein polyubiquitination</a>	20	0.0031	2	0.0063	0.1853410	E
<input type="checkbox"/>	GO:0006826	7,8,9	<a href="#">iron ion transport</a>	20	0.0031	2	0.0063	0.1853410	E
<input type="checkbox"/>	GO:0006308	5,6	<a href="#">DNA catabolic process</a>	20	0.0031	2	0.0063	0.1853410	E
<input type="checkbox"/>	GO:0007094	9,11,10,8	<a href="#">mitotic cell cycle spindle assembly checkpoint</a>	20	0.0031	2	0.0063	0.1853410	E
<input type="checkbox"/>	GO:0045053	7,6,5,4	<a href="#">protein retention in Golgi</a>	20	0.0031	2	0.0063	0.1853410	E
<input type="checkbox"/>	GO:0042440	4	<a href="#">pigment metabolic process</a>	20	0.0031	2	0.0063	0.1853410	E
<input type="checkbox"/>	GO:0006614	11,10,9,8,7	<a href="#">SRP-dependent cotranslational protein targeting to membrane</a>	20	0.0031	2	0.0063	0.1853410	E
<input type="checkbox"/>	GO:0042724	7	<a href="#">thiamin and derivative biosynthetic process</a>	20	0.0031	2	0.0063	0.1853410	E
<input type="checkbox"/>	GO:0051052	7,6	<a href="#">regulation of DNA metabolic process</a>	41	0.0063	3	0.0094	0.1868461	E
<input type="checkbox"/>	GO:0016311	6	<a href="#">dephosphorylation</a>	41	0.0063	3	0.0094	0.1868461	E
<input type="checkbox"/>	GO:0006769	8,7	<a href="#">nicotinamide metabolic process</a>	42	0.0065	3	0.0094	0.1913690	E
<input type="checkbox"/>	GO:0019674	9,8	<a href="#">NAD metabolic process</a>	21	0.0032	2	0.0063	0.1948238	E
<input type="checkbox"/>	GO:0006081	4	<a href="#">aldehyde metabolic process</a>	21	0.0032	2	0.0063	0.1948238	E
<input type="checkbox"/>	GO:0006401	6	<a href="#">RNA catabolic process</a>	74	0.0114	4	0.0126	0.1983130	E
<input type="checkbox"/>	GO:0046365	6,7	<a href="#">monosaccharide catabolic process</a>	44	0.0068	3	0.0094	0.1996844	E
<input type="checkbox"/>	GO:0006367	8,9,7	<a href="#">transcription initiation from RNA polymerase II promoter</a>	44	0.0068	3	0.0094	0.1996844	E
<input type="checkbox"/>	GO:0046483	4	<a href="#">heterocycle metabolic process</a>	76	0.0117	4	0.0126	0.1999630	E
<input type="checkbox"/>	GO:0000338	8	<a href="#">protein deneddylation</a>	5	0.0008	1	0.0031	0.2008488	E
<input type="checkbox"/>	GO:0000092	8,9,10,7	<a href="#">mitotic anaphase B</a>	5	0.0008	1	0.0031	0.2008488	E
<input type="checkbox"/>	GO:0006639	6,5,7	<a href="#">acylglycerol metabolic process</a>	5	0.0008	1	0.0031	0.2008488	E

<input type="checkbox"/>	GO:0046486	5,6	<a href="#">glycerolipid metabolic process</a>	5	0.0008	1	0.0031	0.2008488	E
<input type="checkbox"/>	GO:0019323	7,8	<a href="#">pentose catabolic process</a>	5	0.0008	1	0.0031	0.2008488	E
<input type="checkbox"/>	GO:0031111	7,10,6	<a href="#">negative regulation of microtubule polymerization or depolymerization</a>	5	0.0008	1	0.0031	0.2008488	E
<input type="checkbox"/>	GO:0031114	7,10,6,8	<a href="#">regulation of microtubule depolymerization</a>	5	0.0008	1	0.0031	0.2008488	E
<input type="checkbox"/>	GO:0006641	7,6,8	<a href="#">triacylglycerol metabolic process</a>	5	0.0008	1	0.0031	0.2008488	E
<input type="checkbox"/>	GO:0016560	8,11,10,7,9	<a href="#">protein import into peroxisome matrix, docking</a>	5	0.0008	1	0.0031	0.2008488	E
<input type="checkbox"/>	GO:0046688	6	<a href="#">response to copper ion</a>	5	0.0008	1	0.0031	0.2008488	E
<input type="checkbox"/>	GO:0001881	5,7	<a href="#">receptor recycling</a>	5	0.0008	1	0.0031	0.2008488	E
<input type="checkbox"/>	GO:0043112	6	<a href="#">receptor metabolic process</a>	5	0.0008	1	0.0031	0.2008488	E
<input type="checkbox"/>	GO:0030026	10,8	<a href="#">cellular manganese ion homeostasis</a>	5	0.0008	1	0.0031	0.2008488	E
<input type="checkbox"/>	GO:0006813	7,8	<a href="#">potassium ion transport</a>	5	0.0008	1	0.0031	0.2008488	E
<input type="checkbox"/>	GO:0009051	10,7,11,12,8	<a href="#">pentose-phosphate shunt, oxidative branch</a>	5	0.0008	1	0.0031	0.2008488	E
<input type="checkbox"/>	GO:0019388	8,9	<a href="#">galactose catabolic process</a>	5	0.0008	1	0.0031	0.2008488	E
<input type="checkbox"/>	GO:0006089	7	<a href="#">lactate metabolic process</a>	5	0.0008	1	0.0031	0.2008488	E
<input type="checkbox"/>	GO:0007026	8,7,11,9,6	<a href="#">negative regulation of microtubule depolymerization</a>	5	0.0008	1	0.0031	0.2008488	E
<input type="checkbox"/>	GO:0055071	9	<a href="#">manganese ion homeostasis</a>	5	0.0008	1	0.0031	0.2008488	E
<input type="checkbox"/>	GO:0046854	7,9,8,10	<a href="#">phosphoinositide phosphorylation</a>	5	0.0008	1	0.0031	0.2008488	E
<input type="checkbox"/>	GO:0046834	6,7	<a href="#">lipid phosphorylation</a>	5	0.0008	1	0.0031	0.2008488	E
<input type="checkbox"/>	GO:0016562	6,11,10,8,9,7	<a href="#">protein import into peroxisome matrix, receptor recycling</a>	5	0.0008	1	0.0031	0.2008488	E
<input type="checkbox"/>	GO:0006638	5,6	<a href="#">neutral lipid metabolic process</a>	5	0.0008	1	0.0031	0.2008488	E
<input type="checkbox"/>	GO:0000076	11,9,8,10	<a href="#">DNA replication checkpoint</a>	5	0.0008	1	0.0031	0.2008488	E
<input type="checkbox"/>	GO:0009268	4	<a href="#">response to pH</a>	5	0.0008	1	0.0031	0.2008488	E
<input type="checkbox"/>	GO:0046487	5,7	<a href="#">glyoxylate metabolic process</a>	5	0.0008	1	0.0031	0.2008488	E
<input type="checkbox"/>	GO:0006662	4	<a href="#">glycerol ether metabolic process</a>	5	0.0008	1	0.0031	0.2008488	E
<input type="checkbox"/>	GO:0051188	5	<a href="#">cofactor biosynthetic process</a>	79	0.0122	4	0.0126	0.2013685	E
<input type="checkbox"/>	GO:0006888	8,6,5,7	<a href="#">ER to Golgi vesicle-mediated transport</a>	81	0.0125	4	0.0126	0.2016238	E
<input type="checkbox"/>	GO:0006312	7	<a href="#">mitotic recombination</a>	45	0.0069	3	0.0094	0.2034697	E
<input type="checkbox"/>	GO:0007231	6,5	<a href="#">osmosensory signaling pathway</a>	22	0.0034	2	0.0063	0.2038150	E
<input type="checkbox"/>	GO:0006513	10	<a href="#">protein monoubiquitination</a>	22	0.0034	2	0.0063	0.2038150	E
<input type="checkbox"/>	GO:0006311	10,8,7,5,9,6,4	<a href="#">meiotic gene conversion</a>	22	0.0034	2	0.0063	0.2038150	E
<input type="checkbox"/>	GO:0042723	6	<a href="#">thiamin and derivative metabolic process</a>	22	0.0034	2	0.0063	0.2038150	E
<input type="checkbox"/>	GO:0042364	6	<a href="#">water-soluble vitamin biosynthetic process</a>	46	0.0071	3	0.0094	0.2070037	E
<input type="checkbox"/>	GO:0009110	5	<a href="#">vitamin biosynthetic process</a>	46	0.0071	3	0.0094	0.2070037	E
<input type="checkbox"/>	GO:0006417	7,6,5	<a href="#">regulation of translation</a>	47	0.0073	3	0.0094	0.2102853	E
<input type="checkbox"/>	GO:0046164	5	<a href="#">alcohol catabolic process</a>	47	0.0073	3	0.0094	0.2102853	E
<input type="checkbox"/>	GO:0007534	6,8,7	<a href="#">gene conversion at mating-type locus</a>	23	0.0036	2	0.0063	0.2122964	E
<input type="checkbox"/>	GO:0051030	5,7,6,8	<a href="#">snRNA transport</a>	23	0.0036	2	0.0063	0.2122964	E
<input type="checkbox"/>	GO:0006613	10,9,8,7,6	<a href="#">cotranslational protein targeting to membrane</a>	23	0.0036	2	0.0063	0.2122964	E
<input type="checkbox"/>	GO:0006607	10,11,8,9,7	<a href="#">NLS-bearing substrate import into nucleus</a>	23	0.0036	2	0.0063	0.2122964	E
<input type="checkbox"/>	GO:0006408	11,9,6,8,10,7	<a href="#">snRNA export from nucleus</a>	23	0.0036	2	0.0063	0.2122964	E
<input type="checkbox"/>	GO:0019748	3	<a href="#">secondary metabolic process</a>	23	0.0036	2	0.0063	0.2122964	E
<input type="checkbox"/>	GO:0007020	8	<a href="#">microtubule nucleation</a>	23	0.0036	2	0.0063	0.2122964	E
<input type="checkbox"/>	GO:0006608	10,11,8,9,7	<a href="#">snRNP protein import into nucleus</a>	23	0.0036	2	0.0063	0.2122964	E
<input type="checkbox"/>	GO:0006610	10,11,8,9,7	<a href="#">ribosomal protein import into nucleus</a>	23	0.0036	2	0.0063	0.2122964	E

<input type="radio"/>	GO:0000288	10,8,9	<a href="#">mRNA catabolic process, deadenylation-dependent decay</a>	24	0.0037	2	0.0063	0.2202549	E
<input type="radio"/>	GO:0006576	5,6	<a href="#">biogenic amine metabolic process</a>	24	0.0037	2	0.0063	0.2202549	E
<input type="radio"/>	GO:0006626	9,8,7,6	<a href="#">protein targeting to mitochondrion</a>	52	0.0080	3	0.0094	0.2229253	E
<input type="radio"/>	GO:0006400	7,8	<a href="#">tRNA modification</a>	52	0.0080	3	0.0094	0.2229253	E
<input type="radio"/>	GO:0007088	7,9,8,6	<a href="#">regulation of mitosis</a>	55	0.0085	3	0.0094	0.2275786	E
<input type="radio"/>	GO:0006352	7,8,6	<a href="#">transcription initiation</a>	55	0.0085	3	0.0094	0.2275786	E
<input type="radio"/>	GO:0042773	8,5	<a href="#">ATP synthesis coupled electron transport</a>	25	0.0039	2	0.0063	0.2276820	E
<input type="radio"/>	GO:0009607	3	<a href="#">response to biotic stimulus</a>	25	0.0039	2	0.0063	0.2276820	E
<input type="radio"/>	GO:0042775	9,6	<a href="#">organelle ATP synthesis coupled electron transport</a>	25	0.0039	2	0.0063	0.2276820	E
<input type="radio"/>	GO:0006609	10,11,8,9,7	<a href="#">mRNA-binding (hnRNP) protein import into nucleus</a>	25	0.0039	2	0.0063	0.2276820	E
<input type="radio"/>	GO:0033214	12,10	<a href="#">iron assimilation by chelation and transport</a>	6	0.0009	1	0.0031	0.2292116	E
<input type="radio"/>	GO:0031327	7,6	<a href="#">negative regulation of cellular biosynthetic process</a>	6	0.0009	1	0.0031	0.2292116	E
<input type="radio"/>	GO:0051058	7,8,6	<a href="#">negative regulation of small GTPase mediated signal transduction</a>	6	0.0009	1	0.0031	0.2292116	E
<input type="radio"/>	GO:0009113	7,6	<a href="#">purine base biosynthetic process</a>	6	0.0009	1	0.0031	0.2292116	E
<input type="radio"/>	GO:0015892	13,11,8,9,5,10,6	<a href="#">siderophore-iron transport</a>	6	0.0009	1	0.0031	0.2292116	E
<input type="radio"/>	GO:0007019	9,7	<a href="#">microtubule depolymerization</a>	6	0.0009	1	0.0031	0.2292116	E
<input type="radio"/>	GO:0051056	6,7,5	<a href="#">regulation of small GTPase mediated signal transduction</a>	6	0.0009	1	0.0031	0.2292116	E
<input type="radio"/>	GO:0046185	5	<a href="#">aldehyde catabolic process</a>	6	0.0009	1	0.0031	0.2292116	E
<input type="radio"/>	GO:0006591	7,8,5,4	<a href="#">ornithine metabolic process</a>	6	0.0009	1	0.0031	0.2292116	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	0.0031	0.2292116	E
<input type="radio"/>	GO:0006627	10,9,8,7	<a href="#">mitochondrial protein processing</a>	6	0.0009	1	0.0031	0.2292116	E
<input type="radio"/>	GO:0031930	6	<a href="#">mitochondrial signaling pathway</a>	6	0.0009	1	0.0031	0.2292116	E
<input type="radio"/>	GO:0051322	6,7,5	<a href="#">anaphase</a>	6	0.0009	1	0.0031	0.2292116	E
<input type="radio"/>	GO:0046580	8,9,7	<a href="#">negative regulation of Ras protein signal transduction</a>	6	0.0009	1	0.0031	0.2292116	E
<input type="radio"/>	GO:0000090	7,8,9,6	<a href="#">mitotic anaphase</a>	6	0.0009	1	0.0031	0.2292116	E
<input type="radio"/>	GO:0032297	10,8,9	<a href="#">negative regulation of DNA replication initiation</a>	6	0.0009	1	0.0031	0.2292116	E
<input type="radio"/>	GO:0005979	8,7,9,10,6	<a href="#">regulation of glycogen biosynthetic process</a>	6	0.0009	1	0.0031	0.2292116	E
<input type="radio"/>	GO:0046578	7,8,6	<a href="#">regulation of Ras protein signal transduction</a>	6	0.0009	1	0.0031	0.2292116	E
<input type="radio"/>	GO:0017148	8,7,6	<a href="#">negative regulation of protein biosynthetic process</a>	6	0.0009	1	0.0031	0.2292116	E
<input type="radio"/>	GO:0045116	9	<a href="#">protein neddylation</a>	6	0.0009	1	0.0031	0.2292116	E
<input type="radio"/>	GO:0006020	7,8	<a href="#">inositol metabolic process</a>	6	0.0009	1	0.0031	0.2292116	E
<input type="radio"/>	GO:0005985	7	<a href="#">sucrose metabolic process</a>	6	0.0009	1	0.0031	0.2292116	E
<input type="radio"/>	GO:0005987	8	<a href="#">sucrose catabolic process</a>	6	0.0009	1	0.0031	0.2292116	E
<input type="radio"/>	GO:0007130	11,9,8,6,5,10,7,4	<a href="#">synaptonemal complex assembly</a>	6	0.0009	1	0.0031	0.2292116	E
<input type="radio"/>	GO:0007015	8	<a href="#">actin filament organization</a>	61	0.0094	3	0.0094	0.2308366	E
<input type="radio"/>	GO:0006696	7,8,9	<a href="#">ergosterol biosynthetic process</a>	26	0.0040	2	0.0063	0.2345732	E
<input type="radio"/>	GO:0010382	6,4	<a href="#">cell wall metabolic process</a>	26	0.0040	2	0.0063	0.2345732	E
<input type="radio"/>	GO:0006407	11,9,6,8,10,7	<a href="#">rRNA export from nucleus</a>	26	0.0040	2	0.0063	0.2345732	E
<input type="radio"/>	GO:0008204	6,7,8	<a href="#">ergosterol metabolic process</a>	26	0.0040	2	0.0063	0.2345732	E
<input type="radio"/>	GO:0051029	5,7,6,8	<a href="#">rRNA transport</a>	26	0.0040	2	0.0063	0.2345732	E
<input type="radio"/>	GO:0043241	6,5	<a href="#">protein complex disassembly</a>	28	0.0043	2	0.0063	0.2467468	E

<input type="checkbox"/>	GO:0043624	7,6	<a href="#">cellular protein complex disassembly</a>	28	0.0043	2	0.0063	0.2467468	E
<input type="checkbox"/>	GO:0007533	5,7,6	<a href="#">mating type switching</a>	29	0.0045	2	0.0063	0.2520362	E
<input type="checkbox"/>	GO:0006999	6	<a href="#">nuclear pore organization and biogenesis</a>	29	0.0045	2	0.0063	0.2520362	E
<input type="checkbox"/>	GO:0051651	5,4,3	<a href="#">maintenance of cellular localization</a>	29	0.0045	2	0.0063	0.2520362	E
<input type="checkbox"/>	GO:0032507	6,5,4	<a href="#">maintenance of cellular protein localization</a>	29	0.0045	2	0.0063	0.2520362	E
<input type="checkbox"/>	GO:0009063	6,7	<a href="#">amino acid catabolic process</a>	29	0.0045	2	0.0063	0.2520362	E
<input type="checkbox"/>	GO:0043331	4	<a href="#">response to dsRNA</a>	7	0.0011	1	0.0031	0.2543115	E
<input type="checkbox"/>	GO:0000710	11,9,8,6,5,10,7,4	<a href="#">meiotic mismatch repair</a>	7	0.0011	1	0.0031	0.2543115	E
<input type="checkbox"/>	GO:0046700	5	<a href="#">heterocycle catabolic process</a>	7	0.0011	1	0.0031	0.2543115	E
<input type="checkbox"/>	GO:0009102	6,7,8	<a href="#">biotin biosynthetic process</a>	7	0.0011	1	0.0031	0.2543115	E
<input type="checkbox"/>	GO:0000727	9,8	<a href="#">double-strand break repair via break-induced replication</a>	7	0.0011	1	0.0031	0.2543115	E
<input type="checkbox"/>	GO:0045332	5,7,6,8	<a href="#">phospholipid translocation</a>	7	0.0011	1	0.0031	0.2543115	E
<input type="checkbox"/>	GO:0009615	4,5	<a href="#">response to virus</a>	7	0.0011	1	0.0031	0.2543115	E
<input type="checkbox"/>	GO:0006768	5,7,6	<a href="#">biotin metabolic process</a>	7	0.0011	1	0.0031	0.2543115	E
<input type="checkbox"/>	GO:0000289	11,9,10	<a href="#">poly(A) tail shortening</a>	7	0.0011	1	0.0031	0.2543115	E
<input type="checkbox"/>	GO:0051129	6,5	<a href="#">negative regulation of cell organization and biogenesis</a>	7	0.0011	1	0.0031	0.2543115	E
<input type="checkbox"/>	GO:0000715	7,8	<a href="#">nucleotide-excision repair, DNA damage recognition</a>	7	0.0011	1	0.0031	0.2543115	E
<input type="checkbox"/>	GO:0019655	6,7	<a href="#">glucose catabolic process to ethanol</a>	7	0.0011	1	0.0031	0.2543115	E
<input type="checkbox"/>	GO:0006617	8,12,11,7,10,9	<a href="#">SRP-dependent cotranslational protein targeting to membrane, signal sequence recognition</a>	7	0.0011	1	0.0031	0.2543115	E
<input type="checkbox"/>	GO:0043330	5,6	<a href="#">response to exogenous dsRNA</a>	7	0.0011	1	0.0031	0.2543115	E
<input type="checkbox"/>	GO:0051707	3,4	<a href="#">response to other organism</a>	7	0.0011	1	0.0031	0.2543115	E
<input type="checkbox"/>	GO:0000256	6	<a href="#">allantoin catabolic process</a>	7	0.0011	1	0.0031	0.2543115	E
<input type="checkbox"/>	GO:0043248	8,7	<a href="#">proteasome assembly</a>	7	0.0011	1	0.0031	0.2543115	E
<input type="checkbox"/>	GO:0006998	5,6	<a href="#">nuclear membrane organization and biogenesis</a>	7	0.0011	1	0.0031	0.2543115	E
<input type="checkbox"/>	GO:0006415	8,7,6	<a href="#">translational termination</a>	7	0.0011	1	0.0031	0.2543115	E
<input type="checkbox"/>	GO:0006265	6	<a href="#">DNA topological change</a>	7	0.0011	1	0.0031	0.2543115	E
<input type="checkbox"/>	GO:0000255	5	<a href="#">allantoin metabolic process</a>	7	0.0011	1	0.0031	0.2543115	E
<input type="checkbox"/>	GO:0006560	7,8	<a href="#">proline metabolic process</a>	7	0.0011	1	0.0031	0.2543115	E
<input type="checkbox"/>	GO:0033205	5,4	<a href="#">cytokinesis during cell cycle</a>	7	0.0011	1	0.0031	0.2543115	E
<input type="checkbox"/>	GO:0043488	9,8,7	<a href="#">regulation of mRNA stability</a>	30	0.0046	2	0.0063	0.2568028	E
<input type="checkbox"/>	GO:0045185	5,4,3	<a href="#">maintenance of protein localization</a>	30	0.0046	2	0.0063	0.2568028	E
<input type="checkbox"/>	GO:0043487	8,7	<a href="#">regulation of RNA stability</a>	30	0.0046	2	0.0063	0.2568028	E
<input type="checkbox"/>	GO:0000002	6	<a href="#">mitochondrial genome maintenance</a>	31	0.0048	2	0.0063	0.2610559	E
<input type="checkbox"/>	GO:0032984	5	<a href="#">macromolecular complex disassembly</a>	32	0.0049	2	0.0063	0.2648067	E
<input type="checkbox"/>	GO:0016126	6,7,8	<a href="#">sterol biosynthetic process</a>	32	0.0049	2	0.0063	0.2648067	E
<input type="checkbox"/>	GO:0006694	6,5,7	<a href="#">steroid biosynthetic process</a>	32	0.0049	2	0.0063	0.2648067	E
<input type="checkbox"/>	GO:0055067	8	<a href="#">monovalent inorganic cation homeostasis</a>	34	0.0053	2	0.0063	0.2708527	E
<input type="checkbox"/>	GO:0030004	9,7	<a href="#">cellular monovalent inorganic cation homeostasis</a>	34	0.0053	2	0.0063	0.2708527	E
<input type="checkbox"/>	GO:0006869	4,5	<a href="#">lipid transport</a>	34	0.0053	2	0.0063	0.2708527	E
<input type="checkbox"/>	GO:0007530	4,5	<a href="#">sex determination</a>	35	0.0054	2	0.0063	0.2731766	E
<input type="checkbox"/>	GO:0000726	7,6	<a href="#">non-recombinational repair</a>	35	0.0054	2	0.0063	0.2731766	E
<input type="checkbox"/>	GO:0007531	4,6,5	<a href="#">mating type determination</a>	35	0.0054	2	0.0063	0.2731766	E
<input type="checkbox"/>	GO:0003006	3,4	<a href="#">reproductive developmental process</a>	35	0.0054	2	0.0063	0.2731766	E



<input type="checkbox"/>	GO:0051252	7,6	<a href="#">regulation of RNA metabolic process</a>	36	0.0056	2	0.0063	0.2750552	E
<input type="checkbox"/>	GO:0022411	4	<a href="#">cellular component disassembly</a>	36	0.0056	2	0.0063	0.2750552	E
<input type="checkbox"/>	GO:0044242	5,6	<a href="#">cellular lipid catabolic process</a>	8	0.0012	1	0.0031	0.2763994	E
<input type="checkbox"/>	GO:0018345	9,8,7	<a href="#">protein palmitoylation</a>	8	0.0012	1	0.0031	0.2763994	E
<input type="checkbox"/>	GO:0008156	9,8	<a href="#">negative regulation of DNA replication</a>	8	0.0012	1	0.0031	0.2763994	E
<input type="checkbox"/>	GO:0033212	11,9	<a href="#">iron assimilation</a>	8	0.0012	1	0.0031	0.2763994	E
<input type="checkbox"/>	GO:0016042	4,5	<a href="#">lipid catabolic process</a>	8	0.0012	1	0.0031	0.2763994	E
<input type="checkbox"/>	GO:0006855	5,6	<a href="#">multidrug transport</a>	8	0.0012	1	0.0031	0.2763994	E
<input type="checkbox"/>	GO:0018318	10,9,8	<a href="#">protein amino acid palmitoylation</a>	8	0.0012	1	0.0031	0.2763994	E
<input type="checkbox"/>	GO:0031146	11,10,12	<a href="#">SCF-dependent proteasomal ubiquitin-dependent protein catabolic process</a>	8	0.0012	1	0.0031	0.2763994	E
<input type="checkbox"/>	GO:0019660	6	<a href="#">glycolytic fermentation</a>	8	0.0012	1	0.0031	0.2763994	E
<input type="checkbox"/>	GO:0019320	7,8	<a href="#">hexose catabolic process</a>	39	0.0060	2	0.0063	0.2781859	E
<input type="checkbox"/>	GO:0048308	5	<a href="#">organelle inheritance</a>	40	0.0062	2	0.0063	0.2784520	E
<input type="checkbox"/>	GO:0019751	5	<a href="#">polyol metabolic process</a>	9	0.0014	1	0.0031	0.2957095	E
<input type="checkbox"/>	GO:0000290	11,8,9,10	<a href="#">deadenylation-dependent decapping</a>	9	0.0014	1	0.0031	0.2957095	E
<input type="checkbox"/>	GO:0006071	6	<a href="#">glycerol metabolic process</a>	9	0.0014	1	0.0031	0.2957095	E
<input type="checkbox"/>	GO:0042375	5	<a href="#">quinone cofactor metabolic process</a>	9	0.0014	1	0.0031	0.2957095	E
<input type="checkbox"/>	GO:0042138	11,9,8,5,6,10,7,4	<a href="#">meiotic DNA double-strand break formation</a>	9	0.0014	1	0.0031	0.2957095	E
<input type="checkbox"/>	GO:0006743	7,6	<a href="#">ubiquinone metabolic process</a>	9	0.0014	1	0.0031	0.2957095	E
<input type="checkbox"/>	GO:0046685	5	<a href="#">response to arsenic</a>	9	0.0014	1	0.0031	0.2957095	E
<input type="checkbox"/>	GO:0031106	7	<a href="#">septin ring organization</a>	9	0.0014	1	0.0031	0.2957095	E
<input type="checkbox"/>	GO:0045426	7,6	<a href="#">quinone cofactor biosynthetic process</a>	9	0.0014	1	0.0031	0.2957095	E
<input type="checkbox"/>	GO:0015891	4,5	<a href="#">siderophore transport</a>	9	0.0014	1	0.0031	0.2957095	E
<input type="checkbox"/>	GO:0006474	10,9	<a href="#">N-terminal protein amino acid acetylation</a>	9	0.0014	1	0.0031	0.2957095	E
<input type="checkbox"/>	GO:0019794	6,7	<a href="#">nonprotein amino acid metabolic process</a>	9	0.0014	1	0.0031	0.2957095	E
<input type="checkbox"/>	GO:0006744	8,7	<a href="#">ubiquinone biosynthetic process</a>	9	0.0014	1	0.0031	0.2957095	E
<input type="checkbox"/>	GO:0008535	8,7	<a href="#">cytochrome c oxidase complex assembly</a>	9	0.0014	1	0.0031	0.2957095	E
<input type="checkbox"/>	GO:0000921	8,7	<a href="#">septin ring assembly</a>	9	0.0014	1	0.0031	0.2957095	E
<input type="checkbox"/>	GO:0032185	6	<a href="#">septin cytoskeleton organization and biogenesis</a>	9	0.0014	1	0.0031	0.2957095	E
<input type="checkbox"/>	GO:0043486	11	<a href="#">histone exchange</a>	9	0.0014	1	0.0031	0.2957095	E
<input type="checkbox"/>	GO:0016925	9	<a href="#">protein sumoylation</a>	10	0.0015	1	0.0031	0.3124605	E
<input type="checkbox"/>	GO:0051181	4,5	<a href="#">cofactor transport</a>	10	0.0015	1	0.0031	0.3124605	E
<input type="checkbox"/>	GO:0007129	10,8,7,5,9,6,4	<a href="#">synapsis</a>	10	0.0015	1	0.0031	0.3124605	E
<input type="checkbox"/>	GO:0006526	8,9,6,5	<a href="#">arginine biosynthetic process</a>	10	0.0015	1	0.0031	0.3124605	E
<input type="checkbox"/>	GO:0006012	7,8	<a href="#">galactose metabolic process</a>	10	0.0015	1	0.0031	0.3124605	E
<input type="checkbox"/>	GO:0008298	5	<a href="#">intracellular mRNA localization</a>	10	0.0015	1	0.0031	0.3124605	E
<input type="checkbox"/>	GO:0006616	9,12,11,7,10,8	<a href="#">SRP-dependent cotranslational protein targeting to membrane, translocation</a>	10	0.0015	1	0.0031	0.3124605	E
<input type="checkbox"/>	GO:0006817	7,8	<a href="#">phosphate transport</a>	10	0.0015	1	0.0031	0.3124605	E
<input type="checkbox"/>	GO:0051261	6	<a href="#">protein depolymerization</a>	10	0.0015	1	0.0031	0.3124605	E
<input type="checkbox"/>	GO:0006098	9,10,11	<a href="#">pentose-phosphate shunt</a>	11	0.0017	1	0.0031	0.3268561	E
<input type="checkbox"/>	GO:0016237	4,6	<a href="#">microautophagy</a>	11	0.0017	1	0.0031	0.3268561	E
<input type="checkbox"/>	GO:0031163	5	<a href="#">metallo-sulfur cluster assembly</a>	11	0.0017	1	0.0031	0.3268561	E
<input type="checkbox"/>	GO:0007109	7,6,5,4	<a href="#">cytokinesis, completion of separation</a>	11	0.0017	1	0.0031	0.3268561	E
<input type="checkbox"/>	GO:0001558	5,6,4,8,9	<a href="#">regulation of cell growth</a>	11	0.0017	1	0.0031	0.3268561	E

<input type="radio"/>	GO:0016226	6	<a href="#">iron-sulfur cluster assembly</a>	11	0.0017	1	0.0031	0.3268561	E
<input type="radio"/>	GO:0065002	8,6,7	<a href="#">intracellular protein transport across a membrane</a>	11	0.0017	1	0.0031	0.3268561	E
<input type="radio"/>	GO:0001101	4	<a href="#">response to acid</a>	11	0.0017	1	0.0031	0.3268561	E
<input type="radio"/>	GO:0008054	7,6,11,10,12	<a href="#">cyclin catabolic process</a>	12	0.0019	1	0.0031	0.3390865	E
<input type="radio"/>	GO:0015846	5,6	<a href="#">polyamine transport</a>	12	0.0019	1	0.0031	0.3390865	E
<input type="radio"/>	GO:0006067	5	<a href="#">ethanol metabolic process</a>	12	0.0019	1	0.0031	0.3390865	E
<input type="radio"/>	GO:0015914	5,6	<a href="#">phospholipid transport</a>	12	0.0019	1	0.0031	0.3390865	E
<input type="radio"/>	GO:0000083	10,9,6,5,7,8,4	<a href="#">G1/S-specific transcription in mitotic cell cycle</a>	12	0.0019	1	0.0031	0.3390865	E
<input type="radio"/>	GO:0000302	5	<a href="#">response to reactive oxygen species</a>	12	0.0019	1	0.0031	0.3390865	E
<input type="radio"/>	GO:0031929	6	<a href="#">TOR signaling pathway</a>	13	0.0020	1	0.0031	0.3493288	E
<input type="radio"/>	GO:0007346	7,5,6	<a href="#">regulation of progression through mitotic cell cycle</a>	13	0.0020	1	0.0031	0.3493288	E
<input type="radio"/>	GO:0007103	6,7,5,8	<a href="#">spindle pole body duplication in nuclear envelope</a>	13	0.0020	1	0.0031	0.3493288	E
<input type="radio"/>	GO:0006779	6,7	<a href="#">porphyrin biosynthetic process</a>	13	0.0020	1	0.0031	0.3493288	E
<input type="radio"/>	GO:0033014	6	<a href="#">tetrapyrrole biosynthetic process</a>	13	0.0020	1	0.0031	0.3493288	E
<input type="radio"/>	GO:0006038	9,10,7,8,11	<a href="#">cell wall chitin biosynthetic process</a>	13	0.0020	1	0.0031	0.3493288	E
<input type="radio"/>	GO:0008219	4,6	<a href="#">cell death</a>	13	0.0020	1	0.0031	0.3493288	E
<input type="radio"/>	GO:0006915	6,8	<a href="#">apoptosis</a>	13	0.0020	1	0.0031	0.3493288	E
<input type="radio"/>	GO:0030258	5,6	<a href="#">lipid modification</a>	13	0.0020	1	0.0031	0.3493288	E
<input type="radio"/>	GO:0012501	5,7	<a href="#">programmed cell death</a>	13	0.0020	1	0.0031	0.3493288	E
<input type="radio"/>	GO:0016265	3	<a href="#">death</a>	13	0.0020	1	0.0031	0.3493288	E
<input type="radio"/>	GO:0006783	7,6,8	<a href="#">heme biosynthetic process</a>	13	0.0020	1	0.0031	0.3493288	E
<input type="radio"/>	GO:0006895	8,9,6,7	<a href="#">Golgi to endosome transport</a>	13	0.0020	1	0.0031	0.3493288	E
<input type="radio"/>	GO:0000920	6,4	<a href="#">cell separation during cytokinesis</a>	13	0.0020	1	0.0031	0.3493288	E
<input type="radio"/>	GO:0015893	4,5	<a href="#">drug transport</a>	13	0.0020	1	0.0031	0.3493288	E
<input type="radio"/>	GO:0040008	4,3	<a href="#">regulation of growth</a>	13	0.0020	1	0.0031	0.3493288	E
<input type="radio"/>	GO:0000147	5,9,8	<a href="#">actin cortical patch assembly</a>	14	0.0022	1	0.0031	0.3577482	E
<input type="radio"/>	GO:0006749	6,5	<a href="#">glutathione metabolic process</a>	14	0.0022	1	0.0031	0.3577482	E
<input type="radio"/>	GO:0006740	10,9	<a href="#">NADPH regeneration</a>	14	0.0022	1	0.0031	0.3577482	E
<input type="radio"/>	GO:0006778	5,6	<a href="#">porphyrin metabolic process</a>	14	0.0022	1	0.0031	0.3577482	E
<input type="radio"/>	GO:0000105	8,9	<a href="#">histidine biosynthetic process</a>	14	0.0022	1	0.0031	0.3577482	E
<input type="radio"/>	GO:0030474	5,6,4,7	<a href="#">spindle pole body duplication</a>	14	0.0022	1	0.0031	0.3577482	E
<input type="radio"/>	GO:0006547	7,8	<a href="#">histidine metabolic process</a>	14	0.0022	1	0.0031	0.3577482	E
<input type="radio"/>	GO:0009076	7,8	<a href="#">histidine family amino acid biosynthetic process</a>	14	0.0022	1	0.0031	0.3577482	E
<input type="radio"/>	GO:0009075	6,7	<a href="#">histidine family amino acid metabolic process</a>	14	0.0022	1	0.0031	0.3577482	E
<input type="radio"/>	GO:0000011	6	<a href="#">vacuole inheritance</a>	14	0.0022	1	0.0031	0.3577482	E
<input type="radio"/>	GO:0042168	6,7,5	<a href="#">heme metabolic process</a>	14	0.0022	1	0.0031	0.3577482	E
<input type="radio"/>	GO:0006144	6	<a href="#">purine base metabolic process</a>	14	0.0022	1	0.0031	0.3577482	E
<input type="radio"/>	GO:0045002	8,7	<a href="#">double-strand break repair via single-strand annealing</a>	14	0.0022	1	0.0031	0.3577482	E
<input type="radio"/>	GO:0033013	5	<a href="#">tetrapyrrole metabolic process</a>	14	0.0022	1	0.0031	0.3577482	E
<input type="radio"/>	GO:0006099	8,7,6	<a href="#">tricarboxylic acid cycle</a>	15	0.0023	1	0.0031	0.3644984	E
<input type="radio"/>	GO:0009894	5,4	<a href="#">regulation of catabolic process</a>	15	0.0023	1	0.0031	0.3644984	E
<input type="radio"/>	GO:0031110	6,9,5	<a href="#">regulation of microtubule polymerization or depolymerization</a>	15	0.0023	1	0.0031	0.3644984	E
<input type="radio"/>	GO:0031145	11,10,12	<a href="#">anaphase-promoting complex-dependent proteasomal ubiquitin-dependent protein</a>	15	0.0023	1	0.0031	0.3644984	E

			<a href="#">catabolic process</a>						
<input type="radio"/>	GO:0018409	9	<a href="#">peptide or protein amino-terminal blocking</a>	15	0.0023	1	0.0031	0.3644984	E
<input type="radio"/>	GO:0030488	8,9	<a href="#">tRNA methylation</a>	15	0.0023	1	0.0031	0.3644984	E
<input type="radio"/>	GO:0007091	9,7,5,8,6,4	<a href="#">mitotic metaphase/anaphase transition</a>	15	0.0023	1	0.0031	0.3644984	E
<input type="radio"/>	GO:0031365	8	<a href="#">N-terminal protein amino acid modification</a>	15	0.0023	1	0.0031	0.3644984	E
<input type="radio"/>	GO:0006031	9,7,8,10	<a href="#">chitin biosynthetic process</a>	15	0.0023	1	0.0031	0.3644984	E
<input type="radio"/>	GO:0046356	7	<a href="#">acetyl-CoA catabolic process</a>	15	0.0023	1	0.0031	0.3644984	E
<input type="radio"/>	GO:0030865	6	<a href="#">cortical cytoskeleton organization and biogenesis</a>	16	0.0025	1	0.0031	0.3697225	E
<input type="radio"/>	GO:0048015	7	<a href="#">phosphoinositide-mediated signaling</a>	16	0.0025	1	0.0031	0.3697225	E
<input type="radio"/>	GO:0048017	8	<a href="#">inositol lipid-mediated signaling</a>	16	0.0025	1	0.0031	0.3697225	E
<input type="radio"/>	GO:0031023	5	<a href="#">microtubule organizing center organization and biogenesis</a>	16	0.0025	1	0.0031	0.3697225	E
<input type="radio"/>	GO:0051300	5,4,6	<a href="#">spindle pole body organization and biogenesis</a>	16	0.0025	1	0.0031	0.3697225	E
<input type="radio"/>	GO:0030866	8,7	<a href="#">cortical actin cytoskeleton organization and biogenesis</a>	16	0.0025	1	0.0031	0.3697225	E
<input type="radio"/>	GO:0015698	6,7	<a href="#">inorganic anion transport</a>	16	0.0025	1	0.0031	0.3697225	E
<input type="radio"/>	GO:0031109	8	<a href="#">microtubule polymerization or depolymerization</a>	16	0.0025	1	0.0031	0.3697225	E
<input type="radio"/>	GO:0006820	5,6	<a href="#">anion transport</a>	17	0.0026	1	0.0031	0.3735535	E
<input type="radio"/>	GO:0046349	6,7	<a href="#">amino sugar biosynthetic process</a>	17	0.0026	1	0.0031	0.3735535	E
<input type="radio"/>	GO:0006045	8,9	<a href="#">N-acetylglucosamine biosynthetic process</a>	17	0.0026	1	0.0031	0.3735535	E
<input type="radio"/>	GO:0006042	7,8	<a href="#">glucosamine biosynthetic process</a>	17	0.0026	1	0.0031	0.3735535	E
<input type="radio"/>	GO:0006739	9,8	<a href="#">NADP metabolic process</a>	17	0.0026	1	0.0031	0.3735535	E
<input type="radio"/>	GO:0006369	9,8	<a href="#">transcription termination from RNA polymerase II promoter</a>	18	0.0028	1	0.0031	0.3761152	E
<input type="radio"/>	GO:0006986	4,5	<a href="#">response to unfolded protein</a>	18	0.0028	1	0.0031	0.3761152	E
<input type="radio"/>	GO:0042401	6,7	<a href="#">biogenic amine biosynthetic process</a>	18	0.0028	1	0.0031	0.3761152	E
<input type="radio"/>	GO:0051789	4	<a href="#">response to protein stimulus</a>	18	0.0028	1	0.0031	0.3761152	E
<input type="radio"/>	GO:0000183	11,7,8,12,10	<a href="#">chromatin silencing at rDNA</a>	18	0.0028	1	0.0031	0.3761152	E
<input type="radio"/>	GO:0055065	8	<a href="#">metal ion homeostasis</a>	19	0.0029	1	0.0031	0.3775227	E
<input type="radio"/>	GO:0043094	4	<a href="#">metabolic compound salvage</a>	19	0.0029	1	0.0031	0.3775227	E
<input type="radio"/>	GO:0000245	7,6,9,11	<a href="#">spliceosome assembly</a>	19	0.0029	1	0.0031	0.3775227	E
<input type="radio"/>	GO:0006875	9,7	<a href="#">cellular metal ion homeostasis</a>	19	0.0029	1	0.0031	0.3775227	E
<input type="radio"/>	GO:0000722	9,8	<a href="#">telomere maintenance via recombination</a>	19	0.0029	1	0.0031	0.3775227	E
<input type="radio"/>	GO:0042398	6,5	<a href="#">amino acid derivative biosynthetic process</a>	20	0.0031	1	0.0031	0.3778827	E
<input type="radio"/>	GO:0051053	8,7	<a href="#">negative regulation of DNA metabolic process</a>	20	0.0031	1	0.0031	0.3778827	E
<input type="radio"/>	GO:0000165	7	<a href="#">MAPKKK cascade</a>	20	0.0031	1	0.0031	0.3778827	E
<input type="radio"/>	GO:0006100	6	<a href="#">tricarboxylic acid cycle intermediate metabolic process</a>	20	0.0031	1	0.0031	0.3778827	E
<input type="radio"/>	GO:0009109	6	<a href="#">coenzyme catabolic process</a>	20	0.0031	1	0.0031	0.3778827	E
<input type="radio"/>	GO:0006353	8,7	<a href="#">transcription termination</a>	20	0.0031	1	0.0031	0.3778827	E
<input type="radio"/>	GO:0008150	1	<a href="#">biological process</a>	6476	1.0000	318	1.0000	1.0000000	D
<input type="radio"/>	GO:0046112	6,5	<a href="#">nucleobase biosynthetic process</a>	21	0.0032	1	0.0031	0.3772945	D
<input type="radio"/>	GO:0051187	5	<a href="#">cofactor catabolic process</a>	21	0.0032	1	0.0031	0.3772945	D
<input type="radio"/>	GO:0044272	5	<a href="#">sulfur compound biosynthetic process</a>	22	0.0034	1	0.0031	0.3758499	D
<input type="radio"/>	GO:0030150	10,9,8,7	<a href="#">protein import into mitochondrial matrix</a>	22	0.0034	1	0.0031	0.3758499	D
<input type="radio"/>	GO:0040020	7,9,8,6	<a href="#">regulation of meiosis</a>	22	0.0034	1	0.0031	0.3758499	D
<input type="radio"/>	GO:0007243	6	<a href="#">protein kinase cascade</a>	23	0.0036	1	0.0031	0.3736343	D

<input type="radio"/>	GO:0006479	9,7	<a href="#">protein amino acid methylation</a>	23	0.0036	1	0.0031	0.3736343	D
<input type="radio"/>	GO:0006303	8,7	<a href="#">double-strand break repair via nonhomologous end joining</a>	23	0.0036	1	0.0031	0.3736343	D
<input type="radio"/>	GO:0043044	10	<a href="#">ATP-dependent chromatin remodeling</a>	23	0.0036	1	0.0031	0.3736343	D
<input type="radio"/>	GO:0008213	8	<a href="#">protein amino acid alkylation</a>	23	0.0036	1	0.0031	0.3736343	D
<input type="radio"/>	GO:0045851	8	<a href="#">pH reduction</a>	24	0.0037	1	0.0031	0.3707267	D
<input type="radio"/>	GO:0051278	8,7	<a href="#">chitin- and beta-glucan-containing cell wall polysaccharide biosynthetic process</a>	24	0.0037	1	0.0031	0.3707267	D
<input type="radio"/>	GO:0009069	6,7	<a href="#">serine family amino acid metabolic process</a>	24	0.0037	1	0.0031	0.3707267	D
<input type="radio"/>	GO:0007035	13,10,6,11	<a href="#">vacuolar acidification</a>	24	0.0037	1	0.0031	0.3707267	D
<input type="radio"/>	GO:0007096	8,10,9,7	<a href="#">regulation of exit from mitosis</a>	24	0.0037	1	0.0031	0.3707267	D
<input type="radio"/>	GO:0007006	5,6	<a href="#">mitochondrial membrane organization and biogenesis</a>	24	0.0037	1	0.0031	0.3707267	D
<input type="radio"/>	GO:0046352	7	<a href="#">disaccharide catabolic process</a>	24	0.0037	1	0.0031	0.3707267	D
<input type="radio"/>	GO:0051452	12,9,10	<a href="#">cellular pH reduction</a>	24	0.0037	1	0.0031	0.3707267	D
<input type="radio"/>	GO:0006555	7,8,6	<a href="#">methionine metabolic process</a>	24	0.0037	1	0.0031	0.3707267	D
<input type="radio"/>	GO:0016575	11,9	<a href="#">histone deacetylation</a>	24	0.0037	1	0.0031	0.3707267	D
<input type="radio"/>	GO:0006890	8,6,5,7	<a href="#">retrograde vesicle-mediated transport, Golgi to ER</a>	24	0.0037	1	0.0031	0.3707267	D
<input type="radio"/>	GO:0030641	10,8	<a href="#">cellular hydrogen ion homeostasis</a>	25	0.0039	1	0.0031	0.3672001	D
<input type="radio"/>	GO:0000724	8,7	<a href="#">double-strand break repair via homologous recombination</a>	25	0.0039	1	0.0031	0.3672001	D
<input type="radio"/>	GO:0045005	8,6	<a href="#">maintenance of fidelity during DNA-dependent DNA replication</a>	25	0.0039	1	0.0031	0.3672001	D
<input type="radio"/>	GO:0051453	11,8,9	<a href="#">regulation of cellular pH</a>	25	0.0039	1	0.0031	0.3672001	D
<input type="radio"/>	GO:0006298	7,9,6	<a href="#">mismatch repair</a>	25	0.0039	1	0.0031	0.3672001	D
<input type="radio"/>	GO:0048311	7,6	<a href="#">mitochondrion distribution</a>	26	0.0040	1	0.0031	0.3631223	D
<input type="radio"/>	GO:0006476	8	<a href="#">protein amino acid deacetylation</a>	26	0.0040	1	0.0031	0.3631223	D
<input type="radio"/>	GO:0000001	8,7,6	<a href="#">mitochondrion inheritance</a>	26	0.0040	1	0.0031	0.3631223	D
<input type="radio"/>	GO:0000080	7,8,6	<a href="#">G1 phase of mitotic cell cycle</a>	27	0.0042	1	0.0031	0.3585557	D
<input type="radio"/>	GO:0051646	6,5	<a href="#">mitochondrion localization</a>	27	0.0042	1	0.0031	0.3585557	D
<input type="radio"/>	GO:0051318	6,7,5	<a href="#">G1 phase</a>	27	0.0042	1	0.0031	0.3585557	D
<input type="radio"/>	GO:0032005	7,6	<a href="#">signal transduction during conjugation with cellular fusion</a>	28	0.0043	1	0.0031	0.3535580	D
<input type="radio"/>	GO:0018193	7	<a href="#">peptidyl-amino acid modification</a>	28	0.0043	1	0.0031	0.3535580	D
<input type="radio"/>	GO:0000750	8,7,6	<a href="#">pheromone-dependent signal transduction during conjugation with cellular fusion</a>	28	0.0043	1	0.0031	0.3535580	D
<input type="radio"/>	GO:0006906	6,5	<a href="#">vesicle fusion</a>	28	0.0043	1	0.0031	0.3535580	D
<input type="radio"/>	GO:0000725	7,6	<a href="#">recombinational repair</a>	29	0.0045	1	0.0031	0.3481824	D
<input type="radio"/>	GO:0006409	11,9,6,8,10,7	<a href="#">tRNA export from nucleus</a>	29	0.0045	1	0.0031	0.3481824	D
<input type="radio"/>	GO:0006885	7	<a href="#">regulation of pH</a>	29	0.0045	1	0.0031	0.3481824	D
<input type="radio"/>	GO:0031137	6,5	<a href="#">regulation of conjugation with cellular fusion</a>	30	0.0046	1	0.0031	0.3424782	D
<input type="radio"/>	GO:0030466	11,7,8,12,10	<a href="#">chromatin silencing at silent mating-type cassette</a>	30	0.0046	1	0.0031	0.3424782	D
<input type="radio"/>	GO:0051128	5,4	<a href="#">regulation of cellular component organization and biogenesis</a>	30	0.0046	1	0.0031	0.3424782	D
<input type="radio"/>	GO:0006665	6,7	<a href="#">sphingolipid metabolic process</a>	30	0.0046	1	0.0031	0.3424782	D
<input type="radio"/>	GO:0051031	5,7,6,8	<a href="#">tRNA transport</a>	30	0.0046	1	0.0031	0.3424782	D
<input type="radio"/>	GO:0046999	5,4	<a href="#">regulation of conjugation</a>	30	0.0046	1	0.0031	0.3424782	D
<input type="radio"/>	GO:0009112	5	<a href="#">nucleobase metabolic process</a>	31	0.0048	1	0.0031	0.3364904	D
<input type="radio"/>	GO:0007121	8,6,10,7,11,5	<a href="#">bipolar cellular bud site selection</a>	32	0.0049	1	0.0031	0.3302606	D
<input type="radio"/>	GO:0015672	6,7	<a href="#">monovalent inorganic cation transport</a>	32	0.0049	1	0.0031	0.3302606	D

<input type="checkbox"/>	GO:0042546	6	<a href="#">cell wall biogenesis</a>	33	0.0051	1	0.0031	0.3238270	D
<input type="checkbox"/>	GO:0000096	6,7,5	<a href="#">sulfur amino acid metabolic process</a>	33	0.0051	1	0.0031	0.3238270	D
<input type="checkbox"/>	GO:0009272	7	<a href="#">chitin- and beta-glucan-containing cell wall biogenesis</a>	33	0.0051	1	0.0031	0.3238270	D
<input type="checkbox"/>	GO:0006007	8,9	<a href="#">glucose catabolic process</a>	34	0.0053	1	0.0031	0.3172247	D
<input type="checkbox"/>	GO:0007117	6,5,4	<a href="#">budding cell bud growth</a>	35	0.0054	1	0.0031	0.3104856	D
<input type="checkbox"/>	GO:0048590	3	<a href="#">non-developmental growth</a>	35	0.0054	1	0.0031	0.3104856	D
<input type="checkbox"/>	GO:0000086	8,5,6,7,4	<a href="#">G2/M transition of mitotic cell cycle</a>	35	0.0054	1	0.0031	0.3104856	D
<input type="checkbox"/>	GO:0030433	9,11,10,12	<a href="#">ER-associated protein catabolic process</a>	35	0.0054	1	0.0031	0.3104856	D
<input type="checkbox"/>	GO:0006865	5,6,7	<a href="#">amino acid transport</a>	39	0.0060	1	0.0031	0.2827122	D
<input type="checkbox"/>	GO:0016125	5,6,7	<a href="#">sterol metabolic process</a>	42	0.0065	2	0.0063	0.2779241	D
<input type="checkbox"/>	GO:0008202	5,6	<a href="#">steroid metabolic process</a>	43	0.0066	2	0.0063	0.2771655	D
<input type="checkbox"/>	GO:0006752	6	<a href="#">group transfer coenzyme metabolic process</a>	44	0.0068	2	0.0063	0.2761007	D
<input type="checkbox"/>	GO:0006289	7,6	<a href="#">nucleotide-excision repair</a>	44	0.0068	2	0.0063	0.2761007	D
<input type="checkbox"/>	GO:0031505	6	<a href="#">chitin- and beta-glucan-containing cell wall organization and biogenesis</a>	44	0.0068	2	0.0063	0.2761007	D
<input type="checkbox"/>	GO:0043681	6,7,8	<a href="#">protein import into mitochondrion</a>	40	0.0062	1	0.0031	0.2756817	D
<input type="checkbox"/>	GO:0050790	4	<a href="#">regulation of catalytic activity</a>	45	0.0069	2	0.0063	0.2747470	D
<input type="checkbox"/>	GO:0065009	3	<a href="#">regulation of a molecular function</a>	46	0.0071	2	0.0063	0.2731216	D
<input type="checkbox"/>	GO:0006119	7,4	<a href="#">oxidative phosphorylation</a>	46	0.0071	2	0.0063	0.2731216	D
<input type="checkbox"/>	GO:0000041	7,8	<a href="#">transition metal ion transport</a>	46	0.0071	2	0.0063	0.2731216	D
<input type="checkbox"/>	GO:0006497	8,7,6	<a href="#">protein amino acid lipidation</a>	48	0.0074	2	0.0063	0.2691227	D
<input type="checkbox"/>	GO:0042158	7,5	<a href="#">lipoprotein biosynthetic process</a>	48	0.0074	2	0.0063	0.2691227	D
<input type="checkbox"/>	GO:0042157	6	<a href="#">lipoprotein metabolic process</a>	48	0.0074	2	0.0063	0.2691227	D
<input type="checkbox"/>	GO:0006606	9,10,7,8,6	<a href="#">protein import into nucleus</a>	50	0.0077	2	0.0063	0.2642340	D
<input type="checkbox"/>	GO:0015837	4,5	<a href="#">amine transport</a>	50	0.0077	2	0.0063	0.2642340	D
<input type="checkbox"/>	GO:0051170	9,7,8	<a href="#">nuclear import</a>	50	0.0077	2	0.0063	0.2642340	D
<input type="checkbox"/>	GO:0000082	8,5,6,7,4	<a href="#">G1/S transition of mitotic cell cycle</a>	52	0.0080	2	0.0063	0.2585793	D
<input type="checkbox"/>	GO:0030384	8,9	<a href="#">phosphoinositide metabolic process</a>	43	0.0066	1	0.0031	0.2546825	D
<input type="checkbox"/>	GO:0006887	8,6,5,7	<a href="#">exocytosis</a>	44	0.0068	1	0.0031	0.2477635	D
<input type="checkbox"/>	GO:0006611	9,10,7,8	<a href="#">protein export from nucleus</a>	56	0.0086	2	0.0063	0.2454279	D
<input type="checkbox"/>	GO:0051640	5,4	<a href="#">organelle localization</a>	56	0.0086	2	0.0063	0.2454279	D
<input type="checkbox"/>	GO:0006302	7,6	<a href="#">double-strand break repair</a>	57	0.0088	2	0.0063	0.2418330	D
<input type="checkbox"/>	GO:0006997	5	<a href="#">nuclear organization and biogenesis</a>	57	0.0088	2	0.0063	0.2418330	D
<input type="checkbox"/>	GO:0009066	6,7	<a href="#">aspartate family amino acid metabolic process</a>	46	0.0071	1	0.0031	0.2341207	D
<input type="checkbox"/>	GO:0051028	5,7,6,8	<a href="#">mRNA transport</a>	66	0.0102	3	0.0094	0.2281601	D
<input type="checkbox"/>	GO:0009108	6	<a href="#">coenzyme biosynthetic process</a>	66	0.0102	3	0.0094	0.2281601	D
<input type="checkbox"/>	GO:0030468	8,5,9	<a href="#">establishment of cell polarity (sensu Fungi)</a>	66	0.0102	3	0.0094	0.2281601	D
<input type="checkbox"/>	GO:0007105	6,4	<a href="#">cytokinesis, site selection</a>	66	0.0102	3	0.0094	0.2281601	D
<input type="checkbox"/>	GO:0000282	7,9,5,6,10	<a href="#">cellular bud site selection</a>	66	0.0102	3	0.0094	0.2281601	D
<input type="checkbox"/>	GO:0030467	7,4,8	<a href="#">establishment and/or maintenance of cell polarity (sensu Fungi)</a>	66	0.0102	3	0.0094	0.2281601	D
<input type="checkbox"/>	GO:0006406	11,9,6,8,10,7	<a href="#">mRNA export from nucleus</a>	66	0.0102	3	0.0094	0.2281601	D
<input type="checkbox"/>	GO:0006790	4	<a href="#">sulfur metabolic process</a>	67	0.0103	3	0.0094	0.2271173	D
<input type="checkbox"/>	GO:0065004	6,5	<a href="#">protein-DNA complex assembly</a>	74	0.0114	3	0.0094	0.2159319	D
<input type="checkbox"/>	GO:0006413	7,6	<a href="#">translational initiation</a>	49	0.0076	1	0.0031	0.2142880	D
<input type="checkbox"/>	GO:0006405	10,8,5,7,9,6	<a href="#">RNA export from nucleus</a>	79	0.0122	3	0.0094	0.2046658	D

<input type="checkbox"/>	GO:0051236	3,4,5	<a href="#">establishment of RNA localization</a>	80	0.0124	3	0.0094	0.2021690	D
<input type="checkbox"/>	GO:0050658	4,6,5,7	<a href="#">RNA transport</a>	80	0.0124	3	0.0094	0.2021690	D
<input type="checkbox"/>	GO:0050657	5,6	<a href="#">nucleic acid transport</a>	80	0.0124	3	0.0094	0.2021690	D
<input type="checkbox"/>	GO:0007033	5	<a href="#">vacuole organization and biogenesis</a>	67	0.0103	2	0.0063	0.2021499	D
<input type="checkbox"/>	GO:0006403	4	<a href="#">RNA localization</a>	90	0.0139	4	0.0126	0.1967719	D
<input type="checkbox"/>	GO:0008033	7	<a href="#">tRNA processing</a>	84	0.0130	3	0.0094	0.1915663	D
<input type="checkbox"/>	GO:0016458	5	<a href="#">gene silencing</a>	95	0.0147	4	0.0126	0.1905154	D
<input type="checkbox"/>	GO:0006342	10,6,7,11,9	<a href="#">chromatin silencing</a>	95	0.0147	4	0.0126	0.1905154	D
<input type="checkbox"/>	GO:0031507	6,10	<a href="#">heterochromatin formation</a>	95	0.0147	4	0.0126	0.1905154	D
<input type="checkbox"/>	GO:0045814	5	<a href="#">negative regulation of gene expression, epigenetic</a>	95	0.0147	4	0.0126	0.1905154	D
<input type="checkbox"/>	GO:0006368	9,7,8	<a href="#">RNA elongation from RNA polymerase II promoter</a>	53	0.0082	1	0.0031	0.1893164	D
<input type="checkbox"/>	GO:0046942	5,6	<a href="#">carboxylic acid transport</a>	54	0.0083	1	0.0031	0.1833686	D
<input type="checkbox"/>	GO:0040029	4	<a href="#">regulation of gene expression, epigenetic</a>	100	0.0154	4	0.0126	0.1823190	D
<input type="checkbox"/>	GO:0031497	5,9	<a href="#">chromatin assembly</a>	104	0.0161	5	0.0157	0.1810502	D
<input type="checkbox"/>	GO:0030036	7	<a href="#">actin cytoskeleton organization and biogenesis</a>	107	0.0165	5	0.0157	0.1799373	D
<input type="checkbox"/>	GO:0007005	5	<a href="#">mitochondrion organization and biogenesis</a>	110	0.0170	5	0.0157	0.1780892	D
<input type="checkbox"/>	GO:0015849	4,5	<a href="#">organic acid transport</a>	55	0.0085	1	0.0031	0.1775453	D
<input type="checkbox"/>	GO:0030010	7,4,8	<a href="#">establishment of cell polarity</a>	103	0.0159	4	0.0126	0.1766647	D
<input type="checkbox"/>	GO:0030029	6	<a href="#">actin filament-based process</a>	112	0.0173	5	0.0157	0.1764792	D
<input type="checkbox"/>	GO:0009309	5,6	<a href="#">amine biosynthetic process</a>	114	0.0176	5	0.0157	0.1745891	D
<input type="checkbox"/>	GO:0015931	4,5	<a href="#">nucleobase, nucleoside, nucleotide and nucleic acid transport</a>	90	0.0139	3	0.0094	0.1743914	D
<input type="checkbox"/>	GO:0044271	5,4	<a href="#">nitrogen compound biosynthetic process</a>	115	0.0178	5	0.0157	0.1735450	D
<input type="checkbox"/>	GO:0006260	6	<a href="#">DNA replication</a>	117	0.0181	5	0.0157	0.1712712	D
<input type="checkbox"/>	GO:0008652	6,7	<a href="#">amino acid biosynthetic process</a>	106	0.0164	4	0.0126	0.1705758	D
<input type="checkbox"/>	GO:0006333	8	<a href="#">chromatin assembly or disassembly</a>	119	0.0184	5	0.0157	0.1687660	D
<input type="checkbox"/>	GO:0008654	7,6,8	<a href="#">phospholipid biosynthetic process</a>	58	0.0090	1	0.0031	0.1608420	D
<input type="checkbox"/>	GO:0051325	6,5	<a href="#">interphase</a>	112	0.0173	4	0.0126	0.1574481	D
<input type="checkbox"/>	GO:0051329	7,5,6	<a href="#">interphase of mitotic cell cycle</a>	112	0.0173	4	0.0126	0.1574481	D
<input type="checkbox"/>	GO:0007067	8,6,7,5	<a href="#">mitosis</a>	127	0.0196	5	0.0157	0.1568210	D
<input type="checkbox"/>	GO:0000070	9,7,5,8,6,4	<a href="#">mitotic sister chromatid segregation</a>	59	0.0091	1	0.0031	0.1555338	D
<input type="checkbox"/>	GO:0006944	5	<a href="#">membrane fusion</a>	59	0.0091	1	0.0031	0.1555338	D
<input type="checkbox"/>	GO:0006354	8,6,7	<a href="#">RNA elongation</a>	59	0.0091	1	0.0031	0.1555338	D
<input type="checkbox"/>	GO:0009165	5,6	<a href="#">nucleotide biosynthetic process</a>	59	0.0091	1	0.0031	0.1555338	D
<input type="checkbox"/>	GO:0006644	6,7	<a href="#">phospholipid metabolic process</a>	97	0.0150	3	0.0094	0.1535754	D
<input type="checkbox"/>	GO:0000087	7,5,6	<a href="#">M phase of mitotic cell cycle</a>	129	0.0199	5	0.0157	0.1534480	D
<input type="checkbox"/>	GO:0007163	6,3,7	<a href="#">establishment and/or maintenance of cell polarity</a>	115	0.0178	4	0.0126	0.1505710	D
<input type="checkbox"/>	GO:0006650	7,8	<a href="#">glycerophospholipid metabolic process</a>	60	0.0093	1	0.0031	0.1503564	D
<input type="checkbox"/>	GO:0031509	7,11	<a href="#">telomeric heterochromatin formation</a>	60	0.0093	1	0.0031	0.1503564	D
<input type="checkbox"/>	GO:0006725	4	<a href="#">aromatic compound metabolic process</a>	60	0.0093	1	0.0031	0.1503564	D
<input type="checkbox"/>	GO:0001510	7	<a href="#">RNA methylation</a>	60	0.0093	1	0.0031	0.1503564	D
<input type="checkbox"/>	GO:0006348	11,7,8,12,10	<a href="#">chromatin silencing at telomere</a>	60	0.0093	1	0.0031	0.1503564	D
<input type="checkbox"/>	GO:0007059	3	<a href="#">chromosome segregation</a>	119	0.0184	4	0.0126	0.1412381	D
<input type="checkbox"/>	GO:0000819	7,4	<a href="#">sister chromatid segregation</a>	62	0.0096	1	0.0031	0.1403936	D
<input type="checkbox"/>	GO:0051168	9,7,8	<a href="#">nuclear export</a>	102	0.0158	3	0.0094	0.1388271	D

<input type="checkbox"/>	GO:0043414	6	<a href="#">biopolymer methylation</a>	83	0.0128	2	0.0063	0.1384136	D
<input type="checkbox"/>	GO:0032259	5	<a href="#">methylation</a>	83	0.0128	2	0.0063	0.1384136	D
<input type="checkbox"/>	GO:0006281	6,5	<a href="#">DNA repair</a>	193	0.0298	9	0.0283	0.1350934	D
<input type="checkbox"/>	GO:0006397	7	<a href="#">mRNA processing</a>	157	0.0242	6	0.0189	0.1327118	D
<input type="checkbox"/>	GO:0019954	3	<a href="#">asexual reproduction</a>	85	0.0131	2	0.0063	0.1312051	D
<input type="checkbox"/>	GO:0007114	5,4	<a href="#">cell budding</a>	85	0.0131	2	0.0063	0.1312051	D
<input type="checkbox"/>	GO:0016071	6	<a href="#">mRNA metabolic process</a>	210	0.0324	10	0.0314	0.1295914	D
<input type="checkbox"/>	GO:0006643	5,6	<a href="#">membrane lipid metabolic process</a>	125	0.0193	4	0.0126	0.1271818	D
<input type="checkbox"/>	GO:0008610	5,4,6	<a href="#">lipid biosynthetic process</a>	129	0.0199	4	0.0126	0.1179497	D
<input type="checkbox"/>	GO:0000902	5,6	<a href="#">cell morphogenesis</a>	248	0.0383	11	0.0346	0.1165641	D
<input type="checkbox"/>	GO:0048856	3	<a href="#">anatomical structure development</a>	248	0.0383	11	0.0346	0.1165641	D
<input type="checkbox"/>	GO:0009653	4,3	<a href="#">anatomical structure morphogenesis</a>	248	0.0383	11	0.0346	0.1165641	D
<input type="checkbox"/>	GO:0032989	4,5	<a href="#">cellular structure morphogenesis</a>	248	0.0383	11	0.0346	0.1165641	D
<input type="checkbox"/>	GO:0006520	5,6	<a href="#">amino acid metabolic process</a>	187	0.0289	7	0.0220	0.1133089	D
<input type="checkbox"/>	GO:0065003	5,4	<a href="#">macromolecular complex assembly</a>	328	0.0506	16	0.0503	0.1043474	D
<input type="checkbox"/>	GO:0000278	4	<a href="#">mitotic cell cycle</a>	266	0.0411	11	0.0346	0.1028672	D
<input type="checkbox"/>	GO:0006730	4	<a href="#">one-carbon compound metabolic process</a>	97	0.0150	2	0.0063	0.0930661	D
<input type="checkbox"/>	GO:0006399	6	<a href="#">tRNA metabolic process</a>	121	0.0187	3	0.0094	0.0887663	D
<input type="checkbox"/>	GO:0000398	8,10	<a href="#">nuclear mRNA splicing, via spliceosome</a>	102	0.0158	2	0.0063	0.0798563	D
<input type="checkbox"/>	GO:0046467	6,5,7	<a href="#">membrane lipid biosynthetic process</a>	78	0.0120	1	0.0031	0.0784193	D
<input type="checkbox"/>	GO:0000377	9	<a href="#">RNA splicing, via transesterification reactions with bulged adenosine as nucleophile</a>	103	0.0159	2	0.0063	0.0774002	D
<input type="checkbox"/>	GO:0009100	6	<a href="#">glycoprotein metabolic process</a>	79	0.0122	1	0.0031	0.0754894	D
<input type="checkbox"/>	GO:0051169	7,5,6	<a href="#">nuclear transport</a>	129	0.0199	3	0.0094	0.0717149	D
<input type="checkbox"/>	GO:0006913	8,6,7	<a href="#">nucleocytoplasmic transport</a>	129	0.0199	3	0.0094	0.0717149	D
<input type="checkbox"/>	GO:0008380	7	<a href="#">RNA splicing</a>	132	0.0204	3	0.0094	0.0659876	D
<input type="checkbox"/>	GO:0000375	8	<a href="#">RNA splicing, via transesterification reactions</a>	110	0.0170	2	0.0063	0.0618650	D
<input type="checkbox"/>	GO:0016070	5	<a href="#">RNA metabolic process</a>	1058	0.1634	49	0.1541	0.0569285	D
<input type="checkbox"/>	GO:0009451	6	<a href="#">RNA modification</a>	139	0.0215	3	0.0094	0.0539992	D
<input type="checkbox"/>	GO:0022618	6,5	<a href="#">protein-RNA complex assembly</a>	144	0.0222	2	0.0063	0.0187299	D
<input type="checkbox"/>	GO:0006996	4	<a href="#">organelle organization and biogenesis</a>	1388	0.2143	56	0.1761	0.0131446	D
<input type="checkbox"/>	GO:0043284	5	<a href="#">biopolymer biosynthetic process</a>	354	0.0547	7	0.0220	0.0019445	D
<input type="checkbox"/>	GO:0006396	6	<a href="#">RNA processing</a>	491	0.0758	10	0.0314	0.0003624	D
<input type="checkbox"/>	GO:0009058	3	<a href="#">biosynthetic process</a>	1249	0.1929	39	0.1226	0.0001940	D
<input type="checkbox"/>	GO:0009059	4	<a href="#">macromolecule biosynthetic process</a>	886	0.1368	22	0.0692	4.274251E-05	D
<input type="checkbox"/>	GO:0006414	7,6	<a href="#">translational elongation</a>	313	0.0483	2	0.0063	1.377373E-05	D
<input type="checkbox"/>	GO:0006412	6,5	<a href="#">translation</a>	688	0.1062	9	0.0283	7.156869E-08	D
<input type="checkbox"/>	GO:0022613	4	<a href="#">ribonucleoprotein complex biogenesis and assembly</a>	483	0.0746	2	0.0063	3.754426E-09	D