

# GO-Stats Results

Your dataset contains **468** 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:0009987	2	<a href="#">cellular process</a>	4654	0.7187	411	0.8782	5.137181E-18	E
<input type="radio"/> GO:0009101	7,5	<a href="#">glycoprotein biosynthetic process</a>	78	0.0120	25	0.0534	6.284208E-11	E
<input type="radio"/> GO:0009100	6	<a href="#">glycoprotein metabolic process</a>	79	0.0122	25	0.0534	8.556998E-11	E
<input type="radio"/> GO:0043413	6	<a href="#">biopolymer glycosylation</a>	73	0.0113	23	0.0491	5.382359E-10	E
<input type="radio"/> GO:0006486	8,7,6	<a href="#">protein amino acid glycosylation</a>	73	0.0113	23	0.0491	5.382359E-10	E
<input type="radio"/> GO:0016043	3	<a href="#">cellular component organization and biogenesis</a>	2264	0.3496	223	0.4765	1.336771E-09	E
<input type="radio"/> GO:0006464	6	<a href="#">protein modification process</a>	520	0.0803	73	0.1560	6.153059E-09	E
<input type="radio"/> GO:0006487	9,8,7	<a href="#">protein amino acid N-linked glycosylation</a>	48	0.0074	17	0.0363	1.362523E-08	E
<input type="radio"/> GO:0044237	3	<a href="#">cellular metabolic process</a>	3403	0.5255	302	0.6453	1.539029E-08	E
<input type="radio"/> GO:0008152	2	<a href="#">metabolic process</a>	3516	0.5429	308	0.6581	4.193818E-08	E
<input type="radio"/> GO:0043412	5	<a href="#">biopolymer modification</a>	664	0.1025	84	0.1795	5.183641E-08	E
<input type="radio"/> GO:0007049	3	<a href="#">cell cycle</a>	458	0.0707	62	0.1325	3.318455E-07	E
<input type="radio"/> GO:0044238	3	<a href="#">primary metabolic process</a>	3247	0.5014	283	0.6047	7.635965E-07	E
<input type="radio"/> GO:0022402	4,3	<a href="#">cell cycle process</a>	439	0.0678	58	0.1239	1.725520E-06	E
<input type="radio"/> GO:0051234	2,3	<a href="#">establishment of localization</a>	1004	0.1550	108	0.2308	2.179504E-06	E
<input type="radio"/> GO:0006810	3,4	<a href="#">transport</a>	981	0.1515	105	0.2244	3.834687E-06	E
<input type="radio"/> GO:0016125	5,6,7	<a href="#">sterol metabolic process</a>	42	0.0065	13	0.0278	3.835038E-06	E
<input type="radio"/> GO:0000074	6,5	<a href="#">regulation of progression through cell cycle</a>	167	0.0258	29	0.0620	4.662559E-06	E
<input type="radio"/> GO:0051726	5,4	<a href="#">regulation of cell cycle</a>	167	0.0258	29	0.0620	4.662559E-06	E
<input type="radio"/> GO:0008202	5,6	<a href="#">steroid metabolic process</a>	43	0.0066	13	0.0278	5.108159E-06	E
<input type="radio"/> GO:0065007	2	<a href="#">biological regulation</a>	948	0.1464	101	0.2158	7.250879E-06	E

<input type="radio"/>	GO:0000278	4	<a href="#">mitotic cell cycle</a>	266	0.0411	39	0.0833	7.997653E-06	E
<input type="radio"/>	GO:0051649	5,3,4	<a href="#">establishment of cellular localization</a>	606	0.0936	71	0.1517	8.821454E-06	E
<input type="radio"/>	GO:0051179	2	<a href="#">localization</a>	1051	0.1623	109	0.2329	9.953972E-06	E
<input type="radio"/>	GO:0046907	6,4,5	<a href="#">intracellular transport</a>	545	0.0842	65	0.1389	1.210270E-05	E
<input type="radio"/>	GO:0050789	3	<a href="#">regulation of biological process</a>	761	0.1175	84	0.1795	1.259138E-05	E
<input type="radio"/>	GO:0050794	4,3	<a href="#">regulation of cellular process</a>	738	0.1140	82	0.1752	1.265243E-05	E
<input type="radio"/>	GO:0022403	5,4	<a href="#">cell cycle phase</a>	353	0.0545	47	0.1004	1.306010E-05	E
<input type="radio"/>	GO:0045045	7,5,4,6	<a href="#">secretory pathway</a>	243	0.0375	36	0.0769	1.387518E-05	E
<input type="radio"/>	GO:0051641	4,3	<a href="#">cellular localization</a>	642	0.0991	73	0.1560	1.787297E-05	E
<input type="radio"/>	GO:0046903	3,4	<a href="#">secretion</a>	250	0.0386	36	0.0769	2.527600E-05	E
<input type="radio"/>	GO:0032940	6,4,5	<a href="#">secretion by cell</a>	250	0.0386	36	0.0769	2.527600E-05	E
<input type="radio"/>	GO:0008610	5,4,6	<a href="#">lipid biosynthetic process</a>	129	0.0199	23	0.0491	2.763700E-05	E
<input type="radio"/>	GO:0006696	7,8,9	<a href="#">ergosterol biosynthetic process</a>	26	0.0040	9	0.0192	4.464816E-05	E
<input type="radio"/>	GO:0008204	6,7,8	<a href="#">ergosterol metabolic process</a>	26	0.0040	9	0.0192	4.464816E-05	E
<input type="radio"/>	GO:0006694	6,5,7	<a href="#">steroid biosynthetic process</a>	32	0.0049	10	0.0214	4.538313E-05	E
<input type="radio"/>	GO:0016126	6,7,8	<a href="#">sterol biosynthetic process</a>	32	0.0049	10	0.0214	4.538313E-05	E
<input type="radio"/>	GO:0043283	4	<a href="#">biopolymer metabolic process</a>	2230	0.3443	197	0.4209	6.629781E-05	E
<input type="radio"/>	GO:0051329	7,5,6	<a href="#">interphase of mitotic cell cycle</a>	112	0.0173	20	0.0427	8.562292E-05	E
<input type="radio"/>	GO:0051325	6,5	<a href="#">interphase</a>	112	0.0173	20	0.0427	8.562292E-05	E
<input type="radio"/>	GO:0019219	6,5	<a href="#">regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process</a>	440	0.0679	52	0.1111	0.0001041	E
<input type="radio"/>	GO:0006888	8,6,5,7	<a href="#">ER to Golgi vesicle-mediated transport</a>	81	0.0125	16	0.0342	0.0001278	E
<input type="radio"/>	GO:0007346	7,5,6	<a href="#">regulation of progression through mitotic cell cycle</a>	13	0.0020	6	0.0128	0.0001412	E
<input type="radio"/>	GO:0006139	4	<a href="#">nucleobase, nucleoside, nucleotide and nucleic acid metabolic process</a>	1532	0.2366	141	0.3013	0.0001624	E
<input type="radio"/>	GO:0044255	4,5	<a href="#">cellular lipid metabolic process</a>	229	0.0354	31	0.0662	0.0002500	E
<input type="radio"/>	GO:0006629	4	<a href="#">lipid metabolic process</a>	242	0.0374	32	0.0684	0.0003018	E
<input type="radio"/>	GO:0006886	7,5,6	<a href="#">intracellular protein transport</a>	274	0.0423	35	0.0748	0.0003112	E
<input type="radio"/>	GO:0045184	3,4,5	<a href="#">establishment of protein localization</a>	296	0.0457	37	0.0791	0.0003240	E
<input type="radio"/>	GO:0045047	9,8,7,6,5	<a href="#">protein targeting to ER</a>	33	0.0051	9	0.0192	0.0003286	E
<input type="radio"/>	GO:0043170	3	<a href="#">macromolecule metabolic process</a>	2841	0.4387	237	0.5064	0.0003622	E
<input type="radio"/>	GO:0006260	6	<a href="#">DNA replication</a>	117	0.0181	19	0.0406	0.0004151	E
<input type="radio"/>	GO:0006605	8,6,7	<a href="#">protein targeting</a>	258	0.0398	33	0.0705	0.0004347	E
<input type="radio"/>	GO:0015031	4,5,6	<a href="#">protein transport</a>	280	0.0432	35	0.0748	0.0004526	E
<input type="radio"/>	GO:0017038	5,6,7	<a href="#">protein import</a>	109	0.0168	18	0.0385	0.0004724	E
<input type="radio"/>	GO:0033036	3	<a href="#">macromolecule localization</a>	382	0.0590	44	0.0940	0.0005321	E
<input type="radio"/>	GO:0000087	7,5,6	<a href="#">M phase of mitotic cell cycle</a>	129	0.0199	20	0.0427	0.0005364	E
<input type="radio"/>	GO:0006350	5	<a href="#">transcription</a>	567	0.0876	60	0.1282	0.0005454	E
<input type="radio"/>	GO:0048519	4	<a href="#">negative regulation of biological process</a>	242	0.0374	31	0.0662	0.0006072	E

<input type="radio"/>	GO:0006259	5	<a href="#">DNA metabolic process</a>	523	0.0808	56	0.1197	0.0006152	E
<input type="radio"/>	GO:0008104	4	<a href="#">protein localization</a>	330	0.0510	39	0.0833	0.0006482	E
<input type="radio"/>	GO:0045449	7,6	<a href="#">regulation of transcription</a>	386	0.0596	44	0.0940	0.0006483	E
<input type="radio"/>	GO:0006996	4	<a href="#">organelle organization and biogenesis</a>	1388	0.2143	125	0.2671	0.0008235	E
<input type="radio"/>	GO:0031323	5,4	<a href="#">regulation of cellular metabolic process</a>	507	0.0783	54	0.1154	0.0008346	E
<input type="radio"/>	GO:0048523	5,4	<a href="#">negative regulation of cellular process</a>	239	0.0369	30	0.0641	0.0009812	E
<input type="radio"/>	GO:0007062	7,4	<a href="#">sister chromatid cohesion</a>	31	0.0048	8	0.0171	0.0010140	E
<input type="radio"/>	GO:0051276	5	<a href="#">chromosome organization and biogenesis</a>	572	0.0883	59	0.1261	0.0010451	E
<input type="radio"/>	GO:0019222	4,3	<a href="#">regulation of metabolic process</a>	538	0.0831	56	0.1197	0.0011151	E
<input type="radio"/>	GO:0015931	4,5	<a href="#">nucleobase, nucleoside, nucleotide and nucleic acid transport</a>	90	0.0139	15	0.0321	0.0011792	E
<input type="radio"/>	GO:0000910	4	<a href="#">cytokinesis</a>	109	0.0168	17	0.0363	0.0012125	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	24	0.0513	0.0012230	E
<input type="radio"/>	GO:0007001	6	<a href="#">chromosome organization and biogenesis (sensu Eukaryota)</a>	567	0.0876	58	0.1239	0.0013472	E
<input type="radio"/>	GO:0015865	6,7	<a href="#">purine nucleotide transport</a>	4	0.0006	3	0.0064	0.0013929	E
<input type="radio"/>	GO:0042158	7,5	<a href="#">lipoprotein biosynthetic process</a>	48	0.0074	10	0.0214	0.0014124	E
<input type="radio"/>	GO:0042157	6	<a href="#">lipoprotein metabolic process</a>	48	0.0074	10	0.0214	0.0014124	E
<input type="radio"/>	GO:0006497	8,7,6	<a href="#">protein amino acid lipidation</a>	48	0.0074	10	0.0214	0.0014124	E
<input type="radio"/>	GO:0006351	7,6	<a href="#">transcription, DNA-dependent</a>	522	0.0806	54	0.1154	0.0014938	E
<input type="radio"/>	GO:0040007	2	<a href="#">growth</a>	141	0.0218	20	0.0427	0.0015156	E
<input type="radio"/>	GO:0006355	8,7	<a href="#">regulation of transcription, DNA-dependent</a>	359	0.0554	40	0.0855	0.0015510	E
<input type="radio"/>	GO:0000279	6,5	<a href="#">M phase</a>	258	0.0398	31	0.0662	0.0015704	E
<input type="radio"/>	GO:0032774	6	<a href="#">RNA biosynthetic process</a>	524	0.0809	54	0.1154	0.0016078	E
<input type="radio"/>	GO:0030447	3	<a href="#">filamentous growth</a>	94	0.0145	15	0.0321	0.0017830	E
<input type="radio"/>	GO:0006614	11,10,9,8,7	<a href="#">SRP-dependent cotranslational protein targeting to membrane</a>	20	0.0031	6	0.0128	0.0018973	E
<input type="radio"/>	GO:0048193	7,5,6	<a href="#">Golgi vesicle transport</a>	166	0.0256	22	0.0470	0.0021052	E
<input type="radio"/>	GO:0000086	8,5,6,7,4	<a href="#">G2/M transition of mitotic cell cycle</a>	35	0.0054	8	0.0171	0.0022496	E
<input type="radio"/>	GO:0007067	8,6,7,5	<a href="#">mitosis</a>	127	0.0196	18	0.0385	0.0024624	E
<input type="radio"/>	GO:0006891	8,6,5,7	<a href="#">intra-Golgi vesicle-mediated transport</a>	21	0.0032	6	0.0128	0.0024661	E
<input type="radio"/>	GO:0018193	7	<a href="#">peptidyl-amino acid modification</a>	28	0.0043	7	0.0150	0.0024685	E
<input type="radio"/>	GO:0032506	5,3	<a href="#">cytokinetic process</a>	88	0.0136	14	0.0299	0.0025082	E
<input type="radio"/>	GO:0007124	6,4,8,9	<a href="#">pseudohyphal growth</a>	61	0.0094	11	0.0235	0.0026524	E
<input type="radio"/>	GO:0030150	10,9,8,7	<a href="#">protein import into mitochondrial matrix</a>	22	0.0034	6	0.0128	0.0031483	E
<input type="radio"/>	GO:0007064	10,8,5,6,9,7,4	<a href="#">mitotic sister chromatid cohesion</a>	22	0.0034	6	0.0128	0.0031483	E
<input type="radio"/>	GO:0007231	6,5	<a href="#">osmosensory signaling pathway</a>	22	0.0034	6	0.0128	0.0031483	E
<input type="radio"/>	GO:0006862	5,6	<a href="#">nucleotide transport</a>	5	0.0008	3	0.0064	0.0032320	E
<input type="radio"/>	GO:0033261	7,8,6	<a href="#">regulation of progression through S phase</a>	5	0.0008	3	0.0064	0.0032320	E
<input type="radio"/>	GO:0006468	8,7	<a href="#">protein amino acid phosphorylation</a>	101	0.0156	15	0.0321	0.0034080	E
<input type="radio"/>	GO:0006366	8,7	<a href="#">transcription from RNA polymerase II promoter</a>	343	0.0530	37	0.0791	0.0034870	E
<input type="radio"/>	GO:0016049	5,3,7,8	<a href="#">cell growth</a>	102	0.0158	15	0.0321	0.0037116	E
<input type="radio"/>	GO:0009058	3	<a href="#">biosynthetic process</a>	1249	0.1929	109	0.2329	0.0037980	E
<input type="radio"/>	GO:0009892	5,4	<a href="#">negative regulation of metabolic process</a>	208	0.0321	25	0.0534	0.0038032	E
<input type="radio"/>	GO:0006613	10,9,8,7,6	<a href="#">cotranslational protein targeting to membrane</a>	23	0.0036	6	0.0128	0.0039545	E
<input type="radio"/>	GO:0031324	6,5	<a href="#">negative regulation of cellular metabolic process</a>	198	0.0306	24	0.0513	0.0040257	E

<input type="radio"/>	GO:0031497	5,9	<a href="#">chromatin assembly</a>	104	0.0161	15	0.0321	0.0043805	E
<input type="radio"/>	GO:0006796	5	<a href="#">phosphate metabolic process</a>	212	0.0327	25	0.0534	0.0047035	E
<input type="radio"/>	GO:0006793	4	<a href="#">phosphorus metabolic process</a>	212	0.0327	25	0.0534	0.0047035	E
<input type="radio"/>	GO:0043681	6,7,8	<a href="#">protein import into mitochondrion</a>	40	0.0062	8	0.0171	0.0050743	E
<input type="radio"/>	GO:0009653	4,3	<a href="#">anatomical structure morphogenesis</a>	248	0.0383	28	0.0598	0.0051980	E
<input type="radio"/>	GO:0048856	3	<a href="#">anatomical structure development</a>	248	0.0383	28	0.0598	0.0051980	E
<input type="radio"/>	GO:0032989	4,5	<a href="#">cellular structure morphogenesis</a>	248	0.0383	28	0.0598	0.0051980	E
<input type="radio"/>	GO:0000902	5,6	<a href="#">cell morphogenesis</a>	248	0.0383	28	0.0598	0.0051980	E
<input type="radio"/>	GO:0006518	4	<a href="#">peptide metabolic process</a>	11	0.0017	4	0.0085	0.0052823	E
<input type="radio"/>	GO:0051049	5,4	<a href="#">regulation of transport</a>	11	0.0017	4	0.0085	0.0052823	E
<input type="radio"/>	GO:0006261	7	<a href="#">DNA-dependent DNA replication</a>	97	0.0150	14	0.0299	0.0056144	E
<input type="radio"/>	GO:0051704	2	<a href="#">multi-organism process</a>	139	0.0215	18	0.0385	0.0057978	E
<input type="radio"/>	GO:0016311	6	<a href="#">dephosphorylation</a>	41	0.0063	8	0.0171	0.0058539	E
<input type="radio"/>	GO:0051052	7,6	<a href="#">regulation of DNA metabolic process</a>	41	0.0063	8	0.0171	0.0058539	E
<input type="radio"/>	GO:0006354	8,6,7	<a href="#">RNA elongation</a>	59	0.0091	10	0.0214	0.0060129	E
<input type="radio"/>	GO:0006913	8,6,7	<a href="#">nucleocytoplasmic transport</a>	129	0.0199	17	0.0363	0.0060407	E
<input type="radio"/>	GO:0051169	7,5,6	<a href="#">nuclear transport</a>	129	0.0199	17	0.0363	0.0060407	E
<input type="radio"/>	GO:0051170	9,7,8	<a href="#">nuclear import</a>	50	0.0077	9	0.0192	0.0060677	E
<input type="radio"/>	GO:0006606	9,10,7,8,6	<a href="#">protein import into nucleus</a>	50	0.0077	9	0.0192	0.0060677	E
<input type="radio"/>	GO:0007059	3	<a href="#">chromosome segregation</a>	119	0.0184	16	0.0342	0.0062614	E
<input type="radio"/>	GO:0016481	8,7	<a href="#">negative regulation of transcription</a>	162	0.0250	20	0.0427	0.0063039	E
<input type="radio"/>	GO:0006402	7	<a href="#">mRNA catabolic process</a>	60	0.0093	10	0.0214	0.0067005	E
<input type="radio"/>	GO:0007165	4	<a href="#">signal transduction</a>	209	0.0323	24	0.0513	0.0071162	E
<input type="radio"/>	GO:0006357	9,8	<a href="#">regulation of transcription from RNA polymerase II promoter</a>	221	0.0341	25	0.0534	0.0073122	E
<input type="radio"/>	GO:0016071	6	<a href="#">mRNA metabolic process</a>	210	0.0324	24	0.0513	0.0074652	E
<input type="radio"/>	GO:0006626	9,8,7,6	<a href="#">protein targeting to mitochondrion</a>	52	0.0080	9	0.0192	0.0076825	E
<input type="radio"/>	GO:0007166	5	<a href="#">cell surface receptor linked signal transduction</a>	52	0.0080	9	0.0192	0.0076825	E
<input type="radio"/>	GO:0006275	8,7	<a href="#">regulation of DNA replication</a>	19	0.0029	5	0.0107	0.0079380	E
<input type="radio"/>	GO:0007047	5	<a href="#">cell wall organization and biogenesis</a>	200	0.0309	23	0.0491	0.0079828	E
<input type="radio"/>	GO:0045229	4	<a href="#">external encapsulating structure organization and biogenesis</a>	200	0.0309	23	0.0491	0.0079828	E
<input type="radio"/>	GO:0006368	9,7,8	<a href="#">RNA elongation from RNA polymerase II promoter</a>	53	0.0082	9	0.0192	0.0085927	E
<input type="radio"/>	GO:0006505	9,10	<a href="#">GPI anchor metabolic process</a>	27	0.0042	6	0.0128	0.0086144	E
<input type="radio"/>	GO:0000080	7,8,6	<a href="#">G1 phase of mitotic cell cycle</a>	27	0.0042	6	0.0128	0.0086144	E
<input type="radio"/>	GO:0051318	6,7,5	<a href="#">G1 phase</a>	27	0.0042	6	0.0128	0.0086144	E
<input type="radio"/>	GO:0016070	5	<a href="#">RNA metabolic process</a>	1058	0.1634	91	0.1944	0.0088346	E
<input type="radio"/>	GO:0009309	5,6	<a href="#">amine biosynthetic process</a>	114	0.0176	15	0.0321	0.0091485	E
<input type="radio"/>	GO:0050896	2	<a href="#">response to stimulus</a>	763	0.1178	68	0.1453	0.0096903	E
<input type="radio"/>	GO:0015833	4,5	<a href="#">peptide transport</a>	7	0.0011	3	0.0064	0.0097446	E
<input type="radio"/>	GO:0001402	5,4	<a href="#">signal transduction during filamentous growth</a>	7	0.0011	3	0.0064	0.0097446	E
<input type="radio"/>	GO:0006465	9,5	<a href="#">signal peptide processing</a>	7	0.0011	3	0.0064	0.0097446	E
<input type="radio"/>	GO:0006617	8,12,11,7,10,9	<a href="#">SRP-dependent cotranslational protein targeting to membrane, signal sequence recognition</a>	7	0.0011	3	0.0064	0.0097446	E
<input type="radio"/>	GO:0044271	5,4	<a href="#">nitrogen compound biosynthetic process</a>	115	0.0178	15	0.0321	0.0097717	E
<input type="radio"/>	GO:0019236	4	<a href="#">response to pheromone</a>	94	0.0145	13	0.0278	0.0098314	E

<input type="radio"/>	GO:0006334	6,7,10	<a href="#">nucleosome assembly</a>	13	0.0020	4	0.0085	0.0098609	E
<input type="radio"/>	GO:0045786	6,7,5	<a href="#">negative regulation of progression through cell cycle</a>	13	0.0020	4	0.0085	0.0098609	E
<input type="radio"/>	GO:0006401	6	<a href="#">RNA catabolic process</a>	74	0.0114	11	0.0235	0.0101362	E
<input type="radio"/>	GO:0007088	7,9,8,6	<a href="#">regulation of mitosis</a>	55	0.0085	9	0.0192	0.0106295	E
<input type="radio"/>	GO:0008652	6,7	<a href="#">amino acid biosynthetic process</a>	106	0.0164	14	0.0299	0.0109150	E
<input type="radio"/>	GO:0006839	7,5,6	<a href="#">mitochondrial transport</a>	65	0.0100	10	0.0214	0.0109846	E
<input type="radio"/>	GO:0043687	7	<a href="#">post-translational protein modification</a>	388	0.0599	38	0.0812	0.0111215	E
<input type="radio"/>	GO:0019953	3	<a href="#">sexual reproduction</a>	118	0.0182	15	0.0321	0.0118159	E
<input type="radio"/>	GO:0000747	4	<a href="#">conjugation with cellular fusion</a>	118	0.0182	15	0.0321	0.0118159	E
<input type="radio"/>	GO:0000746	3	<a href="#">conjugation</a>	118	0.0182	15	0.0321	0.0118159	E
<input type="radio"/>	GO:0008361	4,6,7	<a href="#">regulation of cell size</a>	129	0.0199	16	0.0342	0.0118542	E
<input type="radio"/>	GO:0006470	8,7	<a href="#">protein amino acid dephosphorylation</a>	29	0.0045	6	0.0128	0.0119140	E
<input type="radio"/>	GO:0009072	6,5,7	<a href="#">aromatic amino acid family metabolic process</a>	21	0.0032	5	0.0107	0.0119705	E
<input type="radio"/>	GO:0007105	6,4	<a href="#">cytokinesis, site selection</a>	66	0.0102	10	0.0214	0.0120213	E
<input type="radio"/>	GO:0030468	8,5,9	<a href="#">establishment of cell polarity (sensu Fungi)</a>	66	0.0102	10	0.0214	0.0120213	E
<input type="radio"/>	GO:0030467	7,4,8	<a href="#">establishment and/or maintenance of cell polarity (sensu Fungi)</a>	66	0.0102	10	0.0214	0.0120213	E
<input type="radio"/>	GO:0051028	5,7,6,8	<a href="#">mRNA transport</a>	66	0.0102	10	0.0214	0.0120213	E
<input type="radio"/>	GO:0006406	11,9,6,8,10,7	<a href="#">mRNA export from nucleus</a>	66	0.0102	10	0.0214	0.0120213	E
<input type="radio"/>	GO:0000282	7,9,5,6,10	<a href="#">cellular bud site selection</a>	66	0.0102	10	0.0214	0.0120213	E
<input type="radio"/>	GO:0006333	8	<a href="#">chromatin assembly or disassembly</a>	119	0.0184	15	0.0321	0.0125568	E
<input type="radio"/>	GO:0006272	9,8	<a href="#">leading strand elongation</a>	14	0.0022	4	0.0085	0.0128142	E
<input type="radio"/>	GO:0044267	5	<a href="#">cellular protein metabolic process</a>	1498	0.2313	122	0.2607	0.0132729	E
<input type="radio"/>	GO:0044260	4	<a href="#">cellular macromolecule metabolic process</a>	1552	0.2397	126	0.2692	0.0132778	E
<input type="radio"/>	GO:0046467	6,5,7	<a href="#">membrane lipid biosynthetic process</a>	78	0.0120	11	0.0235	0.0140260	E
<input type="radio"/>	GO:0007120	8,6,10,7,11,5	<a href="#">axial cellular bud site selection</a>	22	0.0034	5	0.0107	0.0143801	E
<input type="radio"/>	GO:0000370	8,9,7,10,11,12,13	<a href="#">U2-type nuclear mRNA branch site recognition</a>	3	0.0005	2	0.0043	0.0145109	E
<input type="radio"/>	GO:0007090	8,9,7,6	<a href="#">regulation of S phase of mitotic cell cycle</a>	3	0.0005	2	0.0043	0.0145109	E
<input type="radio"/>	GO:0017157	6,9,5,7,8	<a href="#">regulation of exocytosis</a>	3	0.0005	2	0.0043	0.0145109	E
<input type="radio"/>	GO:0015867	8,9	<a href="#">ATP transport</a>	3	0.0005	2	0.0043	0.0145109	E
<input type="radio"/>	GO:0051503	7,8	<a href="#">adenine nucleotide transport</a>	3	0.0005	2	0.0043	0.0145109	E
<input type="radio"/>	GO:0000117	10,9,6,5,7,8,4	<a href="#">G2/M-specific transcription in mitotic cell cycle</a>	3	0.0005	2	0.0043	0.0145109	E
<input type="radio"/>	GO:0045787	6,7,5	<a href="#">positive regulation of progression through cell cycle</a>	3	0.0005	2	0.0043	0.0145109	E
<input type="radio"/>	GO:0019538	4	<a href="#">protein metabolic process</a>	1547	0.2389	125	0.2671	0.0147550	E
<input type="radio"/>	GO:0040029	4	<a href="#">regulation of gene expression, epigenetic</a>	100	0.0154	13	0.0278	0.0148876	E
<input type="radio"/>	GO:0045892	9,8	<a href="#">negative regulation of transcription, DNA-dependent</a>	156	0.0241	18	0.0385	0.0150430	E
<input type="radio"/>	GO:0006405	10,8,5,7,9,6	<a href="#">RNA export from nucleus</a>	79	0.0122	11	0.0235	0.0151310	E
<input type="radio"/>	GO:0006807	3	<a href="#">nitrogen compound metabolic process</a>	251	0.0388	26	0.0556	0.0153421	E
<input type="radio"/>	GO:0000002	6	<a href="#">mitochondrial genome maintenance</a>	31	0.0048	6	0.0128	0.0159147	E
<input type="radio"/>	GO:0007154	3	<a href="#">cell communication</a>	240	0.0371	25	0.0534	0.0159498	E
<input type="radio"/>	GO:0018409	9	<a href="#">peptide or protein amino-terminal blocking</a>	15	0.0023	4	0.0085	0.0162192	E
<input type="radio"/>	GO:0031365	8	<a href="#">N-terminal protein amino acid modification</a>	15	0.0023	4	0.0085	0.0162192	E
<input type="radio"/>	GO:0051236	3,4,5	<a href="#">establishment of RNA localization</a>	80	0.0124	11	0.0235	0.0162899	E
<input type="radio"/>	GO:0050658	4,6,5,7	<a href="#">RNA transport</a>	80	0.0124	11	0.0235	0.0162899	E

<input type="checkbox"/>	GO:0050657	5,6	<a href="#">nucleic acid transport</a>	80	0.0124	11	0.0235	0.0162899	E
<input type="checkbox"/>	GO:0006281	6,5	<a href="#">DNA repair</a>	193	0.0298	21	0.0449	0.0164650	E
<input type="checkbox"/>	GO:0016192	4,5	<a href="#">vesicle-mediated transport</a>	328	0.0506	32	0.0684	0.0170148	E
<input type="checkbox"/>	GO:0007243	6	<a href="#">protein kinase cascade</a>	23	0.0036	5	0.0107	0.0170565	E
<input type="checkbox"/>	GO:0007020	8	<a href="#">microtubule nucleation</a>	23	0.0036	5	0.0107	0.0170565	E
<input type="checkbox"/>	GO:0006643	5,6	<a href="#">membrane lipid metabolic process</a>	125	0.0193	15	0.0321	0.0176444	E
<input type="checkbox"/>	GO:0042221	3	<a href="#">response to chemical stimulus</a>	382	0.0590	36	0.0769	0.0187843	E
<input type="checkbox"/>	GO:0007163	6,3,7	<a href="#">establishment and/or maintenance of cell polarity</a>	115	0.0178	14	0.0299	0.0188853	E
<input type="checkbox"/>	GO:0051300	5,4,6	<a href="#">spindle pole body organization and biogenesis</a>	16	0.0025	4	0.0085	0.0200726	E
<input type="checkbox"/>	GO:0031023	5	<a href="#">microtubule organizing center organization and biogenesis</a>	16	0.0025	4	0.0085	0.0200726	E
<input type="checkbox"/>	GO:0006493	9,8,7	<a href="#">protein amino acid O-linked glycosylation</a>	16	0.0025	4	0.0085	0.0200726	E
<input type="checkbox"/>	GO:0009073	7,6,8	<a href="#">aromatic amino acid family biosynthetic process</a>	16	0.0025	4	0.0085	0.0200726	E
<input type="checkbox"/>	GO:0015802	6,7,8	<a href="#">basic amino acid transport</a>	9	0.0014	3	0.0064	0.0201454	E
<input type="checkbox"/>	GO:0000819	7,4	<a href="#">sister chromatid segregation</a>	62	0.0096	9	0.0192	0.0201738	E
<input type="checkbox"/>	GO:0043543	7	<a href="#">protein amino acid acylation</a>	62	0.0096	9	0.0192	0.0201738	E
<input type="checkbox"/>	GO:0000082	8,5,6,7,4	<a href="#">G1/S transition of mitotic cell cycle</a>	52	0.0080	8	0.0171	0.0203773	E
<input type="checkbox"/>	GO:0006400	7,8	<a href="#">tRNA modification</a>	52	0.0080	8	0.0171	0.0203773	E
<input type="checkbox"/>	GO:0032200	7	<a href="#">telomere organization and biogenesis</a>	274	0.0423	27	0.0577	0.0217455	E
<input type="checkbox"/>	GO:0000723	8	<a href="#">telomere maintenance</a>	274	0.0423	27	0.0577	0.0217455	E
<input type="checkbox"/>	GO:0030384	8,9	<a href="#">phosphoinositide metabolic process</a>	43	0.0066	7	0.0150	0.0220529	E
<input type="checkbox"/>	GO:0000075	7,6	<a href="#">cell cycle checkpoint</a>	53	0.0082	8	0.0171	0.0222813	E
<input type="checkbox"/>	GO:0019954	3	<a href="#">asexual reproduction</a>	85	0.0131	11	0.0235	0.0228941	E
<input type="checkbox"/>	GO:0007114	5,4	<a href="#">cell budding</a>	85	0.0131	11	0.0235	0.0228941	E
<input type="checkbox"/>	GO:0006298	7,9,6	<a href="#">mismatch repair</a>	25	0.0039	5	0.0107	0.0232050	E
<input type="checkbox"/>	GO:0006609	10,11,8,9,7	<a href="#">mRNA-binding (hnRNP) protein import into nucleus</a>	25	0.0039	5	0.0107	0.0232050	E
<input type="checkbox"/>	GO:0045005	8,6	<a href="#">maintenance of fidelity during DNA-dependent DNA replication</a>	25	0.0039	5	0.0107	0.0232050	E
<input type="checkbox"/>	GO:0045859	7	<a href="#">regulation of protein kinase activity</a>	25	0.0039	5	0.0107	0.0232050	E
<input type="checkbox"/>	GO:0043549	6	<a href="#">regulation of kinase activity</a>	25	0.0039	5	0.0107	0.0232050	E
<input type="checkbox"/>	GO:0009968	6,5	<a href="#">negative regulation of signal transduction</a>	17	0.0026	4	0.0085	0.0243634	E
<input type="checkbox"/>	GO:0006325	7	<a href="#">establishment and/or maintenance of chromatin architecture</a>	253	0.0391	25	0.0534	0.0244868	E
<input type="checkbox"/>	GO:0006323	6	<a href="#">DNA packaging</a>	253	0.0391	25	0.0534	0.0244868	E
<input type="checkbox"/>	GO:0007005	5	<a href="#">mitochondrion organization and biogenesis</a>	110	0.0170	13	0.0278	0.0264636	E
<input type="checkbox"/>	GO:0006506	10,9,8,7,11	<a href="#">GPI anchor biosynthetic process</a>	26	0.0040	5	0.0107	0.0266680	E
<input type="checkbox"/>	GO:0010382	6,4	<a href="#">cell wall metabolic process</a>	26	0.0040	5	0.0107	0.0266680	E
<input type="checkbox"/>	GO:0051338	5	<a href="#">regulation of transferase activity</a>	26	0.0040	5	0.0107	0.0266680	E
<input type="checkbox"/>	GO:0030174	9,7,8	<a href="#">regulation of DNA replication initiation</a>	10	0.0015	3	0.0064	0.0267099	E
<input type="checkbox"/>	GO:0009373	9,8,5	<a href="#">regulation of transcription by pheromones</a>	10	0.0015	3	0.0064	0.0267099	E
<input type="checkbox"/>	GO:0046019	10,9,6	<a href="#">regulation of transcription from RNA polymerase II promoter by pheromones</a>	10	0.0015	3	0.0064	0.0267099	E
<input type="checkbox"/>	GO:0006592	8,9,6,5	<a href="#">ornithine biosynthetic process</a>	4	0.0006	2	0.0043	0.0269325	E
<input type="checkbox"/>	GO:0000135	9,8	<a href="#">septin checkpoint</a>	4	0.0006	2	0.0043	0.0269325	E
<input type="checkbox"/>	GO:0050000	6,5	<a href="#">chromosome localization</a>	4	0.0006	2	0.0043	0.0269325	E
<input type="checkbox"/>	GO:0032147	8,9	<a href="#">activation of protein kinase activity</a>	4	0.0006	2	0.0043	0.0269325	E
<input type="checkbox"/>	GO:0000301	9,7,6,8	<a href="#">retrograde transport, vesicle recycling within Golgi</a>	4	0.0006	2	0.0043	0.0269325	E

<input type="radio"/>	GO:0031565	8,7	<a href="#">cytokinesis checkpoint</a>	4	0.0006	2	0.0043	0.0269325	E
<input type="radio"/>	GO:0000348	7,8,6,10,12	<a href="#">nuclear mRNA branch site recognition</a>	4	0.0006	2	0.0043	0.0269325	E
<input type="radio"/>	GO:0009164	5,6	<a href="#">nucleoside catabolic process</a>	4	0.0006	2	0.0043	0.0269325	E
<input type="radio"/>	GO:0051301	3	<a href="#">cell division</a>	246	0.0380	24	0.0513	0.0288149	E
<input type="radio"/>	GO:0009116	5	<a href="#">nucleoside metabolic process</a>	18	0.0028	4	0.0085	0.0290741	E
<input type="radio"/>	GO:0019438	5	<a href="#">aromatic compound biosynthetic process</a>	18	0.0028	4	0.0085	0.0290741	E
<input type="radio"/>	GO:0006403	4	<a href="#">RNA localization</a>	90	0.0139	11	0.0235	0.0308042	E
<input type="radio"/>	GO:0051168	9,7,8	<a href="#">nuclear export</a>	102	0.0158	12	0.0256	0.0316625	E
<input type="radio"/>	GO:0006950	3	<a href="#">response to stress</a>	488	0.0754	42	0.0897	0.0330105	E
<input type="radio"/>	GO:0008654	7,6,8	<a href="#">phospholipid biosynthetic process</a>	58	0.0090	8	0.0171	0.0332283	E
<input type="radio"/>	GO:0030010	7,4,8	<a href="#">establishment of cell polarity</a>	103	0.0159	12	0.0256	0.0332740	E
<input type="radio"/>	GO:0032502	2	<a href="#">developmental process</a>	436	0.0673	38	0.0812	0.0339022	E
<input type="radio"/>	GO:0007109	7,6,5,4	<a href="#">cytokinesis, completion of separation</a>	11	0.0017	3	0.0064	0.0340849	E
<input type="radio"/>	GO:0006488	10,9,8	<a href="#">dolichol-linked oligosaccharide biosynthetic process</a>	11	0.0017	3	0.0064	0.0340849	E
<input type="radio"/>	GO:0006972	5	<a href="#">hyperosmotic response</a>	11	0.0017	3	0.0064	0.0340849	E
<input type="radio"/>	GO:0046489	9,8,10	<a href="#">phosphoinositide biosynthetic process</a>	28	0.0043	5	0.0107	0.0343286	E
<input type="radio"/>	GO:0000750	8,7,6	<a href="#">pheromone-dependent signal transduction during conjugation with cellular fusion</a>	28	0.0043	5	0.0107	0.0343286	E
<input type="radio"/>	GO:0032005	7,6	<a href="#">signal transduction during conjugation with cellular fusion</a>	28	0.0043	5	0.0107	0.0343286	E
<input type="radio"/>	GO:0009308	4	<a href="#">amine metabolic process</a>	228	0.0352	22	0.0470	0.0354368	E
<input type="radio"/>	GO:0000070	9,7,5,8,6,4	<a href="#">mitotic sister chromatid segregation</a>	59	0.0091	8	0.0171	0.0356854	E
<input type="radio"/>	GO:0006650	7,8	<a href="#">glycerophospholipid metabolic process</a>	60	0.0093	8	0.0171	0.0382238	E
<input type="radio"/>	GO:0000003	2	<a href="#">reproduction</a>	323	0.0499	29	0.0620	0.0385487	E
<input type="radio"/>	GO:0006338	9	<a href="#">chromatin remodeling</a>	155	0.0239	16	0.0342	0.0386389	E
<input type="radio"/>	GO:0046474	8,7,9	<a href="#">glycerophospholipid biosynthetic process</a>	39	0.0060	6	0.0128	0.0388816	E
<input type="radio"/>	GO:0006612	9,7,8	<a href="#">protein targeting to membrane</a>	39	0.0060	6	0.0128	0.0388816	E
<input type="radio"/>	GO:0000165	7	<a href="#">MAPKKK cascade</a>	20	0.0031	4	0.0085	0.0396561	E
<input type="radio"/>	GO:0051320	7,6,5	<a href="#">S phase</a>	20	0.0031	4	0.0085	0.0396561	E
<input type="radio"/>	GO:0051053	8,7	<a href="#">negative regulation of DNA metabolic process</a>	20	0.0031	4	0.0085	0.0396561	E
<input type="radio"/>	GO:0045814	5	<a href="#">negative regulation of gene expression, epigenetic</a>	95	0.0147	11	0.0235	0.0398784	E
<input type="radio"/>	GO:0031507	6,10	<a href="#">heterochromatin formation</a>	95	0.0147	11	0.0235	0.0398784	E
<input type="radio"/>	GO:0016458	5	<a href="#">gene silencing</a>	95	0.0147	11	0.0235	0.0398784	E
<input type="radio"/>	GO:0006342	10,6,7,11,9	<a href="#">chromatin silencing</a>	95	0.0147	11	0.0235	0.0398784	E
<input type="radio"/>	GO:0065008	3	<a href="#">regulation of biological quality</a>	260	0.0401	24	0.0513	0.0411622	E
<input type="radio"/>	GO:0006397	7	<a href="#">mRNA processing</a>	157	0.0242	16	0.0342	0.0413289	E
<input type="radio"/>	GO:0006974	4	<a href="#">response to DNA damage stimulus</a>	234	0.0361	22	0.0470	0.0413630	E
<input type="radio"/>	GO:0000076	11,9,8,10	<a href="#">DNA replication checkpoint</a>	5	0.0008	2	0.0043	0.0416555	E
<input type="radio"/>	GO:0007232	7,6	<a href="#">osmosensory signaling pathway via Sho1 osmosensor</a>	5	0.0008	2	0.0043	0.0416555	E
<input type="radio"/>	GO:0007329	11,10,7	<a href="#">positive regulation of transcription from RNA polymerase II promoter by pheromones</a>	5	0.0008	2	0.0043	0.0416555	E
<input type="radio"/>	GO:0009371	10,9,6	<a href="#">positive regulation of transcription by pheromones</a>	5	0.0008	2	0.0043	0.0416555	E
<input type="radio"/>	GO:0018377	9,8,7	<a href="#">protein myristoylation</a>	5	0.0008	2	0.0043	0.0416555	E
<input type="radio"/>	GO:0018319	10,9,8	<a href="#">protein amino acid myristoylation</a>	5	0.0008	2	0.0043	0.0416555	E
<input type="radio"/>	GO:0006499	10,11,9,8	<a href="#">N-terminal protein myristoylation</a>	5	0.0008	2	0.0043	0.0416555	E

<input type="checkbox"/>	GO:0015693	7,8	<a href="#">magnesium ion transport</a>	5	0.0008	2	0.0043	0.0416555	E
<input type="checkbox"/>	GO:0055075	9	<a href="#">potassium ion homeostasis</a>	5	0.0008	2	0.0043	0.0416555	E
<input type="checkbox"/>	GO:0016255	11,10,8,9,12	<a href="#">attachment of GPI anchor to protein</a>	5	0.0008	2	0.0043	0.0416555	E
<input type="checkbox"/>	GO:0006498	9,10,8,7	<a href="#">N-terminal protein lipidation</a>	5	0.0008	2	0.0043	0.0416555	E
<input type="checkbox"/>	GO:0030007	10,8	<a href="#">cellular potassium ion homeostasis</a>	5	0.0008	2	0.0043	0.0416555	E
<input type="checkbox"/>	GO:0006396	6	<a href="#">RNA processing</a>	491	0.0758	41	0.0876	0.0420575	E
<input type="checkbox"/>	GO:0000083	10,9,6,5,7,8,4	<a href="#">G1/S-specific transcription in mitotic cell cycle</a>	12	0.0019	3	0.0064	0.0421778	E
<input type="checkbox"/>	GO:0042278	6	<a href="#">purine nucleoside metabolic process</a>	12	0.0019	3	0.0064	0.0421778	E
<input type="checkbox"/>	GO:0006057	8,6	<a href="#">mannoprotein biosynthetic process</a>	12	0.0019	3	0.0064	0.0421778	E
<input type="checkbox"/>	GO:0031506	7,5,8,6	<a href="#">cell wall glycoprotein biosynthetic process</a>	12	0.0019	3	0.0064	0.0421778	E
<input type="checkbox"/>	GO:0000032	8,6,9,7	<a href="#">cell wall mannoprotein biosynthetic process</a>	12	0.0019	3	0.0064	0.0421778	E
<input type="checkbox"/>	GO:0006056	7	<a href="#">mannoprotein metabolic process</a>	12	0.0019	3	0.0064	0.0421778	E
<input type="checkbox"/>	GO:0046999	5,4	<a href="#">regulation of conjugation</a>	30	0.0046	5	0.0107	0.0428841	E
<input type="checkbox"/>	GO:0030466	11,7,8,12,10	<a href="#">chromatin silencing at silent mating-type cassette</a>	30	0.0046	5	0.0107	0.0428841	E
<input type="checkbox"/>	GO:0031137	6,5	<a href="#">regulation of conjugation with cellular fusion</a>	30	0.0046	5	0.0107	0.0428841	E
<input type="checkbox"/>	GO:0006644	6,7	<a href="#">phospholipid metabolic process</a>	97	0.0150	11	0.0235	0.0437835	E
<input type="checkbox"/>	GO:0007010	5	<a href="#">cytoskeleton organization and biogenesis</a>	227	0.0351	21	0.0449	0.0478019	E
<input type="checkbox"/>	GO:0048522	5,4	<a href="#">positive regulation of cellular process</a>	124	0.0191	13	0.0278	0.0484329	E
<input type="checkbox"/>	GO:0048518	4	<a href="#">positive regulation of biological process</a>	124	0.0191	13	0.0278	0.0484329	E
<input type="checkbox"/>	GO:0007242	5	<a href="#">intracellular signaling cascade</a>	137	0.0212	14	0.0299	0.0491193	E
<input type="checkbox"/>	GO:0006066	4	<a href="#">alcohol metabolic process</a>	163	0.0252	16	0.0342	0.0497117	E
<input type="checkbox"/>	GO:0001403	6,4,8,9	<a href="#">invasive growth (sensu Saccharomyces)</a>	42	0.0065	6	0.0128	0.0499960	E
<input type="checkbox"/>	GO:0009719	3	<a href="#">response to endogenous stimulus</a>	243	0.0375	22	0.0470	0.0506003	E
<input type="checkbox"/>	GO:0009082	7,8	<a href="#">branched chain family amino acid biosynthetic process</a>	13	0.0020	3	0.0064	0.0508867	E
<input type="checkbox"/>	GO:0000920	6,4	<a href="#">cell separation during cytokinesis</a>	13	0.0020	3	0.0064	0.0508867	E
<input type="checkbox"/>	GO:0007103	6,7,5,8	<a href="#">spindle pole body duplication in nuclear envelope</a>	13	0.0020	3	0.0064	0.0508867	E
<input type="checkbox"/>	GO:0015893	4,5	<a href="#">drug transport</a>	13	0.0020	3	0.0064	0.0508867	E
<input type="checkbox"/>	GO:0006970	4	<a href="#">response to osmotic stress</a>	89	0.0137	10	0.0214	0.0525040	E
<input type="checkbox"/>	GO:0022607	4	<a href="#">cellular component assembly</a>	471	0.0727	38	0.0812	0.0541690	E
<input type="checkbox"/>	GO:0009059	4	<a href="#">macromolecule biosynthetic process</a>	886	0.1368	65	0.1389	0.0548117	E
<input type="checkbox"/>	GO:0016310	6	<a href="#">phosphorylation</a>	155	0.0239	15	0.0321	0.0572115	E
<input type="checkbox"/>	GO:0006607	10,11,8,9,7	<a href="#">NLS-bearing substrate import into nucleus</a>	23	0.0036	4	0.0085	0.0579448	E
<input type="checkbox"/>	GO:0051030	5,7,6,8	<a href="#">snRNA transport</a>	23	0.0036	4	0.0085	0.0579448	E
<input type="checkbox"/>	GO:0006608	10,11,8,9,7	<a href="#">snRNP protein import into nucleus</a>	23	0.0036	4	0.0085	0.0579448	E
<input type="checkbox"/>	GO:0006610	10,11,8,9,7	<a href="#">ribosomal protein import into nucleus</a>	23	0.0036	4	0.0085	0.0579448	E
<input type="checkbox"/>	GO:0006408	11,9,6,8,10,7	<a href="#">snRNA export from nucleus</a>	23	0.0036	4	0.0085	0.0579448	E
<input type="checkbox"/>	GO:0006289	7,6	<a href="#">nucleotide-excision repair</a>	44	0.0068	6	0.0128	0.0579620	E
<input type="checkbox"/>	GO:0045996	10,9,6	<a href="#">negative regulation of transcription by pheromones</a>	6	0.0009	2	0.0043	0.0579836	E
<input type="checkbox"/>	GO:0046020	11,10,7	<a href="#">negative regulation of transcription from RNA polymerase II promoter by pheromones</a>	6	0.0009	2	0.0043	0.0579836	E
<input type="checkbox"/>	GO:0006591	7,8,5,4	<a href="#">ornithine metabolic process</a>	6	0.0009	2	0.0043	0.0579836	E
<input type="checkbox"/>	GO:0015695	6,7	<a href="#">organic cation transport</a>	6	0.0009	2	0.0043	0.0579836	E
<input type="checkbox"/>	GO:0008299	6,5,7	<a href="#">isoprenoid biosynthetic process</a>	6	0.0009	2	0.0043	0.0579836	E
<input type="checkbox"/>	GO:0015696	7,8	<a href="#">ammonium transport</a>	6	0.0009	2	0.0043	0.0579836	E



<input type="checkbox"/>	GO:0006720	5,6	<a href="#">isoprenoid metabolic process</a>	6	0.0009	2	0.0043	0.0579836	E
<input type="checkbox"/>	GO:0019795	7,8	<a href="#">nonprotein amino acid biosynthetic process</a>	6	0.0009	2	0.0043	0.0579836	E
<input type="checkbox"/>	GO:0032297	10,8,9	<a href="#">negative regulation of DNA replication initiation</a>	6	0.0009	2	0.0043	0.0579836	E
<input type="checkbox"/>	GO:0051347	6	<a href="#">positive regulation of transferase activity</a>	6	0.0009	2	0.0043	0.0579836	E
<input type="checkbox"/>	GO:0045860	7,8	<a href="#">positive regulation of protein kinase activity</a>	6	0.0009	2	0.0043	0.0579836	E
<input type="checkbox"/>	GO:0016568	8	<a href="#">chromatin modification</a>	223	0.0344	20	0.0427	0.0583214	E
<input type="checkbox"/>	GO:0009628	3	<a href="#">response to abiotic stimulus</a>	117	0.0181	12	0.0256	0.0589178	E
<input type="checkbox"/>	GO:0030474	5,6,4,7	<a href="#">spindle pole body duplication</a>	14	0.0022	3	0.0064	0.0601052	E
<input type="checkbox"/>	GO:0044249	4	<a href="#">cellular biosynthetic process</a>	366	0.0565	30	0.0641	0.0602588	E
<input type="checkbox"/>	GO:0007186	6	<a href="#">G-protein coupled receptor protein signaling pathway</a>	34	0.0053	5	0.0107	0.0621429	E
<input type="checkbox"/>	GO:0006869	4,5	<a href="#">lipid transport</a>	34	0.0053	5	0.0107	0.0621429	E
<input type="checkbox"/>	GO:0015674	6,7	<a href="#">di-, tri-valent inorganic cation transport</a>	34	0.0053	5	0.0107	0.0621429	E
<input type="checkbox"/>	GO:0000749	5	<a href="#">response to pheromone during conjugation with cellular fusion</a>	57	0.0088	7	0.0150	0.0638170	E
<input type="checkbox"/>	GO:0043623	7,6	<a href="#">cellular protein complex assembly</a>	69	0.0107	8	0.0171	0.0639197	E
<input type="checkbox"/>	GO:0007006	5,6	<a href="#">mitochondrial membrane organization and biogenesis</a>	24	0.0037	4	0.0085	0.0645339	E
<input type="checkbox"/>	GO:0007096	8,10,9,7	<a href="#">regulation of exit from mitosis</a>	24	0.0037	4	0.0085	0.0645339	E
<input type="checkbox"/>	GO:0030433	9,11,10,12	<a href="#">ER-associated protein catabolic process</a>	35	0.0054	5	0.0107	0.0672893	E
<input type="checkbox"/>	GO:0000754	8,7,5	<a href="#">adaptation to pheromone during conjugation with cellular fusion</a>	15	0.0023	3	0.0064	0.0697251	E
<input type="checkbox"/>	GO:0022401	7,6	<a href="#">adaptation of signaling pathway</a>	15	0.0023	3	0.0064	0.0697251	E
<input type="checkbox"/>	GO:0000114	10,8,9,5,7,4	<a href="#">G1-specific transcription in mitotic cell cycle</a>	15	0.0023	3	0.0064	0.0697251	E
<input type="checkbox"/>	GO:0043285	5	<a href="#">biopolymer catabolic process</a>	277	0.0428	23	0.0491	0.0698083	E
<input type="checkbox"/>	GO:0008033	7	<a href="#">tRNA processing</a>	84	0.0130	9	0.0192	0.0712758	E
<input type="checkbox"/>	GO:0006812	5,6	<a href="#">cation transport</a>	97	0.0150	10	0.0214	0.0715793	E
<input type="checkbox"/>	GO:0048280	7,6	<a href="#">vesicle fusion with Golgi apparatus</a>	1	0.0002	1	0.0021	0.0722668	E
<input type="checkbox"/>	GO:0015871	5,6	<a href="#">choline transport</a>	1	0.0002	1	0.0021	0.0722668	E
<input type="checkbox"/>	GO:0019346	8,9,7	<a href="#">transsulfuration</a>	1	0.0002	1	0.0021	0.0722668	E
<input type="checkbox"/>	GO:0045117	5,6	<a href="#">azole transport</a>	1	0.0002	1	0.0021	0.0722668	E
<input type="checkbox"/>	GO:0000115	10,9,8,5,7,4	<a href="#">S-phase-specific transcription in mitotic cell cycle</a>	1	0.0002	1	0.0021	0.0722668	E
<input type="checkbox"/>	GO:0019985	7,6	<a href="#">bypass DNA synthesis</a>	1	0.0002	1	0.0021	0.0722668	E
<input type="checkbox"/>	GO:0032377	7,8,6	<a href="#">regulation of intracellular lipid transport</a>	1	0.0002	1	0.0021	0.0722668	E
<input type="checkbox"/>	GO:0032365	7,5,6	<a href="#">intracellular lipid transport</a>	1	0.0002	1	0.0021	0.0722668	E
<input type="checkbox"/>	GO:0000273	6,5	<a href="#">lipoic acid metabolic process</a>	1	0.0002	1	0.0021	0.0722668	E
<input type="checkbox"/>	GO:0032979	8,7,6	<a href="#">protein insertion into mitochondrial membrane from inner side</a>	1	0.0002	1	0.0021	0.0722668	E
<input type="checkbox"/>	GO:0043171	5	<a href="#">peptide catabolic process</a>	1	0.0002	1	0.0021	0.0722668	E
<input type="checkbox"/>	GO:0009305	8	<a href="#">protein amino acid biotinylation</a>	1	0.0002	1	0.0021	0.0722668	E
<input type="checkbox"/>	GO:0019408	9,8,10	<a href="#">dolichol biosynthetic process</a>	1	0.0002	1	0.0021	0.0722668	E
<input type="checkbox"/>	GO:0000046	5,6	<a href="#">autophagic vacuole fusion</a>	1	0.0002	1	0.0021	0.0722668	E
<input type="checkbox"/>	GO:0030970	8,6,7	<a href="#">retrograde protein transport, ER to cytosol</a>	1	0.0002	1	0.0021	0.0722668	E
<input type="checkbox"/>	GO:0006655	9,8,10	<a href="#">phosphatidylglycerol biosynthetic process</a>	1	0.0002	1	0.0021	0.0722668	E
<input type="checkbox"/>	GO:0043007	7	<a href="#">maintenance of rDNA</a>	1	0.0002	1	0.0021	0.0722668	E
<input type="checkbox"/>	GO:0006152	6,7	<a href="#">purine nucleoside catabolic process</a>	1	0.0002	1	0.0021	0.0722668	E
<input type="checkbox"/>	GO:0046471	8,9	<a href="#">phosphatidylglycerol metabolic process</a>	1	0.0002	1	0.0021	0.0722668	E
<input type="checkbox"/>	GO:0015950	6	<a href="#">diadenosine polyphosphate metabolic</a>	1	0.0002	1	0.0021	0.0722668	E

<input type="radio"/>	GO:0013939	7	<a href="#">process</a>	1	0.0002	1	0.0021	0.0722668	E
<input type="radio"/>	GO:0000373	10	<a href="#">Group II intron splicing</a>	1	0.0002	1	0.0021	0.0722668	E
<input type="radio"/>	GO:0000185	9,10,8	<a href="#">activation of MAPKKK activity</a>	1	0.0002	1	0.0021	0.0722668	E
<input type="radio"/>	GO:0019348	8,9	<a href="#">dolichol metabolic process</a>	1	0.0002	1	0.0021	0.0722668	E
<input type="radio"/>	GO:0045490	8,7	<a href="#">pectin catabolic process</a>	1	0.0002	1	0.0021	0.0722668	E
<input type="radio"/>	GO:0018201	8	<a href="#">peptidyl-glycine modification</a>	1	0.0002	1	0.0021	0.0722668	E
<input type="radio"/>	GO:0015785	7,8	<a href="#">UDP-galactose transport</a>	1	0.0002	1	0.0021	0.0722668	E
<input type="radio"/>	GO:0043570	6	<a href="#">maintenance of DNA repeat elements</a>	1	0.0002	1	0.0021	0.0722668	E
<input type="radio"/>	GO:0000770	5,6	<a href="#">peptide pheromone export</a>	1	0.0002	1	0.0021	0.0722668	E
<input type="radio"/>	GO:0006570	7,6,8	<a href="#">tyrosine metabolic process</a>	1	0.0002	1	0.0021	0.0722668	E
<input type="radio"/>	GO:0043111	10,9	<a href="#">replication fork blocking</a>	1	0.0002	1	0.0021	0.0722668	E
<input type="radio"/>	GO:0018008	11,12,9,10	<a href="#">N-terminal peptidyl-glycine N-myristoylation</a>	1	0.0002	1	0.0021	0.0722668	E
<input type="radio"/>	GO:0045488	6,7	<a href="#">pectin metabolic process</a>	1	0.0002	1	0.0021	0.0722668	E
<input type="radio"/>	GO:0032978	7,6,5	<a href="#">protein insertion into membrane from inner side</a>	1	0.0002	1	0.0021	0.0722668	E
<input type="radio"/>	GO:0001408	7,8	<a href="#">guanine nucleotide transport</a>	1	0.0002	1	0.0021	0.0722668	E
<input type="radio"/>	GO:0043433	9,8	<a href="#">negative regulation of transcription factor activity</a>	1	0.0002	1	0.0021	0.0722668	E
<input type="radio"/>	GO:0045736	8,9,7,6	<a href="#">negative regulation of cyclin-dependent protein kinase activity</a>	1	0.0002	1	0.0021	0.0722668	E
<input type="radio"/>	GO:0015720	6,7	<a href="#">allantoin transport</a>	1	0.0002	1	0.0021	0.0722668	E
<input type="radio"/>	GO:0009105	7,6	<a href="#">lipoic acid biosynthetic process</a>	1	0.0002	1	0.0021	0.0722668	E
<input type="radio"/>	GO:0032368	6,5	<a href="#">regulation of lipid transport</a>	1	0.0002	1	0.0021	0.0722668	E
<input type="radio"/>	GO:0051090	8,7	<a href="#">regulation of transcription factor activity</a>	1	0.0002	1	0.0021	0.0722668	E
<input type="radio"/>	GO:0065003	5,4	<a href="#">macromolecular complex assembly</a>	328	0.0506	26	0.0556	0.0739427	E
<input type="radio"/>	GO:0031509	7,11	<a href="#">telomeric heterochromatin formation</a>	60	0.0093	7	0.0150	0.0745421	E
<input type="radio"/>	GO:0006725	4	<a href="#">aromatic compound metabolic process</a>	60	0.0093	7	0.0150	0.0745421	E
<input type="radio"/>	GO:0006348	11,7,8,12,10	<a href="#">chromatin silencing at telomere</a>	60	0.0093	7	0.0150	0.0745421	E
<input type="radio"/>	GO:0043633	7	<a href="#">modification-dependent RNA catabolic process</a>	7	0.0011	2	0.0043	0.0753303	E
<input type="radio"/>	GO:0006415	8,7,6	<a href="#">translational termination</a>	7	0.0011	2	0.0043	0.0753303	E
<input type="radio"/>	GO:0000289	11,9,10	<a href="#">poly(A) tail shortening</a>	7	0.0011	2	0.0043	0.0753303	E
<input type="radio"/>	GO:0043634	8	<a href="#">polyadenylation-dependent ncRNA catabolic process</a>	7	0.0011	2	0.0043	0.0753303	E
<input type="radio"/>	GO:0006469	7,8	<a href="#">negative regulation of protein kinase activity</a>	7	0.0011	2	0.0043	0.0753303	E
<input type="radio"/>	GO:0051348	6	<a href="#">negative regulation of transferase activity</a>	7	0.0011	2	0.0043	0.0753303	E
<input type="radio"/>	GO:0009966	5,4	<a href="#">regulation of signal transduction</a>	26	0.0040	4	0.0085	0.0782040	E
<input type="radio"/>	GO:0051029	5,7,6,8	<a href="#">rRNA transport</a>	26	0.0040	4	0.0085	0.0782040	E
<input type="radio"/>	GO:0006407	11,9,6,8,10,7	<a href="#">rRNA export from nucleus</a>	26	0.0040	4	0.0085	0.0782040	E
<input type="radio"/>	GO:0065004	6,5	<a href="#">protein-DNA complex assembly</a>	74	0.0114	8	0.0171	0.0793729	E
<input type="radio"/>	GO:0009081	6,7	<a href="#">branched chain family amino acid metabolic process</a>	16	0.0025	3	0.0064	0.0796394	E
<input type="radio"/>	GO:0030001	6,7	<a href="#">metal ion transport</a>	62	0.0096	7	0.0150	0.0817705	E
<input type="radio"/>	GO:0006811	4,5	<a href="#">ion transport</a>	115	0.0178	11	0.0235	0.0820149	E
<input type="radio"/>	GO:0006520	5,6	<a href="#">amino acid metabolic process</a>	187	0.0289	16	0.0342	0.0829393	E
<input type="radio"/>	GO:0006519	4	<a href="#">amino acid and derivative metabolic process</a>	202	0.0312	17	0.0363	0.0830611	E
<input type="radio"/>	GO:0016485	8	<a href="#">protein processing</a>	38	0.0059	5	0.0107	0.0831765	E
<input type="radio"/>	GO:0006515	8,9	<a href="#">misfolded or incompletely synthesized protein catabolic process</a>	38	0.0059	5	0.0107	0.0831765	E

<input type="radio"/>	GO:0015837	4,5	<a href="#">amine transport</a>	50	0.0077	6	0.0128	0.0834125	E
<input type="radio"/>	GO:0007093	8,10,9,7	<a href="#">mitotic cell cycle checkpoint</a>	27	0.0042	4	0.0085	0.0852005	E
<input type="radio"/>	GO:0000122	10,9	<a href="#">negative regulation of transcription from RNA polymerase II promoter</a>	63	0.0097	7	0.0150	0.0853800	E
<input type="radio"/>	GO:0046483	4	<a href="#">heterocycle metabolic process</a>	76	0.0117	8	0.0171	0.0855444	E
<input type="radio"/>	GO:0000377	9	<a href="#">RNA splicing, via transesterification reactions with bulged adenosine as nucleophile</a>	103	0.0159	10	0.0214	0.0858530	E
<input type="radio"/>	GO:0008380	7	<a href="#">RNA splicing</a>	132	0.0204	12	0.0256	0.0877600	E
<input type="radio"/>	GO:0019752	5	<a href="#">carboxylic acid metabolic process</a>	314	0.0485	23	0.0491	0.0880812	E
<input type="radio"/>	GO:0006082	4	<a href="#">organic acid metabolic process</a>	314	0.0485	23	0.0491	0.0880812	E
<input type="radio"/>	GO:0006865	5,6,7	<a href="#">amino acid transport</a>	39	0.0060	5	0.0107	0.0885469	E
<input type="radio"/>	GO:0006045	8,9	<a href="#">N-acetylglucosamine biosynthetic process</a>	17	0.0026	3	0.0064	0.0897440	E
<input type="radio"/>	GO:0006042	7,8	<a href="#">glucosamine biosynthetic process</a>	17	0.0026	3	0.0064	0.0897440	E
<input type="radio"/>	GO:0045132	9,7,8,6,4	<a href="#">meiotic chromosome segregation</a>	17	0.0026	3	0.0064	0.0897440	E
<input type="radio"/>	GO:0019740	4	<a href="#">nitrogen utilization</a>	17	0.0026	3	0.0064	0.0897440	E
<input type="radio"/>	GO:0046349	6,7	<a href="#">amino sugar biosynthetic process</a>	17	0.0026	3	0.0064	0.0897440	E
<input type="radio"/>	GO:0007126	8,6,7,5	<a href="#">meiosis</a>	148	0.0229	13	0.0278	0.0901857	E
<input type="radio"/>	GO:0051327	7,5,6	<a href="#">M phase of meiotic cell cycle</a>	148	0.0229	13	0.0278	0.0901857	E
<input type="radio"/>	GO:0051321	4	<a href="#">meiotic cell cycle</a>	148	0.0229	13	0.0278	0.0901857	E
<input type="radio"/>	GO:0000335	10,9,6	<a href="#">negative regulation of DNA transposition</a>	8	0.0012	2	0.0043	0.0932050	E
<input type="radio"/>	GO:0018345	9,8,7	<a href="#">protein palmitoylation</a>	8	0.0012	2	0.0043	0.0932050	E
<input type="radio"/>	GO:0015940	7,8	<a href="#">pantothenate biosynthetic process</a>	8	0.0012	2	0.0043	0.0932050	E
<input type="radio"/>	GO:0015939	7	<a href="#">pantothenate metabolic process</a>	8	0.0012	2	0.0043	0.0932050	E
<input type="radio"/>	GO:0008156	9,8	<a href="#">negative regulation of DNA replication</a>	8	0.0012	2	0.0043	0.0932050	E
<input type="radio"/>	GO:0018318	10,9,8	<a href="#">protein amino acid palmitoylation</a>	8	0.0012	2	0.0043	0.0932050	E
<input type="radio"/>	GO:0000903	6,4,8,7,9	<a href="#">cellular morphogenesis during vegetative growth</a>	8	0.0012	2	0.0043	0.0932050	E
<input type="radio"/>	GO:0016973	12,10,7,9,11,8	<a href="#">poly(A)+ mRNA export from nucleus</a>	8	0.0012	2	0.0043	0.0932050	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	0.0214	0.0970449	E
<input type="radio"/>	GO:0051186	4	<a href="#">cofactor metabolic process</a>	170	0.0263	14	0.0299	0.0988908	E
<input type="radio"/>	GO:0006999	6	<a href="#">nuclear pore organization and biogenesis</a>	29	0.0045	4	0.0085	0.0993082	E
<input type="radio"/>	GO:0006409	11,9,6,8,10,7	<a href="#">tRNA export from nucleus</a>	29	0.0045	4	0.0085	0.0993082	E
<input type="radio"/>	GO:0042401	6,7	<a href="#">biogenic amine biosynthetic process</a>	18	0.0028	3	0.0064	0.0999397	E
<input type="radio"/>	GO:0000084	8,7,6	<a href="#">S phase of mitotic cell cycle</a>	18	0.0028	3	0.0064	0.0999397	E
<input type="radio"/>	GO:0046942	5,6	<a href="#">carboxylic acid transport</a>	54	0.0083	6	0.0128	0.1005822	E
<input type="radio"/>	GO:0000375	8	<a href="#">RNA splicing, via transesterification reactions</a>	110	0.0170	10	0.0214	0.1012325	E
<input type="radio"/>	GO:0015849	4,5	<a href="#">organic acid transport</a>	55	0.0085	6	0.0128	0.1047765	E
<input type="radio"/>	GO:0007131	10,8,7,5,9,6,4	<a href="#">meiotic recombination</a>	55	0.0085	6	0.0128	0.1047765	E
<input type="radio"/>	GO:0006665	6,7	<a href="#">sphingolipid metabolic process</a>	30	0.0046	4	0.0085	0.1063394	E
<input type="radio"/>	GO:0051031	5,7,6,8	<a href="#">tRNA transport</a>	30	0.0046	4	0.0085	0.1063394	E
<input type="radio"/>	GO:0006611	9,10,7,8	<a href="#">protein export from nucleus</a>	56	0.0086	6	0.0128	0.1089062	E
<input type="radio"/>	GO:0006040	5,6	<a href="#">amino sugar metabolic process</a>	19	0.0029	3	0.0064	0.1101331	E
<input type="radio"/>	GO:0009228	7,8	<a href="#">thiamin biosynthetic process</a>	19	0.0029	3	0.0064	0.1101331	E
<input type="radio"/>	GO:0046148	5	<a href="#">pigment biosynthetic process</a>	19	0.0029	3	0.0064	0.1101331	E
<input type="radio"/>	GO:0006041	6,7	<a href="#">glucosamine metabolic process</a>	19	0.0029	3	0.0064	0.1101331	E
<input type="radio"/>	GO:0006044	7,8	<a href="#">N-acetylglucosamine metabolic process</a>	19	0.0029	3	0.0064	0.1101331	E

<input type="radio"/>	GO:0000245	7,6,9,11	<a href="#">spliceosome assembly</a>	19	0.0029	3	0.0064	0.1101331	E
<input type="radio"/>	GO:0016044	4	<a href="#">membrane organization and biogenesis</a>	188	0.0290	14	0.0299	0.1110749	E
<input type="radio"/>	GO:0000921	8,7	<a href="#">septin ring assembly</a>	9	0.0014	2	0.0043	0.1112013	E
<input type="radio"/>	GO:0032185	6	<a href="#">septin cytoskeleton organization and biogenesis</a>	9	0.0014	2	0.0043	0.1112013	E
<input type="radio"/>	GO:0000128	3	<a href="#">flocculation</a>	9	0.0014	2	0.0043	0.1112013	E
<input type="radio"/>	GO:0006280	6	<a href="#">mutagenesis</a>	9	0.0014	2	0.0043	0.1112013	E
<input type="radio"/>	GO:0031106	7	<a href="#">septin ring organization</a>	9	0.0014	2	0.0043	0.1112013	E
<input type="radio"/>	GO:0006474	10,9	<a href="#">N-terminal protein amino acid acetylation</a>	9	0.0014	2	0.0043	0.1112013	E
<input type="radio"/>	GO:0042138	11,9,8,5,6,10,7,4	<a href="#">meiotic DNA double-strand break formation</a>	9	0.0014	2	0.0043	0.1112013	E
<input type="radio"/>	GO:0007076	10,8,5,6,9,7,4	<a href="#">mitotic chromosome condensation</a>	9	0.0014	2	0.0043	0.1112013	E
<input type="radio"/>	GO:0006345	10,6,9	<a href="#">loss of chromatin silencing</a>	9	0.0014	2	0.0043	0.1112013	E
<input type="radio"/>	GO:0046685	5	<a href="#">response to arsenic</a>	9	0.0014	2	0.0043	0.1112013	E
<input type="radio"/>	GO:0051180	4,5	<a href="#">vitamin transport</a>	9	0.0014	2	0.0043	0.1112013	E
<input type="radio"/>	GO:0006283	8,7	<a href="#">transcription-coupled nucleotide-excision repair</a>	9	0.0014	2	0.0043	0.1112013	E
<input type="radio"/>	GO:0019794	6,7	<a href="#">nonprotein amino acid metabolic process</a>	9	0.0014	2	0.0043	0.1112013	E
<input type="radio"/>	GO:0045815	5	<a href="#">positive regulation of gene expression, epigenetic</a>	9	0.0014	2	0.0043	0.1112013	E
<input type="radio"/>	GO:0000501	4	<a href="#">flocculation via cell wall protein-carbohydrate interaction</a>	9	0.0014	2	0.0043	0.1112013	E
<input type="radio"/>	GO:0009893	5,4	<a href="#">positive regulation of metabolic process</a>	116	0.0179	10	0.0214	0.1124804	E
<input type="radio"/>	GO:0006461	6,5	<a href="#">protein complex assembly</a>	116	0.0179	10	0.0214	0.1124804	E
<input type="radio"/>	GO:0031325	6,5	<a href="#">positive regulation of cellular metabolic process</a>	116	0.0179	10	0.0214	0.1124804	E
<input type="radio"/>	GO:0006997	5	<a href="#">nuclear organization and biogenesis</a>	57	0.0088	6	0.0128	0.1129595	E
<input type="radio"/>	GO:0006887	8,6,5,7	<a href="#">exocytosis</a>	44	0.0068	5	0.0107	0.1149803	E
<input type="radio"/>	GO:0031505	6	<a href="#">chitin- and beta-glucan-containing cell wall organization and biogenesis</a>	44	0.0068	5	0.0107	0.1149803	E
<input type="radio"/>	GO:0000398	8,10	<a href="#">nuclear mRNA splicing, via spliceosome</a>	102	0.0158	9	0.0192	0.1157492	E
<input type="radio"/>	GO:0050790	4	<a href="#">regulation of catalytic activity</a>	45	0.0069	5	0.0107	0.1200415	E
<input type="radio"/>	GO:0006399	6	<a href="#">tRNA metabolic process</a>	121	0.0187	10	0.0214	0.1200510	E
<input type="radio"/>	GO:0042493	4	<a href="#">response to drug</a>	121	0.0187	10	0.0214	0.1200510	E
<input type="radio"/>	GO:0006271	8,7	<a href="#">DNA strand elongation during DNA replication</a>	32	0.0049	4	0.0085	0.1201687	E
<input type="radio"/>	GO:0022616	6	<a href="#">DNA strand elongation</a>	32	0.0049	4	0.0085	0.1201687	E
<input type="radio"/>	GO:0006772	7	<a href="#">thiamin metabolic process</a>	20	0.0031	3	0.0064	0.1202375	E
<input type="radio"/>	GO:0030148	7,6,8	<a href="#">sphingolipid biosynthetic process</a>	20	0.0031	3	0.0064	0.1202375	E
<input type="radio"/>	GO:0042398	6,5	<a href="#">amino acid derivative biosynthetic process</a>	20	0.0031	3	0.0064	0.1202375	E
<input type="radio"/>	GO:0042440	4	<a href="#">pigment metabolic process</a>	20	0.0031	3	0.0064	0.1202375	E
<input type="radio"/>	GO:0042724	7	<a href="#">thiamin and derivative biosynthetic process</a>	20	0.0031	3	0.0064	0.1202375	E
<input type="radio"/>	GO:0006310	6	<a href="#">DNA recombination</a>	122	0.0188	10	0.0214	0.1213454	E
<input type="radio"/>	GO:0065009	3	<a href="#">regulation of a molecular function</a>	46	0.0071	5	0.0107	0.1249843	E
<input type="radio"/>	GO:0007127	9,7,6,8,5	<a href="#">meiosis I</a>	75	0.0116	7	0.0150	0.1250303	E
<input type="radio"/>	GO:0009272	7	<a href="#">chitin- and beta-glucan-containing cell wall biogenesis</a>	33	0.0051	4	0.0085	0.1268974	E
<input type="radio"/>	GO:0006270	8,6	<a href="#">DNA replication initiation</a>	33	0.0051	4	0.0085	0.1268974	E
<input type="radio"/>	GO:0042546	6	<a href="#">cell wall biogenesis</a>	33	0.0051	4	0.0085	0.1268974	E
<input type="radio"/>	GO:0042430	5	<a href="#">indole and derivative metabolic process</a>	10	0.0015	2	0.0043	0.1289854	E
<input type="radio"/>	GO:0009096	8,7,9	<a href="#">aromatic amino acid family biosynthetic process, anthranilate pathway</a>	10	0.0015	2	0.0043	0.1289854	E
<input type="radio"/>	GO:0006817	7,8	<a href="#">phosphate transport</a>	10	0.0015	2	0.0043	0.1289854	E

<input type="radio"/>	GO:0006313	7,4	<a href="#">transposition, DNA-mediated</a>	10	0.0015	2	0.0043	0.1289854	E
<input type="radio"/>	GO:0055069	9	<a href="#">zinc ion homeostasis</a>	10	0.0015	2	0.0043	0.1289854	E
<input type="radio"/>	GO:0006882	10,8	<a href="#">cellular zinc ion homeostasis</a>	10	0.0015	2	0.0043	0.1289854	E
<input type="radio"/>	GO:0042434	6	<a href="#">indole derivative metabolic process</a>	10	0.0015	2	0.0043	0.1289854	E
<input type="radio"/>	GO:0042435	7,5	<a href="#">indole derivative biosynthetic process</a>	10	0.0015	2	0.0043	0.1289854	E
<input type="radio"/>	GO:0000337	9,8,5	<a href="#">regulation of DNA transposition</a>	10	0.0015	2	0.0043	0.1289854	E
<input type="radio"/>	GO:0006586	6,7	<a href="#">indolalkylamine metabolic process</a>	10	0.0015	2	0.0043	0.1289854	E
<input type="radio"/>	GO:0006526	8,9,6,5	<a href="#">arginine biosynthetic process</a>	10	0.0015	2	0.0043	0.1289854	E
<input type="radio"/>	GO:0000162	9,8,7,10	<a href="#">tryptophan biosynthetic process</a>	10	0.0015	2	0.0043	0.1289854	E
<input type="radio"/>	GO:0046219	7,8,6	<a href="#">indolalkylamine biosynthetic process</a>	10	0.0015	2	0.0043	0.1289854	E
<input type="radio"/>	GO:0006568	7,8,6	<a href="#">tryptophan metabolic process</a>	10	0.0015	2	0.0043	0.1289854	E
<input type="radio"/>	GO:0006732	5	<a href="#">coenzyme metabolic process</a>	136	0.0210	10	0.0214	0.1311668	E
<input type="radio"/>	GO:0045893	9,8	<a href="#">positive regulation of transcription, DNA-dependent</a>	95	0.0147	8	0.0171	0.1333908	E
<input type="radio"/>	GO:0045016	8,6,7,9	<a href="#">mitochondrial magnesium ion transport</a>	2	0.0003	1	0.0021	0.1341094	E
<input type="radio"/>	GO:0006533	8,9	<a href="#">aspartate catabolic process</a>	2	0.0003	1	0.0021	0.1341094	E
<input type="radio"/>	GO:0019266	9,10,7,8	<a href="#">asparagine biosynthetic process from oxaloacetate</a>	2	0.0003	1	0.0021	0.1341094	E
<input type="radio"/>	GO:0010032	7	<a href="#">meiotic chromosome condensation</a>	2	0.0003	1	0.0021	0.1341094	E
<input type="radio"/>	GO:0009895	6,5	<a href="#">negative regulation of catabolic process</a>	2	0.0003	1	0.0021	0.1341094	E
<input type="radio"/>	GO:0009847	5	<a href="#">spore germination</a>	2	0.0003	1	0.0021	0.1341094	E
<input type="radio"/>	GO:0042990	9,8,11,12,10,7	<a href="#">regulation of transcription factor import into nucleus</a>	2	0.0003	1	0.0021	0.1341094	E
<input type="radio"/>	GO:0033260	8,7,6	<a href="#">DNA replication during S phase</a>	2	0.0003	1	0.0021	0.1341094	E
<input type="radio"/>	GO:0042992	9,10,12,13,11,8	<a href="#">negative regulation of transcription factor import into nucleus</a>	2	0.0003	1	0.0021	0.1341094	E
<input type="radio"/>	GO:0006531	7,8	<a href="#">aspartate metabolic process</a>	2	0.0003	1	0.0021	0.1341094	E
<input type="radio"/>	GO:0018279	10,9,8	<a href="#">protein amino acid N-linked glycosylation via asparagine</a>	2	0.0003	1	0.0021	0.1341094	E
<input type="radio"/>	GO:0018195	8	<a href="#">peptidyl-arginine modification</a>	2	0.0003	1	0.0021	0.1341094	E
<input type="radio"/>	GO:0008215	7,8	<a href="#">spermine metabolic process</a>	2	0.0003	1	0.0021	0.1341094	E
<input type="radio"/>	GO:0018196	8	<a href="#">peptidyl-asparagine modification</a>	2	0.0003	1	0.0021	0.1341094	E
<input type="radio"/>	GO:0006597	8,9	<a href="#">spermine biosynthetic process</a>	2	0.0003	1	0.0021	0.1341094	E
<input type="radio"/>	GO:0000078	9,11,10,8,6,7	<a href="#">cell morphogenesis checkpoint</a>	2	0.0003	1	0.0021	0.1341094	E
<input type="radio"/>	GO:0032465	6,5	<a href="#">regulation of cytokinesis</a>	2	0.0003	1	0.0021	0.1341094	E
<input type="radio"/>	GO:0043649	6,7	<a href="#">dicarboxylic acid catabolic process</a>	2	0.0003	1	0.0021	0.1341094	E
<input type="radio"/>	GO:0042177	7,8,6	<a href="#">negative regulation of protein catabolic process</a>	2	0.0003	1	0.0021	0.1341094	E
<input type="radio"/>	GO:0030969	8,6,7	<a href="#">UFP-specific transcription factor mRNA processing during unfolded protein response</a>	2	0.0003	1	0.0021	0.1341094	E
<input type="radio"/>	GO:0046823	7,10,6,8,9	<a href="#">negative regulation of nucleocytoplasmic transport</a>	2	0.0003	1	0.0021	0.1341094	E
<input type="radio"/>	GO:0006666	5,8,9	<a href="#">3-keto-sphinganine metabolic process</a>	2	0.0003	1	0.0021	0.1341094	E
<input type="radio"/>	GO:0006532	8,9	<a href="#">aspartate biosynthetic process</a>	2	0.0003	1	0.0021	0.1341094	E
<input type="radio"/>	GO:0051666	5,4	<a href="#">actin cortical patch localization</a>	2	0.0003	1	0.0021	0.1341094	E
<input type="radio"/>	GO:0006282	8,7,6	<a href="#">regulation of DNA repair</a>	2	0.0003	1	0.0021	0.1341094	E
<input type="radio"/>	GO:0042308	8,9,11,12,10,7	<a href="#">negative regulation of protein import into nucleus</a>	2	0.0003	1	0.0021	0.1341094	E
<input type="radio"/>	GO:0031055	10	<a href="#">chromatin remodeling at centromere</a>	2	0.0003	1	0.0021	0.1341094	E
<input type="radio"/>	GO:0043409	7,9,6	<a href="#">negative regulation of MAPKKK cascade</a>	2	0.0003	1	0.0021	0.1341094	E
<input type="radio"/>	GO:0015781	6,7	<a href="#">pyrimidine nucleotide-sugar transport</a>	2	0.0003	1	0.0021	0.1341094	E

<input type="radio"/>	GO:0045740	9,8	<a href="#">positive regulation of DNA replication</a>	2	0.0003	1	0.0021	0.1341094	E
<input type="radio"/>	GO:0033262	8,9,7	<a href="#">regulation of DNA replication during S phase</a>	2	0.0003	1	0.0021	0.1341094	E
<input type="radio"/>	GO:0006107	7	<a href="#">oxaloacetate metabolic process</a>	2	0.0003	1	0.0021	0.1341094	E
<input type="radio"/>	GO:0000168	10,11,8,9,7	<a href="#">activation of MAPKK activity during osmolarity sensing</a>	2	0.0003	1	0.0021	0.1341094	E
<input type="radio"/>	GO:0042991	10,11,8,9,7	<a href="#">transcription factor import into nucleus</a>	2	0.0003	1	0.0021	0.1341094	E
<input type="radio"/>	GO:0006047	8,6,9	<a href="#">UDP-N-acetylglucosamine metabolic process</a>	2	0.0003	1	0.0021	0.1341094	E
<input type="radio"/>	GO:0006048	9,7,10	<a href="#">UDP-N-acetylglucosamine biosynthetic process</a>	2	0.0003	1	0.0021	0.1341094	E
<input type="radio"/>	GO:0006473	8	<a href="#">protein amino acid acetylation</a>	48	0.0074	5	0.0107	0.1344503	E
<input type="radio"/>	GO:0043161	10,9,11	<a href="#">proteasomal ubiquitin-dependent protein catabolic process</a>	63	0.0097	6	0.0128	0.1350828	E
<input type="radio"/>	GO:0051188	5	<a href="#">cofactor biosynthetic process</a>	79	0.0122	7	0.0150	0.1354023	E
<input type="radio"/>	GO:0007117	6,5,4	<a href="#">budding cell bud growth</a>	35	0.0054	4	0.0085	0.1398275	E
<input type="radio"/>	GO:0048590	3	<a href="#">non-developmental growth</a>	35	0.0054	4	0.0085	0.1398275	E
<input type="radio"/>	GO:0048284	5	<a href="#">organelle fusion</a>	22	0.0034	3	0.0064	0.1398693	E
<input type="radio"/>	GO:0042723	6	<a href="#">thiamin and derivative metabolic process</a>	22	0.0034	3	0.0064	0.1398693	E
<input type="radio"/>	GO:0045941	8,7	<a href="#">positive regulation of transcription</a>	101	0.0156	8	0.0171	0.1415411	E
<input type="radio"/>	GO:0006457	6	<a href="#">protein folding</a>	84	0.0130	7	0.0150	0.1455416	E
<input type="radio"/>	GO:0051252	7,6	<a href="#">regulation of RNA metabolic process</a>	36	0.0056	4	0.0085	0.1459738	E
<input type="radio"/>	GO:0043086	5	<a href="#">negative regulation of enzyme activity</a>	11	0.0017	2	0.0043	0.1462872	E
<input type="radio"/>	GO:0007050	7,8,6	<a href="#">cell cycle arrest</a>	11	0.0017	2	0.0043	0.1462872	E
<input type="radio"/>	GO:0043085	5	<a href="#">positive regulation of enzyme activity</a>	11	0.0017	2	0.0043	0.1462872	E
<input type="radio"/>	GO:0031163	5	<a href="#">metallo-sulfur cluster assembly</a>	11	0.0017	2	0.0043	0.1462872	E
<input type="radio"/>	GO:0016226	6	<a href="#">iron-sulfur cluster assembly</a>	11	0.0017	2	0.0043	0.1462872	E
<input type="radio"/>	GO:0030261	6	<a href="#">chromosome condensation</a>	11	0.0017	2	0.0043	0.1462872	E
<input type="radio"/>	GO:0000161	7,8,6	<a href="#">MAPKKK cascade during osmolarity sensing</a>	11	0.0017	2	0.0043	0.1462872	E
<input type="radio"/>	GO:0046128	7	<a href="#">purine ribonucleoside metabolic process</a>	11	0.0017	2	0.0043	0.1462872	E
<input type="radio"/>	GO:0019748	3	<a href="#">secondary metabolic process</a>	23	0.0036	3	0.0064	0.1492607	E
<input type="radio"/>	GO:0006979	4	<a href="#">response to oxidative stress</a>	71	0.0110	6	0.0128	0.1565028	E
<input type="radio"/>	GO:0006576	5,6	<a href="#">biogenic amine metabolic process</a>	24	0.0037	3	0.0064	0.1582915	E
<input type="radio"/>	GO:0000288	10,8,9	<a href="#">mRNA catabolic process, deadenylation-dependent decay</a>	24	0.0037	3	0.0064	0.1582915	E
<input type="radio"/>	GO:0051278	8,7	<a href="#">chitin- and beta-glucan-containing cell wall polysaccharide biosynthetic process</a>	24	0.0037	3	0.0064	0.1582915	E
<input type="radio"/>	GO:0001302	5	<a href="#">replicative cell aging</a>	39	0.0060	4	0.0085	0.1628630	E
<input type="radio"/>	GO:0045910	9,8	<a href="#">negative regulation of DNA recombination</a>	12	0.0019	2	0.0043	0.1628913	E
<input type="radio"/>	GO:0007007	6,7	<a href="#">inner mitochondrial membrane organization and biogenesis</a>	12	0.0019	2	0.0043	0.1628913	E
<input type="radio"/>	GO:0015914	5,6	<a href="#">phospholipid transport</a>	12	0.0019	2	0.0043	0.1628913	E
<input type="radio"/>	GO:0006284	7,6	<a href="#">base-excision repair</a>	12	0.0019	2	0.0043	0.1628913	E
<input type="radio"/>	GO:0009607	3	<a href="#">response to biotic stimulus</a>	25	0.0039	3	0.0064	0.1669129	E
<input type="radio"/>	GO:0000226	7	<a href="#">microtubule cytoskeleton organization and biogenesis</a>	81	0.0125	6	0.0128	0.1676558	E
<input type="radio"/>	GO:0006302	7,6	<a href="#">double-strand break repair</a>	57	0.0088	5	0.0107	0.1676939	E
<input type="radio"/>	GO:0006379	8	<a href="#">mRNA cleavage</a>	26	0.0040	3	0.0064	0.1750834	E
<input type="radio"/>	GO:0007264	6	<a href="#">small GTPase mediated signal transduction</a>	61	0.0094	5	0.0107	0.1765939	E
<input type="radio"/>	GO:0033014	6	<a href="#">tetrapyrrole biosynthetic process</a>	13	0.0020	2	0.0043	0.1786297	E
<input type="radio"/>	GO:0006783	7,6,8	<a href="#">heme biosynthetic process</a>	13	0.0020	2	0.0043	0.1786297	E

<input type="checkbox"/>	GO:0009119	6	<a href="#">ribonucleoside metabolic process</a>	13	0.0020	2	0.0043	0.1786297	E
<input type="checkbox"/>	GO:0006779	6,7	<a href="#">porphyrin biosynthetic process</a>	13	0.0020	2	0.0043	0.1786297	E
<input type="checkbox"/>	GO:0006038	9,10,7,8,11	<a href="#">cell wall chitin biosynthetic process</a>	13	0.0020	2	0.0043	0.1786297	E
<input type="checkbox"/>	GO:0055066	8	<a href="#">di-, tri-valent inorganic cation homeostasis</a>	64	0.0099	5	0.0107	0.1807657	E
<input type="checkbox"/>	GO:0030005	9,7	<a href="#">cellular di-, tri-valent inorganic cation homeostasis</a>	64	0.0099	5	0.0107	0.1807657	E
<input type="checkbox"/>	GO:0005976	5	<a href="#">polysaccharide metabolic process</a>	65	0.0100	5	0.0107	0.1816889	E
<input type="checkbox"/>	GO:0044264	5,6	<a href="#">cellular polysaccharide metabolic process</a>	65	0.0100	5	0.0107	0.1816889	E
<input type="checkbox"/>	GO:0009108	6	<a href="#">coenzyme biosynthetic process</a>	66	0.0102	5	0.0107	0.1823844	E
<input type="checkbox"/>	GO:0009084	7,8	<a href="#">glutamine family amino acid biosynthetic process</a>	27	0.0042	3	0.0064	0.1827688	E
<input type="checkbox"/>	GO:0006752	6	<a href="#">group transfer coenzyme metabolic process</a>	44	0.0068	4	0.0085	0.1848915	E
<input type="checkbox"/>	GO:0006367	8,9,7	<a href="#">transcription initiation from RNA polymerase II promoter</a>	44	0.0068	4	0.0085	0.1848915	E
<input type="checkbox"/>	GO:0043408	6,8,5	<a href="#">regulation of MAPKKK cascade</a>	3	0.0005	1	0.0021	0.1866532	E
<input type="checkbox"/>	GO:0006658	8,9	<a href="#">phosphatidylserine metabolic process</a>	3	0.0005	1	0.0021	0.1866532	E
<input type="checkbox"/>	GO:0016090	6,7	<a href="#">prenol metabolic process</a>	3	0.0005	1	0.0021	0.1866532	E
<input type="checkbox"/>	GO:0000186	9,10,8	<a href="#">activation of MAPKK activity</a>	3	0.0005	1	0.0021	0.1866532	E
<input type="checkbox"/>	GO:0051302	5,4	<a href="#">regulation of cell division</a>	3	0.0005	1	0.0021	0.1866532	E
<input type="checkbox"/>	GO:0000917	6,4	<a href="#">barrier septum formation</a>	3	0.0005	1	0.0021	0.1866532	E
<input type="checkbox"/>	GO:0006449	8,7,9,6	<a href="#">regulation of translational termination</a>	3	0.0005	1	0.0021	0.1866532	E
<input type="checkbox"/>	GO:0051205	6,5,4	<a href="#">protein insertion into membrane</a>	3	0.0005	1	0.0021	0.1866532	E
<input type="checkbox"/>	GO:0042306	8,7,10,11,9,6	<a href="#">regulation of protein import into nucleus</a>	3	0.0005	1	0.0021	0.1866532	E
<input type="checkbox"/>	GO:0051054	8,7	<a href="#">positive regulation of DNA metabolic process</a>	3	0.0005	1	0.0021	0.1866532	E
<input type="checkbox"/>	GO:0046822	6,9,5,7,8	<a href="#">regulation of nucleocytoplasmic transport</a>	3	0.0005	1	0.0021	0.1866532	E
<input type="checkbox"/>	GO:0051225	5,9	<a href="#">spindle assembly</a>	3	0.0005	1	0.0021	0.1866532	E
<input type="checkbox"/>	GO:0051204	7,6,5	<a href="#">protein insertion into mitochondrial membrane</a>	3	0.0005	1	0.0021	0.1866532	E
<input type="checkbox"/>	GO:0016584	6,10	<a href="#">nucleosome positioning</a>	3	0.0005	1	0.0021	0.1866532	E
<input type="checkbox"/>	GO:0051383	6	<a href="#">kinetochore organization and biogenesis</a>	3	0.0005	1	0.0021	0.1866532	E
<input type="checkbox"/>	GO:0043065	7,8,10,6	<a href="#">positive regulation of apoptosis</a>	3	0.0005	1	0.0021	0.1866532	E
<input type="checkbox"/>	GO:0032786	9,8,10	<a href="#">positive regulation of RNA elongation</a>	3	0.0005	1	0.0021	0.1866532	E
<input type="checkbox"/>	GO:0015888	5,6	<a href="#">thiamin transport</a>	3	0.0005	1	0.0021	0.1866532	E
<input type="checkbox"/>	GO:0016094	8,7,9	<a href="#">polyprenol biosynthetic process</a>	3	0.0005	1	0.0021	0.1866532	E
<input type="checkbox"/>	GO:0015851	5,6	<a href="#">nucleobase transport</a>	3	0.0005	1	0.0021	0.1866532	E
<input type="checkbox"/>	GO:0033157	7,8,6	<a href="#">regulation of intracellular protein transport</a>	3	0.0005	1	0.0021	0.1866532	E
<input type="checkbox"/>	GO:0016093	7,8	<a href="#">polyprenol metabolic process</a>	3	0.0005	1	0.0021	0.1866532	E
<input type="checkbox"/>	GO:0016091	7,6,8	<a href="#">prenol biosynthetic process</a>	3	0.0005	1	0.0021	0.1866532	E
<input type="checkbox"/>	GO:0051668	5,4	<a href="#">localization within membrane</a>	3	0.0005	1	0.0021	0.1866532	E
<input type="checkbox"/>	GO:0051382	8,7	<a href="#">kinetochore assembly</a>	3	0.0005	1	0.0021	0.1866532	E
<input type="checkbox"/>	GO:0032386	6,7,5	<a href="#">regulation of intracellular transport</a>	3	0.0005	1	0.0021	0.1866532	E
<input type="checkbox"/>	GO:0030100	6,7,5	<a href="#">regulation of endocytosis</a>	3	0.0005	1	0.0021	0.1866532	E
<input type="checkbox"/>	GO:0007234	7,6	<a href="#">osmosensory signaling pathway via two-component system</a>	3	0.0005	1	0.0021	0.1866532	E
<input type="checkbox"/>	GO:0032784	8,7,9	<a href="#">regulation of RNA elongation</a>	3	0.0005	1	0.0021	0.1866532	E
<input type="checkbox"/>	GO:0006857	5,6	<a href="#">oligopeptide transport</a>	3	0.0005	1	0.0021	0.1866532	E
<input type="checkbox"/>	GO:0006452	8,7,6	<a href="#">translational frameshifting</a>	3	0.0005	1	0.0021	0.1866532	E
<input type="checkbox"/>	GO:0018206	8	<a href="#">peptidyl-methionine modification</a>	3	0.0005	1	0.0021	0.1866532	E
<input type="checkbox"/>	GO:0000160	5	<a href="#">two-component signal transduction system</a>	3	0.0005	1	0.0021	0.1866532	E

<input type="radio"/>	GO:0000180	5	<a href="#">(phosphorelay)</a>	5	0.0005	1	0.0021	0.1866532	E
<input type="radio"/>	GO:0051224	7,6,8	<a href="#">negative regulation of protein transport</a>	3	0.0005	1	0.0021	0.1866532	E
<input type="radio"/>	GO:0006561	8,9	<a href="#">proline biosynthetic process</a>	3	0.0005	1	0.0021	0.1866532	E
<input type="radio"/>	GO:0043068	6,7,9,5	<a href="#">positive regulation of programmed cell death</a>	3	0.0005	1	0.0021	0.1866532	E
<input type="radio"/>	GO:0017196	11,9,10	<a href="#">N-terminal peptidyl-methionine acetylation</a>	3	0.0005	1	0.0021	0.1866532	E
<input type="radio"/>	GO:0006906	6,5	<a href="#">vesicle fusion</a>	28	0.0043	3	0.0064	0.1899412	E
<input type="radio"/>	GO:0043241	6,5	<a href="#">protein complex disassembly</a>	28	0.0043	3	0.0064	0.1899412	E
<input type="radio"/>	GO:0043624	7,6	<a href="#">cellular protein complex disassembly</a>	28	0.0043	3	0.0064	0.1899412	E
<input type="radio"/>	GO:0000041	7,8	<a href="#">transition metal ion transport</a>	46	0.0071	4	0.0085	0.1913438	E
<input type="radio"/>	GO:0009110	5	<a href="#">vitamin biosynthetic process</a>	46	0.0071	4	0.0085	0.1913438	E
<input type="radio"/>	GO:0042364	6	<a href="#">water-soluble vitamin biosynthetic process</a>	46	0.0071	4	0.0085	0.1913438	E
<input type="radio"/>	GO:0006778	5,6	<a href="#">porphyrin metabolic process</a>	14	0.0022	2	0.0043	0.1933750	E
<input type="radio"/>	GO:0006037	8,9,6,7,10	<a href="#">cell wall chitin metabolic process</a>	14	0.0022	2	0.0043	0.1933750	E
<input type="radio"/>	GO:0042168	6,7,5	<a href="#">heme metabolic process</a>	14	0.0022	2	0.0043	0.1933750	E
<input type="radio"/>	GO:0000105	8,9	<a href="#">histidine biosynthetic process</a>	14	0.0022	2	0.0043	0.1933750	E
<input type="radio"/>	GO:0006547	7,8	<a href="#">histidine metabolic process</a>	14	0.0022	2	0.0043	0.1933750	E
<input type="radio"/>	GO:0009075	6,7	<a href="#">histidine family amino acid metabolic process</a>	14	0.0022	2	0.0043	0.1933750	E
<input type="radio"/>	GO:0009076	7,8	<a href="#">histidine family amino acid biosynthetic process</a>	14	0.0022	2	0.0043	0.1933750	E
<input type="radio"/>	GO:0033013	5	<a href="#">tetrapyrrole metabolic process</a>	14	0.0022	2	0.0043	0.1933750	E
<input type="radio"/>	GO:0000725	7,6	<a href="#">recombinational repair</a>	29	0.0045	3	0.0064	0.1965793	E
<input type="radio"/>	GO:0007569	4	<a href="#">cell aging</a>	49	0.0076	4	0.0085	0.1984344	E
<input type="radio"/>	GO:0007568	3	<a href="#">aging</a>	49	0.0076	4	0.0085	0.1984344	E
<input type="radio"/>	GO:0043488	9,8,7	<a href="#">regulation of mRNA stability</a>	30	0.0046	3	0.0064	0.2026675	E
<input type="radio"/>	GO:0043487	8,7	<a href="#">regulation of RNA stability</a>	30	0.0046	3	0.0064	0.2026675	E
<input type="radio"/>	GO:0006352	7,8,6	<a href="#">transcription initiation</a>	55	0.0085	4	0.0085	0.2037135	E
<input type="radio"/>	GO:0015918	5,6	<a href="#">sterol transport</a>	15	0.0023	2	0.0043	0.2070346	E
<input type="radio"/>	GO:0006031	9,7,8,10	<a href="#">chitin biosynthetic process</a>	15	0.0023	2	0.0043	0.2070346	E
<input type="radio"/>	GO:0006525	7,8,5,4	<a href="#">arginine metabolic process</a>	15	0.0023	2	0.0043	0.2070346	E
<input type="radio"/>	GO:0000051	4,3	<a href="#">urea cycle intermediate metabolic process</a>	15	0.0023	2	0.0043	0.2070346	E
<input type="radio"/>	GO:0000737	6,7	<a href="#">DNA catabolic process, endonucleolytic</a>	15	0.0023	2	0.0043	0.2070346	E
<input type="radio"/>	GO:0030488	8,9	<a href="#">tRNA methylation</a>	15	0.0023	2	0.0043	0.2070346	E
<input type="radio"/>	GO:0006374	9,11	<a href="#">nuclear mRNA splicing via U2-type spliceosome</a>	15	0.0023	2	0.0043	0.2070346	E
<input type="radio"/>	GO:0000079	8,7,6	<a href="#">regulation of cyclin-dependent protein kinase activity</a>	15	0.0023	2	0.0043	0.2070346	E
<input type="radio"/>	GO:0009112	5	<a href="#">nucleobase metabolic process</a>	31	0.0048	3	0.0064	0.2081955	E
<input type="radio"/>	GO:0006575	5	<a href="#">amino acid derivative metabolic process</a>	31	0.0048	3	0.0064	0.2081955	E
<input type="radio"/>	GO:0032984	5	<a href="#">macromolecular complex disassembly</a>	32	0.0049	3	0.0064	0.2131579	E
<input type="radio"/>	GO:0007121	8,6,10,7,11,5	<a href="#">bipolar cellular bud site selection</a>	32	0.0049	3	0.0064	0.2131579	E
<input type="radio"/>	GO:0019932	6	<a href="#">second-messenger-mediated signaling</a>	32	0.0049	3	0.0064	0.2131579	E
<input type="radio"/>	GO:0016050	5	<a href="#">vesicle organization and biogenesis</a>	16	0.0025	2	0.0043	0.2195454	E
<input type="radio"/>	GO:0010383	7,5,6	<a href="#">cell wall polysaccharide metabolic process</a>	16	0.0025	2	0.0043	0.2195454	E
<input type="radio"/>	GO:0015698	6,7	<a href="#">inorganic anion transport</a>	16	0.0025	2	0.0043	0.2195454	E
<input type="radio"/>	GO:0009127	7,8	<a href="#">purine nucleoside monophosphate biosynthetic process</a>	16	0.0025	2	0.0043	0.2195454	E
<input type="radio"/>	GO:0006360	8,7	<a href="#">transcription from RNA polymerase I promoter</a>	34	0.0053	3	0.0064	0.2213870	E
<input type="radio"/>	GO:0022411	4	<a href="#">cellular component disassembly</a>	36	0.0056	3	0.0064	0.2273938	E



<input type="checkbox"/>	GO:0006030	8,6,7,9	<a href="#">chitin metabolic process</a>	17	0.0026	2	0.0043	0.2308694	E
<input type="checkbox"/>	GO:0006820	5,6	<a href="#">anion transport</a>	17	0.0026	2	0.0043	0.2308694	E
<input type="checkbox"/>	GO:0007004	9	<a href="#">telomere maintenance via telomerase</a>	17	0.0026	2	0.0043	0.2308694	E
<input type="checkbox"/>	GO:0007266	8	<a href="#">Rho protein signal transduction</a>	17	0.0026	2	0.0043	0.2308694	E
<input type="checkbox"/>	GO:0000742	7,5	<a href="#">karyogamy during conjugation with cellular fusion</a>	17	0.0026	2	0.0043	0.2308694	E
<input type="checkbox"/>	GO:0006206	6	<a href="#">pyrimidine base metabolic process</a>	17	0.0026	2	0.0043	0.2308694	E
<input type="checkbox"/>	GO:0000741	6	<a href="#">karyogamy</a>	17	0.0026	2	0.0043	0.2308694	E
<input type="checkbox"/>	GO:0009124	6,7	<a href="#">nucleoside monophosphate biosynthetic process</a>	17	0.0026	2	0.0043	0.2308694	E
<input type="checkbox"/>	GO:0006085	7	<a href="#">acetyl-CoA biosynthetic process</a>	4	0.0006	1	0.0021	0.2309159	E
<input type="checkbox"/>	GO:0007135	9,7,6,8,5	<a href="#">meiosis II</a>	4	0.0006	1	0.0021	0.2309159	E
<input type="checkbox"/>	GO:0006534	7,8,6	<a href="#">cysteine metabolic process</a>	4	0.0006	1	0.0021	0.2309159	E
<input type="checkbox"/>	GO:0051223	6,5,7	<a href="#">regulation of protein transport</a>	4	0.0006	1	0.0021	0.2309159	E
<input type="checkbox"/>	GO:0042180	4	<a href="#">ketone metabolic process</a>	4	0.0006	1	0.0021	0.2309159	E
<input type="checkbox"/>	GO:0031119	8,9	<a href="#">tRNA pseudouridine synthesis</a>	4	0.0006	1	0.0021	0.2309159	E
<input type="checkbox"/>	GO:0018348	11,10,9	<a href="#">protein amino acid geranylgeranylation</a>	4	0.0006	1	0.0021	0.2309159	E
<input type="checkbox"/>	GO:0042542	6	<a href="#">response to hydrogen peroxide</a>	4	0.0006	1	0.0021	0.2309159	E
<input type="checkbox"/>	GO:0006596	7,8	<a href="#">polyamine biosynthetic process</a>	4	0.0006	1	0.0021	0.2309159	E
<input type="checkbox"/>	GO:0045144	10,8,7,5,9,6,4	<a href="#">meiotic sister chromatid segregation</a>	4	0.0006	1	0.0021	0.2309159	E
<input type="checkbox"/>	GO:0018344	10,9,8	<a href="#">protein geranylgeranylation</a>	4	0.0006	1	0.0021	0.2309159	E
<input type="checkbox"/>	GO:0000731	7,6	<a href="#">DNA synthesis during DNA repair</a>	4	0.0006	1	0.0021	0.2309159	E
<input type="checkbox"/>	GO:0042981	6,7,9,5	<a href="#">regulation of apoptosis</a>	4	0.0006	1	0.0021	0.2309159	E
<input type="checkbox"/>	GO:0031578	9,11,10,8	<a href="#">mitotic cell cycle spindle orientation checkpoint</a>	4	0.0006	1	0.0021	0.2309159	E
<input type="checkbox"/>	GO:0051051	6,5	<a href="#">negative regulation of transport</a>	4	0.0006	1	0.0021	0.2309159	E
<input type="checkbox"/>	GO:0046686	6	<a href="#">response to cadmium ion</a>	4	0.0006	1	0.0021	0.2309159	E
<input type="checkbox"/>	GO:0006529	8,9	<a href="#">asparagine biosynthetic process</a>	4	0.0006	1	0.0021	0.2309159	E
<input type="checkbox"/>	GO:0000059	8,10,11,7,9	<a href="#">protein import into nucleus, docking</a>	4	0.0006	1	0.0021	0.2309159	E
<input type="checkbox"/>	GO:0006491	10,9,8	<a href="#">N-glycan processing</a>	4	0.0006	1	0.0021	0.2309159	E
<input type="checkbox"/>	GO:0001100	9,11,10,8	<a href="#">negative regulation of exit from mitosis</a>	4	0.0006	1	0.0021	0.2309159	E
<input type="checkbox"/>	GO:0043067	5,6,8,4	<a href="#">regulation of programmed cell death</a>	4	0.0006	1	0.0021	0.2309159	E
<input type="checkbox"/>	GO:0015780	5,6	<a href="#">nucleotide-sugar transport</a>	4	0.0006	1	0.0021	0.2309159	E
<input type="checkbox"/>	GO:0031204	9,11,10,7,8	<a href="#">posttranslational protein targeting to membrane, translocation</a>	4	0.0006	1	0.0021	0.2309159	E
<input type="checkbox"/>	GO:0007265	7	<a href="#">Ras protein signal transduction</a>	39	0.0060	3	0.0064	0.2324446	E
<input type="checkbox"/>	GO:0016573	11,9	<a href="#">histone acetylation</a>	40	0.0062	3	0.0064	0.2331385	E
<input type="checkbox"/>	GO:0007031	5	<a href="#">peroxisome organization and biogenesis</a>	40	0.0062	3	0.0064	0.2331385	E
<input type="checkbox"/>	GO:0000271	6,7	<a href="#">polysaccharide biosynthetic process</a>	41	0.0063	3	0.0064	0.2333702	E
<input type="checkbox"/>	GO:0051789	4	<a href="#">response to protein stimulus</a>	18	0.0028	2	0.0043	0.2409893	E
<input type="checkbox"/>	GO:0000018	8,7	<a href="#">regulation of DNA recombination</a>	18	0.0028	2	0.0043	0.2409893	E
<input type="checkbox"/>	GO:0009126	7	<a href="#">purine nucleoside monophosphate metabolic process</a>	18	0.0028	2	0.0043	0.2409893	E
<input type="checkbox"/>	GO:0031570	8,7	<a href="#">DNA integrity checkpoint</a>	18	0.0028	2	0.0043	0.2409893	E
<input type="checkbox"/>	GO:0006378	9	<a href="#">mRNA polyadenylation</a>	18	0.0028	2	0.0043	0.2409893	E
<input type="checkbox"/>	GO:0006986	4,5	<a href="#">response to unfolded protein</a>	18	0.0028	2	0.0043	0.2409893	E
<input type="checkbox"/>	GO:0006273	9,8	<a href="#">lagging strand elongation</a>	18	0.0028	2	0.0043	0.2409893	E
<input type="checkbox"/>	GO:0000753	7,8,6	<a href="#">cellular morphogenesis during conjugation with cellular fusion</a>	18	0.0028	2	0.0043	0.2409893	E

<input type="radio"/>	GO:0006875	9,7	<a href="#">cellular metal ion homeostasis</a>	19	0.0029	2	0.0043	0.2499057	E
<input type="radio"/>	GO:0000722	9,8	<a href="#">telomere maintenance via recombination</a>	19	0.0029	2	0.0043	0.2499057	E
<input type="radio"/>	GO:0009123	6	<a href="#">nucleoside monophosphate metabolic process</a>	19	0.0029	2	0.0043	0.2499057	E
<input type="radio"/>	GO:0055065	8	<a href="#">metal ion homeostasis</a>	19	0.0029	2	0.0043	0.2499057	E
<input type="radio"/>	GO:0043094	4	<a href="#">metabolic compound salvage</a>	19	0.0029	2	0.0043	0.2499057	E
<input type="radio"/>	GO:0009067	7,8	<a href="#">aspartate family amino acid biosynthetic process</a>	20	0.0031	2	0.0043	0.2576335	E
<input type="radio"/>	GO:0051647	6,5	<a href="#">nucleus localization</a>	20	0.0031	2	0.0043	0.2576335	E
<input type="radio"/>	GO:0006308	5,6	<a href="#">DNA catabolic process</a>	20	0.0031	2	0.0043	0.2576335	E
<input type="radio"/>	GO:0040023	6,7,4,5	<a href="#">establishment of nucleus localization</a>	20	0.0031	2	0.0043	0.2576335	E
<input type="radio"/>	GO:0006826	7,8,9	<a href="#">iron ion transport</a>	20	0.0031	2	0.0043	0.2576335	E
<input type="radio"/>	GO:0007097	7,8,5,6	<a href="#">nuclear migration</a>	20	0.0031	2	0.0043	0.2576335	E
<input type="radio"/>	GO:0000767	6,7	<a href="#">cellular morphogenesis during conjugation</a>	20	0.0031	2	0.0043	0.2576335	E
<input type="radio"/>	GO:0046112	6,5	<a href="#">nucleobase biosynthetic process</a>	21	0.0032	2	0.0043	0.2641991	E
<input type="radio"/>	GO:0017183	10,4	<a href="#">peptidyl-diphthamide biosynthetic process from peptidyl-histidine</a>	5	0.0008	1	0.0021	0.2678171	E
<input type="radio"/>	GO:0045991	10,8,9,6	<a href="#">positive regulation of transcription by carbon catabolites</a>	5	0.0008	1	0.0021	0.2678171	E
<input type="radio"/>	GO:0017182	9	<a href="#">peptidyl-diphthamide metabolic process</a>	5	0.0008	1	0.0021	0.2678171	E
<input type="radio"/>	GO:0016562	6,11,10,8,9,7	<a href="#">protein import into peroxisome matrix, receptor recycling</a>	5	0.0008	1	0.0021	0.2678171	E
<input type="radio"/>	GO:0009051	10,7,11,12,8	<a href="#">pentose-phosphate shunt, oxidative branch</a>	5	0.0008	1	0.0021	0.2678171	E
<input type="radio"/>	GO:0006816	7,8	<a href="#">calcium ion transport</a>	5	0.0008	1	0.0021	0.2678171	E
<input type="radio"/>	GO:0006279	7	<a href="#">premeiotic DNA synthesis</a>	5	0.0008	1	0.0021	0.2678171	E
<input type="radio"/>	GO:0055071	9	<a href="#">manganese ion homeostasis</a>	5	0.0008	1	0.0021	0.2678171	E
<input type="radio"/>	GO:0043001	10,8,7,9	<a href="#">Golgi to plasma membrane protein transport</a>	5	0.0008	1	0.0021	0.2678171	E
<input type="radio"/>	GO:0000173	10,11,8,9,7	<a href="#">inactivation of MAPK activity during osmolarity sensing</a>	5	0.0008	1	0.0021	0.2678171	E
<input type="radio"/>	GO:0051083	8	<a href="#">cotranslational protein folding</a>	5	0.0008	1	0.0021	0.2678171	E
<input type="radio"/>	GO:0018202	8	<a href="#">peptidyl-histidine modification</a>	5	0.0008	1	0.0021	0.2678171	E
<input type="radio"/>	GO:0000188	9,10,8	<a href="#">inactivation of MAPK activity</a>	5	0.0008	1	0.0021	0.2678171	E
<input type="radio"/>	GO:0006336	7,8,11	<a href="#">DNA replication-independent nucleosome assembly</a>	5	0.0008	1	0.0021	0.2678171	E
<input type="radio"/>	GO:0000411	11,9,10,7	<a href="#">positive regulation of transcription by galactose</a>	5	0.0008	1	0.0021	0.2678171	E
<input type="radio"/>	GO:0018346	10,9,8	<a href="#">protein amino acid prenylation</a>	5	0.0008	1	0.0021	0.2678171	E
<input type="radio"/>	GO:0006089	7	<a href="#">lactate metabolic process</a>	5	0.0008	1	0.0021	0.2678171	E
<input type="radio"/>	GO:0009098	8,9	<a href="#">leucine biosynthetic process</a>	5	0.0008	1	0.0021	0.2678171	E
<input type="radio"/>	GO:0016078	7	<a href="#">tRNA catabolic process</a>	5	0.0008	1	0.0021	0.2678171	E
<input type="radio"/>	GO:0042176	6,7,5	<a href="#">regulation of protein catabolic process</a>	5	0.0008	1	0.0021	0.2678171	E
<input type="radio"/>	GO:0006797	6	<a href="#">polyphosphate metabolic process</a>	5	0.0008	1	0.0021	0.2678171	E
<input type="radio"/>	GO:0030026	10,8	<a href="#">cellular manganese ion homeostasis</a>	5	0.0008	1	0.0021	0.2678171	E
<input type="radio"/>	GO:0008655	5	<a href="#">pyrimidine salvage</a>	5	0.0008	1	0.0021	0.2678171	E
<input type="radio"/>	GO:0018342	9,8,7	<a href="#">protein prenylation</a>	5	0.0008	1	0.0021	0.2678171	E
<input type="radio"/>	GO:0007535	6,8,4,7	<a href="#">donor selection</a>	5	0.0008	1	0.0021	0.2678171	E
<input type="radio"/>	GO:0043112	6	<a href="#">receptor metabolic process</a>	5	0.0008	1	0.0021	0.2678171	E
<input type="radio"/>	GO:0051254	8,7	<a href="#">positive regulation of RNA metabolic process</a>	5	0.0008	1	0.0021	0.2678171	E
<input type="radio"/>	GO:0000409	10,8,9,6	<a href="#">regulation of transcription by galactose</a>	5	0.0008	1	0.0021	0.2678171	E
<input type="radio"/>	GO:0043407	8,9	<a href="#">negative regulation of MAPK activity</a>	5	0.0008	1	0.0021	0.2678171	E

<input type="checkbox"/>	GO:0001881	5,7	<a href="#">receptor recycling</a>	5	0.0008	1	0.0021	0.2678171	E
<input type="checkbox"/>	GO:0000266	6	<a href="#">mitochondrial fission</a>	5	0.0008	1	0.0021	0.2678171	E
<input type="checkbox"/>	GO:0040020	7,9,8,6	<a href="#">regulation of meiosis</a>	22	0.0034	2	0.0043	0.2696386	E
<input type="checkbox"/>	GO:0006311	10,8,7,5,9,6,4	<a href="#">meiotic gene conversion</a>	22	0.0034	2	0.0043	0.2696386	E
<input type="checkbox"/>	GO:0043044	10	<a href="#">ATP-dependent chromatin remodeling</a>	23	0.0036	2	0.0043	0.2739955	E
<input type="checkbox"/>	GO:0009069	6,7	<a href="#">serine family amino acid metabolic process</a>	24	0.0037	2	0.0043	0.2773189	E
<input type="checkbox"/>	GO:0010035	4	<a href="#">response to inorganic substance</a>	24	0.0037	2	0.0043	0.2773189	E
<input type="checkbox"/>	GO:0043631	8	<a href="#">RNA polyadenylation</a>	24	0.0037	2	0.0043	0.2773189	E
<input type="checkbox"/>	GO:0031577	8,7	<a href="#">spindle checkpoint</a>	24	0.0037	2	0.0043	0.2773189	E
<input type="checkbox"/>	GO:0006890	8,6,5,7	<a href="#">retrograde vesicle-mediated transport, Golgi to ER</a>	24	0.0037	2	0.0043	0.2773189	E
<input type="checkbox"/>	GO:0000724	8,7	<a href="#">double-strand break repair via homologous recombination</a>	25	0.0039	2	0.0043	0.2796624	E
<input type="checkbox"/>	GO:0016054	5	<a href="#">organic acid catabolic process</a>	6	0.0009	1	0.0021	0.2981871	E
<input type="checkbox"/>	GO:0007089	8,9,7,6	<a href="#">traversing start control point of mitotic cell cycle</a>	6	0.0009	1	0.0021	0.2981871	E
<input type="checkbox"/>	GO:0006627	10,9,8,7	<a href="#">mitochondrial protein processing</a>	6	0.0009	1	0.0021	0.2981871	E
<input type="checkbox"/>	GO:0001323	4,5,6	<a href="#">age-dependent general metabolic decline during chronological cell aging</a>	6	0.0009	1	0.0021	0.2981871	E
<input type="checkbox"/>	GO:0009231	7,8	<a href="#">riboflavin biosynthetic process</a>	6	0.0009	1	0.0021	0.2981871	E
<input type="checkbox"/>	GO:0001306	4,5	<a href="#">age-dependent response to oxidative stress</a>	6	0.0009	1	0.0021	0.2981871	E
<input type="checkbox"/>	GO:0045041	10,9,8,7	<a href="#">protein import into mitochondrial intermembrane space</a>	6	0.0009	1	0.0021	0.2981871	E
<input type="checkbox"/>	GO:0045143	10,8,7,5,9,6,4	<a href="#">homologous chromosome segregation</a>	6	0.0009	1	0.0021	0.2981871	E
<input type="checkbox"/>	GO:0043174	5	<a href="#">nucleoside salvage</a>	6	0.0009	1	0.0021	0.2981871	E
<input type="checkbox"/>	GO:0051691	6	<a href="#">cellular oligosaccharide metabolic process</a>	6	0.0009	1	0.0021	0.2981871	E
<input type="checkbox"/>	GO:0009113	7,6	<a href="#">purine base biosynthetic process</a>	6	0.0009	1	0.0021	0.2981871	E
<input type="checkbox"/>	GO:0006020	7,8	<a href="#">inositol metabolic process</a>	6	0.0009	1	0.0021	0.2981871	E
<input type="checkbox"/>	GO:0016236	4	<a href="#">macroautophagy</a>	6	0.0009	1	0.0021	0.2981871	E
<input type="checkbox"/>	GO:0046021	10,8,5,6,9,7,4	<a href="#">regulation of transcription from RNA polymerase II promoter, mitotic</a>	6	0.0009	1	0.0021	0.2981871	E
<input type="checkbox"/>	GO:0045040	10,9,7,8	<a href="#">protein import into mitochondrial outer membrane</a>	6	0.0009	1	0.0021	0.2981871	E
<input type="checkbox"/>	GO:0043405	8	<a href="#">regulation of MAPK activity</a>	6	0.0009	1	0.0021	0.2981871	E
<input type="checkbox"/>	GO:0006166	6,8	<a href="#">purine ribonucleoside salvage</a>	6	0.0009	1	0.0021	0.2981871	E
<input type="checkbox"/>	GO:0007070	11,9,6,7,10,8,5	<a href="#">negative regulation of transcription from RNA polymerase II promoter, mitotic</a>	6	0.0009	1	0.0021	0.2981871	E
<input type="checkbox"/>	GO:0006771	7	<a href="#">riboflavin metabolic process</a>	6	0.0009	1	0.0021	0.2981871	E
<input type="checkbox"/>	GO:0001324	5,6,7	<a href="#">age-dependent response to oxidative stress during chronological cell aging</a>	6	0.0009	1	0.0021	0.2981871	E
<input type="checkbox"/>	GO:0006490	5,11,10,9,7,6	<a href="#">oligosaccharide-lipid intermediate assembly</a>	6	0.0009	1	0.0021	0.2981871	E
<input type="checkbox"/>	GO:0031935	11,7,4,8,12,10	<a href="#">regulation of chromatin silencing</a>	6	0.0009	1	0.0021	0.2981871	E
<input type="checkbox"/>	GO:0031938	12,8,5,9,13,11	<a href="#">regulation of chromatin silencing at telomere</a>	6	0.0009	1	0.0021	0.2981871	E
<input type="checkbox"/>	GO:0048285	5	<a href="#">organelle fission</a>	6	0.0009	1	0.0021	0.2981871	E
<input type="checkbox"/>	GO:0007008	6,7	<a href="#">outer mitochondrial membrane organization and biogenesis</a>	7	0.0011	1	0.0021	0.3227749	E
<input type="checkbox"/>	GO:0015936	7	<a href="#">coenzyme A metabolic process</a>	7	0.0011	1	0.0021	0.3227749	E
<input type="checkbox"/>	GO:0000256	6	<a href="#">allantoin catabolic process</a>	7	0.0011	1	0.0021	0.3227749	E
<input type="checkbox"/>	GO:0006829	8,9	<a href="#">zinc ion transport</a>	7	0.0011	1	0.0021	0.3227749	E
<input type="checkbox"/>	GO:0006078	9,8,10	<a href="#">1,6-beta-glucan biosynthetic process</a>	7	0.0011	1	0.0021	0.3227749	E
<input type="checkbox"/>	GO:0006621	7,6,5,4	<a href="#">protein retention in ER</a>	7	0.0011	1	0.0021	0.3227749	E
<input type="checkbox"/>	GO:0045896	9,7,5,8,6,4	<a href="#">regulation of transcription, mitotic</a>	7	0.0011	1	0.0021	0.3227749	E

<input type="checkbox"/>	GO:0043331	4	<a href="#">response to dsRNA</a>	7	0.0011	1	0.0021	0.3227749	E
<input type="checkbox"/>	GO:0019722	7	<a href="#">calcium-mediated signaling</a>	7	0.0011	1	0.0021	0.3227749	E
<input type="checkbox"/>	GO:0006551	7,8	<a href="#">leucine metabolic process</a>	7	0.0011	1	0.0021	0.3227749	E
<input type="checkbox"/>	GO:0000255	5	<a href="#">allantoin metabolic process</a>	7	0.0011	1	0.0021	0.3227749	E
<input type="checkbox"/>	GO:0009225	5	<a href="#">nucleotide-sugar metabolic process</a>	7	0.0011	1	0.0021	0.3227749	E
<input type="checkbox"/>	GO:0007068	10,8,6,9,7,5	<a href="#">negative regulation of transcription, mitotic</a>	7	0.0011	1	0.0021	0.3227749	E
<input type="checkbox"/>	GO:0043330	5,6	<a href="#">response to exogenous dsRNA</a>	7	0.0011	1	0.0021	0.3227749	E
<input type="checkbox"/>	GO:0031120	8	<a href="#">snRNA pseudouridine synthesis</a>	7	0.0011	1	0.0021	0.3227749	E
<input type="checkbox"/>	GO:0015937	7,8	<a href="#">coenzyme A biosynthetic process</a>	7	0.0011	1	0.0021	0.3227749	E
<input type="checkbox"/>	GO:0000715	7,8	<a href="#">nucleotide-excision repair, DNA damage recognition</a>	7	0.0011	1	0.0021	0.3227749	E
<input type="checkbox"/>	GO:0006359	9,8	<a href="#">regulation of transcription from RNA polymerase III promoter</a>	7	0.0011	1	0.0021	0.3227749	E
<input type="checkbox"/>	GO:0006560	7,8	<a href="#">proline metabolic process</a>	7	0.0011	1	0.0021	0.3227749	E
<input type="checkbox"/>	GO:0046839	6,7	<a href="#">phospholipid dephosphorylation</a>	7	0.0011	1	0.0021	0.3227749	E
<input type="checkbox"/>	GO:0046700	5	<a href="#">heterocycle catabolic process</a>	7	0.0011	1	0.0021	0.3227749	E
<input type="checkbox"/>	GO:0045332	5,7,6,8	<a href="#">phospholipid translocation</a>	7	0.0011	1	0.0021	0.3227749	E
<input type="checkbox"/>	GO:0007571	3,4	<a href="#">age-dependent general metabolic decline</a>	7	0.0011	1	0.0021	0.3227749	E
<input type="checkbox"/>	GO:0009615	4,5	<a href="#">response to virus</a>	7	0.0011	1	0.0021	0.3227749	E
<input type="checkbox"/>	GO:0046856	7,9,8,10	<a href="#">phosphoinositide dephosphorylation</a>	7	0.0011	1	0.0021	0.3227749	E
<input type="checkbox"/>	GO:0006265	6	<a href="#">DNA topological change</a>	7	0.0011	1	0.0021	0.3227749	E
<input type="checkbox"/>	GO:0009092	7,8	<a href="#">homoserine metabolic process</a>	7	0.0011	1	0.0021	0.3227749	E
<input type="checkbox"/>	GO:0009311	5	<a href="#">oligosaccharide metabolic process</a>	7	0.0011	1	0.0021	0.3227749	E
<input type="checkbox"/>	GO:0040031	7	<a href="#">snRNA modification</a>	7	0.0011	1	0.0021	0.3227749	E
<input type="checkbox"/>	GO:0006595	6,7	<a href="#">polyamine metabolic process</a>	7	0.0011	1	0.0021	0.3227749	E
<input type="checkbox"/>	GO:0051707	3,4	<a href="#">response to other organism</a>	7	0.0011	1	0.0021	0.3227749	E
<input type="checkbox"/>	GO:0001308	11,7,10	<a href="#">loss of chromatin silencing during replicative cell aging</a>	8	0.0012	1	0.0021	0.3422555	E
<input type="checkbox"/>	GO:0030011	7,4,8	<a href="#">maintenance of cell polarity</a>	8	0.0012	1	0.0021	0.3422555	E
<input type="checkbox"/>	GO:0006077	8,9	<a href="#">1,6-beta-glucan metabolic process</a>	8	0.0012	1	0.0021	0.3422555	E
<input type="checkbox"/>	GO:0006828	8,9	<a href="#">manganese ion transport</a>	8	0.0012	1	0.0021	0.3422555	E
<input type="checkbox"/>	GO:0045039	10,9,7,8	<a href="#">protein import into mitochondrial inner membrane</a>	8	0.0012	1	0.0021	0.3422555	E
<input type="checkbox"/>	GO:0019878	9,10	<a href="#">lysine biosynthetic process via aminoadipic acid</a>	8	0.0012	1	0.0021	0.3422555	E
<input type="checkbox"/>	GO:0031146	11,10,12	<a href="#">SCF-dependent proteasomal ubiquitin-dependent protein catabolic process</a>	8	0.0012	1	0.0021	0.3422555	E
<input type="checkbox"/>	GO:0042816	6	<a href="#">vitamin B6 metabolic process</a>	8	0.0012	1	0.0021	0.3422555	E
<input type="checkbox"/>	GO:0006356	9,8	<a href="#">regulation of transcription from RNA polymerase I promoter</a>	8	0.0012	1	0.0021	0.3422555	E
<input type="checkbox"/>	GO:0051171	5,4	<a href="#">regulation of nitrogen metabolic process</a>	8	0.0012	1	0.0021	0.3422555	E
<input type="checkbox"/>	GO:0006808	6,5	<a href="#">regulation of nitrogen utilization</a>	8	0.0012	1	0.0021	0.3422555	E
<input type="checkbox"/>	GO:0007323	9	<a href="#">peptide pheromone maturation</a>	8	0.0012	1	0.0021	0.3422555	E
<input type="checkbox"/>	GO:0042727	7	<a href="#">riboflavin and derivative biosynthetic process</a>	8	0.0012	1	0.0021	0.3422555	E
<input type="checkbox"/>	GO:0042726	6	<a href="#">riboflavin and derivative metabolic process</a>	8	0.0012	1	0.0021	0.3422555	E
<input type="checkbox"/>	GO:0015677	9,10	<a href="#">copper ion import</a>	8	0.0012	1	0.0021	0.3422555	E
<input type="checkbox"/>	GO:0006620	10,9,8,7,6	<a href="#">posttranslational protein targeting to membrane</a>	8	0.0012	1	0.0021	0.3422555	E
<input type="checkbox"/>	GO:0008614	7	<a href="#">pyridoxine metabolic process</a>	8	0.0012	1	0.0021	0.3422555	E
<input type="checkbox"/>	GO:0043144	7	<a href="#">snoRNA processing</a>	8	0.0012	1	0.0021	0.3422555	E

<input type="checkbox"/>	GO:0006855	5,6	<a href="#">multidrug transport</a>	8	0.0012	1	0.0021	0.3422555	E
<input type="checkbox"/>	GO:0006760	5,7	<a href="#">folic acid and derivative metabolic process</a>	9	0.0014	1	0.0021	0.3572372	E
<input type="checkbox"/>	GO:0043101	5	<a href="#">purine salvage</a>	9	0.0014	1	0.0021	0.3572372	E
<input type="checkbox"/>	GO:0045426	7,6	<a href="#">quinone cofactor biosynthetic process</a>	9	0.0014	1	0.0021	0.3572372	E
<input type="checkbox"/>	GO:0019933	8	<a href="#">cAMP-mediated signaling</a>	9	0.0014	1	0.0021	0.3572372	E
<input type="checkbox"/>	GO:0030968	7,5,6	<a href="#">unfolded protein response</a>	9	0.0014	1	0.0021	0.3572372	E
<input type="checkbox"/>	GO:0001304	10,6	<a href="#">progressive alteration of chromatin during replicative cell aging</a>	9	0.0014	1	0.0021	0.3572372	E
<input type="checkbox"/>	GO:0006635	7,9,8	<a href="#">fatty acid beta-oxidation</a>	9	0.0014	1	0.0021	0.3572372	E
<input type="checkbox"/>	GO:0043648	6	<a href="#">dicarboxylic acid metabolic process</a>	9	0.0014	1	0.0021	0.3572372	E
<input type="checkbox"/>	GO:0009085	8,9	<a href="#">lysine biosynthetic process</a>	9	0.0014	1	0.0021	0.3572372	E
<input type="checkbox"/>	GO:0006553	7,8	<a href="#">lysine metabolic process</a>	9	0.0014	1	0.0021	0.3572372	E
<input type="checkbox"/>	GO:0019935	7	<a href="#">cyclic-nucleotide-mediated signaling</a>	9	0.0014	1	0.0021	0.3572372	E
<input type="checkbox"/>	GO:0006743	7,6	<a href="#">ubiquinone metabolic process</a>	9	0.0014	1	0.0021	0.3572372	E
<input type="checkbox"/>	GO:0006984	6	<a href="#">ER-nuclear signaling pathway</a>	9	0.0014	1	0.0021	0.3572372	E
<input type="checkbox"/>	GO:0030491	7,9,10,6,8	<a href="#">heteroduplex formation</a>	9	0.0014	1	0.0021	0.3572372	E
<input type="checkbox"/>	GO:0006744	8,7	<a href="#">ubiquinone biosynthetic process</a>	9	0.0014	1	0.0021	0.3572372	E
<input type="checkbox"/>	GO:0042375	5	<a href="#">quinone cofactor metabolic process</a>	9	0.0014	1	0.0021	0.3572372	E
<input type="checkbox"/>	GO:0000184	8	<a href="#">mRNA catabolic process, nonsense-mediated decay</a>	9	0.0014	1	0.0021	0.3572372	E
<input type="checkbox"/>	GO:0006528	7,8	<a href="#">asparagine metabolic process</a>	9	0.0014	1	0.0021	0.3572372	E
<input type="checkbox"/>	GO:0001301	9,5	<a href="#">progressive alteration of chromatin during cell aging</a>	10	0.0015	1	0.0021	0.3682668	E
<input type="checkbox"/>	GO:0006012	7,8	<a href="#">galactose metabolic process</a>	10	0.0015	1	0.0021	0.3682668	E
<input type="checkbox"/>	GO:0015718	6,7	<a href="#">monocarboxylic acid transport</a>	10	0.0015	1	0.0021	0.3682668	E
<input type="checkbox"/>	GO:0006268	8	<a href="#">DNA unwinding during replication</a>	10	0.0015	1	0.0021	0.3682668	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	0.0021	0.3682668	E
<input type="checkbox"/>	GO:0046519	7,8	<a href="#">sphingoid metabolic process</a>	10	0.0015	1	0.0021	0.3682668	E
<input type="checkbox"/>	GO:0009068	7,8	<a href="#">aspartate family amino acid catabolic process</a>	10	0.0015	1	0.0021	0.3682668	E
<input type="checkbox"/>	GO:0065002	8,6,7	<a href="#">intracellular protein transport across a membrane</a>	11	0.0017	1	0.0021	0.3758360	E
<input type="checkbox"/>	GO:0051274	8,9	<a href="#">beta-glucan biosynthetic process</a>	11	0.0017	1	0.0021	0.3758360	E
<input type="checkbox"/>	GO:0019321	6,7	<a href="#">pentose metabolic process</a>	11	0.0017	1	0.0021	0.3758360	E
<input type="checkbox"/>	GO:0006098	9,10,11	<a href="#">pentose-phosphate shunt</a>	11	0.0017	1	0.0021	0.3758360	E
<input type="checkbox"/>	GO:0000055	11,12,7,9,10	<a href="#">ribosomal large subunit export from nucleus</a>	11	0.0017	1	0.0021	0.3758360	E
<input type="checkbox"/>	GO:0019395	6,8,7	<a href="#">fatty acid oxidation</a>	11	0.0017	1	0.0021	0.3758360	E
<input type="checkbox"/>	GO:0044247	7,6	<a href="#">cellular polysaccharide catabolic process</a>	12	0.0019	1	0.0021	0.3803863	E
<input type="checkbox"/>	GO:0051273	7,8	<a href="#">beta-glucan metabolic process</a>	12	0.0019	1	0.0021	0.3803863	E
<input type="checkbox"/>	GO:0000302	5	<a href="#">response to reactive oxygen species</a>	12	0.0019	1	0.0021	0.3803863	E
<input type="checkbox"/>	GO:0009070	7,8	<a href="#">serine family amino acid biosynthetic process</a>	12	0.0019	1	0.0021	0.3803863	E
<input type="checkbox"/>	GO:0000272	6	<a href="#">polysaccharide catabolic process</a>	12	0.0019	1	0.0021	0.3803863	E
<input type="checkbox"/>	GO:0012501	5,7	<a href="#">programmed cell death</a>	13	0.0020	1	0.0021	0.3823135	E
<input type="checkbox"/>	GO:0001300	5	<a href="#">chronological cell aging</a>	13	0.0020	1	0.0021	0.3823135	E
<input type="checkbox"/>	GO:0006301	7,6	<a href="#">postreplication repair</a>	13	0.0020	1	0.0021	0.3823135	E
<input type="checkbox"/>	GO:0006633	7,6,8,5	<a href="#">fatty acid biosynthetic process</a>	13	0.0020	1	0.0021	0.3823135	E
<input type="checkbox"/>	GO:0006915	6,8	<a href="#">apoptosis</a>	13	0.0020	1	0.0021	0.3823135	E
<input type="checkbox"/>	GO:0030258	5,6	<a href="#">lipid modification</a>	13	0.0020	1	0.0021	0.3823135	E

<input type="checkbox"/>	GO:0008219	4,6	<a href="#">cell death</a>	13	0.0020	1	0.0021	0.3823135	E
<input type="checkbox"/>	GO:0031929	6	<a href="#">TOR signaling pathway</a>	13	0.0020	1	0.0021	0.3823135	E
<input type="checkbox"/>	GO:0006450	8,7,6	<a href="#">regulation of translational fidelity</a>	13	0.0020	1	0.0021	0.3823135	E
<input type="checkbox"/>	GO:0016265	3	<a href="#">death</a>	13	0.0020	1	0.0021	0.3823135	E
<input type="checkbox"/>	GO:0008150	1	<a href="#">biological process</a>	6476	1.0000	468	1.0000	1.0000000	D
<input type="checkbox"/>	GO:0000394	8	<a href="#">RNA splicing, via endonucleolytic cleavage and ligation</a>	14	0.0022	1	0.0021	0.3819723	D
<input type="checkbox"/>	GO:0006734	9,8	<a href="#">NADH metabolic process</a>	14	0.0022	1	0.0021	0.3819723	D
<input type="checkbox"/>	GO:0000011	6	<a href="#">vacuole inheritance</a>	14	0.0022	1	0.0021	0.3819723	D
<input type="checkbox"/>	GO:0006749	6,5	<a href="#">glutathione metabolic process</a>	14	0.0022	1	0.0021	0.3819723	D
<input type="checkbox"/>	GO:0000028	9,7,8,6	<a href="#">ribosomal small subunit assembly and maintenance</a>	14	0.0022	1	0.0021	0.3819723	D
<input type="checkbox"/>	GO:0042787	10,9,11	<a href="#">protein ubiquitination during ubiquitin-dependent protein catabolic process</a>	14	0.0022	1	0.0021	0.3819723	D
<input type="checkbox"/>	GO:0006825	8,9	<a href="#">copper ion transport</a>	14	0.0022	1	0.0021	0.3819723	D
<input type="checkbox"/>	GO:0048278	4,5,6	<a href="#">vesicle docking</a>	14	0.0022	1	0.0021	0.3819723	D
<input type="checkbox"/>	GO:0006740	10,9	<a href="#">NADPH regeneration</a>	14	0.0022	1	0.0021	0.3819723	D
<input type="checkbox"/>	GO:0046040	9	<a href="#">IMP metabolic process</a>	14	0.0022	1	0.0021	0.3819723	D
<input type="checkbox"/>	GO:0006188	9,10	<a href="#">IMP biosynthetic process</a>	14	0.0022	1	0.0021	0.3819723	D
<input type="checkbox"/>	GO:0006388	9,8	<a href="#">tRNA splicing</a>	14	0.0022	1	0.0021	0.3819723	D
<input type="checkbox"/>	GO:0022406	3	<a href="#">membrane docking</a>	14	0.0022	1	0.0021	0.3819723	D
<input type="checkbox"/>	GO:0006144	6	<a href="#">purine base metabolic process</a>	14	0.0022	1	0.0021	0.3819723	D
<input type="checkbox"/>	GO:0045990	9,7,8,5	<a href="#">regulation of transcription by carbon catabolites</a>	14	0.0022	1	0.0021	0.3819723	D
<input type="checkbox"/>	GO:0019856	7,6	<a href="#">pyrimidine base biosynthetic process</a>	15	0.0023	1	0.0021	0.3796796	D
<input type="checkbox"/>	GO:0030473	8,9,6,7	<a href="#">nuclear migration, microtubule-mediated</a>	15	0.0023	1	0.0021	0.3796796	D
<input type="checkbox"/>	GO:0009894	5,4	<a href="#">regulation of catabolic process</a>	15	0.0023	1	0.0021	0.3796796	D
<input type="checkbox"/>	GO:0009168	8,9	<a href="#">purine ribonucleoside monophosphate biosynthetic process</a>	15	0.0023	1	0.0021	0.3796796	D
<input type="checkbox"/>	GO:0006267	8,7	<a href="#">pre-replicative complex assembly</a>	15	0.0023	1	0.0021	0.3796796	D
<input type="checkbox"/>	GO:0016073	6	<a href="#">snRNA metabolic process</a>	15	0.0023	1	0.0021	0.3796796	D
<input type="checkbox"/>	GO:0009651	5	<a href="#">response to salt stress</a>	15	0.0023	1	0.0021	0.3796796	D
<input type="checkbox"/>	GO:0007018	8,7,6	<a href="#">microtubule-based movement</a>	15	0.0023	1	0.0021	0.3796796	D
<input type="checkbox"/>	GO:0009156	7,8	<a href="#">ribonucleoside monophosphate biosynthetic process</a>	15	0.0023	1	0.0021	0.3796796	D
<input type="checkbox"/>	GO:0048015	7	<a href="#">phosphoinositide-mediated signaling</a>	16	0.0025	1	0.0021	0.3757189	D
<input type="checkbox"/>	GO:0048017	8	<a href="#">inositol lipid-mediated signaling</a>	16	0.0025	1	0.0021	0.3757189	D
<input type="checkbox"/>	GO:0032508	7	<a href="#">DNA duplex unwinding</a>	16	0.0025	1	0.0021	0.3757189	D
<input type="checkbox"/>	GO:0032392	6	<a href="#">DNA geometric change</a>	16	0.0025	1	0.0021	0.3757189	D
<input type="checkbox"/>	GO:0016558	10,9,7,8,6	<a href="#">protein import into peroxisome matrix</a>	17	0.0026	1	0.0021	0.3703426	D
<input type="checkbox"/>	GO:0045003	9,8	<a href="#">double-strand break repair via synthesis-dependent strand annealing</a>	17	0.0026	1	0.0021	0.3703426	D
<input type="checkbox"/>	GO:0016053	5	<a href="#">organic acid biosynthetic process</a>	17	0.0026	1	0.0021	0.3703426	D
<input type="checkbox"/>	GO:0009167	8	<a href="#">purine ribonucleoside monophosphate metabolic process</a>	17	0.0026	1	0.0021	0.3703426	D
<input type="checkbox"/>	GO:0046394	6	<a href="#">carboxylic acid biosynthetic process</a>	17	0.0026	1	0.0021	0.3703426	D
<input type="checkbox"/>	GO:0030705	7,5,6	<a href="#">cytoskeleton-dependent intracellular transport</a>	17	0.0026	1	0.0021	0.3703426	D
<input type="checkbox"/>	GO:0009161	7	<a href="#">ribonucleoside monophosphate metabolic process</a>	17	0.0026	1	0.0021	0.3703426	D
<input type="checkbox"/>	GO:0016074	6	<a href="#">snoRNA metabolic process</a>	17	0.0026	1	0.0021	0.3703426	D
<input type="checkbox"/>	GO:0006739	9,8	<a href="#">NADP metabolic process</a>	17	0.0026	1	0.0021	0.3703426	D

<input type="checkbox"/>	GO:0042147	8,6,7	<a href="#">retrograde transport, endosome to Golgi</a>	17	0.0026	1	0.0021	0.3703426	D
<input type="checkbox"/>	GO:0016571	11,9,10,8	<a href="#">histone methylation</a>	18	0.0028	1	0.0021	0.3637758	D
<input type="checkbox"/>	GO:0007584	6,4	<a href="#">response to nutrient</a>	18	0.0028	1	0.0021	0.3637758	D
<input type="checkbox"/>	GO:0051248	6,5	<a href="#">negative regulation of protein metabolic process</a>	18	0.0028	1	0.0021	0.3637758	D
<input type="checkbox"/>	GO:0006369	9,8	<a href="#">transcription termination from RNA polymerase II promoter</a>	18	0.0028	1	0.0021	0.3637758	D
<input type="checkbox"/>	GO:0010038	5	<a href="#">response to metal ion</a>	18	0.0028	1	0.0021	0.3637758	D
<input type="checkbox"/>	GO:0006353	8,7	<a href="#">transcription termination</a>	20	0.0031	1	0.0021	0.3478473	D
<input type="checkbox"/>	GO:0016579	9	<a href="#">protein deubiquitination</a>	20	0.0031	1	0.0021	0.3478473	D
<input type="checkbox"/>	GO:0000209	10	<a href="#">protein polyubiquitination</a>	20	0.0031	1	0.0021	0.3478473	D
<input type="checkbox"/>	GO:0006625	9,8,6,7	<a href="#">protein targeting to peroxisome</a>	20	0.0031	1	0.0021	0.3478473	D
<input type="checkbox"/>	GO:0006084	6	<a href="#">acetyl-CoA metabolic process</a>	20	0.0031	1	0.0021	0.3478473	D
<input type="checkbox"/>	GO:0000447	9,10	<a href="#">endonucleolytic cleavage between SSU-rRNA and 5.8S rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)</a>	20	0.0031	1	0.0021	0.3478473	D
<input type="checkbox"/>	GO:0000478	7,8	<a href="#">endonucleolytic cleavages during rRNA processing</a>	20	0.0031	1	0.0021	0.3478473	D
<input type="checkbox"/>	GO:0006100	6	<a href="#">tricarboxylic acid cycle intermediate metabolic process</a>	20	0.0031	1	0.0021	0.3478473	D
<input type="checkbox"/>	GO:0043574	7,5,6	<a href="#">peroxisomal transport</a>	20	0.0031	1	0.0021	0.3478473	D
<input type="checkbox"/>	GO:0007094	9,11,10,8	<a href="#">mitotic cell cycle spindle assembly checkpoint</a>	20	0.0031	1	0.0021	0.3478473	D
<input type="checkbox"/>	GO:0000479	8,9	<a href="#">endonucleolytic cleavage of tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)</a>	20	0.0031	1	0.0021	0.3478473	D
<input type="checkbox"/>	GO:0006081	4	<a href="#">aldehyde metabolic process</a>	21	0.0032	1	0.0021	0.3388197	D
<input type="checkbox"/>	GO:0030472	6,5,10	<a href="#">mitotic spindle organization and biogenesis in nucleus</a>	22	0.0034	1	0.0021	0.3292741	D
<input type="checkbox"/>	GO:0006513	10	<a href="#">protein monoubiquitination</a>	22	0.0034	1	0.0021	0.3292741	D
<input type="checkbox"/>	GO:0007534	6,8,7	<a href="#">gene conversion at mating-type locus</a>	23	0.0036	1	0.0021	0.3193325	D
<input type="checkbox"/>	GO:0009408	5,4	<a href="#">response to heat</a>	23	0.0036	1	0.0021	0.3193325	D
<input type="checkbox"/>	GO:0006479	9,7	<a href="#">protein amino acid methylation</a>	23	0.0036	1	0.0021	0.3193325	D
<input type="checkbox"/>	GO:0008213	8	<a href="#">protein amino acid alkylation</a>	23	0.0036	1	0.0021	0.3193325	D
<input type="checkbox"/>	GO:0006896	9,8,7,6	<a href="#">Golgi to vacuole transport</a>	24	0.0037	1	0.0021	0.3091018	D
<input type="checkbox"/>	GO:0009250	7,8	<a href="#">glucan biosynthetic process</a>	25	0.0039	1	0.0021	0.2986758	D
<input type="checkbox"/>	GO:0000001	8,7,6	<a href="#">mitochondrion inheritance</a>	26	0.0040	1	0.0021	0.2881363	D
<input type="checkbox"/>	GO:0048311	7,6	<a href="#">mitochondrion distribution</a>	26	0.0040	1	0.0021	0.2881363	D
<input type="checkbox"/>	GO:0042274	6,5	<a href="#">ribosomal small subunit biogenesis and assembly</a>	26	0.0040	1	0.0021	0.2881363	D
<input type="checkbox"/>	GO:0009636	4	<a href="#">response to toxin</a>	28	0.0043	2	0.0043	0.2813845	D
<input type="checkbox"/>	GO:0000054	10,11,6,8,9	<a href="#">ribosome export from nucleus</a>	28	0.0043	2	0.0043	0.2813845	D
<input type="checkbox"/>	GO:0009266	4	<a href="#">response to temperature stimulus</a>	28	0.0043	2	0.0043	0.2813845	D
<input type="checkbox"/>	GO:0051656	6,3,5,4	<a href="#">establishment of organelle localization</a>	29	0.0045	2	0.0043	0.2803857	D
<input type="checkbox"/>	GO:0007533	5,7,6	<a href="#">mating type switching</a>	29	0.0045	2	0.0043	0.2803857	D
<input type="checkbox"/>	GO:0006893	9,7,6,8	<a href="#">Golgi to plasma membrane transport</a>	30	0.0046	2	0.0043	0.2786989	D
<input type="checkbox"/>	GO:0051646	6,5	<a href="#">mitochondrion localization</a>	27	0.0042	1	0.0021	0.2775541	D
<input type="checkbox"/>	GO:0006118	4	<a href="#">electron transport</a>	33	0.0051	2	0.0043	0.2700827	D
<input type="checkbox"/>	GO:0042144	6	<a href="#">vacuole fusion, non-autophagic</a>	28	0.0043	1	0.0021	0.2669906	D
<input type="checkbox"/>	GO:0055067	8	<a href="#">monovalent inorganic cation homeostasis</a>	34	0.0053	2	0.0043	0.2662078	D
<input type="checkbox"/>	GO:0030004	9,7	<a href="#">cellular monovalent inorganic cation homeostasis</a>	34	0.0053	2	0.0043	0.2662078	D

<input type="checkbox"/>	GO:0007530	4,5	<a href="#">sex determination</a>	35	0.0054	2	0.0043	0.2619177	D
<input type="checkbox"/>	GO:0007531	4,6,5	<a href="#">mating type determination</a>	35	0.0054	2	0.0043	0.2619177	D
<input type="checkbox"/>	GO:0003006	3,4	<a href="#">reproductive developmental process</a>	35	0.0054	2	0.0043	0.2619177	D
<input type="checkbox"/>	GO:0051651	5,4,3	<a href="#">maintenance of cellular localization</a>	29	0.0045	1	0.0021	0.2564984	D
<input type="checkbox"/>	GO:0006109	5,4	<a href="#">regulation of carbohydrate metabolic process</a>	29	0.0045	1	0.0021	0.2564984	D
<input type="checkbox"/>	GO:0032507	6,5,4	<a href="#">maintenance of cellular protein localization</a>	29	0.0045	1	0.0021	0.2564984	D
<input type="checkbox"/>	GO:0009063	6,7	<a href="#">amino acid catabolic process</a>	29	0.0045	1	0.0021	0.2564984	D
<input type="checkbox"/>	GO:0008643	4,5	<a href="#">carbohydrate transport</a>	38	0.0059	2	0.0043	0.2470252	D
<input type="checkbox"/>	GO:0006879	10,8	<a href="#">cellular iron ion homeostasis</a>	38	0.0059	2	0.0043	0.2470252	D
<input type="checkbox"/>	GO:0006383	8,7	<a href="#">transcription from RNA polymerase III promoter</a>	38	0.0059	2	0.0043	0.2470252	D
<input type="checkbox"/>	GO:0006090	7	<a href="#">pyruvate metabolic process</a>	38	0.0059	2	0.0043	0.2470252	D
<input type="checkbox"/>	GO:0055072	9	<a href="#">iron ion homeostasis</a>	38	0.0059	2	0.0043	0.2470252	D
<input type="checkbox"/>	GO:0045185	5,4,3	<a href="#">maintenance of protein localization</a>	30	0.0046	1	0.0021	0.2461226	D
<input type="checkbox"/>	GO:0048308	5	<a href="#">organelle inheritance</a>	40	0.0062	2	0.0043	0.2358375	D
<input type="checkbox"/>	GO:0009064	6,7	<a href="#">glutamine family amino acid metabolic process</a>	43	0.0066	3	0.0064	0.2325331	D
<input type="checkbox"/>	GO:0006914	3	<a href="#">autophagy</a>	45	0.0069	3	0.0064	0.2301135	D
<input type="checkbox"/>	GO:0006164	6,7	<a href="#">purine nucleotide biosynthetic process</a>	41	0.0063	2	0.0043	0.2299802	D
<input type="checkbox"/>	GO:0006417	7,6,5	<a href="#">regulation of translation</a>	47	0.0073	3	0.0064	0.2262981	D
<input type="checkbox"/>	GO:0044270	5,4	<a href="#">nitrogen compound catabolic process</a>	32	0.0049	1	0.0021	0.2258663	D
<input type="checkbox"/>	GO:0009310	5,6	<a href="#">amine catabolic process</a>	32	0.0049	1	0.0021	0.2258663	D
<input type="checkbox"/>	GO:0030476	8,6,7	<a href="#">spore wall assembly (sensu Fungi)</a>	42	0.0065	2	0.0043	0.2239921	D
<input type="checkbox"/>	GO:0006769	8,7	<a href="#">nicotinamide metabolic process</a>	42	0.0065	2	0.0043	0.2239921	D
<input type="checkbox"/>	GO:0042244	5,6	<a href="#">spore wall assembly</a>	42	0.0065	2	0.0043	0.2239921	D
<input type="checkbox"/>	GO:0006413	7,6	<a href="#">translational initiation</a>	49	0.0076	3	0.0064	0.2212743	D
<input type="checkbox"/>	GO:0051235	3,2	<a href="#">maintenance of localization</a>	33	0.0051	1	0.0021	0.2160445	D
<input type="checkbox"/>	GO:0000096	6,7,5	<a href="#">sulfur amino acid metabolic process</a>	33	0.0051	1	0.0021	0.2160445	D
<input type="checkbox"/>	GO:0048468	3,5	<a href="#">cell development</a>	52	0.0080	3	0.0064	0.2118725	D
<input type="checkbox"/>	GO:0000466	8,9	<a href="#">maturation of 5.8S rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)</a>	34	0.0053	1	0.0021	0.2064575	D
<input type="checkbox"/>	GO:0006007	8,9	<a href="#">glucose catabolic process</a>	34	0.0053	1	0.0021	0.2064575	D
<input type="checkbox"/>	GO:0006312	7	<a href="#">mitotic recombination</a>	45	0.0069	2	0.0043	0.2055380	D
<input type="checkbox"/>	GO:0019362	7,6	<a href="#">pyridine nucleotide metabolic process</a>	45	0.0069	2	0.0043	0.2055380	D
<input type="checkbox"/>	GO:0051640	5,4	<a href="#">organelle localization</a>	56	0.0086	4	0.0085	0.2035304	D
<input type="checkbox"/>	GO:0006944	5	<a href="#">membrane fusion</a>	59	0.0091	4	0.0085	0.2013702	D
<input type="checkbox"/>	GO:0009066	6,7	<a href="#">aspartate family amino acid metabolic process</a>	46	0.0071	2	0.0043	0.1993101	D
<input type="checkbox"/>	GO:0006073	6,7	<a href="#">glucan metabolic process</a>	46	0.0071	2	0.0043	0.1993101	D
<input type="checkbox"/>	GO:0006733	6	<a href="#">oxidoreduction coenzyme metabolic process</a>	56	0.0086	3	0.0064	0.1967502	D
<input type="checkbox"/>	GO:0006163	6	<a href="#">purine nucleotide metabolic process</a>	47	0.0073	2	0.0043	0.1930818	D
<input type="checkbox"/>	GO:0006631	5,7,6	<a href="#">fatty acid metabolic process</a>	47	0.0073	2	0.0043	0.1930818	D
<input type="checkbox"/>	GO:0007051	8	<a href="#">spindle organization and biogenesis</a>	47	0.0073	2	0.0043	0.1930818	D
<input type="checkbox"/>	GO:0016567	9	<a href="#">protein ubiquitination</a>	66	0.0102	4	0.0085	0.1885151	D
<input type="checkbox"/>	GO:0000460	7,8	<a href="#">maturation of 5.8S rRNA</a>	36	0.0056	1	0.0021	0.1880543	D
<input type="checkbox"/>	GO:0009991	4	<a href="#">response to extracellular stimulus</a>	37	0.0057	1	0.0021	0.1792624	D
<input type="checkbox"/>	GO:0009605	3	<a href="#">response to external stimulus</a>	37	0.0057	1	0.0021	0.1792624	D



<input type="radio"/>	GO:0031667	5	<a href="#">response to nutrient levels</a>	37	0.0057	1	0.0021	0.1792624	D
<input type="radio"/>	GO:0045944	10,9	<a href="#">positive regulation of transcription from RNA polymerase II promoter</a>	76	0.0117	5	0.0107	0.1780499	D
<input type="radio"/>	GO:0051246	5,4	<a href="#">regulation of protein metabolic process</a>	72	0.0111	4	0.0085	0.1714068	D
<input type="radio"/>	GO:0009152	7,8	<a href="#">purine ribonucleotide biosynthetic process</a>	38	0.0059	1	0.0021	0.1707546	D
<input type="radio"/>	GO:0006767	5	<a href="#">water-soluble vitamin metabolic process</a>	89	0.0137	6	0.0128	0.1647132	D
<input type="radio"/>	GO:0006766	4	<a href="#">vitamin metabolic process</a>	89	0.0137	6	0.0128	0.1647132	D
<input type="radio"/>	GO:0009060	6	<a href="#">aerobic respiration</a>	84	0.0130	5	0.0107	0.1631076	D
<input type="radio"/>	GO:0019320	7,8	<a href="#">hexose catabolic process</a>	39	0.0060	1	0.0021	0.1625360	D
<input type="radio"/>	GO:0001522	7	<a href="#">pseudouridine synthesis</a>	39	0.0060	1	0.0021	0.1625360	D
<input type="radio"/>	GO:0006897	6,5	<a href="#">endocytosis</a>	86	0.0133	5	0.0107	0.1583072	D
<input type="radio"/>	GO:0016051	5	<a href="#">carbohydrate biosynthetic process</a>	77	0.0119	4	0.0085	0.1547783	D
<input type="radio"/>	GO:0009260	6,7	<a href="#">ribonucleotide biosynthetic process</a>	40	0.0062	1	0.0021	0.1546093	D
<input type="radio"/>	GO:0007017	6	<a href="#">microtubule-based process</a>	101	0.0156	7	0.0150	0.1545605	D
<input type="radio"/>	GO:0055080	7	<a href="#">cation homeostasis</a>	102	0.0158	7	0.0150	0.1539488	D
<input type="radio"/>	GO:0030003	8,6	<a href="#">cellular cation homeostasis</a>	102	0.0158	7	0.0150	0.1539488	D
<input type="radio"/>	GO:0006512	8	<a href="#">ubiquitin cycle</a>	88	0.0136	5	0.0107	0.1532052	D
<input type="radio"/>	GO:0045333	5	<a href="#">cellular respiration</a>	89	0.0137	5	0.0107	0.1505593	D
<input type="radio"/>	GO:0030036	7	<a href="#">actin cytoskeleton organization and biogenesis</a>	107	0.0165	7	0.0150	0.1493301	D
<input type="radio"/>	GO:0007033	5	<a href="#">vacuole organization and biogenesis</a>	67	0.0103	3	0.0064	0.1486025	D
<input type="radio"/>	GO:0006623	9,8,7,6	<a href="#">protein targeting to vacuole</a>	67	0.0103	3	0.0064	0.1486025	D
<input type="radio"/>	GO:0031326	6,5	<a href="#">regulation of cellular biosynthetic process</a>	67	0.0103	3	0.0064	0.1486025	D
<input type="radio"/>	GO:0009150	7	<a href="#">purine ribonucleotide metabolic process</a>	41	0.0063	1	0.0021	0.1469756	D
<input type="radio"/>	GO:0000027	9,7,8,6	<a href="#">ribosomal large subunit assembly and maintenance</a>	41	0.0063	1	0.0021	0.1469756	D
<input type="radio"/>	GO:0042257	8,7	<a href="#">ribosomal subunit assembly</a>	55	0.0085	2	0.0043	0.1452330	D
<input type="radio"/>	GO:0055082	6,4	<a href="#">cellular chemical homeostasis</a>	115	0.0178	8	0.0171	0.1450212	D
<input type="radio"/>	GO:0006873	7,5	<a href="#">cellular ion homeostasis</a>	115	0.0178	8	0.0171	0.1450212	D
<input type="radio"/>	GO:0030029	6	<a href="#">actin filament-based process</a>	112	0.0173	7	0.0150	0.1424764	D
<input type="radio"/>	GO:0050801	6	<a href="#">ion homeostasis</a>	119	0.0184	8	0.0171	0.1423992	D
<input type="radio"/>	GO:0048878	5	<a href="#">chemical homeostasis</a>	121	0.0187	8	0.0171	0.1405821	D
<input type="radio"/>	GO:0006892	8,6,5,7	<a href="#">post-Golgi vesicle-mediated transport</a>	69	0.0107	3	0.0064	0.1397972	D
<input type="radio"/>	GO:0009889	5,4	<a href="#">regulation of biosynthetic process</a>	69	0.0107	3	0.0064	0.1397972	D
<input type="radio"/>	GO:0009259	6	<a href="#">ribonucleotide metabolic process</a>	43	0.0066	1	0.0021	0.1325821	D
<input type="radio"/>	GO:0019725	5,3	<a href="#">cellular homeostasis</a>	128	0.0198	8	0.0171	0.1319836	D
<input type="radio"/>	GO:0009451	6	<a href="#">RNA modification</a>	139	0.0215	10	0.0214	0.1312581	D
<input type="radio"/>	GO:0010324	5	<a href="#">membrane invagination</a>	96	0.0148	5	0.0107	0.1308902	D
<input type="radio"/>	GO:0032446	8	<a href="#">protein modification by small protein conjugation</a>	84	0.0130	4	0.0085	0.1302620	D
<input type="radio"/>	GO:0046365	6,7	<a href="#">monosaccharide catabolic process</a>	44	0.0068	1	0.0021	0.1258169	D
<input type="radio"/>	GO:0007052	5,4,9	<a href="#">mitotic spindle organization and biogenesis</a>	44	0.0068	1	0.0021	0.1258169	D
<input type="radio"/>	GO:0043632	6	<a href="#">modification-dependent macromolecule catabolic process</a>	155	0.0239	11	0.0235	0.1250803	D
<input type="radio"/>	GO:0009165	5,6	<a href="#">nucleotide biosynthetic process</a>	59	0.0091	2	0.0043	0.1237865	D
<input type="radio"/>	GO:0042592	4	<a href="#">homeostatic process</a>	134	0.0207	8	0.0171	0.1224636	D
<input type="radio"/>	GO:0030490	7,8	<a href="#">maturation of SSU-rRNA</a>	45	0.0069	1	0.0021	0.1193337	D
<input type="radio"/>	GO:0000462	8,9	<a href="#">maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)</a>	45	0.0069	1	0.0021	0.1193337	D

<input type="radio"/>	GO:0001510	7	<a href="#">RNA methylation</a>	60	0.0093	2	0.0043	0.1187557	D
<input type="radio"/>	GO:0006511	9,8,10	<a href="#">ubiquitin-dependent protein catabolic process</a>	148	0.0229	9	0.0192	0.1174732	D
<input type="radio"/>	GO:0019941	8,7,9	<a href="#">modification-dependent protein catabolic process</a>	148	0.0229	9	0.0192	0.1174732	D
<input type="radio"/>	GO:0007015	8	<a href="#">actin filament organization</a>	61	0.0094	2	0.0043	0.1138636	D
<input type="radio"/>	GO:0051603	7,8	<a href="#">proteolysis involved in cellular protein catabolic process</a>	151	0.0233	9	0.0192	0.1128326	D
<input type="radio"/>	GO:0032505	4,3	<a href="#">reproduction of a single-celled organism</a>	194	0.0300	14	0.0299	0.1117116	D
<input type="radio"/>	GO:0046164	5	<a href="#">alcohol catabolic process</a>	47	0.0073	1	0.0021	0.1071918	D
<input type="radio"/>	GO:0006508	6	<a href="#">proteolysis</a>	178	0.0275	11	0.0235	0.1066561	D
<input type="radio"/>	GO:0016569	9	<a href="#">covalent chromatin modification</a>	91	0.0141	4	0.0085	0.1064404	D
<input type="radio"/>	GO:0016570	10,8	<a href="#">histone modification</a>	91	0.0141	4	0.0085	0.1064404	D
<input type="radio"/>	GO:0022618	6,5	<a href="#">protein-RNA complex assembly</a>	144	0.0222	8	0.0171	0.1040768	D
<input type="radio"/>	GO:0042273	6,5	<a href="#">ribosomal large subunit biogenesis and assembly</a>	64	0.0099	2	0.0043	0.1000346	D
<input type="radio"/>	GO:0044257	6,7	<a href="#">cellular protein catabolic process</a>	160	0.0247	9	0.0192	0.0977480	D
<input type="radio"/>	GO:0030163	6,5	<a href="#">protein catabolic process</a>	173	0.0267	10	0.0214	0.0969454	D
<input type="radio"/>	GO:0030154	4	<a href="#">cell differentiation</a>	173	0.0267	10	0.0214	0.0969454	D
<input type="radio"/>	GO:0048869	3	<a href="#">cellular developmental process</a>	173	0.0267	10	0.0214	0.0969454	D
<input type="radio"/>	GO:0016197	7,5,6	<a href="#">endosome transport</a>	49	0.0076	1	0.0021	0.0961062	D
<input type="radio"/>	GO:0048610	3,4	<a href="#">reproductive cellular process</a>	149	0.0230	8	0.0171	0.0944170	D
<input type="radio"/>	GO:0022413	5,4	<a href="#">reproductive process in single-celled organism</a>	149	0.0230	8	0.0171	0.0944170	D
<input type="radio"/>	GO:0030435	5	<a href="#">sporulation</a>	123	0.0190	6	0.0128	0.0931374	D
<input type="radio"/>	GO:0042255	7,6	<a href="#">ribosome assembly</a>	66	0.0102	2	0.0043	0.0915260	D
<input type="radio"/>	GO:0044265	5	<a href="#">cellular macromolecule catabolic process</a>	314	0.0485	22	0.0470	0.0889327	D
<input type="radio"/>	GO:0006730	4	<a href="#">one-carbon compound metabolic process</a>	97	0.0150	4	0.0085	0.0877343	D
<input type="radio"/>	GO:0006790	4	<a href="#">sulfur metabolic process</a>	67	0.0103	2	0.0043	0.0874837	D
<input type="radio"/>	GO:0032787	6	<a href="#">monocarboxylic acid metabolic process</a>	126	0.0195	6	0.0128	0.0860658	D
<input type="radio"/>	GO:0032259	5	<a href="#">methylation</a>	83	0.0128	3	0.0064	0.0852806	D
<input type="radio"/>	GO:0043414	6	<a href="#">biopolymer methylation</a>	83	0.0128	3	0.0064	0.0852806	D
<input type="radio"/>	GO:0009057	4	<a href="#">macromolecule catabolic process</a>	345	0.0533	24	0.0513	0.0846640	D
<input type="radio"/>	GO:0022414	3,2	<a href="#">reproductive process</a>	183	0.0283	10	0.0214	0.0811163	D
<input type="radio"/>	GO:0007034	7,5,6	<a href="#">vacuolar transport</a>	114	0.0176	5	0.0107	0.0808482	D
<input type="radio"/>	GO:0019318	6,7	<a href="#">hexose metabolic process</a>	85	0.0131	3	0.0064	0.0788227	D
<input type="radio"/>	GO:0044248	4	<a href="#">cellular catabolic process</a>	425	0.0656	28	0.0598	0.0696131	D
<input type="radio"/>	GO:0009056	3	<a href="#">catabolic process</a>	438	0.0676	29	0.0620	0.0692008	D
<input type="radio"/>	GO:0030437	7,6	<a href="#">sporulation (sensu Fungi)</a>	108	0.0167	4	0.0085	0.0590890	D
<input type="radio"/>	GO:0048622	6,5	<a href="#">reproductive sporulation</a>	108	0.0167	4	0.0085	0.0590890	D
<input type="radio"/>	GO:0005996	5,6	<a href="#">monosaccharide metabolic process</a>	92	0.0142	3	0.0064	0.0590452	D
<input type="radio"/>	GO:0044262	5	<a href="#">cellular carbohydrate metabolic process</a>	213	0.0329	11	0.0235	0.0575650	D
<input type="radio"/>	GO:0009117	5	<a href="#">nucleotide metabolic process</a>	111	0.0171	4	0.0085	0.0526240	D
<input type="radio"/>	GO:0005975	4	<a href="#">carbohydrate metabolic process</a>	233	0.0360	12	0.0256	0.0506204	D
<input type="radio"/>	GO:0006364	6,7	<a href="#">rRNA processing</a>	249	0.0384	13	0.0278	0.0489057	D
<input type="radio"/>	GO:0016052	5	<a href="#">carbohydrate catabolic process</a>	80	0.0124	2	0.0043	0.0468178	D
<input type="radio"/>	GO:0044275	6	<a href="#">cellular carbohydrate catabolic process</a>	80	0.0124	2	0.0043	0.0468178	D
<input type="radio"/>	GO:0016072	6	<a href="#">rRNA metabolic process</a>	256	0.0395	13	0.0278	0.0415864	D
<input type="radio"/>	GO:0006006	7,8	<a href="#">glucose metabolic process</a>	65	0.0100	1	0.0021	0.0380750	D

<input type="radio"/>	GO:0000154	7,8	<a href="#">rRNA modification</a>	85	0.0131	2	0.0043	0.0362302	D
<input type="radio"/>	GO:0015980	4	<a href="#">energy derivation by oxidation of organic compounds</a>	145	0.0224	5	0.0107	0.0262153	D
<input type="radio"/>	GO:0006091	3	<a href="#">generation of precursor metabolites and energy</a>	183	0.0283	7	0.0150	0.0222315	D
<input type="radio"/>	GO:0022613	4	<a href="#">ribonucleoprotein complex biogenesis and assembly</a>	483	0.0746	25	0.0534	0.0140121	D
<input type="radio"/>	GO:0032196	3	<a href="#">transposition</a>	105	0.0162	2	0.0043	0.0121610	D
<input type="radio"/>	GO:0042254	5	<a href="#">ribosome biogenesis and assembly</a>	410	0.0633	19	0.0406	0.0080477	D
<input type="radio"/>	GO:0006412	6,5	<a href="#">translation</a>	688	0.1062	27	0.0577	5.509595E-05	D
<input type="radio"/>	GO:0043284	5	<a href="#">biopolymer biosynthetic process</a>	354	0.0547	3	0.0064	5.547249E-09	D