

# GO-Stats Results

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

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

Color codes			
<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:0022613	4	<a href="#">ribonucleoprotein complex biogenesis and assembly</a>	483	0.0746	174	0.1968	6.323328E-39	E
<input type="radio"/> GO:0042254	5	<a href="#">ribosome biogenesis and assembly</a>	410	0.0633	154	0.1742	9.405645E-37	E
<input type="radio"/> GO:0006139	4	<a href="#">nucleobase, nucleoside, nucleotide and nucleic acid metabolic process</a>	1532	0.2366	345	0.3903	1.086021E-28	E
<input type="radio"/> GO:0009987	2	<a href="#">cellular process</a>	4654	0.7187	764	0.8643	1.785442E-28	E
<input type="radio"/> GO:0016070	5	<a href="#">RNA metabolic process</a>	1058	0.1634	263	0.2975	1.106726E-27	E
<input type="radio"/> GO:0016043	3	<a href="#">cellular component organization and biogenesis</a>	2264	0.3496	448	0.5068	1.879484E-25	E
<input type="radio"/> GO:0006996	4	<a href="#">organelle organization and biogenesis</a>	1388	0.2143	312	0.3529	3.771544E-25	E
<input type="radio"/> GO:0006396	6	<a href="#">RNA processing</a>	491	0.0758	144	0.1629	1.328513E-21	E
<input type="radio"/> GO:0016072	6	<a href="#">rRNA metabolic process</a>	256	0.0395	90	0.1018	3.131783E-19	E
<input type="radio"/> GO:0006364	6,7	<a href="#">rRNA processing</a>	249	0.0384	86	0.0973	7.310371E-18	E
<input type="radio"/> GO:0008152	2	<a href="#">metabolic process</a>	3516	0.5429	584	0.6606	6.594483E-15	E
<input type="radio"/> GO:0044237	3	<a href="#">cellular metabolic process</a>	3403	0.5255	562	0.6357	3.069123E-13	E
<input type="radio"/> GO:0044238	3	<a href="#">primary metabolic process</a>	3247	0.5014	541	0.6120	3.251095E-13	E
<input type="radio"/> GO:0022607	4	<a href="#">cellular component assembly</a>	471	0.0727	118	0.1335	2.227130E-12	E
<input type="radio"/> GO:0042273	6,5	<a href="#">ribosomal large subunit biogenesis and assembly</a>	64	0.0099	32	0.0362	2.503119E-12	E
<input type="radio"/> GO:0022618	6,5	<a href="#">protein-RNA complex assembly</a>	144	0.0222	50	0.0566	5.388651E-11	E
<input type="radio"/> GO:0043283	4	<a href="#">biopolymer metabolic process</a>	2230	0.3443	387	0.4378	1.325072E-10	E
<input type="radio"/> GO:0065003	5,4	<a href="#">macromolecular complex assembly</a>	328	0.0506	85	0.0962	5.393963E-10	E
<input type="radio"/> 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	20	0.0226	7.776078E-10	E
<input type="radio"/> GO:0006399	6	<a href="#">tRNA metabolic process</a>	121	0.0187	42	0.0475	1.858972E-09	E
<input type="radio"/> GO:0000460	7,8	<a href="#">maturation of 5.8S rRNA</a>	26	0.0056	20	0.0226	3.060730E-	E

<input type="radio"/>	GO:0000460	7,9	<a href="#">maturation of 5.8S rRNA</a>	30	0.0030	20	0.0220	09	E
<input type="radio"/>	GO:0006360	8,7	<a href="#">transcription from RNA polymerase I promoter</a>	34	0.0053	18	0.0204	5.113028E-08	E
<input type="radio"/>	GO:0043170	3	<a href="#">macromolecule metabolic process</a>	2841	0.4387	458	0.5181	6.485669E-08	E
<input type="radio"/>	GO:0000463	8,9	<a href="#">maturation of LSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)</a>	14	0.0022	11	0.0124	6.842703E-08	E
<input type="radio"/>	GO:0000470	7,8	<a href="#">maturation of LSU-rRNA</a>	14	0.0022	11	0.0124	6.842703E-08	E
<input type="radio"/>	GO:0042255	7,6	<a href="#">ribosome assembly</a>	66	0.0102	26	0.0294	1.274073E-07	E
<input type="radio"/>	GO:0000027	9,7,8,6	<a href="#">ribosomal large subunit assembly and maintenance</a>	41	0.0063	19	0.0215	3.210693E-07	E
<input type="radio"/>	GO:0051168	9,7,8	<a href="#">nuclear export</a>	102	0.0158	32	0.0362	1.817682E-06	E
<input type="radio"/>	GO:0006351	7,6	<a href="#">transcription, DNA-dependent</a>	522	0.0806	107	0.1210	1.821465E-06	E
<input type="radio"/>	GO:0032774	6	<a href="#">RNA biosynthetic process</a>	524	0.0809	107	0.1210	2.175465E-06	E
<input type="radio"/>	GO:0006350	5	<a href="#">transcription</a>	567	0.0876	113	0.1278	3.666825E-06	E
<input type="radio"/>	GO:0000054	10,11,6,8,9	<a href="#">ribosome export from nucleus</a>	28	0.0043	14	0.0158	3.770343E-06	E
<input type="radio"/>	GO:0016071	6	<a href="#">mRNA metabolic process</a>	210	0.0324	52	0.0588	4.545593E-06	E
<input type="radio"/>	GO:0000398	8,10	<a href="#">nuclear mRNA splicing, via spliceosome</a>	102	0.0158	31	0.0351	5.303430E-06	E
<input type="radio"/>	GO:0000377	9	<a href="#">RNA splicing, via transesterification reactions with bulged adenosine as nucleophile</a>	103	0.0159	31	0.0351	6.571541E-06	E
<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	18	0.0204	8.122845E-06	E
<input type="radio"/>	GO:0030490	7,8	<a href="#">maturation of SSU-rRNA</a>	45	0.0069	18	0.0204	8.122845E-06	E
<input type="radio"/>	GO:0051169	7,5,6	<a href="#">nuclear transport</a>	129	0.0199	36	0.0407	8.127317E-06	E
<input type="radio"/>	GO:0006913	8,6,7	<a href="#">nucleocytoplasmic transport</a>	129	0.0199	36	0.0407	8.127317E-06	E
<input type="radio"/>	GO:0000375	8	<a href="#">RNA splicing, via transesterification reactions</a>	110	0.0170	32	0.0362	1.007128E-05	E
<input type="radio"/>	GO:0042257	8,7	<a href="#">ribosomal subunit assembly</a>	55	0.0085	20	0.0226	1.364169E-05	E
<input type="radio"/>	GO:0006611	9,10,7,8	<a href="#">protein export from nucleus</a>	56	0.0086	20	0.0226	1.836502E-05	E
<input type="radio"/>	GO:0008033	7	<a href="#">tRNA processing</a>	84	0.0130	26	0.0294	2.019380E-05	E
<input type="radio"/>	GO:0006082	4	<a href="#">organic acid metabolic process</a>	314	0.0485	68	0.0769	2.128670E-05	E
<input type="radio"/>	GO:0019752	5	<a href="#">carboxylic acid metabolic process</a>	314	0.0485	68	0.0769	2.128670E-05	E
<input type="radio"/>	GO:0043039	7,8	<a href="#">tRNA aminoacylation</a>	32	0.0049	14	0.0158	2.481018E-05	E
<input type="radio"/>	GO:0043038	6,7	<a href="#">amino acid activation</a>	32	0.0049	14	0.0158	2.481018E-05	E
<input type="radio"/>	GO:0006418	8,7,9,6	<a href="#">tRNA aminoacylation for protein translation</a>	32	0.0049	14	0.0158	2.481018E-05	E
<input type="radio"/>	GO:0006397	7	<a href="#">mRNA processing</a>	157	0.0242	40	0.0452	2.601986E-05	E
<input type="radio"/>	GO:0006519	4	<a href="#">amino acid and derivative metabolic process</a>	202	0.0312	48	0.0543	3.024353E-05	E
<input type="radio"/>	GO:0006400	7,8	<a href="#">tRNA modification</a>	52	0.0080	18	0.0204	7.335819E-05	E
<input type="radio"/>	GO:0006520	5,6	<a href="#">amino acid metabolic process</a>	187	0.0289	44	0.0498	7.715308E-05	E
<input type="radio"/>	GO:0006355	8,7	<a href="#">regulation of transcription, DNA-dependent</a>	359	0.0554	72	0.0814	0.0001424	E

<input type="radio"/>	GO:0022403	5,4	<a href="#">cell cycle phase</a>	353	0.0545	71	0.0803	0.0001441	E
<input type="radio"/>	GO:0008380	7	<a href="#">RNA splicing</a>	132	0.0204	33	0.0373	0.0001704	E
<input type="radio"/>	GO:0006725	4	<a href="#">aromatic compound metabolic process</a>	60	0.0093	19	0.0215	0.0001721	E
<input type="radio"/>	GO:0007049	3	<a href="#">cell cycle</a>	458	0.0707	87	0.0984	0.0002107	E
<input type="radio"/>	GO:0006997	5	<a href="#">nuclear organization and biogenesis</a>	57	0.0088	18	0.0204	0.0002586	E
<input type="radio"/>	GO:0045449	7,6	<a href="#">regulation of transcription</a>	386	0.0596	75	0.0848	0.0002716	E
<input type="radio"/>	GO:0019856	7,6	<a href="#">pyrimidine base biosynthetic process</a>	15	0.0023	8	0.0090	0.0002724	E
<input type="radio"/>	GO:0000279	6,5	<a href="#">M phase</a>	258	0.0398	54	0.0611	0.0002963	E
<input type="radio"/>	GO:0022402	4,3	<a href="#">cell cycle process</a>	439	0.0678	83	0.0939	0.0003244	E
<input type="radio"/>	GO:0006413	7,6	<a href="#">translational initiation</a>	49	0.0076	16	0.0181	0.0003651	E
<input type="radio"/>	GO:0044249	4	<a href="#">cellular biosynthetic process</a>	366	0.0565	71	0.0803	0.0003925	E
<input type="radio"/>	GO:0009308	4	<a href="#">amine metabolic process</a>	228	0.0352	48	0.0543	0.0005154	E
<input type="radio"/>	GO:0018193	7	<a href="#">peptidyl-amino acid modification</a>	28	0.0043	11	0.0124	0.0005280	E
<input type="radio"/>	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	9	0.0102	0.0005384	E
<input type="radio"/>	GO:0000479	8,9	<a href="#">endonucleolytic cleavage of tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)</a>	20	0.0031	9	0.0102	0.0005384	E
<input type="radio"/>	GO:0000478	7,8	<a href="#">endonucleolytic cleavages during rRNA processing</a>	20	0.0031	9	0.0102	0.0005384	E
<input type="radio"/>	GO:0007126	8,6,7,5	<a href="#">meiosis</a>	148	0.0229	34	0.0385	0.0006500	E
<input type="radio"/>	GO:0051321	4	<a href="#">meiotic cell cycle</a>	148	0.0229	34	0.0385	0.0006500	E
<input type="radio"/>	GO:0051327	7,5,6	<a href="#">M phase of meiotic cell cycle</a>	148	0.0229	34	0.0385	0.0006500	E
<input type="radio"/>	GO:0030476	8,6,7	<a href="#">spore wall assembly (sensu Fungi)</a>	42	0.0065	14	0.0158	0.0006516	E
<input type="radio"/>	GO:0042244	5,6	<a href="#">spore wall assembly</a>	42	0.0065	14	0.0158	0.0006516	E
<input type="radio"/>	GO:0048610	3,4	<a href="#">reproductive cellular process</a>	149	0.0230	34	0.0385	0.0007291	E
<input type="radio"/>	GO:0022413	5,4	<a href="#">reproductive process in single-celled organism</a>	149	0.0230	34	0.0385	0.0007291	E
<input type="radio"/>	GO:0006206	6	<a href="#">pyrimidine base metabolic process</a>	17	0.0026	8	0.0090	0.0007688	E
<input type="radio"/>	GO:0019219	6,5	<a href="#">regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process</a>	440	0.0679	81	0.0916	0.0007813	E
<input type="radio"/>	GO:0006357	9,8	<a href="#">regulation of transcription from RNA polymerase II promoter</a>	221	0.0341	46	0.0520	0.0008139	E
<input type="radio"/>	GO:0065007	2	<a href="#">biological regulation</a>	948	0.1464	157	0.1776	0.0008453	E
<input type="radio"/>	GO:0031323	5,4	<a href="#">regulation of cellular metabolic process</a>	507	0.0783	91	0.1029	0.0008808	E
<input type="radio"/>	GO:0006401	6	<a href="#">RNA catabolic process</a>	74	0.0114	20	0.0226	0.0010171	E
<input type="radio"/>	GO:0019222	4,3	<a href="#">regulation of metabolic process</a>	538	0.0831	95	0.1075	0.0011342	E
<input type="radio"/>	GO:0048284	5	<a href="#">organelle fusion</a>	22	0.0034	9	0.0102	0.0011916	E
<input type="radio"/>	GO:0048622	6,5	<a href="#">reproductive sporulation</a>	108	0.0167	26	0.0294	0.0012469	E
<input type="radio"/>	GO:0030437	7,6	<a href="#">sporulation (sensu Fungi)</a>	108	0.0167	26	0.0294	0.0012469	E
<input type="radio"/>	GO:0006807	3	<a href="#">nitrogen compound metabolic process</a>	251	0.0388	50	0.0566	0.0012883	E
<input type="radio"/>	GO:0009112	5	<a href="#">nucleobase metabolic process</a>	31	0.0048	11	0.0124	0.0013455	E
<input type="radio"/>	GO:0046483	4	<a href="#">heterocycle metabolic process</a>	76	0.0117	20	0.0226	0.0014085	E
<input type="radio"/>	GO:0051234	2,3	<a href="#">establishment of localization</a>	1004	0.1550	163	0.1844	0.0014840	E
<input type="radio"/>	GO:0006406	11,9,6,8,10,7	<a href="#">mRNA export from nucleus</a>	66	0.0102	18	0.0204	0.0015472	E
<input type="radio"/>	GO:0051028	5,7,6,8	<a href="#">mRNA transport</a>	66	0.0102	18	0.0204	0.0015472	E
<input type="radio"/>	GO:0006366	8,7	<a href="#">transcription from RNA polymerase II promoter</a>	343	0.0530	64	0.0724	0.0016644	E
<input type="radio"/>	GO:0042816	6	<a href="#">vitamin B6 metabolic process</a>	8	0.0012	5	0.0057	0.0016960	E

<input type="checkbox"/>	GO:0008614	7	<a href="#">pyridoxine metabolic process</a>	8	0.0012	5	0.0057	0.0016960	E
<input type="checkbox"/>	GO:0009890	6,5	<a href="#">negative regulation of biosynthetic process</a>	8	0.0012	5	0.0057	0.0016960	E
<input type="checkbox"/>	GO:0016073	6	<a href="#">snRNA metabolic process</a>	15	0.0023	7	0.0079	0.0017345	E
<input type="checkbox"/>	GO:0006810	3,4	<a href="#">transport</a>	981	0.1515	159	0.1799	0.0017452	E
<input type="checkbox"/>	GO:0051179	2	<a href="#">localization</a>	1051	0.1623	169	0.1912	0.0018013	E
<input type="checkbox"/>	GO:0022414	3,2	<a href="#">reproductive process</a>	183	0.0283	38	0.0430	0.0020484	E
<input type="checkbox"/>	GO:0006403	4	<a href="#">RNA localization</a>	90	0.0139	22	0.0249	0.0022049	E
<input type="checkbox"/>	GO:0007010	5	<a href="#">cytoskeleton organization and biogenesis</a>	227	0.0351	45	0.0509	0.0022146	E
<input type="checkbox"/>	GO:0006405	10,8,5,7,9,6	<a href="#">RNA export from nucleus</a>	79	0.0122	20	0.0226	0.0022173	E
<input type="checkbox"/>	GO:0051276	5	<a href="#">chromosome organization and biogenesis</a>	572	0.0883	98	0.1109	0.0022325	E
<input type="checkbox"/>	GO:0051301	3	<a href="#">cell division</a>	246	0.0380	48	0.0543	0.0022577	E
<input type="checkbox"/>	GO:0000096	6,7,5	<a href="#">sulfur amino acid metabolic process</a>	33	0.0051	11	0.0124	0.0022986	E
<input type="checkbox"/>	GO:0006555	7,8,6	<a href="#">methionine metabolic process</a>	24	0.0037	9	0.0102	0.0023404	E
<input type="checkbox"/>	GO:0007001	6	<a href="#">chromosome organization and biogenesis (sensu Eukaryota)</a>	567	0.0876	97	0.1097	0.0024091	E
<input type="checkbox"/>	GO:0006383	8,7	<a href="#">transcription from RNA polymerase III promoter</a>	38	0.0059	12	0.0136	0.0024348	E
<input type="checkbox"/>	GO:0050657	5,6	<a href="#">nucleic acid transport</a>	80	0.0124	20	0.0226	0.0025571	E
<input type="checkbox"/>	GO:0050658	4,6,5,7	<a href="#">RNA transport</a>	80	0.0124	20	0.0226	0.0025571	E
<input type="checkbox"/>	GO:0051236	3,4,5	<a href="#">establishment of RNA localization</a>	80	0.0124	20	0.0226	0.0025571	E
<input type="checkbox"/>	GO:0043412	5	<a href="#">biopolymer modification</a>	664	0.1025	111	0.1256	0.0026815	E
<input type="checkbox"/>	GO:0000003	2	<a href="#">reproduction</a>	323	0.0499	59	0.0667	0.0034766	E
<input type="checkbox"/>	GO:0046112	6,5	<a href="#">nucleobase biosynthetic process</a>	21	0.0032	8	0.0090	0.0035920	E
<input type="checkbox"/>	GO:0030435	5	<a href="#">sporulation</a>	123	0.0190	27	0.0305	0.0036059	E
<input type="checkbox"/>	GO:0015837	4,5	<a href="#">amine transport</a>	50	0.0077	14	0.0158	0.0036135	E
<input type="checkbox"/>	GO:0017148	8,7,6	<a href="#">negative regulation of protein biosynthetic process</a>	6	0.0009	4	0.0045	0.0038652	E
<input type="checkbox"/>	GO:0031327	7,6	<a href="#">negative regulation of cellular biosynthetic process</a>	6	0.0009	4	0.0045	0.0038652	E
<input type="checkbox"/>	GO:0016074	6	<a href="#">snoRNA metabolic process</a>	17	0.0026	7	0.0079	0.0039155	E
<input type="checkbox"/>	GO:0000097	7,8,6	<a href="#">sulfur amino acid biosynthetic process</a>	13	0.0020	6	0.0068	0.0039394	E
<input type="checkbox"/>	GO:0006259	5	<a href="#">DNA metabolic process</a>	523	0.0808	88	0.0995	0.0048930	E
<input type="checkbox"/>	GO:0032505	4,3	<a href="#">reproduction of a single-celled organism</a>	194	0.0300	38	0.0430	0.0049413	E
<input type="checkbox"/>	GO:0006631	5,7,6	<a href="#">fatty acid metabolic process</a>	47	0.0073	13	0.0147	0.0053515	E
<input type="checkbox"/>	GO:0050794	4,3	<a href="#">regulation of cellular process</a>	738	0.1140	119	0.1346	0.0053737	E
<input type="checkbox"/>	GO:0000183	11,7,8,12,10	<a href="#">chromatin silencing at rDNA</a>	18	0.0028	7	0.0079	0.0055372	E
<input type="checkbox"/>	GO:0050789	3	<a href="#">regulation of biological process</a>	761	0.1175	122	0.1380	0.0057694	E
<input type="checkbox"/>	GO:0009117	5	<a href="#">nucleotide metabolic process</a>	111	0.0171	24	0.0271	0.0064678	E
<input type="checkbox"/>	GO:0051649	5,3,4	<a href="#">establishment of cellular localization</a>	606	0.0936	99	0.1120	0.0065730	E
<input type="checkbox"/>	GO:0046907	6,4,5	<a href="#">intracellular transport</a>	545	0.0842	90	0.1018	0.0067574	E
<input type="checkbox"/>	GO:0006402	7	<a href="#">mRNA catabolic process</a>	60	0.0093	15	0.0170	0.0074966	E
<input type="checkbox"/>	GO:0045892	9,8	<a href="#">negative regulation of transcription, DNA-dependent</a>	156	0.0241	31	0.0351	0.0076816	E
<input type="checkbox"/>	GO:0043331	4	<a href="#">response to dsRNA</a>	7	0.0011	4	0.0045	0.0077921	E
<input type="checkbox"/>	GO:0051707	3,4	<a href="#">response to other organism</a>	7	0.0011	4	0.0045	0.0077921	E
<input type="checkbox"/>	GO:0009615	4,5	<a href="#">response to virus</a>	7	0.0011	4	0.0045	0.0077921	E
<input type="checkbox"/>	GO:0043330	5,6	<a href="#">response to exogenous dsRNA</a>	7	0.0011	4	0.0045	0.0077921	E
<input type="checkbox"/>	GO:0030488	8,9	<a href="#">tRNA methylation</a>	15	0.0023	6	0.0068	0.0085799	E
<input type="checkbox"/>	GO:0015021	4,5	<a href="#">nucleobase, nucleoside, nucleotide and</a>	90	0.0130	20	0.0226	0.0086206	E

<input type="radio"/>	GO:0015951	4,3	<a href="#">nucleic acid transport</a>	90	0.0139	20	0.0220	0.0080290	E
<input type="radio"/>	GO:0051641	4,3	<a href="#">cellular localization</a>	642	0.0991	103	0.1165	0.0086414	E
<input type="radio"/>	GO:0045943	10,9	<a href="#">positive regulation of transcription from RNA polymerase I promoter</a>	4	0.0006	3	0.0034	0.0087636	E
<input type="radio"/>	GO:0008053	6	<a href="#">mitochondrial fusion</a>	4	0.0006	3	0.0034	0.0087636	E
<input type="radio"/>	GO:0032502	2	<a href="#">developmental process</a>	436	0.0673	73	0.0826	0.0088412	E
<input type="radio"/>	GO:0033036	3	<a href="#">macromolecule localization</a>	382	0.0590	65	0.0735	0.0089594	E
<input type="radio"/>	GO:0006629	4	<a href="#">lipid metabolic process</a>	242	0.0374	44	0.0498	0.0090056	E
<input type="radio"/>	GO:0000055	11,12,7,9,10	<a href="#">ribosomal large subunit export from nucleus</a>	11	0.0017	5	0.0057	0.0090268	E
<input type="radio"/>	GO:0019395	6,8,7	<a href="#">fatty acid oxidation</a>	11	0.0017	5	0.0057	0.0090268	E
<input type="radio"/>	GO:0031324	6,5	<a href="#">negative regulation of cellular metabolic process</a>	198	0.0306	37	0.0419	0.0099057	E
<input type="radio"/>	GO:0007097	7,8,5,6	<a href="#">nuclear migration</a>	20	0.0031	7	0.0079	0.0100732	E
<input type="radio"/>	GO:0040023	6,7,4,5	<a href="#">establishment of nucleus localization</a>	20	0.0031	7	0.0079	0.0100732	E
<input type="radio"/>	GO:0051647	6,5	<a href="#">nucleus localization</a>	20	0.0031	7	0.0079	0.0100732	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	34	0.0385	0.0101349	E
<input type="radio"/>	GO:0031497	5,9	<a href="#">chromatin assembly</a>	104	0.0161	22	0.0249	0.0104487	E
<input type="radio"/>	GO:0006605	8,6,7	<a href="#">protein targeting</a>	258	0.0398	46	0.0520	0.0104630	E
<input type="radio"/>	GO:0000278	4	<a href="#">mitotic cell cycle</a>	266	0.0411	47	0.0532	0.0111992	E
<input type="radio"/>	GO:0016481	8,7	<a href="#">negative regulation of transcription</a>	162	0.0250	31	0.0351	0.0117682	E
<input type="radio"/>	GO:0006464	6	<a href="#">protein modification process</a>	520	0.0803	84	0.0950	0.0118289	E
<input type="radio"/>	GO:0015698	6,7	<a href="#">inorganic anion transport</a>	16	0.0025	6	0.0068	0.0118624	E
<input type="radio"/>	GO:0006886	7,5,6	<a href="#">intracellular protein transport</a>	274	0.0423	48	0.0543	0.0119377	E
<input type="radio"/>	GO:0009892	5,4	<a href="#">negative regulation of metabolic process</a>	208	0.0321	38	0.0430	0.0121517	E
<input type="radio"/>	GO:0007062	7,4	<a href="#">sister chromatid cohesion</a>	31	0.0048	9	0.0102	0.0130033	E
<input type="radio"/>	GO:0007059	3	<a href="#">chromosome segregation</a>	119	0.0184	24	0.0271	0.0130563	E
<input type="radio"/>	GO:0000083	10,9,6,5,7,8,4	<a href="#">G1/S-specific transcription in mitotic cell cycle</a>	12	0.0019	5	0.0057	0.0133706	E
<input type="radio"/>	GO:0015677	9,10	<a href="#">copper ion import</a>	8	0.0012	4	0.0045	0.0134642	E
<input type="radio"/>	GO:0032787	6	<a href="#">monocarboxylic acid metabolic process</a>	126	0.0195	25	0.0283	0.0137824	E
<input type="radio"/>	GO:0007017	6	<a href="#">microtubule-based process</a>	101	0.0156	21	0.0238	0.0138038	E
<input type="radio"/>	GO:0009165	5,6	<a href="#">nucleotide biosynthetic process</a>	59	0.0091	14	0.0158	0.0138235	E
<input type="radio"/>	GO:0006767	5	<a href="#">water-soluble vitamin metabolic process</a>	89	0.0137	19	0.0215	0.0141598	E
<input type="radio"/>	GO:0006766	4	<a href="#">vitamin metabolic process</a>	89	0.0137	19	0.0215	0.0141598	E
<input type="radio"/>	GO:0015031	4,5,6	<a href="#">protein transport</a>	280	0.0432	48	0.0543	0.0156450	E
<input type="radio"/>	GO:0016053	5	<a href="#">organic acid biosynthetic process</a>	17	0.0026	6	0.0068	0.0158411	E
<input type="radio"/>	GO:0006820	5,6	<a href="#">anion transport</a>	17	0.0026	6	0.0068	0.0158411	E
<input type="radio"/>	GO:0000742	7,5	<a href="#">karyogamy during conjugation with cellular fusion</a>	17	0.0026	6	0.0068	0.0158411	E
<input type="radio"/>	GO:0000741	6	<a href="#">karyogamy</a>	17	0.0026	6	0.0068	0.0158411	E
<input type="radio"/>	GO:0046394	6	<a href="#">carboxylic acid biosynthetic process</a>	17	0.0026	6	0.0068	0.0158411	E
<input type="radio"/>	GO:0044272	5	<a href="#">sulfur compound biosynthetic process</a>	22	0.0034	7	0.0079	0.0165487	E
<input type="radio"/>	GO:0007064	10,8,5,6,9,7,4	<a href="#">mitotic sister chromatid cohesion</a>	22	0.0034	7	0.0079	0.0165487	E
<input type="radio"/>	GO:0015849	4,5	<a href="#">organic acid transport</a>	55	0.0085	13	0.0147	0.0172138	E
<input type="radio"/>	GO:0008643	4,5	<a href="#">carbohydrate transport</a>	38	0.0059	10	0.0113	0.0172585	E
<input type="radio"/>	GO:0044255	4,5	<a href="#">cellular lipid metabolic process</a>	229	0.0354	40	0.0452	0.0180052	E
<input type="radio"/>	GO:0043687	7	<a href="#">post-translational protein modification</a>	388	0.0599	63	0.0713	0.0185824	E

<input type="checkbox"/>	GO:0046516	6	<a href="#">hypusine metabolic process</a>	2	0.0003	2	0.0023	0.0186151	E
<input type="checkbox"/>	GO:0046039	9	<a href="#">GTP metabolic process</a>	2	0.0003	2	0.0023	0.0186151	E
<input type="checkbox"/>	GO:0045141	9,7,5,8,6,4	<a href="#">telomere clustering</a>	2	0.0003	2	0.0023	0.0186151	E
<input type="checkbox"/>	GO:0007000	6	<a href="#">nucleolus organization and biogenesis</a>	2	0.0003	2	0.0023	0.0186151	E
<input type="checkbox"/>	GO:0006426	9,8,10,7	<a href="#">glycyl-tRNA aminoacylation</a>	2	0.0003	2	0.0023	0.0186151	E
<input type="checkbox"/>	GO:0015824	7,8,9	<a href="#">proline transport</a>	2	0.0003	2	0.0023	0.0186151	E
<input type="checkbox"/>	GO:0006183	9,10	<a href="#">GTP biosynthetic process</a>	2	0.0003	2	0.0023	0.0186151	E
<input type="checkbox"/>	GO:0046515	7,6	<a href="#">hypusine biosynthetic process</a>	2	0.0003	2	0.0023	0.0186151	E
<input type="checkbox"/>	GO:0015723	7,8	<a href="#">bilirubin transport</a>	2	0.0003	2	0.0023	0.0186151	E
<input type="checkbox"/>	GO:0015804	6,7,8	<a href="#">neutral amino acid transport</a>	2	0.0003	2	0.0023	0.0186151	E
<input type="checkbox"/>	GO:0000316	7,8	<a href="#">sulfite transport</a>	2	0.0003	2	0.0023	0.0186151	E
<input type="checkbox"/>	GO:0015691	7,8,9	<a href="#">cadmium ion transport</a>	2	0.0003	2	0.0023	0.0186151	E
<input type="checkbox"/>	GO:0006633	7,6,8,5	<a href="#">fatty acid biosynthetic process</a>	13	0.0020	5	0.0057	0.0187727	E
<input type="checkbox"/>	GO:0043630	9,10	<a href="#">ncRNA polyadenylation during polyadenylation-dependent ncRNA catabolic process</a>	5	0.0008	3	0.0034	0.0189267	E
<input type="checkbox"/>	GO:0017182	9	<a href="#">peptidyl-diphthamide metabolic process</a>	5	0.0008	3	0.0034	0.0189267	E
<input type="checkbox"/>	GO:0043629	9	<a href="#">ncRNA polyadenylation</a>	5	0.0008	3	0.0034	0.0189267	E
<input type="checkbox"/>	GO:0016075	7	<a href="#">rRNA catabolic process</a>	5	0.0008	3	0.0034	0.0189267	E
<input type="checkbox"/>	GO:0017183	10,4	<a href="#">peptidyl-diphthamide biosynthetic process from peptidyl-histidine</a>	5	0.0008	3	0.0034	0.0189267	E
<input type="checkbox"/>	GO:0006221	6,7	<a href="#">pyrimidine nucleotide biosynthetic process</a>	5	0.0008	3	0.0034	0.0189267	E
<input type="checkbox"/>	GO:0018202	8	<a href="#">peptidyl-histidine modification</a>	5	0.0008	3	0.0034	0.0189267	E
<input type="checkbox"/>	GO:0065004	6,5	<a href="#">protein-DNA complex assembly</a>	74	0.0114	16	0.0181	0.0193592	E
<input type="checkbox"/>	GO:0030001	6,7	<a href="#">metal ion transport</a>	62	0.0096	14	0.0158	0.0195227	E
<input type="checkbox"/>	GO:0006865	5,6,7	<a href="#">amino acid transport</a>	39	0.0060	10	0.0113	0.0200589	E
<input type="checkbox"/>	GO:0006635	7,9,8	<a href="#">fatty acid beta-oxidation</a>	9	0.0014	4	0.0045	0.0209383	E
<input type="checkbox"/>	GO:0006325	7	<a href="#">establishment and/or maintenance of chromatin architecture</a>	253	0.0391	43	0.0486	0.0210468	E
<input type="checkbox"/>	GO:0006323	6	<a href="#">DNA packaging</a>	253	0.0391	43	0.0486	0.0210468	E
<input type="checkbox"/>	GO:0009451	6	<a href="#">RNA modification</a>	139	0.0215	26	0.0294	0.0214705	E
<input type="checkbox"/>	GO:0007154	3	<a href="#">cell communication</a>	240	0.0371	41	0.0464	0.0216630	E
<input type="checkbox"/>	GO:0015674	6,7	<a href="#">di-, tri-valent inorganic cation transport</a>	34	0.0053	9	0.0102	0.0218365	E
<input type="checkbox"/>	GO:0045184	3,4,5	<a href="#">establishment of protein localization</a>	296	0.0457	49	0.0554	0.0223517	E
<input type="checkbox"/>	GO:0048869	3	<a href="#">cellular developmental process</a>	173	0.0267	31	0.0351	0.0224732	E
<input type="checkbox"/>	GO:0030154	4	<a href="#">cell differentiation</a>	173	0.0267	31	0.0351	0.0224732	E
<input type="checkbox"/>	GO:0006468	8,7	<a href="#">protein amino acid phosphorylation</a>	101	0.0156	20	0.0226	0.0228312	E
<input type="checkbox"/>	GO:0006342	10,6,7,11,9	<a href="#">chromatin silencing</a>	95	0.0147	19	0.0215	0.0235007	E
<input type="checkbox"/>	GO:0045814	5	<a href="#">negative regulation of gene expression, epigenetic</a>	95	0.0147	19	0.0215	0.0235007	E
<input type="checkbox"/>	GO:0016458	5	<a href="#">gene silencing</a>	95	0.0147	19	0.0215	0.0235007	E
<input type="checkbox"/>	GO:0031507	6,10	<a href="#">heterochromatin formation</a>	95	0.0147	19	0.0215	0.0235007	E
<input type="checkbox"/>	GO:0051656	6,3,5,4	<a href="#">establishment of organelle localization</a>	29	0.0045	8	0.0090	0.0235748	E
<input type="checkbox"/>	GO:0042364	6	<a href="#">water-soluble vitamin biosynthetic process</a>	46	0.0071	11	0.0124	0.0238249	E
<input type="checkbox"/>	GO:0009110	5	<a href="#">vitamin biosynthetic process</a>	46	0.0071	11	0.0124	0.0238249	E
<input type="checkbox"/>	GO:0009066	6,7	<a href="#">aspartate family amino acid metabolic process</a>	46	0.0071	11	0.0124	0.0238249	E
<input type="checkbox"/>	GO:0007165	4	<a href="#">signal transduction</a>	209	0.0323	36	0.0407	0.0248329	E
<input type="checkbox"/>	GO:0016568	8	<a href="#">chromatin modification</a>	223	0.0344	38	0.0430	0.0251235	E

<input type="radio"/>	GO:0006825	8,9	<a href="#">copper ion transport</a>	14	0.0022	5	0.0057	0.0252303	E
<input type="radio"/>	GO:0009123	6	<a href="#">nucleoside monophosphate metabolic process</a>	19	0.0029	6	0.0068	0.0259281	E
<input type="radio"/>	GO:0000245	7,6,9,11	<a href="#">spliceosome assembly</a>	19	0.0029	6	0.0068	0.0259281	E
<input type="radio"/>	GO:0030466	11,7,8,12,10	<a href="#">chromatin silencing at silent mating-type cassette</a>	30	0.0046	8	0.0090	0.0277793	E
<input type="radio"/>	GO:0006665	6,7	<a href="#">sphingolipid metabolic process</a>	30	0.0046	8	0.0090	0.0277793	E
<input type="radio"/>	GO:0007242	5	<a href="#">intracellular signaling cascade</a>	137	0.0212	25	0.0283	0.0280672	E
<input type="radio"/>	GO:0000747	4	<a href="#">conjugation with cellular fusion</a>	118	0.0182	22	0.0249	0.0297083	E
<input type="radio"/>	GO:0019953	3	<a href="#">sexual reproduction</a>	118	0.0182	22	0.0249	0.0297083	E
<input type="radio"/>	GO:0000746	3	<a href="#">conjugation</a>	118	0.0182	22	0.0249	0.0297083	E
<input type="radio"/>	GO:0046942	5,6	<a href="#">carboxylic acid transport</a>	54	0.0083	12	0.0136	0.0299649	E
<input type="radio"/>	GO:0007129	10,8,7,5,9,6,4	<a href="#">synapsis</a>	10	0.0015	4	0.0045	0.0301485	E
<input type="radio"/>	GO:0006281	6,5	<a href="#">DNA repair</a>	193	0.0298	33	0.0373	0.0302044	E
<input type="radio"/>	GO:0045229	4	<a href="#">external encapsulating structure organization and biogenesis</a>	200	0.0309	34	0.0385	0.0303044	E
<input type="radio"/>	GO:0007047	5	<a href="#">cell wall organization and biogenesis</a>	200	0.0309	34	0.0385	0.0303044	E
<input type="radio"/>	GO:0051704	2	<a href="#">multi-organism process</a>	139	0.0215	25	0.0283	0.0312334	E
<input type="radio"/>	GO:0006333	8	<a href="#">chromatin assembly or disassembly</a>	119	0.0184	22	0.0249	0.0315049	E
<input type="radio"/>	GO:0006790	4	<a href="#">sulfur metabolic process</a>	67	0.0103	14	0.0158	0.0316914	E
<input type="radio"/>	GO:0042724	7	<a href="#">thiamin and derivative biosynthetic process</a>	20	0.0031	6	0.0068	0.0320035	E
<input type="radio"/>	GO:0008652	6,7	<a href="#">amino acid biosynthetic process</a>	106	0.0164	20	0.0226	0.0320663	E
<input type="radio"/>	GO:0030473	8,9,6,7	<a href="#">nuclear migration, microtubule-mediated</a>	15	0.0023	5	0.0057	0.0326975	E
<input type="radio"/>	GO:0031365	8	<a href="#">N-terminal protein amino acid modification</a>	15	0.0023	5	0.0057	0.0326975	E
<input type="radio"/>	GO:0007018	8,7,6	<a href="#">microtubule-based movement</a>	15	0.0023	5	0.0057	0.0326975	E
<input type="radio"/>	GO:0018409	9	<a href="#">peptide or protein amino-terminal blocking</a>	15	0.0023	5	0.0057	0.0326975	E
<input type="radio"/>	GO:0007089	8,9,7,6	<a href="#">traversing start control point of mitotic cell cycle</a>	6	0.0009	3	0.0034	0.0326998	E
<input type="radio"/>	GO:0040029	4	<a href="#">regulation of gene expression, epigenetic</a>	100	0.0154	19	0.0215	0.0333249	E
<input type="radio"/>	GO:0007067	8,6,7,5	<a href="#">mitosis</a>	127	0.0196	23	0.0260	0.0338261	E
<input type="radio"/>	GO:0009309	5,6	<a href="#">amine biosynthetic process</a>	114	0.0176	21	0.0238	0.0347167	E
<input type="radio"/>	GO:0048523	5,4	<a href="#">negative regulation of cellular process</a>	239	0.0369	39	0.0441	0.0349082	E
<input type="radio"/>	GO:0045941	8,7	<a href="#">positive regulation of transcription</a>	101	0.0156	19	0.0215	0.0354779	E
<input type="radio"/>	GO:0051029	5,7,6,8	<a href="#">rRNA transport</a>	26	0.0040	7	0.0079	0.0355831	E
<input type="radio"/>	GO:0006407	11,9,6,8,10,7	<a href="#">rRNA export from nucleus</a>	26	0.0040	7	0.0079	0.0355831	E
<input type="radio"/>	GO:0051640	5,4	<a href="#">organelle localization</a>	56	0.0086	12	0.0136	0.0364315	E
<input type="radio"/>	GO:0006796	5	<a href="#">phosphate metabolic process</a>	212	0.0327	35	0.0396	0.0365099	E
<input type="radio"/>	GO:0006793	4	<a href="#">phosphorus metabolic process</a>	212	0.0327	35	0.0396	0.0365099	E
<input type="radio"/>	GO:0044271	5,4	<a href="#">nitrogen compound biosynthetic process</a>	115	0.0178	21	0.0238	0.0367112	E
<input type="radio"/>	GO:0006811	4,5	<a href="#">ion transport</a>	115	0.0178	21	0.0238	0.0367112	E
<input type="radio"/>	GO:0045893	9,8	<a href="#">positive regulation of transcription, DNA-dependent</a>	95	0.0147	18	0.0204	0.0369360	E
<input type="radio"/>	GO:0009653	4,3	<a href="#">anatomical structure morphogenesis</a>	248	0.0383	40	0.0452	0.0369959	E
<input type="radio"/>	GO:0000902	5,6	<a href="#">cell morphogenesis</a>	248	0.0383	40	0.0452	0.0369959	E
<input type="radio"/>	GO:0032989	4,5	<a href="#">cellular structure morphogenesis</a>	248	0.0383	40	0.0452	0.0369959	E
<input type="radio"/>	GO:0048856	3	<a href="#">anatomical structure development</a>	248	0.0383	40	0.0452	0.0369959	E
<input type="radio"/>	GO:0006310	6	<a href="#">DNA recombination</a>	122	0.0188	22	0.0249	0.0371499	E
<input type="radio"/>	GO:0019932	6	<a href="#">second-messenger-mediated signaling</a>	32	0.0049	8	0.0090	0.0372746	E

<input type="checkbox"/>	GO:0000087	7,5,6	<a href="#">M phase of mitotic cell cycle</a>	129	0.0199	23	0.0260	0.0374941	E
<input type="checkbox"/>	GO:0008610	5,4,6	<a href="#">lipid biosynthetic process</a>	129	0.0199	23	0.0260	0.0374941	E
<input type="checkbox"/>	GO:0030003	8,6	<a href="#">cellular cation homeostasis</a>	102	0.0158	19	0.0215	0.0376835	E
<input type="checkbox"/>	GO:0055080	7	<a href="#">cation homeostasis</a>	102	0.0158	19	0.0215	0.0376835	E
<input type="checkbox"/>	GO:0048519	4	<a href="#">negative regulation of biological process</a>	242	0.0374	39	0.0441	0.0383016	E
<input type="checkbox"/>	GO:0031325	6,5	<a href="#">positive regulation of cellular metabolic process</a>	116	0.0179	21	0.0238	0.0387447	E
<input type="checkbox"/>	GO:0009893	5,4	<a href="#">positive regulation of metabolic process</a>	116	0.0179	21	0.0238	0.0387447	E
<input type="checkbox"/>	GO:0008104	4	<a href="#">protein localization</a>	330	0.0510	51	0.0577	0.0392515	E
<input type="checkbox"/>	GO:0050896	2	<a href="#">response to stimulus</a>	763	0.1178	108	0.1222	0.0402680	E
<input type="checkbox"/>	GO:0007021	7	<a href="#">tubulin folding</a>	11	0.0017	4	0.0045	0.0409284	E
<input type="checkbox"/>	GO:0009081	6,7	<a href="#">branched chain family amino acid metabolic process</a>	16	0.0025	5	0.0057	0.0410896	E
<input type="checkbox"/>	GO:0000080	7,8,6	<a href="#">G1 phase of mitotic cell cycle</a>	27	0.0042	7	0.0079	0.0415057	E
<input type="checkbox"/>	GO:0051318	6,7,5	<a href="#">G1 phase</a>	27	0.0042	7	0.0079	0.0415057	E
<input type="checkbox"/>	GO:0006261	7	<a href="#">DNA-dependent DNA replication</a>	97	0.0150	18	0.0204	0.0416941	E
<input type="checkbox"/>	GO:0030005	9,7	<a href="#">cellular di-, tri-valent inorganic cation homeostasis</a>	64	0.0099	13	0.0147	0.0419254	E
<input type="checkbox"/>	GO:0055066	8	<a href="#">di-, tri-valent inorganic cation homeostasis</a>	64	0.0099	13	0.0147	0.0419254	E
<input type="checkbox"/>	GO:0065008	3	<a href="#">regulation of biological quality</a>	260	0.0401	41	0.0464	0.0422275	E
<input type="checkbox"/>	GO:0006270	8,6	<a href="#">DNA replication initiation</a>	33	0.0051	8	0.0090	0.0425139	E
<input type="checkbox"/>	GO:0016570	10,8	<a href="#">histone modification</a>	91	0.0141	17	0.0192	0.0435586	E
<input type="checkbox"/>	GO:0016569	9	<a href="#">covalent chromatin modification</a>	91	0.0141	17	0.0192	0.0435586	E
<input type="checkbox"/>	GO:0042723	6	<a href="#">thiamin and derivative metabolic process</a>	22	0.0034	6	0.0068	0.0459884	E
<input type="checkbox"/>	GO:0000041	7,8	<a href="#">transition metal ion transport</a>	46	0.0071	10	0.0113	0.0462861	E
<input type="checkbox"/>	GO:0000070	9,7,5,8,6,4	<a href="#">mitotic sister chromatid segregation</a>	59	0.0091	12	0.0136	0.0471341	E
<input type="checkbox"/>	GO:0006432	9,8,10,7	<a href="#">phenylalanyl-tRNA aminoacylation</a>	3	0.0005	2	0.0023	0.0482372	E
<input type="checkbox"/>	GO:0046083	7	<a href="#">adenine metabolic process</a>	3	0.0005	2	0.0023	0.0482372	E
<input type="checkbox"/>	GO:0000912	6,5,9,4	<a href="#">cytokinesis, formation of actomyosin apparatus</a>	3	0.0005	2	0.0023	0.0482372	E
<input type="checkbox"/>	GO:0000915	7,6,10,5	<a href="#">cytokinesis, contractile ring formation</a>	3	0.0005	2	0.0023	0.0482372	E
<input type="checkbox"/>	GO:0031032	8	<a href="#">actomyosin structure organization and biogenesis</a>	3	0.0005	2	0.0023	0.0482372	E
<input type="checkbox"/>	GO:0046500	6,5	<a href="#">S-adenosylmethionine metabolic process</a>	3	0.0005	2	0.0023	0.0482372	E
<input type="checkbox"/>	GO:0000056	11,12,7,9,10	<a href="#">ribosomal small subunit export from nucleus</a>	7	0.0011	3	0.0034	0.0494326	E
<input type="checkbox"/>	GO:0006560	7,8	<a href="#">proline metabolic process</a>	7	0.0011	3	0.0034	0.0494326	E
<input type="checkbox"/>	GO:0009086	8,9,7	<a href="#">methionine biosynthetic process</a>	7	0.0011	3	0.0034	0.0494326	E
<input type="checkbox"/>	GO:0006220	6	<a href="#">pyrimidine nucleotide metabolic process</a>	7	0.0011	3	0.0034	0.0494326	E
<input type="checkbox"/>	GO:0043633	7	<a href="#">modification-dependent RNA catabolic process</a>	7	0.0011	3	0.0034	0.0494326	E
<input type="checkbox"/>	GO:0031120	8	<a href="#">snRNA pseudouridine synthesis</a>	7	0.0011	3	0.0034	0.0494326	E
<input type="checkbox"/>	GO:0000755	6,5	<a href="#">cytogamy</a>	7	0.0011	3	0.0034	0.0494326	E
<input type="checkbox"/>	GO:0043634	8	<a href="#">polyadenylation-dependent ncRNA catabolic process</a>	7	0.0011	3	0.0034	0.0494326	E
<input type="checkbox"/>	GO:0040031	7	<a href="#">snRNA modification</a>	7	0.0011	3	0.0034	0.0494326	E
<input type="checkbox"/>	GO:0030705	7,5,6	<a href="#">cytoskeleton-dependent intracellular transport</a>	17	0.0026	5	0.0057	0.0502897	E
<input type="checkbox"/>	GO:0009124	6,7	<a href="#">nucleoside monophosphate biosynthetic process</a>	17	0.0026	5	0.0057	0.0502897	E
<input type="checkbox"/>	GO:0009167	8	<a href="#">purine ribonucleoside monophosphate metabolic process</a>	17	0.0026	5	0.0057	0.0502897	E
<input type="checkbox"/>	GO:0009161	7	<a href="#">ribonucleoside monophosphate metabolic</a>	17	0.0026	5	0.0057	0.0502897	E



<input type="radio"/>	GO:0009101	7	<a href="#">process</a>	17	0.0020	5	0.0037	0.0502097	E
<input type="radio"/>	GO:0055082	6,4	<a href="#">cellular chemical homeostasis</a>	115	0.0178	20	0.0226	0.0516399	E
<input type="radio"/>	GO:0006873	7,5	<a href="#">cellular ion homeostasis</a>	115	0.0178	20	0.0226	0.0516399	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	19	0.0215	0.0517059	E
<input type="radio"/>	GO:0007007	6,7	<a href="#">inner mitochondrial membrane organization and biogenesis</a>	12	0.0019	4	0.0045	0.0530360	E
<input type="radio"/>	GO:0015846	5,6	<a href="#">polyamine transport</a>	12	0.0019	4	0.0045	0.0530360	E
<input type="radio"/>	GO:0006461	6,5	<a href="#">protein complex assembly</a>	116	0.0179	20	0.0226	0.0539228	E
<input type="radio"/>	GO:0006999	6	<a href="#">nuclear pore organization and biogenesis</a>	29	0.0045	7	0.0079	0.0544563	E
<input type="radio"/>	GO:0042221	3	<a href="#">response to chemical stimulus</a>	382	0.0590	55	0.0622	0.0545053	E
<input type="radio"/>	GO:0006974	4	<a href="#">response to DNA damage stimulus</a>	234	0.0361	36	0.0407	0.0545367	E
<input type="radio"/>	GO:0006473	8	<a href="#">protein amino acid acetylation</a>	48	0.0074	10	0.0113	0.0554493	E
<input type="radio"/>	GO:0048522	5,4	<a href="#">positive regulation of cellular process</a>	124	0.0191	21	0.0238	0.0558298	E
<input type="radio"/>	GO:0048518	4	<a href="#">positive regulation of biological process</a>	124	0.0191	21	0.0238	0.0558298	E
<input type="radio"/>	GO:0009719	3	<a href="#">response to endogenous stimulus</a>	243	0.0375	37	0.0419	0.0560638	E
<input type="radio"/>	GO:0007127	9,7,6,8,5	<a href="#">meiosis I</a>	75	0.0116	14	0.0158	0.0564747	E
<input type="radio"/>	GO:0006352	7,8,6	<a href="#">transcription initiation</a>	55	0.0085	11	0.0124	0.0574193	E
<input type="radio"/>	GO:0007131	10,8,7,5,9,6,4	<a href="#">meiotic recombination</a>	55	0.0085	11	0.0124	0.0574193	E
<input type="radio"/>	GO:0006769	8,7	<a href="#">nicotinamide metabolic process</a>	42	0.0065	9	0.0102	0.0576984	E
<input type="radio"/>	GO:0000819	7,4	<a href="#">sister chromatid segregation</a>	62	0.0096	12	0.0136	0.0586783	E
<input type="radio"/>	GO:0043543	7	<a href="#">protein amino acid acylation</a>	62	0.0096	12	0.0136	0.0586783	E
<input type="radio"/>	GO:0016310	6	<a href="#">phosphorylation</a>	155	0.0239	25	0.0283	0.0593150	E
<input type="radio"/>	GO:0006338	9	<a href="#">chromatin remodeling</a>	155	0.0239	25	0.0283	0.0593150	E
<input type="radio"/>	GO:0019438	5	<a href="#">aromatic compound biosynthetic process</a>	18	0.0028	5	0.0057	0.0601557	E
<input type="radio"/>	GO:0009126	7	<a href="#">purine nucleoside monophosphate metabolic process</a>	18	0.0028	5	0.0057	0.0601557	E
<input type="radio"/>	GO:0051248	6,5	<a href="#">negative regulation of protein metabolic process</a>	18	0.0028	5	0.0057	0.0601557	E
<input type="radio"/>	GO:0050801	6	<a href="#">ion homeostasis</a>	119	0.0184	20	0.0226	0.0607423	E
<input type="radio"/>	GO:0000723	8	<a href="#">telomere maintenance</a>	274	0.0423	40	0.0452	0.0626091	E
<input type="radio"/>	GO:0032200	7	<a href="#">telomere organization and biogenesis</a>	274	0.0423	40	0.0452	0.0626091	E
<input type="radio"/>	GO:0000122	10,9	<a href="#">negative regulation of transcription from RNA polymerase II promoter</a>	63	0.0097	12	0.0136	0.0626305	E
<input type="radio"/>	GO:0009259	6	<a href="#">ribonucleotide metabolic process</a>	43	0.0066	9	0.0102	0.0630477	E
<input type="radio"/>	GO:0019725	5,3	<a href="#">cellular homeostasis</a>	128	0.0198	21	0.0238	0.0643450	E
<input type="radio"/>	GO:0048878	5	<a href="#">chemical homeostasis</a>	121	0.0187	20	0.0226	0.0651989	E
<input type="radio"/>	GO:0009082	7,8	<a href="#">branched chain family amino acid biosynthetic process</a>	13	0.0020	4	0.0045	0.0661784	E
<input type="radio"/>	GO:0006334	6,7,10	<a href="#">nucleosome assembly</a>	13	0.0020	4	0.0045	0.0661784	E
<input type="radio"/>	GO:0030258	5,6	<a href="#">lipid modification</a>	13	0.0020	4	0.0045	0.0661784	E
<input type="radio"/>	GO:0030036	7	<a href="#">actin cytoskeleton organization and biogenesis</a>	107	0.0165	18	0.0204	0.0668996	E
<input type="radio"/>	GO:0006620	10,9,8,7,6	<a href="#">posttranslational protein targeting to membrane</a>	8	0.0012	3	0.0034	0.0683207	E
<input type="radio"/>	GO:0045039	10,9,7,8	<a href="#">protein import into mitochondrial inner membrane</a>	8	0.0012	3	0.0034	0.0683207	E
<input type="radio"/>	GO:0006356	9,8	<a href="#">regulation of transcription from RNA polymerase I promoter</a>	8	0.0012	3	0.0034	0.0683207	E
<input type="radio"/>	GO:0043144	7	<a href="#">snoRNA processing</a>	8	0.0012	3	0.0034	0.0683207	E
<input type="radio"/>	GO:0006367	8,9,7	<a href="#">transcription initiation from RNA polymerase II promoter</a>	44	0.0068	9	0.0102	0.0684792	E

<input type="checkbox"/>	GO:0006289	7,6	<a href="#">nucleotide-excision repair</a>	44	0.0068	9	0.0102	0.0684792	E
<input type="checkbox"/>	GO:0006575	5	<a href="#">amino acid derivative metabolic process</a>	31	0.0048	7	0.0079	0.0684820	E
<input type="checkbox"/>	GO:0009607	3	<a href="#">response to biotic stimulus</a>	25	0.0039	6	0.0068	0.0703885	E
<input type="checkbox"/>	GO:0009228	7,8	<a href="#">thiamin biosynthetic process</a>	19	0.0029	5	0.0057	0.0705279	E
<input type="checkbox"/>	GO:0043094	4	<a href="#">metabolic compound salvage</a>	19	0.0029	5	0.0057	0.0705279	E
<input type="checkbox"/>	GO:0006879	10,8	<a href="#">cellular iron ion homeostasis</a>	38	0.0059	8	0.0090	0.0720959	E
<input type="checkbox"/>	GO:0055072	9	<a href="#">iron ion homeostasis</a>	38	0.0059	8	0.0090	0.0720959	E
<input type="checkbox"/>	GO:0006260	6	<a href="#">DNA replication</a>	117	0.0181	19	0.0215	0.0728672	E
<input type="checkbox"/>	GO:0006643	5,6	<a href="#">membrane lipid metabolic process</a>	125	0.0193	20	0.0226	0.0736641	E
<input type="checkbox"/>	GO:0019362	7,6	<a href="#">pyridine nucleotide metabolic process</a>	45	0.0069	9	0.0102	0.0739543	E
<input type="checkbox"/>	GO:0040007	2	<a href="#">growth</a>	141	0.0218	22	0.0249	0.0745906	E
<input type="checkbox"/>	GO:0030010	7,4,8	<a href="#">establishment of cell polarity</a>	103	0.0159	17	0.0192	0.0754834	E
<input type="checkbox"/>	GO:0042592	4	<a href="#">homeostatic process</a>	134	0.0207	21	0.0238	0.0760438	E
<input type="checkbox"/>	GO:0000226	7	<a href="#">microtubule cytoskeleton organization and biogenesis</a>	81	0.0125	14	0.0158	0.0764162	E
<input type="checkbox"/>	GO:0051325	6,5	<a href="#">interphase</a>	112	0.0173	18	0.0204	0.0787152	E
<input type="checkbox"/>	GO:0030029	6	<a href="#">actin filament-based process</a>	112	0.0173	18	0.0204	0.0787152	E
<input type="checkbox"/>	GO:0051329	7,5,6	<a href="#">interphase of mitotic cell cycle</a>	112	0.0173	18	0.0204	0.0787152	E
<input type="checkbox"/>	GO:0006348	11,7,8,12,10	<a href="#">chromatin silencing at telomere</a>	60	0.0093	11	0.0124	0.0791789	E
<input type="checkbox"/>	GO:0031509	7,11	<a href="#">telomeric heterochromatin formation</a>	60	0.0093	11	0.0124	0.0791789	E
<input type="checkbox"/>	GO:0006730	4	<a href="#">one-carbon compound metabolic process</a>	97	0.0150	16	0.0181	0.0795022	E
<input type="checkbox"/>	GO:0008361	4,6,7	<a href="#">regulation of cell size</a>	129	0.0199	20	0.0226	0.0812076	E
<input type="checkbox"/>	GO:0030148	7,6,8	<a href="#">sphingolipid biosynthetic process</a>	20	0.0031	5	0.0057	0.0812358	E
<input type="checkbox"/>	GO:0006772	7	<a href="#">thiamin metabolic process</a>	20	0.0031	5	0.0057	0.0812358	E
<input type="checkbox"/>	GO:0015780	5,6	<a href="#">nucleotide-sugar transport</a>	4	0.0006	2	0.0023	0.0833290	E
<input type="checkbox"/>	GO:0015793	5,6	<a href="#">glycerol transport</a>	4	0.0006	2	0.0023	0.0833290	E
<input type="checkbox"/>	GO:0016180	7	<a href="#">snRNA processing</a>	4	0.0006	2	0.0023	0.0833290	E
<input type="checkbox"/>	GO:0006562	8,9	<a href="#">proline catabolic process</a>	4	0.0006	2	0.0023	0.0833290	E
<input type="checkbox"/>	GO:0016077	7	<a href="#">snoRNA catabolic process</a>	4	0.0006	2	0.0023	0.0833290	E
<input type="checkbox"/>	GO:0016076	7	<a href="#">snRNA catabolic process</a>	4	0.0006	2	0.0023	0.0833290	E
<input type="checkbox"/>	GO:0000059	8,10,11,7,9	<a href="#">protein import into nucleus, docking</a>	4	0.0006	2	0.0023	0.0833290	E
<input type="checkbox"/>	GO:0006814	7,8	<a href="#">sodium ion transport</a>	4	0.0006	2	0.0023	0.0833290	E
<input type="checkbox"/>	GO:0000743	9,10,8,7,6	<a href="#">nuclear migration during conjugation with cellular fusion</a>	4	0.0006	2	0.0023	0.0833290	E
<input type="checkbox"/>	GO:0000196	8,6	<a href="#">MAPKKK cascade during cell wall biogenesis</a>	4	0.0006	2	0.0023	0.0833290	E
<input type="checkbox"/>	GO:0018205	8	<a href="#">peptidyl-lysine modification</a>	4	0.0006	2	0.0023	0.0833290	E
<input type="checkbox"/>	GO:0009260	6,7	<a href="#">ribonucleotide biosynthetic process</a>	40	0.0062	8	0.0090	0.0846200	E
<input type="checkbox"/>	GO:0016573	11,9	<a href="#">histone acetylation</a>	40	0.0062	8	0.0090	0.0846200	E
<input type="checkbox"/>	GO:0006417	7,6,5	<a href="#">regulation of translation</a>	47	0.0073	9	0.0102	0.0848771	E
<input type="checkbox"/>	GO:0006163	6	<a href="#">purine nucleotide metabolic process</a>	47	0.0073	9	0.0102	0.0848771	E
<input type="checkbox"/>	GO:0007163	6,3,7	<a href="#">establishment and/or maintenance of cell polarity</a>	115	0.0178	18	0.0204	0.0849894	E
<input type="checkbox"/>	GO:0032446	8	<a href="#">protein modification by small protein conjugation</a>	84	0.0130	14	0.0158	0.0857716	E
<input type="checkbox"/>	GO:0009889	5,4	<a href="#">regulation of biosynthetic process</a>	69	0.0107	12	0.0136	0.0860515	E
<input type="checkbox"/>	GO:0043623	7,6	<a href="#">cellular protein complex assembly</a>	69	0.0107	12	0.0136	0.0860515	E
<input type="checkbox"/>	GO:0006760	5,7	<a href="#">folic acid and derivative metabolic process</a>	9	0.0014	3	0.0034	0.0885222	E
<input type="checkbox"/>	GO:0006474	10,9	<a href="#">N-terminal protein amino acid acetylation</a>	9	0.0014	3	0.0034	0.0885222	E

<input type="checkbox"/>	GO:0006280	6	<a href="#">mutagenesis</a>	9	0.0014	3	0.0034	0.0885222	E
<input type="checkbox"/>	GO:0009262	6	<a href="#">deoxyribonucleotide metabolic process</a>	9	0.0014	3	0.0034	0.0885222	E
<input type="checkbox"/>	GO:0015802	6,7,8	<a href="#">basic amino acid transport</a>	9	0.0014	3	0.0034	0.0885222	E
<input type="checkbox"/>	GO:0043101	5	<a href="#">purine salvage</a>	9	0.0014	3	0.0034	0.0885222	E
<input type="checkbox"/>	GO:0009150	7	<a href="#">purine ribonucleotide metabolic process</a>	41	0.0063	8	0.0090	0.0908242	E
<input type="checkbox"/>	GO:0007005	5	<a href="#">mitochondrion organization and biogenesis</a>	110	0.0170	17	0.0192	0.0910501	E
<input type="checkbox"/>	GO:0006891	8,6,5,7	<a href="#">intra-Golgi vesicle-mediated transport</a>	21	0.0032	5	0.0057	0.0921051	E
<input type="checkbox"/>	GO:0009156	7,8	<a href="#">ribonucleoside monophosphate biosynthetic process</a>	15	0.0023	4	0.0045	0.0942755	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	4	0.0045	0.0942755	E
<input type="checkbox"/>	GO:0009168	8,9	<a href="#">purine ribonucleoside monophosphate biosynthetic process</a>	15	0.0023	4	0.0045	0.0942755	E
<input type="checkbox"/>	GO:0051246	5,4	<a href="#">regulation of protein metabolic process</a>	72	0.0111	12	0.0136	0.0966881	E
<input type="checkbox"/>	GO:0006512	8	<a href="#">ubiquitin cycle</a>	88	0.0136	14	0.0158	0.0968037	E
<input type="checkbox"/>	GO:0006812	5,6	<a href="#">cation transport</a>	97	0.0150	15	0.0170	0.0983776	E
<input type="checkbox"/>	GO:0040020	7,9,8,6	<a href="#">regulation of meiosis</a>	22	0.0034	5	0.0057	0.1029637	E
<input type="checkbox"/>	GO:0016567	9	<a href="#">protein ubiquitination</a>	66	0.0102	11	0.0124	0.1031468	E
<input type="checkbox"/>	GO:0000910	4	<a href="#">cytokinesis</a>	109	0.0168	16	0.0181	0.1032171	E
<input type="checkbox"/>	GO:0017038	5,6,7	<a href="#">protein import</a>	109	0.0168	16	0.0181	0.1032171	E
<input type="checkbox"/>	GO:0043414	6	<a href="#">biopolymer methylation</a>	83	0.0128	13	0.0147	0.1049250	E
<input type="checkbox"/>	GO:0032259	5	<a href="#">methylation</a>	83	0.0128	13	0.0147	0.1049250	E
<input type="checkbox"/>	GO:0006409	11,9,6,8,10,7	<a href="#">tRNA export from nucleus</a>	29	0.0045	6	0.0068	0.1051427	E
<input type="checkbox"/>	GO:0031326	6,5	<a href="#">regulation of cellular biosynthetic process</a>	67	0.0103	11	0.0124	0.1066005	E
<input type="checkbox"/>	GO:0016049	5,3,7,8	<a href="#">cell growth</a>	102	0.0158	15	0.0170	0.1066037	E
<input type="checkbox"/>	GO:0007034	7,5,6	<a href="#">vacuolar transport</a>	114	0.0176	16	0.0181	0.1071975	E
<input type="checkbox"/>	GO:0009073	7,6,8	<a href="#">aromatic amino acid family biosynthetic process</a>	16	0.0025	4	0.0045	0.1085800	E
<input type="checkbox"/>	GO:0030866	8,7	<a href="#">cortical actin cytoskeleton organization and biogenesis</a>	16	0.0025	4	0.0045	0.1085800	E
<input type="checkbox"/>	GO:0048017	8	<a href="#">inositol lipid-mediated signaling</a>	16	0.0025	4	0.0045	0.1085800	E
<input type="checkbox"/>	GO:0030865	6	<a href="#">cortical cytoskeleton organization and biogenesis</a>	16	0.0025	4	0.0045	0.1085800	E
<input type="checkbox"/>	GO:0048015	7	<a href="#">phosphoinositide-mediated signaling</a>	16	0.0025	4	0.0045	0.1085800	E
<input type="checkbox"/>	GO:0009127	7,8	<a href="#">purine nucleoside monophosphate biosynthetic process</a>	16	0.0025	4	0.0045	0.1085800	E
<input type="checkbox"/>	GO:0045944	10,9	<a href="#">positive regulation of transcription from RNA polymerase II promoter</a>	76	0.0117	12	0.0136	0.1086975	E
<input type="checkbox"/>	GO:0019236	4	<a href="#">response to pheromone</a>	94	0.0145	14	0.0158	0.1089248	E
<input type="checkbox"/>	GO:0000103	6	<a href="#">sulfate assimilation</a>	10	0.0015	3	0.0034	0.1092326	E
<input type="checkbox"/>	GO:0019363	7,6,8	<a href="#">pyridine nucleotide biosynthetic process</a>	10	0.0015	3	0.0034	0.1092326	E
<input type="checkbox"/>	GO:0006791	5	<a href="#">sulfur utilization</a>	10	0.0015	3	0.0034	0.1092326	E
<input type="checkbox"/>	GO:0006882	10,8	<a href="#">cellular zinc ion homeostasis</a>	10	0.0015	3	0.0034	0.1092326	E
<input type="checkbox"/>	GO:0001301	9,5	<a href="#">progressive alteration of chromatin during cell aging</a>	10	0.0015	3	0.0034	0.1092326	E
<input type="checkbox"/>	GO:0030846	10,9	<a href="#">transcription termination from Pol II promoter, RNA polymerase(A) coupled</a>	10	0.0015	3	0.0034	0.1092326	E
<input type="checkbox"/>	GO:0055069	9	<a href="#">zinc ion homeostasis</a>	10	0.0015	3	0.0034	0.1092326	E
<input type="checkbox"/>	GO:0006817	7,8	<a href="#">phosphate transport</a>	10	0.0015	3	0.0034	0.1092326	E
<input type="checkbox"/>	GO:0051336	5	<a href="#">regulation of hydrolase activity</a>	10	0.0015	3	0.0034	0.1092326	E
<input type="checkbox"/>	GO:0051031	5,7,6,8	<a href="#">tRNA transport</a>	30	0.0046	6	0.0068	0.1135295	E
<input type="checkbox"/>	GO:0046467	6,5,7	<a href="#">membrane lipid biosynthetic process</a>	78	0.0120	12	0.0136	0.1135306	E

<input type="checkbox"/>	GO:0007243	6	<a href="#">protein kinase cascade</a>	23	0.0036	5	0.0057	0.1136463	E
<input type="checkbox"/>	GO:0006479	9,7	<a href="#">protein amino acid methylation</a>	23	0.0036	5	0.0057	0.1136463	E
<input type="checkbox"/>	GO:0051030	5,7,6,8	<a href="#">snRNA transport</a>	23	0.0036	5	0.0057	0.1136463	E
<input type="checkbox"/>	GO:0006610	10,11,8,9,7	<a href="#">ribosomal protein import into nucleus</a>	23	0.0036	5	0.0057	0.1136463	E
<input type="checkbox"/>	GO:0006408	11,9,6,8,10,7	<a href="#">snRNA export from nucleus</a>	23	0.0036	5	0.0057	0.1136463	E
<input type="checkbox"/>	GO:0006608	10,11,8,9,7	<a href="#">snRNP protein import into nucleus</a>	23	0.0036	5	0.0057	0.1136463	E
<input type="checkbox"/>	GO:0006607	10,11,8,9,7	<a href="#">NLS-bearing substrate import into nucleus</a>	23	0.0036	5	0.0057	0.1136463	E
<input type="checkbox"/>	GO:0008213	8	<a href="#">protein amino acid alkylation</a>	23	0.0036	5	0.0057	0.1136463	E
<input type="checkbox"/>	GO:0009152	7,8	<a href="#">purine ribonucleotide biosynthetic process</a>	38	0.0059	7	0.0079	0.1179968	E
<input type="checkbox"/>	GO:0030447	3	<a href="#">filamentous growth</a>	94	0.0145	13	0.0147	0.1191409	E
<input type="checkbox"/>	GO:0065009	3	<a href="#">regulation of a molecular function</a>	46	0.0071	8	0.0090	0.1193004	E
<input type="checkbox"/>	GO:0016078	7	<a href="#">tRNA catabolic process</a>	5	0.0008	2	0.0023	0.1199549	E
<input type="checkbox"/>	GO:0007023	8	<a href="#">post-chaperonin tubulin folding pathway</a>	5	0.0008	2	0.0023	0.1199549	E
<input type="checkbox"/>	GO:0043137	7,10,6,9	<a href="#">DNA replication, removal of RNA primer</a>	5	0.0008	2	0.0023	0.1199549	E
<input type="checkbox"/>	GO:0006797	6	<a href="#">polyphosphate metabolic process</a>	5	0.0008	2	0.0023	0.1199549	E
<input type="checkbox"/>	GO:0009268	4	<a href="#">response to pH</a>	5	0.0008	2	0.0023	0.1199549	E
<input type="checkbox"/>	GO:0046854	7,9,8,10	<a href="#">phosphoinositide phosphorylation</a>	5	0.0008	2	0.0023	0.1199549	E
<input type="checkbox"/>	GO:0016233	9	<a href="#">telomere capping</a>	5	0.0008	2	0.0023	0.1199549	E
<input type="checkbox"/>	GO:0046834	6,7	<a href="#">lipid phosphorylation</a>	5	0.0008	2	0.0023	0.1199549	E
<input type="checkbox"/>	GO:0000092	8,9,10,7	<a href="#">mitotic anaphase B</a>	5	0.0008	2	0.0023	0.1199549	E
<input type="checkbox"/>	GO:0000017	6,7	<a href="#">alpha-glucoside transport</a>	5	0.0008	2	0.0023	0.1199549	E
<input type="checkbox"/>	GO:0043087	6	<a href="#">regulation of GTPase activity</a>	5	0.0008	2	0.0023	0.1199549	E
<input type="checkbox"/>	GO:0006336	7,8,11	<a href="#">DNA replication-independent nucleosome assembly</a>	5	0.0008	2	0.0023	0.1199549	E
<input type="checkbox"/>	GO:0042946	5,6	<a href="#">glucoside transport</a>	5	0.0008	2	0.0023	0.1199549	E
<input type="checkbox"/>	GO:0015680	7,5,9,6,10	<a href="#">intracellular copper ion transport</a>	5	0.0008	2	0.0023	0.1199549	E
<input type="checkbox"/>	GO:0006739	9,8	<a href="#">NADP metabolic process</a>	17	0.0026	4	0.0045	0.1226471	E
<input type="checkbox"/>	GO:0045132	9,7,8,6,4	<a href="#">meiotic chromosome segregation</a>	17	0.0026	4	0.0045	0.1226471	E
<input type="checkbox"/>	GO:0051452	12,9,10	<a href="#">cellular pH reduction</a>	24	0.0037	5	0.0057	0.1239990	E
<input type="checkbox"/>	GO:0043631	8	<a href="#">RNA polyadenylation</a>	24	0.0037	5	0.0057	0.1239990	E
<input type="checkbox"/>	GO:0007006	5,6	<a href="#">mitochondrial membrane organization and biogenesis</a>	24	0.0037	5	0.0057	0.1239990	E
<input type="checkbox"/>	GO:0045851	8	<a href="#">pH reduction</a>	24	0.0037	5	0.0057	0.1239990	E
<input type="checkbox"/>	GO:0007035	13,10,6,11	<a href="#">vacuolar acidification</a>	24	0.0037	5	0.0057	0.1239990	E
<input type="checkbox"/>	GO:0007265	7	<a href="#">Ras protein signal transduction</a>	39	0.0060	7	0.0079	0.1242187	E
<input type="checkbox"/>	GO:0006839	7,5,6	<a href="#">mitochondrial transport</a>	65	0.0100	10	0.0113	0.1261011	E
<input type="checkbox"/>	GO:0006733	6	<a href="#">oxidoreduction coenzyme metabolic process</a>	56	0.0086	9	0.0102	0.1263639	E
<input type="checkbox"/>	GO:0006694	6,5,7	<a href="#">steroid biosynthetic process</a>	32	0.0049	6	0.0068	0.1292749	E
<input type="checkbox"/>	GO:0016126	6,7,8	<a href="#">sterol biosynthetic process</a>	32	0.0049	6	0.0068	0.1292749	E
<input type="checkbox"/>	GO:0006302	7,6	<a href="#">double-strand break repair</a>	57	0.0088	9	0.0102	0.1296054	E
<input type="checkbox"/>	GO:0000749	5	<a href="#">response to pheromone during conjugation with cellular fusion</a>	57	0.0088	9	0.0102	0.1296054	E
<input type="checkbox"/>	GO:0006972	5	<a href="#">hyperosmotic response</a>	11	0.0017	3	0.0034	0.1297306	E
<input type="checkbox"/>	GO:0006098	9,10,11	<a href="#">pentose-phosphate shunt</a>	11	0.0017	3	0.0034	0.1297306	E
<input type="checkbox"/>	GO:0006623	9,8,7,6	<a href="#">protein targeting to vacuole</a>	67	0.0103	10	0.0113	0.1303052	E
<input type="checkbox"/>	GO:0030641	10,8	<a href="#">cellular hydrogen ion homeostasis</a>	25	0.0039	5	0.0057	0.1338823	E
<input type="checkbox"/>	GO:0051453	11,8,9	<a href="#">regulation of cellular pH</a>	25	0.0039	5	0.0057	0.1338823	E
<input type="checkbox"/>	GO:0006600	10,11,8,9,7	<a href="#">mRNA-binding (hnRNP) protein import</a>	25	0.0039	5	0.0057	0.1338823	E

<input type="checkbox"/>	GO:0006609	10,11,0,9,7	<a href="#">into nucleus</a>	23	0.0039	3	0.0037	0.1330823	E
<input type="checkbox"/>	GO:0006164	6,7	<a href="#">purine nucleotide biosynthetic process</a>	41	0.0063	7	0.0079	0.1354596	E
<input type="checkbox"/>	GO:0016571	11,9,10,8	<a href="#">histone methylation</a>	18	0.0028	4	0.0045	0.1362049	E
<input type="checkbox"/>	GO:0007584	6,4	<a href="#">response to nutrient</a>	18	0.0028	4	0.0045	0.1362049	E
<input type="checkbox"/>	GO:0009129	7	<a href="#">pyrimidine nucleoside monophosphate metabolic process</a>	1	0.0002	1	0.0011	0.1365040	E
<input type="checkbox"/>	GO:0046098	7	<a href="#">guanine metabolic process</a>	1	0.0002	1	0.0011	0.1365040	E
<input type="checkbox"/>	GO:0018004	10,9	<a href="#">N-terminal protein formylation</a>	1	0.0002	1	0.0011	0.1365040	E
<input type="checkbox"/>	GO:0001718	8,7,11,10,9	<a href="#">conversion of met-tRNAf to fmet-tRNA</a>	1	0.0002	1	0.0011	0.1365040	E
<input type="checkbox"/>	GO:0006676	8,10,9,11	<a href="#">mannosyl diphosphorylinositol ceramide metabolic process</a>	1	0.0002	1	0.0011	0.1365040	E
<input type="checkbox"/>	GO:0031060	7,9,12,6,10,11,8	<a href="#">regulation of histone methylation</a>	1	0.0002	1	0.0011	0.1365040	E
<input type="checkbox"/>	GO:0006145	7,6	<a href="#">purine base catabolic process</a>	1	0.0002	1	0.0011	0.1365040	E
<input type="checkbox"/>	GO:0030259	6,7	<a href="#">lipid glycosylation</a>	1	0.0002	1	0.0011	0.1365040	E
<input type="checkbox"/>	GO:0051568	12,10,11,9	<a href="#">histone H3-K4 methylation</a>	1	0.0002	1	0.0011	0.1365040	E
<input type="checkbox"/>	GO:0032264	7,8	<a href="#">IMP salvage</a>	1	0.0002	1	0.0011	0.1365040	E
<input type="checkbox"/>	GO:0018256	8	<a href="#">protein amino acid formylation</a>	1	0.0002	1	0.0011	0.1365040	E
<input type="checkbox"/>	GO:0006168	8,7	<a href="#">adenine salvage</a>	1	0.0002	1	0.0011	0.1365040	E
<input type="checkbox"/>	GO:0032218	5,6	<a href="#">riboflavin transport</a>	1	0.0002	1	0.0011	0.1365040	E
<input type="checkbox"/>	GO:0006427	9,8,10,7	<a href="#">histidyl-tRNA aminoacylation</a>	1	0.0002	1	0.0011	0.1365040	E
<input type="checkbox"/>	GO:0016578	11,9,10	<a href="#">histone deubiquitination</a>	1	0.0002	1	0.0011	0.1365040	E
<input type="checkbox"/>	GO:0043096	7,6	<a href="#">purine base salvage</a>	1	0.0002	1	0.0011	0.1365040	E
<input type="checkbox"/>	GO:0006231	9,10	<a href="#">dTMP biosynthetic process</a>	1	0.0002	1	0.0011	0.1365040	E
<input type="checkbox"/>	GO:0006973	6,4	<a href="#">intracellular accumulation of glycerol</a>	1	0.0002	1	0.0011	0.1365040	E
<input type="checkbox"/>	GO:0032092	6	<a href="#">positive regulation of protein binding</a>	1	0.0002	1	0.0011	0.1365040	E
<input type="checkbox"/>	GO:0006387	8	<a href="#">snRNA capping</a>	1	0.0002	1	0.0011	0.1365040	E
<input type="checkbox"/>	GO:0048025	10,9,12	<a href="#">negative regulation of nuclear mRNA splicing, via spliceosome</a>	1	0.0002	1	0.0011	0.1365040	E
<input type="checkbox"/>	GO:0006438	9,8,10,7	<a href="#">valyl-tRNA aminoacylation</a>	1	0.0002	1	0.0011	0.1365040	E
<input type="checkbox"/>	GO:0008612	8,7,9	<a href="#">hypusine biosynthetic process from peptidyl-lysine</a>	1	0.0002	1	0.0011	0.1365040	E
<input type="checkbox"/>	GO:0033353	7,6	<a href="#">S-adenosylmethionine cycle</a>	1	0.0002	1	0.0011	0.1365040	E
<input type="checkbox"/>	GO:0006660	9,10	<a href="#">phosphatidylserine catabolic process</a>	1	0.0002	1	0.0011	0.1365040	E
<input type="checkbox"/>	GO:0018027	10,11,9	<a href="#">peptidyl-lysine di-methylation</a>	1	0.0002	1	0.0011	0.1365040	E
<input type="checkbox"/>	GO:0015819	7,8,9	<a href="#">lysine transport</a>	1	0.0002	1	0.0011	0.1365040	E
<input type="checkbox"/>	GO:0015700	7,8	<a href="#">arsenite transport</a>	1	0.0002	1	0.0011	0.1365040	E
<input type="checkbox"/>	GO:0051253	8,7	<a href="#">negative regulation of RNA metabolic process</a>	1	0.0002	1	0.0011	0.1365040	E
<input type="checkbox"/>	GO:0051123	10,7,9,6	<a href="#">transcriptional preinitiation complex assembly</a>	1	0.0002	1	0.0011	0.1365040	E
<input type="checkbox"/>	GO:0000459	7,8	<a href="#">exonucleolytic trimming during rRNA processing</a>	1	0.0002	1	0.0011	0.1365040	E
<input type="checkbox"/>	GO:0000415	9,11,14,8,12,13,10	<a href="#">negative regulation of histone H3-K36 methylation</a>	1	0.0002	1	0.0011	0.1365040	E
<input type="checkbox"/>	GO:0042762	6,5	<a href="#">regulation of sulfur metabolic process</a>	1	0.0002	1	0.0011	0.1365040	E
<input type="checkbox"/>	GO:0032263	7,8	<a href="#">GMP salvage</a>	1	0.0002	1	0.0011	0.1365040	E
<input type="checkbox"/>	GO:0009130	7,8	<a href="#">pyrimidine nucleoside monophosphate biosynthetic process</a>	1	0.0002	1	0.0011	0.1365040	E
<input type="checkbox"/>	GO:0006146	8,7	<a href="#">adenine catabolic process</a>	1	0.0002	1	0.0011	0.1365040	E
<input type="checkbox"/>	GO:0042819	7	<a href="#">vitamin B6 biosynthetic process</a>	1	0.0002	1	0.0011	0.1365040	E
<input type="checkbox"/>	GO:0006428	9,8,10,7	<a href="#">isoleucyl-tRNA aminoacylation</a>	1	0.0002	1	0.0011	0.1365040	E
<input type="checkbox"/>	GO:0050686	9,8	<a href="#">negative regulation of mRNA processing</a>	1	0.0002	1	0.0011	0.1365040	E

<input type="radio"/>	GO:0046498	6	<a href="#">S-adenosylhomocysteine metabolic process</a>	1	0.0002	1	0.0011	0.1365040	E
<input type="radio"/>	GO:0019284	9,7,8,6,10	<a href="#">methionine biosynthetic process from S-adenosylmethionine</a>	1	0.0002	1	0.0011	0.1365040	E
<input type="radio"/>	GO:0015788	7,8	<a href="#">UDP-N-acetylglucosamine transport</a>	1	0.0002	1	0.0011	0.1365040	E
<input type="radio"/>	GO:0000414	8,10,13,7,11,12,9	<a href="#">regulation of histone H3-K36 methylation</a>	1	0.0002	1	0.0011	0.1365040	E
<input type="radio"/>	GO:0018283	9,7	<a href="#">iron incorporation into metallo-sulfur cluster</a>	1	0.0002	1	0.0011	0.1365040	E
<input type="radio"/>	GO:0051098	4	<a href="#">regulation of binding</a>	1	0.0002	1	0.0011	0.1365040	E
<input type="radio"/>	GO:0006831	9,10	<a href="#">low-affinity zinc ion transport</a>	1	0.0002	1	0.0011	0.1365040	E
<input type="radio"/>	GO:0000040	8,9,10	<a href="#">low affinity iron ion transport</a>	1	0.0002	1	0.0011	0.1365040	E
<input type="radio"/>	GO:0046073	9	<a href="#">dTMP metabolic process</a>	1	0.0002	1	0.0011	0.1365040	E
<input type="radio"/>	GO:0016259	7,8,6	<a href="#">selenocysteine metabolic process</a>	1	0.0002	1	0.0011	0.1365040	E
<input type="radio"/>	GO:0048228	6,9,8,5	<a href="#">actin cortical patch distribution</a>	1	0.0002	1	0.0011	0.1365040	E
<input type="radio"/>	GO:0009157	7,8	<a href="#">deoxyribonucleoside monophosphate biosynthetic process</a>	1	0.0002	1	0.0011	0.1365040	E
<input type="radio"/>	GO:0046033	9	<a href="#">AMP metabolic process</a>	1	0.0002	1	0.0011	0.1365040	E
<input type="radio"/>	GO:0042357	6,7	<a href="#">thiamin diphosphate metabolic process</a>	1	0.0002	1	0.0011	0.1365040	E
<input type="radio"/>	GO:0033559	6,8,7	<a href="#">unsaturated fatty acid metabolic process</a>	1	0.0002	1	0.0011	0.1365040	E
<input type="radio"/>	GO:0000413	8	<a href="#">protein peptidyl-prolyl isomerization</a>	1	0.0002	1	0.0011	0.1365040	E
<input type="radio"/>	GO:0018282	8,6	<a href="#">metal incorporation into metallo-sulfur cluster</a>	1	0.0002	1	0.0011	0.1365040	E
<input type="radio"/>	GO:0009162	7	<a href="#">deoxyribonucleoside monophosphate metabolic process</a>	1	0.0002	1	0.0011	0.1365040	E
<input type="radio"/>	GO:0009177	8,9	<a href="#">pyrimidine deoxyribonucleoside monophosphate biosynthetic process</a>	1	0.0002	1	0.0011	0.1365040	E
<input type="radio"/>	GO:0006636	8,7,9,6	<a href="#">unsaturated fatty acid biosynthetic process</a>	1	0.0002	1	0.0011	0.1365040	E
<input type="radio"/>	GO:0032220	7,6	<a href="#">plasma membrane fusion during cytogamy</a>	1	0.0002	1	0.0011	0.1365040	E
<input type="radio"/>	GO:0042790	9,8	<a href="#">transcription of nuclear rRNA large RNA polymerase I transcript</a>	1	0.0002	1	0.0011	0.1365040	E
<input type="radio"/>	GO:0009176	8	<a href="#">pyrimidine deoxyribonucleoside monophosphate metabolic process</a>	1	0.0002	1	0.0011	0.1365040	E
<input type="radio"/>	GO:0015887	5,6	<a href="#">pantothenate transport</a>	1	0.0002	1	0.0011	0.1365040	E
<input type="radio"/>	GO:0006167	9,10	<a href="#">AMP biosynthetic process</a>	1	0.0002	1	0.0011	0.1365040	E
<input type="radio"/>	GO:0008615	8	<a href="#">pyridoxine biosynthetic process</a>	1	0.0002	1	0.0011	0.1365040	E
<input type="radio"/>	GO:0006286	8,7	<a href="#">base-excision repair, base-free sugar-phosphate removal</a>	1	0.0002	1	0.0011	0.1365040	E
<input type="radio"/>	GO:0045898	11,4,8,10,7	<a href="#">regulation of transcriptional preinitiation complex assembly</a>	1	0.0002	1	0.0011	0.1365040	E
<input type="radio"/>	GO:0009302	8,7	<a href="#">snoRNA transcription</a>	1	0.0002	1	0.0011	0.1365040	E
<input type="radio"/>	GO:0000412	11,9	<a href="#">histone peptidyl-prolyl isomerization</a>	1	0.0002	1	0.0011	0.1365040	E
<input type="radio"/>	GO:0018216	9,10,8	<a href="#">peptidyl-arginine methylation</a>	1	0.0002	1	0.0011	0.1365040	E
<input type="radio"/>	GO:0000734	7,9,8	<a href="#">gene conversion at mating-type locus, DNA repair synthesis</a>	1	0.0002	1	0.0011	0.1365040	E
<input type="radio"/>	GO:0006425	9,8,10,7	<a href="#">glutaminyl-tRNA aminoacylation</a>	1	0.0002	1	0.0011	0.1365040	E
<input type="radio"/>	GO:0015771	6,7,8	<a href="#">trehalose transport</a>	1	0.0002	1	0.0011	0.1365040	E
<input type="radio"/>	GO:0006421	9,8,10,7	<a href="#">asparaginylyl-tRNA aminoacylation</a>	1	0.0002	1	0.0011	0.1365040	E
<input type="radio"/>	GO:0009229	7,8	<a href="#">thiamin diphosphate biosynthetic process</a>	1	0.0002	1	0.0011	0.1365040	E
<input type="radio"/>	GO:0046113	6,5	<a href="#">nucleobase catabolic process</a>	1	0.0002	1	0.0011	0.1365040	E
<input type="radio"/>	GO:0043393	5	<a href="#">regulation of protein binding</a>	1	0.0002	1	0.0011	0.1365040	E
<input type="radio"/>	GO:0047484	4,5	<a href="#">regulation of response to osmotic stress</a>	1	0.0002	1	0.0011	0.1365040	E
<input type="radio"/>	GO:0051099	5	<a href="#">positive regulation of binding</a>	1	0.0002	1	0.0011	0.1365040	E
<input type="radio"/>	GO:0006606	9,10,7,8,6	<a href="#">protein import into nucleus</a>	50	0.0077	8	0.0090	0.1366171	E

<input type="checkbox"/>	GO:0051170	9,7,8	<a href="#">nuclear import</a>	50	0.0077	8	0.0090	0.1366171	E
<input type="checkbox"/>	GO:0007264	6	<a href="#">small GTPase mediated signal transduction</a>	61	0.0094	9	0.0102	0.1389965	E
<input type="checkbox"/>	GO:0030004	9,7	<a href="#">cellular monovalent inorganic cation homeostasis</a>	34	0.0053	6	0.0068	0.1431364	E
<input type="checkbox"/>	GO:0055067	8	<a href="#">monovalent inorganic cation homeostasis</a>	34	0.0053	6	0.0068	0.1431364	E
<input type="checkbox"/>	GO:0006696	7,8,9	<a href="#">ergosterol biosynthetic process</a>	26	0.0040	5	0.0057	0.1431730	E
<input type="checkbox"/>	GO:0015749	5,6	<a href="#">monosaccharide transport</a>	26	0.0040	5	0.0057	0.1431730	E
<input type="checkbox"/>	GO:0008204	6,7,8	<a href="#">ergosterol metabolic process</a>	26	0.0040	5	0.0057	0.1431730	E
<input type="checkbox"/>	GO:0008645	6,7	<a href="#">hexose transport</a>	26	0.0040	5	0.0057	0.1431730	E
<input type="checkbox"/>	GO:0006379	8	<a href="#">mRNA cleavage</a>	26	0.0040	5	0.0057	0.1431730	E
<input type="checkbox"/>	GO:0030384	8,9	<a href="#">phosphoinositide metabolic process</a>	43	0.0066	7	0.0079	0.1448393	E
<input type="checkbox"/>	GO:0009064	6,7	<a href="#">glutamine family amino acid metabolic process</a>	43	0.0066	7	0.0079	0.1448393	E
<input type="checkbox"/>	GO:0055065	8	<a href="#">metal ion homeostasis</a>	19	0.0029	4	0.0045	0.1490169	E
<input type="checkbox"/>	GO:0006875	9,7	<a href="#">cellular metal ion homeostasis</a>	19	0.0029	4	0.0045	0.1490169	E
<input type="checkbox"/>	GO:0006284	7,6	<a href="#">base-excision repair</a>	12	0.0019	3	0.0034	0.1494026	E
<input type="checkbox"/>	GO:0050790	4	<a href="#">regulation of catalytic activity</a>	45	0.0069	7	0.0079	0.1521433	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	2	0.0023	0.1554075	E
<input type="checkbox"/>	GO:0051438	6	<a href="#">regulation of ubiquitin ligase activity</a>	6	0.0009	2	0.0023	0.1554075	E
<input type="checkbox"/>	GO:0000090	7,8,9,6	<a href="#">mitotic anaphase</a>	6	0.0009	2	0.0023	0.1554075	E
<input type="checkbox"/>	GO:0051322	6,7,5	<a href="#">anaphase</a>	6	0.0009	2	0.0023	0.1554075	E
<input type="checkbox"/>	GO:0008299	6,5,7	<a href="#">isoprenoid biosynthetic process</a>	6	0.0009	2	0.0023	0.1554075	E
<input type="checkbox"/>	GO:0015791	4,5	<a href="#">polyol transport</a>	6	0.0009	2	0.0023	0.1554075	E
<input type="checkbox"/>	GO:0007130	11,9,8,6,5,10,7,4	<a href="#">synaptonemal complex assembly</a>	6	0.0009	2	0.0023	0.1554075	E
<input type="checkbox"/>	GO:0009396	6,7,8	<a href="#">folic acid and derivative biosynthetic process</a>	6	0.0009	2	0.0023	0.1554075	E
<input type="checkbox"/>	GO:0000717	8,7	<a href="#">nucleotide-excision repair, DNA duplex unwinding</a>	6	0.0009	2	0.0023	0.1554075	E
<input type="checkbox"/>	GO:0006376	8,7,10,12,3	<a href="#">mRNA splice site selection</a>	6	0.0009	2	0.0023	0.1554075	E
<input type="checkbox"/>	GO:0006720	5,6	<a href="#">isoprenoid metabolic process</a>	6	0.0009	2	0.0023	0.1554075	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	2	0.0023	0.1554075	E
<input type="checkbox"/>	GO:0045116	9	<a href="#">protein neddylation</a>	6	0.0009	2	0.0023	0.1554075	E
<input type="checkbox"/>	GO:0015758	7,8	<a href="#">glucose transport</a>	6	0.0009	2	0.0023	0.1554075	E
<input type="checkbox"/>	GO:0045041	10,9,8,7	<a href="#">protein import into mitochondrial intermembrane space</a>	6	0.0009	2	0.0023	0.1554075	E
<input type="checkbox"/>	GO:0051340	5	<a href="#">regulation of ligase activity</a>	6	0.0009	2	0.0023	0.1554075	E
<input type="checkbox"/>	GO:0009991	4	<a href="#">response to extracellular stimulus</a>	37	0.0057	6	0.0068	0.1594075	E
<input type="checkbox"/>	GO:0031667	5	<a href="#">response to nutrient levels</a>	37	0.0057	6	0.0068	0.1594075	E
<input type="checkbox"/>	GO:0009605	3	<a href="#">response to external stimulus</a>	37	0.0057	6	0.0068	0.1594075	E
<input type="checkbox"/>	GO:0006353	8,7	<a href="#">transcription termination</a>	20	0.0031	4	0.0045	0.1608849	E
<input type="checkbox"/>	GO:0042398	6,5	<a href="#">amino acid derivative biosynthetic process</a>	20	0.0031	4	0.0045	0.1608849	E
<input type="checkbox"/>	GO:0051053	8,7	<a href="#">negative regulation of DNA metabolic process</a>	20	0.0031	4	0.0045	0.1608849	E
<input type="checkbox"/>	GO:0006826	7,8,9	<a href="#">iron ion transport</a>	20	0.0031	4	0.0045	0.1608849	E
<input type="checkbox"/>	GO:0000725	7,6	<a href="#">recombinational repair</a>	29	0.0045	5	0.0057	0.1665358	E
<input type="checkbox"/>	GO:0009063	6,7	<a href="#">amino acid catabolic process</a>	29	0.0045	5	0.0057	0.1665358	E
<input type="checkbox"/>	GO:0006885	7	<a href="#">regulation of pH</a>	29	0.0045	5	0.0057	0.1665358	E
<input type="checkbox"/>	GO:0006612	9,7,8	<a href="#">protein targeting to membrane</a>	39	0.0060	6	0.0068	0.1668596	E
<input type="checkbox"/>	GO:0001302	5	<a href="#">replicative cell aging</a>	39	0.0060	6	0.0068	0.1668596	E

<input type="radio"/>	GO:0009065	7,8	<a href="#">glutamine family amino acid catabolic process</a>	13	0.0020	3	0.0034	0.1677520	E
<input type="radio"/>	GO:0006779	6,7	<a href="#">porphyrin biosynthetic process</a>	13	0.0020	3	0.0034	0.1677520	E
<input type="radio"/>	GO:0033014	6	<a href="#">tetrapyrrole biosynthetic process</a>	13	0.0020	3	0.0034	0.1677520	E
<input type="radio"/>	GO:0006783	7,6,8	<a href="#">heme biosynthetic process</a>	13	0.0020	3	0.0034	0.1677520	E
<input type="radio"/>	GO:0007346	7,5,6	<a href="#">regulation of progression through mitotic cell cycle</a>	13	0.0020	3	0.0034	0.1677520	E
<input type="radio"/>	GO:0006450	8,7,6	<a href="#">regulation of translational fidelity</a>	13	0.0020	3	0.0034	0.1677520	E
<input type="radio"/>	GO:0043681	6,7,8	<a href="#">protein import into mitochondrion</a>	40	0.0062	6	0.0068	0.1695296	E
<input type="radio"/>	GO:0009072	6,5,7	<a href="#">aromatic amino acid family metabolic process</a>	21	0.0032	4	0.0045	0.1716505	E
<input type="radio"/>	GO:0019674	9,8	<a href="#">NAD metabolic process</a>	21	0.0032	4	0.0045	0.1716505	E
<input type="radio"/>	GO:0051128	5,4	<a href="#">regulation of cellular component organization and biogenesis</a>	30	0.0046	5	0.0057	0.1725959	E
<input type="radio"/>	GO:0001403	6,4,8,9	<a href="#">invasive growth (sensu Saccharomyces)</a>	42	0.0065	6	0.0068	0.1727836	E
<input type="radio"/>	GO:0016125	5,6,7	<a href="#">sterol metabolic process</a>	42	0.0065	6	0.0068	0.1727836	E
<input type="radio"/>	GO:0008202	5,6	<a href="#">steroid metabolic process</a>	43	0.0066	6	0.0068	0.1734005	E
<input type="radio"/>	GO:0006513	10	<a href="#">protein monoubiquitination</a>	22	0.0034	4	0.0045	0.1811940	E
<input type="radio"/>	GO:0030472	6,5,10	<a href="#">mitotic spindle organization and biogenesis in nucleus</a>	22	0.0034	4	0.0045	0.1811940	E
<input type="radio"/>	GO:0032984	5	<a href="#">macromolecular complex disassembly</a>	32	0.0049	5	0.0057	0.1819098	E
<input type="radio"/>	GO:0044270	5,4	<a href="#">nitrogen compound catabolic process</a>	32	0.0049	5	0.0057	0.1819098	E
<input type="radio"/>	GO:0009310	5,6	<a href="#">amine catabolic process</a>	32	0.0049	5	0.0057	0.1819098	E
<input type="radio"/>	GO:0000147	5,9,8	<a href="#">actin cortical patch assembly</a>	14	0.0022	3	0.0034	0.1843991	E
<input type="radio"/>	GO:0009076	7,8	<a href="#">histidine family amino acid biosynthetic process</a>	14	0.0022	3	0.0034	0.1843991	E
<input type="radio"/>	GO:0009075	6,7	<a href="#">histidine family amino acid metabolic process</a>	14	0.0022	3	0.0034	0.1843991	E
<input type="radio"/>	GO:0006547	7,8	<a href="#">histidine metabolic process</a>	14	0.0022	3	0.0034	0.1843991	E
<input type="radio"/>	GO:0006778	5,6	<a href="#">porphyrin metabolic process</a>	14	0.0022	3	0.0034	0.1843991	E
<input type="radio"/>	GO:0042168	6,7,5	<a href="#">heme metabolic process</a>	14	0.0022	3	0.0034	0.1843991	E
<input type="radio"/>	GO:0045990	9,7,8,5	<a href="#">regulation of transcription by carbon catabolites</a>	14	0.0022	3	0.0034	0.1843991	E
<input type="radio"/>	GO:0006740	10,9	<a href="#">NADPH regeneration</a>	14	0.0022	3	0.0034	0.1843991	E
<input type="radio"/>	GO:0046040	9	<a href="#">IMP metabolic process</a>	14	0.0022	3	0.0034	0.1843991	E
<input type="radio"/>	GO:0006144	6	<a href="#">purine base metabolic process</a>	14	0.0022	3	0.0034	0.1843991	E
<input type="radio"/>	GO:0042787	10,9,11	<a href="#">protein ubiquitination during ubiquitin-dependent protein catabolic process</a>	14	0.0022	3	0.0034	0.1843991	E
<input type="radio"/>	GO:0006188	9,10	<a href="#">IMP biosynthetic process</a>	14	0.0022	3	0.0034	0.1843991	E
<input type="radio"/>	GO:0000105	8,9	<a href="#">histidine biosynthetic process</a>	14	0.0022	3	0.0034	0.1843991	E
<input type="radio"/>	GO:0033013	5	<a href="#">tetrapyrrole metabolic process</a>	14	0.0022	3	0.0034	0.1843991	E
<input type="radio"/>	GO:0042546	6	<a href="#">cell wall biogenesis</a>	33	0.0051	5	0.0057	0.1851492	E
<input type="radio"/>	GO:0006118	4	<a href="#">electron transport</a>	33	0.0051	5	0.0057	0.1851492	E
<input type="radio"/>	GO:0045047	9,8,7,6,5	<a href="#">protein targeting to ER</a>	33	0.0051	5	0.0057	0.1851492	E
<input type="radio"/>	GO:0009272	7	<a href="#">chitin- and beta-glucan-containing cell wall biogenesis</a>	33	0.0051	5	0.0057	0.1851492	E
<input type="radio"/>	GO:0007186	6	<a href="#">G-protein coupled receptor protein signaling pathway</a>	34	0.0053	5	0.0057	0.1874570	E
<input type="radio"/>	GO:0033205	5,4	<a href="#">cytokinesis during cell cycle</a>	7	0.0011	2	0.0023	0.1879110	E
<input type="radio"/>	GO:0045896	9,7,5,8,6,4	<a href="#">regulation of transcription, mitotic</a>	7	0.0011	2	0.0023	0.1879110	E
<input type="radio"/>	GO:0045913	6,5	<a href="#">positive regulation of carbohydrate metabolic process</a>	7	0.0011	2	0.0023	0.1879110	E
<input type="radio"/>	GO:0006829	8,9	<a href="#">zinc ion transport</a>	7	0.0011	2	0.0023	0.1879110	E



<input type="radio"/>	GO:0007068	10,8,6,9,7,5	<a href="#">negative regulation of transcription, mitotic</a>	7	0.0011	2	0.0023	0.1879110	E
<input type="radio"/>	GO:0051174	6,5	<a href="#">regulation of phosphorus metabolic process</a>	7	0.0011	2	0.0023	0.1879110	E
<input type="radio"/>	GO:0000433	12,10,11,8	<a href="#">negative regulation of transcription from RNA polymerase II promoter by glucose</a>	7	0.0011	2	0.0023	0.1879110	E
<input type="radio"/>	GO:0000429	10,8,9,6	<a href="#">regulation of transcription from RNA polymerase II promoter by carbon catabolites</a>	7	0.0011	2	0.0023	0.1879110	E
<input type="radio"/>	GO:0000715	7,8	<a href="#">nucleotide-excision repair, DNA damage recognition</a>	7	0.0011	2	0.0023	0.1879110	E
<input type="radio"/>	GO:0000430	11,9,10,7	<a href="#">regulation of transcription from RNA polymerase II promoter by glucose</a>	7	0.0011	2	0.0023	0.1879110	E
<input type="radio"/>	GO:0009092	7,8	<a href="#">homoserine metabolic process</a>	7	0.0011	2	0.0023	0.1879110	E
<input type="radio"/>	GO:0009435	8,7,10,9	<a href="#">NAD biosynthetic process</a>	7	0.0011	2	0.0023	0.1879110	E
<input type="radio"/>	GO:0045014	11,9,10,7	<a href="#">negative regulation of transcription by glucose</a>	7	0.0011	2	0.0023	0.1879110	E
<input type="radio"/>	GO:0019220	7,6	<a href="#">regulation of phosphate metabolic process</a>	7	0.0011	2	0.0023	0.1879110	E
<input type="radio"/>	GO:0019722	7	<a href="#">calcium-mediated signaling</a>	7	0.0011	2	0.0023	0.1879110	E
<input type="radio"/>	GO:0000710	11,9,8,6,5,10,7,4	<a href="#">meiotic mismatch repair</a>	7	0.0011	2	0.0023	0.1879110	E
<input type="radio"/>	GO:0000437	11,9,10,7	<a href="#">negative regulation of transcription from RNA polymerase II promoter by carbon catabolites</a>	7	0.0011	2	0.0023	0.1879110	E
<input type="radio"/>	GO:0000726	7,6	<a href="#">non-recombinational repair</a>	35	0.0054	5	0.0057	0.1888586	E
<input type="radio"/>	GO:0007117	6,5,4	<a href="#">budding cell bud growth</a>	35	0.0054	5	0.0057	0.1888586	E
<input type="radio"/>	GO:0048590	3	<a href="#">non-developmental growth</a>	35	0.0054	5	0.0057	0.1888586	E
<input type="radio"/>	GO:0022411	4	<a href="#">cellular component disassembly</a>	36	0.0056	5	0.0057	0.1893892	E
<input type="radio"/>	GO:0019748	3	<a href="#">secondary metabolic process</a>	23	0.0036	4	0.0045	0.1894332	E
<input type="radio"/>	GO:0006303	8,7	<a href="#">double-strand break repair via nonhomologous end joining</a>	23	0.0036	4	0.0045	0.1894332	E
<input type="radio"/>	GO:0009069	6,7	<a href="#">serine family amino acid metabolic process</a>	24	0.0037	4	0.0045	0.1963201	E
<input type="radio"/>	GO:0009201	7,8	<a href="#">ribonucleoside triphosphate biosynthetic process</a>	24	0.0037	4	0.0045	0.1963201	E
<input type="radio"/>	GO:0031145	11,10,12	<a href="#">anaphase-promoting complex-dependent proteasomal ubiquitin-dependent protein catabolic process</a>	15	0.0023	3	0.0034	0.1990736	E
<input type="radio"/>	GO:0006267	8,7	<a href="#">pre-replicative complex assembly</a>	15	0.0023	3	0.0034	0.1990736	E
<input type="radio"/>	GO:0007091	9,7,5,8,6,4	<a href="#">mitotic metaphase/anaphase transition</a>	15	0.0023	3	0.0034	0.1990736	E
<input type="radio"/>	GO:0031110	6,9,5	<a href="#">regulation of microtubule polymerization or depolymerization</a>	15	0.0023	3	0.0034	0.1990736	E
<input type="radio"/>	GO:0015918	5,6	<a href="#">sterol transport</a>	15	0.0023	3	0.0034	0.1990736	E
<input type="radio"/>	GO:0009199	7	<a href="#">ribonucleoside triphosphate metabolic process</a>	25	0.0039	4	0.0045	0.2018376	E
<input type="radio"/>	GO:0045005	8,6	<a href="#">maintenance of fidelity during DNA-dependent DNA replication</a>	25	0.0039	4	0.0045	0.2018376	E
<input type="radio"/>	GO:0006298	7,9,6	<a href="#">mismatch repair</a>	25	0.0039	4	0.0045	0.2018376	E
<input type="radio"/>	GO:0048311	7,6	<a href="#">mitochondrion distribution</a>	26	0.0040	4	0.0045	0.2059961	E
<input type="radio"/>	GO:0042274	6,5	<a href="#">ribosomal small subunit biogenesis and assembly</a>	26	0.0040	4	0.0045	0.2059961	E
<input type="radio"/>	GO:0000001	8,7,6	<a href="#">mitochondrion inheritance</a>	26	0.0040	4	0.0045	0.2059961	E
<input type="radio"/>	GO:0051646	6,5	<a href="#">mitochondrion localization</a>	27	0.0042	4	0.0045	0.2088288	E
<input type="radio"/>	GO:0009142	6,7	<a href="#">nucleoside triphosphate biosynthetic process</a>	27	0.0042	4	0.0045	0.2088288	E
<input type="radio"/>	GO:0032005	7,6	<a href="#">signal transduction during conjugation with cellular fusion</a>	28	0.0043	4	0.0045	0.2103885	E
<input type="radio"/>	GO:0000750	8,7,6	<a href="#">pheromone-dependent signal transduction during conjugation with cellular fusion</a>	28	0.0043	4	0.0045	0.2103885	E
<input type="radio"/>	GO:0043241	6,5	<a href="#">protein complex disassembly</a>	28	0.0043	4	0.0045	0.2103885	E

<input type="radio"/>	GO:0009636	4	<a href="#">response to toxin</a>	28	0.0043	4	0.0045	0.2103885	E
<input type="radio"/>	GO:0043624	7,6	<a href="#">cellular protein complex disassembly</a>	28	0.0043	4	0.0045	0.2103885	E
<input type="radio"/>	GO:0006109	5,4	<a href="#">regulation of carbohydrate metabolic process</a>	29	0.0045	4	0.0045	0.2107435	E
<input type="radio"/>	GO:0031109	8	<a href="#">microtubule polymerization or depolymerization</a>	16	0.0025	3	0.0034	0.2116045	E
<input type="radio"/>	GO:0032392	6	<a href="#">DNA geometric change</a>	16	0.0025	3	0.0034	0.2116045	E
<input type="radio"/>	GO:0032508	7	<a href="#">DNA duplex unwinding</a>	16	0.0025	3	0.0034	0.2116045	E
<input type="radio"/>	GO:0007532	9,5,7,8,6	<a href="#">regulation of transcription, mating-type specific</a>	8	0.0012	2	0.0023	0.2163876	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	0.0023	0.2163876	E
<input type="radio"/>	GO:0001308	11,7,10	<a href="#">loss of chromatin silencing during replicative cell aging</a>	8	0.0012	2	0.0023	0.2163876	E
<input type="radio"/>	GO:0045013	10,8,9,6	<a href="#">negative regulation of transcription by carbon catabolites</a>	8	0.0012	2	0.0023	0.2163876	E
<input type="radio"/>	GO:0008156	9,8	<a href="#">negative regulation of DNA replication</a>	8	0.0012	2	0.0023	0.2163876	E
<input type="radio"/>	GO:0016042	4,5	<a href="#">lipid catabolic process</a>	8	0.0012	2	0.0023	0.2163876	E
<input type="radio"/>	GO:0000335	10,9,6	<a href="#">negative regulation of DNA transposition</a>	8	0.0012	2	0.0023	0.2163876	E
<input type="radio"/>	GO:0044242	5,6	<a href="#">cellular lipid catabolic process</a>	8	0.0012	2	0.0023	0.2163876	E
<input type="radio"/>	GO:0046015	10,8,9,6	<a href="#">regulation of transcription by glucose</a>	8	0.0012	2	0.0023	0.2163876	E
<input type="radio"/>	GO:0006566	7,8	<a href="#">threonine metabolic process</a>	8	0.0012	2	0.0023	0.2163876	E
<input type="radio"/>	GO:0007004	9	<a href="#">telomere maintenance via telomerase</a>	17	0.0026	3	0.0034	0.2219063	E
<input type="radio"/>	GO:0007266	8	<a href="#">Rho protein signal transduction</a>	17	0.0026	3	0.0034	0.2219063	E
<input type="radio"/>	GO:0006273	9,8	<a href="#">lagging strand elongation</a>	18	0.0028	3	0.0034	0.2299662	E
<input type="radio"/>	GO:0000753	7,8,6	<a href="#">cellular morphogenesis during conjugation with cellular fusion</a>	18	0.0028	3	0.0034	0.2299662	E
<input type="radio"/>	GO:0006369	9,8	<a href="#">transcription termination from RNA polymerase II promoter</a>	18	0.0028	3	0.0034	0.2299662	E
<input type="radio"/>	GO:0000084	8,7,6	<a href="#">S phase of mitotic cell cycle</a>	18	0.0028	3	0.0034	0.2299662	E
<input type="radio"/>	GO:0015781	6,7	<a href="#">pyrimidine nucleotide-sugar transport</a>	2	0.0003	1	0.0011	0.2357777	E
<input type="radio"/>	GO:0009061	6	<a href="#">anaerobic respiration</a>	2	0.0003	1	0.0011	0.2357777	E
<input type="radio"/>	GO:0043132	5,6	<a href="#">NAD transport</a>	2	0.0003	1	0.0011	0.2357777	E
<input type="radio"/>	GO:0006429	9,8,10,7	<a href="#">leucyl-tRNA aminoacylation</a>	2	0.0003	1	0.0011	0.2357777	E
<input type="radio"/>	GO:0010043	6	<a href="#">response to zinc ion</a>	2	0.0003	1	0.0011	0.2357777	E
<input type="radio"/>	GO:0009221	7,8	<a href="#">pyrimidine deoxyribonucleotide biosynthetic process</a>	2	0.0003	1	0.0011	0.2357777	E
<input type="radio"/>	GO:0030808	8,6,7,5	<a href="#">regulation of nucleotide biosynthetic process</a>	2	0.0003	1	0.0011	0.2357777	E
<input type="radio"/>	GO:0031055	10	<a href="#">chromatin remodeling at centromere</a>	2	0.0003	1	0.0011	0.2357777	E
<input type="radio"/>	GO:0009187	6	<a href="#">cyclic nucleotide metabolic process</a>	2	0.0003	1	0.0011	0.2357777	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	0.0011	0.2357777	E
<input type="radio"/>	GO:0006467	7,8	<a href="#">protein thiol-disulfide exchange</a>	2	0.0003	1	0.0011	0.2357777	E
<input type="radio"/>	GO:0009220	7,8	<a href="#">pyrimidine ribonucleotide biosynthetic process</a>	2	0.0003	1	0.0011	0.2357777	E
<input type="radio"/>	GO:0009209	8,9	<a href="#">pyrimidine ribonucleoside triphosphate biosynthetic process</a>	2	0.0003	1	0.0011	0.2357777	E
<input type="radio"/>	GO:0031056	6,8,11,5,9,7	<a href="#">regulation of histone modification</a>	2	0.0003	1	0.0011	0.2357777	E
<input type="radio"/>	GO:0046037	9	<a href="#">GMP metabolic process</a>	2	0.0003	1	0.0011	0.2357777	E
<input type="radio"/>	GO:0015757	7,8	<a href="#">galactose transport</a>	2	0.0003	1	0.0011	0.2357777	E
<input type="radio"/>	GO:0010133	9,8,10	<a href="#">proline catabolic process to glutamate</a>	2	0.0003	1	0.0011	0.2357777	E
<input type="radio"/>	GO:0006541	7,8	<a href="#">glutamine metabolic process</a>	2	0.0003	1	0.0011	0.2357777	E
<input type="radio"/>	GO:0032318	7,8,9	<a href="#">regulation of Ras GTPase activity</a>	2	0.0003	1	0.0011	0.2357777	E

<input type="radio"/>	GO:0045980	8,7	<a href="#">negative regulation of nucleotide metabolic process</a>	2	0.0003	1	0.0011	0.2357777	E
<input type="radio"/>	GO:0046156	7,8,6	<a href="#">siroheme metabolic process</a>	2	0.0003	1	0.0011	0.2357777	E
<input type="radio"/>	GO:0046656	7,8,9	<a href="#">folic acid biosynthetic process</a>	2	0.0003	1	0.0011	0.2357777	E
<input type="radio"/>	GO:0019354	8,7,9	<a href="#">siroheme biosynthetic process</a>	2	0.0003	1	0.0011	0.2357777	E
<input type="radio"/>	GO:0006975	9,8,5	<a href="#">DNA damage induced protein phosphorylation</a>	2	0.0003	1	0.0011	0.2357777	E
<input type="radio"/>	GO:0030817	10,8,9,7	<a href="#">regulation of cAMP biosynthetic process</a>	2	0.0003	1	0.0011	0.2357777	E
<input type="radio"/>	GO:0015840	5,6	<a href="#">urea transport</a>	2	0.0003	1	0.0011	0.2357777	E
<input type="radio"/>	GO:0015805	7,8,9	<a href="#">S-adenosylmethionine transport</a>	2	0.0003	1	0.0011	0.2357777	E
<input type="radio"/>	GO:0006241	9,10	<a href="#">CTP biosynthetic process</a>	2	0.0003	1	0.0011	0.2357777	E
<input type="radio"/>	GO:0032261	6,7	<a href="#">purine nucleotide salvage</a>	2	0.0003	1	0.0011	0.2357777	E
<input type="radio"/>	GO:0046058	7	<a href="#">cAMP metabolic process</a>	2	0.0003	1	0.0011	0.2357777	E
<input type="radio"/>	GO:0042558	5	<a href="#">pteridine and derivative metabolic process</a>	2	0.0003	1	0.0011	0.2357777	E
<input type="radio"/>	GO:0006430	9,8,10,7	<a href="#">lysyl-tRNA aminoacylation</a>	2	0.0003	1	0.0011	0.2357777	E
<input type="radio"/>	GO:0006140	7,6	<a href="#">regulation of nucleotide metabolic process</a>	2	0.0003	1	0.0011	0.2357777	E
<input type="radio"/>	GO:0009190	6,7	<a href="#">cyclic nucleotide biosynthetic process</a>	2	0.0003	1	0.0011	0.2357777	E
<input type="radio"/>	GO:0009314	4	<a href="#">response to radiation</a>	2	0.0003	1	0.0011	0.2357777	E
<input type="radio"/>	GO:0051666	5,4	<a href="#">actin cortical patch localization</a>	2	0.0003	1	0.0011	0.2357777	E
<input type="radio"/>	GO:0030803	10,8,9,7	<a href="#">negative regulation of cyclic nucleotide biosynthetic process</a>	2	0.0003	1	0.0011	0.2357777	E
<input type="radio"/>	GO:0006171	7,8	<a href="#">cAMP biosynthetic process</a>	2	0.0003	1	0.0011	0.2357777	E
<input type="radio"/>	GO:0006673	7,9,8,10	<a href="#">inositolphosphoceramide metabolic process</a>	2	0.0003	1	0.0011	0.2357777	E
<input type="radio"/>	GO:0046655	6,8	<a href="#">folic acid metabolic process</a>	2	0.0003	1	0.0011	0.2357777	E
<input type="radio"/>	GO:0030814	9,8	<a href="#">regulation of cAMP metabolic process</a>	2	0.0003	1	0.0011	0.2357777	E
<input type="radio"/>	GO:0006824	7,8,9	<a href="#">cobalt ion transport</a>	2	0.0003	1	0.0011	0.2357777	E
<input type="radio"/>	GO:0006424	9,8,10,7	<a href="#">glutamyl-tRNA aminoacylation</a>	2	0.0003	1	0.0011	0.2357777	E
<input type="radio"/>	GO:0000358	9,8,10,11,12,13	<a href="#">formation of catalytic U2-type spliceosome for second transesterification step</a>	2	0.0003	1	0.0011	0.2357777	E
<input type="radio"/>	GO:0032320	8,9,10	<a href="#">positive regulation of Ras GTPase activity</a>	2	0.0003	1	0.0011	0.2357777	E
<input type="radio"/>	GO:0009208	8	<a href="#">pyrimidine ribonucleoside triphosphate metabolic process</a>	2	0.0003	1	0.0011	0.2357777	E
<input type="radio"/>	GO:0030815	10,9	<a href="#">negative regulation of cAMP metabolic process</a>	2	0.0003	1	0.0011	0.2357777	E
<input type="radio"/>	GO:0006556	8,7,6,9,5	<a href="#">S-adenosylmethionine biosynthetic process</a>	2	0.0003	1	0.0011	0.2357777	E
<input type="radio"/>	GO:0006721	6,7,4	<a href="#">terpenoid metabolic process</a>	2	0.0003	1	0.0011	0.2357777	E
<input type="radio"/>	GO:0033108	8,7	<a href="#">mitochondrial respiratory chain complex assembly</a>	2	0.0003	1	0.0011	0.2357777	E
<input type="radio"/>	GO:0042559	6	<a href="#">pteridine and derivative biosynthetic process</a>	2	0.0003	1	0.0011	0.2357777	E
<input type="radio"/>	GO:0018195	8	<a href="#">peptidyl-arginine modification</a>	2	0.0003	1	0.0011	0.2357777	E
<input type="radio"/>	GO:0050667	7,8,6	<a href="#">homocysteine metabolic process</a>	2	0.0003	1	0.0011	0.2357777	E
<input type="radio"/>	GO:0007024	8	<a href="#">alpha-tubulin folding</a>	2	0.0003	1	0.0011	0.2357777	E
<input type="radio"/>	GO:0009218	7	<a href="#">pyrimidine ribonucleotide metabolic process</a>	2	0.0003	1	0.0011	0.2357777	E
<input type="radio"/>	GO:0030800	9,8	<a href="#">negative regulation of cyclic nucleotide metabolic process</a>	2	0.0003	1	0.0011	0.2357777	E
<input type="radio"/>	GO:0009062	6,7,8	<a href="#">fatty acid catabolic process</a>	2	0.0003	1	0.0011	0.2357777	E
<input type="radio"/>	GO:0030818	11,9,10,8	<a href="#">negative regulation of cAMP biosynthetic process</a>	2	0.0003	1	0.0011	0.2357777	E
<input type="radio"/>	GO:0030799	8,7	<a href="#">regulation of cyclic nucleotide metabolic process</a>	2	0.0003	1	0.0011	0.2357777	E

<input type="radio"/>	GO:0051339	5	<a href="#">regulation of lyase activity</a>	2	0.0003	1	0.0011	0.2357777	E
<input type="radio"/>	GO:0030809	9,7,8,6	<a href="#">negative regulation of nucleotide biosynthetic process</a>	2	0.0003	1	0.0011	0.2357777	E
<input type="radio"/>	GO:0015809	7,8,9	<a href="#">arginine transport</a>	2	0.0003	1	0.0011	0.2357777	E
<input type="radio"/>	GO:0016572	11,9,8	<a href="#">histone phosphorylation</a>	2	0.0003	1	0.0011	0.2357777	E
<input type="radio"/>	GO:0006434	9,8,10,7	<a href="#">seryl-tRNA aminoacylation</a>	2	0.0003	1	0.0011	0.2357777	E
<input type="radio"/>	GO:0016114	7,6,8,5	<a href="#">terpenoid biosynthetic process</a>	2	0.0003	1	0.0011	0.2357777	E
<input type="radio"/>	GO:0015766	5,6	<a href="#">disaccharide transport</a>	2	0.0003	1	0.0011	0.2357777	E
<input type="radio"/>	GO:0046036	9	<a href="#">CTP metabolic process</a>	2	0.0003	1	0.0011	0.2357777	E
<input type="radio"/>	GO:0045761	6,9,10	<a href="#">regulation of adenylate cyclase activity</a>	2	0.0003	1	0.0011	0.2357777	E
<input type="radio"/>	GO:0006545	8,9	<a href="#">glycine biosynthetic process</a>	2	0.0003	1	0.0011	0.2357777	E
<input type="radio"/>	GO:0007580	10,6	<a href="#">extrachromosomal circular DNA accumulation during cell aging</a>	2	0.0003	1	0.0011	0.2357777	E
<input type="radio"/>	GO:0045016	8,6,7,9	<a href="#">mitochondrial magnesium ion transport</a>	2	0.0003	1	0.0011	0.2357777	E
<input type="radio"/>	GO:0030802	9,7,8,6	<a href="#">regulation of cyclic nucleotide biosynthetic process</a>	2	0.0003	1	0.0011	0.2357777	E
<input type="radio"/>	GO:0019988	7,8,9,6	<a href="#">charged-tRNA modification</a>	2	0.0003	1	0.0011	0.2357777	E
<input type="radio"/>	GO:0031279	5	<a href="#">regulation of cyclase activity</a>	2	0.0003	1	0.0011	0.2357777	E
<input type="radio"/>	GO:0042886	4,5	<a href="#">amide transport</a>	2	0.0003	1	0.0011	0.2357777	E
<input type="radio"/>	GO:0000280	3	<a href="#">nuclear division</a>	2	0.0003	1	0.0011	0.2357777	E
<input type="radio"/>	GO:0046148	5	<a href="#">pigment biosynthetic process</a>	19	0.0029	3	0.0034	0.2358307	E
<input type="radio"/>	GO:0042440	4	<a href="#">pigment metabolic process</a>	20	0.0031	3	0.0034	0.2395926	E
<input type="radio"/>	GO:0016579	9	<a href="#">protein deubiquitination</a>	20	0.0031	3	0.0034	0.2395926	E
<input type="radio"/>	GO:0000022	6,5,10,8	<a href="#">mitotic spindle elongation</a>	20	0.0031	3	0.0034	0.2395926	E
<input type="radio"/>	GO:0000767	6,7	<a href="#">cellular morphogenesis during conjugation</a>	20	0.0031	3	0.0034	0.2395926	E
<input type="radio"/>	GO:0000209	10	<a href="#">protein polyubiquitination</a>	20	0.0031	3	0.0034	0.2395926	E
<input type="radio"/>	GO:0051320	7,6,5	<a href="#">S phase</a>	20	0.0031	3	0.0034	0.2395926	E
<input type="radio"/>	GO:0051231	5,4,9,7	<a href="#">spindle elongation</a>	20	0.0031	3	0.0034	0.2395926	E
<input type="radio"/>	GO:0000165	7	<a href="#">MAPKKK cascade</a>	20	0.0031	3	0.0034	0.2395926	E
<input type="radio"/>	GO:0009067	7,8	<a href="#">aspartate family amino acid biosynthetic process</a>	20	0.0031	3	0.0034	0.2395926	E
<input type="radio"/>	GO:0055074	9	<a href="#">calcium ion homeostasis</a>	9	0.0014	2	0.0023	0.2402746	E
<input type="radio"/>	GO:0019935	7	<a href="#">cyclic-nucleotide-mediated signaling</a>	9	0.0014	2	0.0023	0.2402746	E
<input type="radio"/>	GO:0000393	7,6,9,11	<a href="#">spliceosomal conformational changes to generate catalytic conformation</a>	9	0.0014	2	0.0023	0.2402746	E
<input type="radio"/>	GO:0045815	5	<a href="#">positive regulation of gene expression, epigenetic</a>	9	0.0014	2	0.0023	0.2402746	E
<input type="radio"/>	GO:0000921	8,7	<a href="#">septin ring assembly</a>	9	0.0014	2	0.0023	0.2402746	E
<input type="radio"/>	GO:0030952	6	<a href="#">establishment and/or maintenance of cytoskeleton polarity</a>	9	0.0014	2	0.0023	0.2402746	E
<input type="radio"/>	GO:0019933	8	<a href="#">cAMP-mediated signaling</a>	9	0.0014	2	0.0023	0.2402746	E
<input type="radio"/>	GO:0032185	6	<a href="#">septin cytoskeleton organization and biogenesis</a>	9	0.0014	2	0.0023	0.2402746	E
<input type="radio"/>	GO:0000184	8	<a href="#">mRNA catabolic process, nonsense-mediated decay</a>	9	0.0014	2	0.0023	0.2402746	E
<input type="radio"/>	GO:0006345	10,6,9	<a href="#">loss of chromatin silencing</a>	9	0.0014	2	0.0023	0.2402746	E
<input type="radio"/>	GO:0030950	8,7	<a href="#">establishment and/or maintenance of actin cytoskeleton polarity</a>	9	0.0014	2	0.0023	0.2402746	E
<input type="radio"/>	GO:0030968	7,5,6	<a href="#">unfolded protein response</a>	9	0.0014	2	0.0023	0.2402746	E
<input type="radio"/>	GO:0001304	10,6	<a href="#">progressive alteration of chromatin during replicative cell aging</a>	9	0.0014	2	0.0023	0.2402746	E
<input type="radio"/>	GO:0031106	7	<a href="#">septin ring organization</a>	9	0.0014	2	0.0023	0.2402746	E
<input type="radio"/>	GO:0006282	8,7	<a href="#">transcription-coupled nucleotide-excision</a>	9	0.0014	2	0.0023	0.2402746	E

<input type="radio"/>	GO:0000263	9,7	<a href="#">repair</a>	9	0.0014	2	0.0023	0.2402746	E
<input type="radio"/>	GO:0008535	8,7	<a href="#">cytochrome c oxidase complex assembly</a>	9	0.0014	2	0.0023	0.2402746	E
<input type="radio"/>	GO:0051180	4,5	<a href="#">vitamin transport</a>	9	0.0014	2	0.0023	0.2402746	E
<input type="radio"/>	GO:0006984	6	<a href="#">ER-nuclear signaling pathway</a>	9	0.0014	2	0.0023	0.2402746	E
<input type="radio"/>	GO:0006874	10,8	<a href="#">cellular calcium ion homeostasis</a>	9	0.0014	2	0.0023	0.2402746	E
<input type="radio"/>	GO:0006081	4	<a href="#">aldehyde metabolic process</a>	21	0.0032	3	0.0034	0.2413801	E
<input type="radio"/>	GO:0009068	7,8	<a href="#">aspartate family amino acid catabolic process</a>	10	0.0015	2	0.0023	0.2593810	E
<input type="radio"/>	GO:0000337	9,8,5	<a href="#">regulation of DNA transposition</a>	10	0.0015	2	0.0023	0.2593810	E
<input type="radio"/>	GO:0015718	6,7	<a href="#">monocarboxylic acid transport</a>	10	0.0015	2	0.0023	0.2593810	E
<input type="radio"/>	GO:0040001	5,4,7,8,9,6	<a href="#">establishment of mitotic spindle localization</a>	10	0.0015	2	0.0023	0.2593810	E
<input type="radio"/>	GO:0051293	6,7,8,4,5	<a href="#">establishment of spindle localization</a>	10	0.0015	2	0.0023	0.2593810	E
<input type="radio"/>	GO:0051653	6,5	<a href="#">spindle localization</a>	10	0.0015	2	0.0023	0.2593810	E
<input type="radio"/>	GO:0008298	5	<a href="#">intracellular mRNA localization</a>	10	0.0015	2	0.0023	0.2593810	E
<input type="radio"/>	GO:0006313	7,4	<a href="#">transposition, DNA-mediated</a>	10	0.0015	2	0.0023	0.2593810	E
<input type="radio"/>	GO:0000132	6,5,8,9,10,7	<a href="#">establishment of mitotic spindle orientation</a>	10	0.0015	2	0.0023	0.2593810	E
<input type="radio"/>	GO:0051294	7,8,9,5,6	<a href="#">establishment of spindle orientation</a>	10	0.0015	2	0.0023	0.2593810	E
<input type="radio"/>	GO:0043085	5	<a href="#">positive regulation of enzyme activity</a>	11	0.0017	2	0.0023	0.2737776	E
<input type="radio"/>	GO:0001558	5,6,4,8,9	<a href="#">regulation of cell growth</a>	11	0.0017	2	0.0023	0.2737776	E
<input type="radio"/>	GO:0006384	8,9,7	<a href="#">transcription initiation from RNA polymerase III promoter</a>	11	0.0017	2	0.0023	0.2737776	E
<input type="radio"/>	GO:0001101	4	<a href="#">response to acid</a>	11	0.0017	2	0.0023	0.2737776	E
<input type="radio"/>	GO:0006116	10,9	<a href="#">NADH oxidation</a>	11	0.0017	2	0.0023	0.2737776	E
<input type="radio"/>	GO:0007109	7,6,5,4	<a href="#">cytokinesis, completion of separation</a>	11	0.0017	2	0.0023	0.2737776	E
<input type="radio"/>	GO:0008054	7,6,11,10,12	<a href="#">cyclin catabolic process</a>	12	0.0019	2	0.0023	0.2837124	E
<input type="radio"/>	GO:0045910	9,8	<a href="#">negative regulation of DNA recombination</a>	12	0.0019	2	0.0023	0.2837124	E
<input type="radio"/>	GO:0007103	6,7,5,8	<a href="#">spindle pole body duplication in nuclear envelope</a>	13	0.0020	2	0.0023	0.2895459	E
<input type="radio"/>	GO:0006895	8,9,6,7	<a href="#">Golgi to endosome transport</a>	13	0.0020	2	0.0023	0.2895459	E
<input type="radio"/>	GO:0031929	6	<a href="#">TOR signaling pathway</a>	13	0.0020	2	0.0023	0.2895459	E
<input type="radio"/>	GO:0006038	9,10,7,8,11	<a href="#">cell wall chitin biosynthetic process</a>	13	0.0020	2	0.0023	0.2895459	E
<input type="radio"/>	GO:0006537	8,9	<a href="#">glutamate biosynthetic process</a>	13	0.0020	2	0.0023	0.2895459	E
<input type="radio"/>	GO:0040008	4,3	<a href="#">regulation of growth</a>	13	0.0020	2	0.0023	0.2895459	E
<input type="radio"/>	GO:0006301	7,6	<a href="#">postreplication repair</a>	13	0.0020	2	0.0023	0.2895459	E
<input type="radio"/>	GO:0000920	6,4	<a href="#">cell separation during cytokinesis</a>	13	0.0020	2	0.0023	0.2895459	E
<input type="radio"/>	GO:0006734	9,8	<a href="#">NADH metabolic process</a>	14	0.0022	2	0.0023	0.2917038	E
<input type="radio"/>	GO:0042770	5	<a href="#">DNA damage response, signal transduction</a>	14	0.0022	2	0.0023	0.2917038	E
<input type="radio"/>	GO:0000077	9,8,6	<a href="#">DNA damage checkpoint</a>	14	0.0022	2	0.0023	0.2917038	E
<input type="radio"/>	GO:0030474	5,6,4,7	<a href="#">spindle pole body duplication</a>	14	0.0022	2	0.0023	0.2917038	E
<input type="radio"/>	GO:0006037	8,9,6,7,10	<a href="#">cell wall chitin metabolic process</a>	14	0.0022	2	0.0023	0.2917038	E
<input type="radio"/>	GO:0030100	6,7,5	<a href="#">regulation of endocytosis</a>	3	0.0005	1	0.0011	0.3054294	E
<input type="radio"/>	GO:0045026	6	<a href="#">plasma membrane fusion</a>	3	0.0005	1	0.0011	0.3054294	E
<input type="radio"/>	GO:0048024	9,8,11	<a href="#">regulation of nuclear mRNA splicing, via spliceosome</a>	3	0.0005	1	0.0011	0.3054294	E
<input type="radio"/>	GO:0042183	6,8	<a href="#">formate catabolic process</a>	3	0.0005	1	0.0011	0.3054294	E
<input type="radio"/>	GO:0009263	6,7	<a href="#">deoxyribonucleotide biosynthetic process</a>	3	0.0005	1	0.0011	0.3054294	E
<input type="radio"/>	GO:0009437	6,7	<a href="#">carnitine metabolic process</a>	3	0.0005	1	0.0011	0.3054294	E
<input type="radio"/>	GO:0042044	4,5	<a href="#">fluid transport</a>	3	0.0005	1	0.0011	0.3054294	E

<input type="checkbox"/>	GO:0018065	8	<a href="#">protein-cofactor linkage</a>	3	0.0005	1	0.0011	0.3054294	E
<input type="checkbox"/>	GO:0051436	8,6,5	<a href="#">negative regulation of ubiquitin ligase activity during mitotic cell cycle</a>	3	0.0005	1	0.0011	0.3054294	E
<input type="checkbox"/>	GO:0019754	5	<a href="#">one-carbon compound catabolic process</a>	3	0.0005	1	0.0011	0.3054294	E
<input type="checkbox"/>	GO:0006452	8,7,6	<a href="#">translational frameshifting</a>	3	0.0005	1	0.0011	0.3054294	E
<input type="checkbox"/>	GO:0050684	8,7	<a href="#">regulation of mRNA processing</a>	3	0.0005	1	0.0011	0.3054294	E
<input type="checkbox"/>	GO:0019509	7,8,6,9	<a href="#">methionine salvage</a>	3	0.0005	1	0.0011	0.3054294	E
<input type="checkbox"/>	GO:0000387	5,9,11	<a href="#">spliceosomal snRNP biogenesis</a>	3	0.0005	1	0.0011	0.3054294	E
<input type="checkbox"/>	GO:0000244	7,6,10,12	<a href="#">assembly of spliceosomal tri-snRNP</a>	3	0.0005	1	0.0011	0.3054294	E
<input type="checkbox"/>	GO:0051443	7	<a href="#">positive regulation of ubiquitin ligase activity</a>	3	0.0005	1	0.0011	0.3054294	E
<input type="checkbox"/>	GO:0051383	6	<a href="#">kinetochore organization and biogenesis</a>	3	0.0005	1	0.0011	0.3054294	E
<input type="checkbox"/>	GO:0045821	7,11,12,6	<a href="#">positive regulation of glycolysis</a>	3	0.0005	1	0.0011	0.3054294	E
<input type="checkbox"/>	GO:0030541	4	<a href="#">plasmid partitioning</a>	3	0.0005	1	0.0011	0.3054294	E
<input type="checkbox"/>	GO:0006285	7,8	<a href="#">base-excision repair, AP site formation</a>	3	0.0005	1	0.0011	0.3054294	E
<input type="checkbox"/>	GO:0006390	8,7	<a href="#">transcription from mitochondrial promoter</a>	3	0.0005	1	0.0011	0.3054294	E
<input type="checkbox"/>	GO:0032974	8,6,7,9	<a href="#">amino acid export from vacuole</a>	3	0.0005	1	0.0011	0.3054294	E
<input type="checkbox"/>	GO:0019413	7,8	<a href="#">acetate biosynthetic process</a>	3	0.0005	1	0.0011	0.3054294	E
<input type="checkbox"/>	GO:0009219	7	<a href="#">pyrimidine deoxyribonucleotide metabolic process</a>	3	0.0005	1	0.0011	0.3054294	E
<input type="checkbox"/>	GO:0030543	5	<a href="#">2-micrometer plasmid partitioning</a>	3	0.0005	1	0.0011	0.3054294	E
<input type="checkbox"/>	GO:0051351	6	<a href="#">positive regulation of ligase activity</a>	3	0.0005	1	0.0011	0.3054294	E
<input type="checkbox"/>	GO:0043461	8,7	<a href="#">F-type ATPase complex assembly</a>	3	0.0005	1	0.0011	0.3054294	E
<input type="checkbox"/>	GO:0006549	7,8	<a href="#">isoleucine metabolic process</a>	3	0.0005	1	0.0011	0.3054294	E
<input type="checkbox"/>	GO:0031684	7	<a href="#">heterotrimeric G-protein complex cycle</a>	3	0.0005	1	0.0011	0.3054294	E
<input type="checkbox"/>	GO:0017196	11,9,10	<a href="#">N-terminal peptidyl-methionine acetylation</a>	3	0.0005	1	0.0011	0.3054294	E
<input type="checkbox"/>	GO:0051352	6	<a href="#">negative regulation of ligase activity</a>	3	0.0005	1	0.0011	0.3054294	E
<input type="checkbox"/>	GO:0009395	7,8	<a href="#">phospholipid catabolic process</a>	3	0.0005	1	0.0011	0.3054294	E
<input type="checkbox"/>	GO:0018206	8	<a href="#">peptidyl-methionine modification</a>	3	0.0005	1	0.0011	0.3054294	E
<input type="checkbox"/>	GO:0043666	6	<a href="#">regulation of phosphoprotein phosphatase activity</a>	3	0.0005	1	0.0011	0.3054294	E
<input type="checkbox"/>	GO:0006561	8,9	<a href="#">proline biosynthetic process</a>	3	0.0005	1	0.0011	0.3054294	E
<input type="checkbox"/>	GO:0000160	5	<a href="#">two-component signal transduction system (phosphorelay)</a>	3	0.0005	1	0.0011	0.3054294	E
<input type="checkbox"/>	GO:0043102	6,5,7	<a href="#">amino acid salvage</a>	3	0.0005	1	0.0011	0.3054294	E
<input type="checkbox"/>	GO:0051382	8,7	<a href="#">kinetochore assembly</a>	3	0.0005	1	0.0011	0.3054294	E
<input type="checkbox"/>	GO:0018022	9,10,8	<a href="#">peptidyl-lysine methylation</a>	3	0.0005	1	0.0011	0.3054294	E
<input type="checkbox"/>	GO:0032973	6,7,8	<a href="#">amino acid export</a>	3	0.0005	1	0.0011	0.3054294	E
<input type="checkbox"/>	GO:0006658	8,9	<a href="#">phosphatidylserine metabolic process</a>	3	0.0005	1	0.0011	0.3054294	E
<input type="checkbox"/>	GO:0007234	7,6	<a href="#">osmosensory signaling pathway via two-component system</a>	3	0.0005	1	0.0011	0.3054294	E
<input type="checkbox"/>	GO:0051444	7	<a href="#">negative regulation of ubiquitin ligase activity</a>	3	0.0005	1	0.0011	0.3054294	E
<input type="checkbox"/>	GO:0006741	8,7,10,9	<a href="#">NADP biosynthetic process</a>	3	0.0005	1	0.0011	0.3054294	E
<input type="checkbox"/>	GO:0006431	9,8,10,7	<a href="#">methionyl-tRNA aminoacylation</a>	3	0.0005	1	0.0011	0.3054294	E
<input type="checkbox"/>	GO:0046475	8,9	<a href="#">glycerophospholipid catabolic process</a>	3	0.0005	1	0.0011	0.3054294	E
<input type="checkbox"/>	GO:0006567	8,9	<a href="#">threonine catabolic process</a>	3	0.0005	1	0.0011	0.3054294	E
<input type="checkbox"/>	GO:0009303	8,7	<a href="#">rRNA transcription</a>	3	0.0005	1	0.0011	0.3054294	E
<input type="checkbox"/>	GO:0006833	5,6	<a href="#">water transport</a>	3	0.0005	1	0.0011	0.3054294	E
<input type="checkbox"/>	GO:0015942	5,7	<a href="#">formate metabolic process</a>	3	0.0005	1	0.0011	0.3054294	E

<input type="checkbox"/>	GO:0006404	10,8,5,7,9,6	<a href="#">RNA import into nucleus</a>	3	0.0005	1	0.0011	0.3054294	E
<input type="checkbox"/>	GO:0016577	11,9,10	<a href="#">histone demethylation</a>	4	0.0006	1	0.0011	0.3516866	E
<input type="checkbox"/>	GO:0009147	7	<a href="#">pyrimidine nucleoside triphosphate metabolic process</a>	4	0.0006	1	0.0011	0.3516866	E
<input type="checkbox"/>	GO:0000135	9,8	<a href="#">septin checkpoint</a>	4	0.0006	1	0.0011	0.3516866	E
<input type="checkbox"/>	GO:0043173	5	<a href="#">nucleotide salvage</a>	4	0.0006	1	0.0011	0.3516866	E
<input type="checkbox"/>	GO:0008214	8	<a href="#">protein amino acid dealkylation</a>	4	0.0006	1	0.0011	0.3516866	E
<input type="checkbox"/>	GO:0031565	8,7	<a href="#">cytokinesis checkpoint</a>	4	0.0006	1	0.0011	0.3516866	E
<input type="checkbox"/>	GO:0000731	7,6	<a href="#">DNA synthesis during DNA repair</a>	4	0.0006	1	0.0011	0.3516866	E
<input type="checkbox"/>	GO:0030497	8,7,9,6	<a href="#">fatty acid elongation</a>	4	0.0006	1	0.0011	0.3516866	E
<input type="checkbox"/>	GO:0045021	7,6	<a href="#">error-free DNA repair</a>	4	0.0006	1	0.0011	0.3516866	E
<input type="checkbox"/>	GO:0031204	9,11,10,7,8	<a href="#">posttranslational protein targeting to membrane, translocation</a>	4	0.0006	1	0.0011	0.3516866	E
<input type="checkbox"/>	GO:0006074	8,9	<a href="#">1,3-beta-glucan metabolic process</a>	4	0.0006	1	0.0011	0.3516866	E
<input type="checkbox"/>	GO:0045722	7,9,8,10,6,11	<a href="#">positive regulation of gluconeogenesis</a>	4	0.0006	1	0.0011	0.3516866	E
<input type="checkbox"/>	GO:0046395	6	<a href="#">carboxylic acid catabolic process</a>	4	0.0006	1	0.0011	0.3516866	E
<input type="checkbox"/>	GO:0009452	7	<a href="#">RNA capping</a>	4	0.0006	1	0.0011	0.3516866	E
<input type="checkbox"/>	GO:0042439	6,7	<a href="#">ethanolamine and derivative metabolic process</a>	4	0.0006	1	0.0011	0.3516866	E
<input type="checkbox"/>	GO:0000390	7,9,11	<a href="#">spliceosome disassembly</a>	4	0.0006	1	0.0011	0.3516866	E
<input type="checkbox"/>	GO:0000349	8,7,10,12	<a href="#">generation of catalytic spliceosome for first transesterification step</a>	4	0.0006	1	0.0011	0.3516866	E
<input type="checkbox"/>	GO:0006646	7,8,9,6,10	<a href="#">phosphatidylethanolamine biosynthetic process</a>	4	0.0006	1	0.0011	0.3516866	E
<input type="checkbox"/>	GO:0018344	10,9,8	<a href="#">protein geranylgeranylation</a>	4	0.0006	1	0.0011	0.3516866	E
<input type="checkbox"/>	GO:0000752	7,5,6	<a href="#">agglutination during conjugation with cellular fusion</a>	4	0.0006	1	0.0011	0.3516866	E
<input type="checkbox"/>	GO:0050000	6,5	<a href="#">chromosome localization</a>	4	0.0006	1	0.0011	0.3516866	E
<input type="checkbox"/>	GO:0000771	6,4	<a href="#">agglutination</a>	4	0.0006	1	0.0011	0.3516866	E
<input type="checkbox"/>	GO:0032258	10,9,8,7	<a href="#">CVT pathway</a>	4	0.0006	1	0.0011	0.3516866	E
<input type="checkbox"/>	GO:0006075	9,8,10	<a href="#">1,3-beta-glucan biosynthetic process</a>	4	0.0006	1	0.0011	0.3516866	E
<input type="checkbox"/>	GO:0000916	6,5,4	<a href="#">cytokinesis, contractile ring contraction</a>	4	0.0006	1	0.0011	0.3516866	E
<input type="checkbox"/>	GO:0000391	8,10,12	<a href="#">U2-dependent spliceosome disassembly</a>	4	0.0006	1	0.0011	0.3516866	E
<input type="checkbox"/>	GO:0006580	5,7,8	<a href="#">ethanolamine metabolic process</a>	4	0.0006	1	0.0011	0.3516866	E
<input type="checkbox"/>	GO:0046337	5,7,8	<a href="#">phosphatidylethanolamine metabolic process</a>	4	0.0006	1	0.0011	0.3516866	E
<input type="checkbox"/>	GO:0046335	6,7,8,9	<a href="#">ethanolamine biosynthetic process</a>	4	0.0006	1	0.0011	0.3516866	E
<input type="checkbox"/>	GO:0032988	6	<a href="#">protein-RNA complex disassembly</a>	4	0.0006	1	0.0011	0.3516866	E
<input type="checkbox"/>	GO:0046466	6,7	<a href="#">membrane lipid catabolic process</a>	4	0.0006	1	0.0011	0.3516866	E
<input type="checkbox"/>	GO:0018348	11,10,9	<a href="#">protein amino acid geranylgeranylation</a>	4	0.0006	1	0.0011	0.3516866	E
<input type="checkbox"/>	GO:0030071	8,10,6,9,7,5	<a href="#">regulation of mitotic metaphase/anaphase transition</a>	4	0.0006	1	0.0011	0.3516866	E
<input type="checkbox"/>	GO:0031384	6,8,11,10,9,7,12	<a href="#">regulation of initiation of mating projection growth</a>	4	0.0006	1	0.0011	0.3516866	E
<input type="checkbox"/>	GO:0006482	9	<a href="#">protein amino acid demethylation</a>	4	0.0006	1	0.0011	0.3516866	E
<input type="checkbox"/>	GO:0006278	7	<a href="#">RNA-dependent DNA replication</a>	4	0.0006	1	0.0011	0.3516866	E
<input type="checkbox"/>	GO:0006624	9	<a href="#">vacuolar protein processing</a>	4	0.0006	1	0.0011	0.3516866	E
<input type="checkbox"/>	GO:0016036	8,7,6	<a href="#">cellular response to phosphate starvation</a>	4	0.0006	1	0.0011	0.3516866	E
<input type="checkbox"/>	GO:0000350	8,7,10,12	<a href="#">generation of catalytic spliceosome for second transesterification step</a>	4	0.0006	1	0.0011	0.3516866	E
<input type="checkbox"/>	GO:0006097	6,8	<a href="#">glyoxylate cycle</a>	4	0.0006	1	0.0011	0.3516866	E
<input type="checkbox"/>	GO:0007157	5	<a href="#">heterophilic cell adhesion</a>	4	0.0006	1	0.0011	0.3516866	E

<input type="radio"/>	GO:0009083	7,8	<a href="#">branched chain family amino acid catabolic process</a>	4	0.0006	1	0.0011	0.3516866	E
<input type="radio"/>	GO:0031578	9,11,10,8	<a href="#">mitotic cell cycle spindle orientation checkpoint</a>	4	0.0006	1	0.0011	0.3516866	E
<input type="radio"/>	GO:0042542	6	<a href="#">response to hydrogen peroxide</a>	4	0.0006	1	0.0011	0.3516866	E
<input type="radio"/>	GO:0006530	8,9	<a href="#">asparagine catabolic process</a>	5	0.0008	1	0.0011	0.3796308	E
<input type="radio"/>	GO:0031385	6,8,11,10,9,7,12	<a href="#">regulation of termination of mating projection growth</a>	5	0.0008	1	0.0011	0.3796308	E
<input type="radio"/>	GO:0042149	8,7,6	<a href="#">cellular response to glucose starvation</a>	5	0.0008	1	0.0011	0.3796308	E
<input type="radio"/>	GO:0000738	6,7	<a href="#">DNA catabolic process, exonucleolytic</a>	5	0.0008	1	0.0011	0.3796308	E
<input type="radio"/>	GO:0043001	10,8,7,9	<a href="#">Golgi to plasma membrane protein transport</a>	5	0.0008	1	0.0011	0.3796308	E
<input type="radio"/>	GO:0032447	9	<a href="#">protein urmylation</a>	5	0.0008	1	0.0011	0.3796308	E
<input type="radio"/>	GO:0018342	9,8,7	<a href="#">protein prenylation</a>	5	0.0008	1	0.0011	0.3796308	E
<input type="radio"/>	GO:0000409	10,8,9,6	<a href="#">regulation of transcription by galactose</a>	5	0.0008	1	0.0011	0.3796308	E
<input type="radio"/>	GO:0008283	3	<a href="#">cell proliferation</a>	5	0.0008	1	0.0011	0.3796308	E
<input type="radio"/>	GO:0031111	7,10,6	<a href="#">negative regulation of microtubule polymerization or depolymerization</a>	5	0.0008	1	0.0011	0.3796308	E
<input type="radio"/>	GO:0007026	8,7,11,9,6	<a href="#">negative regulation of microtubule depolymerization</a>	5	0.0008	1	0.0011	0.3796308	E
<input type="radio"/>	GO:0009749	7,6	<a href="#">response to glucose stimulus</a>	5	0.0008	1	0.0011	0.3796308	E
<input type="radio"/>	GO:0051439	7,5,4	<a href="#">regulation of ubiquitin ligase activity during mitotic cell cycle</a>	5	0.0008	1	0.0011	0.3796308	E
<input type="radio"/>	GO:0000266	6	<a href="#">mitochondrial fission</a>	5	0.0008	1	0.0011	0.3796308	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	1	0.0011	0.3796308	E
<input type="radio"/>	GO:0018346	10,9,8	<a href="#">protein amino acid prenylation</a>	5	0.0008	1	0.0011	0.3796308	E
<input type="radio"/>	GO:0006813	7,8	<a href="#">potassium ion transport</a>	5	0.0008	1	0.0011	0.3796308	E
<input type="radio"/>	GO:0000411	11,9,10,7	<a href="#">positive regulation of transcription by galactose</a>	5	0.0008	1	0.0011	0.3796308	E
<input type="radio"/>	GO:0000101	6,7,8	<a href="#">sulfur amino acid transport</a>	5	0.0008	1	0.0011	0.3796308	E
<input type="radio"/>	GO:0051083	8	<a href="#">cotranslational protein folding</a>	5	0.0008	1	0.0011	0.3796308	E
<input type="radio"/>	GO:0051017	9	<a href="#">actin filament bundle formation</a>	5	0.0008	1	0.0011	0.3796308	E
<input type="radio"/>	GO:0007232	7,6	<a href="#">osmosensory signaling pathway via Sho1 osmosensor</a>	5	0.0008	1	0.0011	0.3796308	E
<input type="radio"/>	GO:0007188	8,9	<a href="#">G-protein signaling, coupled to cAMP nucleotide second messenger</a>	5	0.0008	1	0.0011	0.3796308	E
<input type="radio"/>	GO:0009264	6,7	<a href="#">deoxyribonucleotide catabolic process</a>	5	0.0008	1	0.0011	0.3796308	E
<input type="radio"/>	GO:0045991	10,8,9,6	<a href="#">positive regulation of transcription by carbon catabolites</a>	5	0.0008	1	0.0011	0.3796308	E
<input type="radio"/>	GO:0006499	10,11,9,8	<a href="#">N-terminal protein myristoylation</a>	5	0.0008	1	0.0011	0.3796308	E
<input type="radio"/>	GO:0009098	8,9	<a href="#">leucine biosynthetic process</a>	5	0.0008	1	0.0011	0.3796308	E
<input type="radio"/>	GO:0045816	11,10	<a href="#">negative regulation of global transcription from RNA polymerase II promoter</a>	5	0.0008	1	0.0011	0.3796308	E
<input type="radio"/>	GO:0007535	6,8,4,7	<a href="#">donor selection</a>	5	0.0008	1	0.0011	0.3796308	E
<input type="radio"/>	GO:0019541	7	<a href="#">propionate metabolic process</a>	5	0.0008	1	0.0011	0.3796308	E
<input type="radio"/>	GO:0030007	10,8	<a href="#">cellular potassium ion homeostasis</a>	5	0.0008	1	0.0011	0.3796308	E
<input type="radio"/>	GO:0006816	7,8	<a href="#">calcium ion transport</a>	5	0.0008	1	0.0011	0.3796308	E
<input type="radio"/>	GO:0018377	9,8,7	<a href="#">protein myristoylation</a>	5	0.0008	1	0.0011	0.3796308	E
<input type="radio"/>	GO:0007187	7,8	<a href="#">G-protein signaling, coupled to cyclic nucleotide second messenger</a>	5	0.0008	1	0.0011	0.3796308	E
<input type="radio"/>	GO:0019388	8,9	<a href="#">galactose catabolic process</a>	5	0.0008	1	0.0011	0.3796308	E
<input type="radio"/>	GO:0009746	6,5	<a href="#">response to hexose stimulus</a>	5	0.0008	1	0.0011	0.3796308	E
<input type="radio"/>	GO:0009371	10,9,6	<a href="#">positive regulation of transcription by pheromones</a>	5	0.0008	1	0.0011	0.3796308	E



<input type="radio"/>	GO:0016337	4	<a href="#">cell-cell adhesion</a>	5	0.0008	1	0.0011	0.3796308	E
<input type="radio"/>	GO:0045011	10	<a href="#">actin cable formation</a>	5	0.0008	1	0.0011	0.3796308	E
<input type="radio"/>	GO:0015693	7,8	<a href="#">magnesium ion transport</a>	5	0.0008	1	0.0011	0.3796308	E
<input type="radio"/>	GO:0008655	5	<a href="#">pyrimidine salvage</a>	5	0.0008	1	0.0011	0.3796308	E
<input type="radio"/>	GO:0006498	9,10,8,7	<a href="#">N-terminal protein lipidation</a>	5	0.0008	1	0.0011	0.3796308	E
<input type="radio"/>	GO:0018319	10,9,8	<a href="#">protein amino acid myristoylation</a>	5	0.0008	1	0.0011	0.3796308	E
<input type="radio"/>	GO:0016560	8,11,10,7,9	<a href="#">protein import into peroxisome matrix, docking</a>	5	0.0008	1	0.0011	0.3796308	E
<input type="radio"/>	GO:0031114	7,10,6,8	<a href="#">regulation of microtubule depolymerization</a>	5	0.0008	1	0.0011	0.3796308	E
<input type="radio"/>	GO:0046487	5,7	<a href="#">glyoxylate metabolic process</a>	5	0.0008	1	0.0011	0.3796308	E
<input type="radio"/>	GO:0055075	9	<a href="#">potassium ion homeostasis</a>	5	0.0008	1	0.0011	0.3796308	E
<input type="radio"/>	GO:0000729	7,8,10,9	<a href="#">DNA double-strand break processing</a>	5	0.0008	1	0.0011	0.3796308	E
<input type="radio"/>	GO:0045040	10,9,7,8	<a href="#">protein import into mitochondrial outer membrane</a>	6	0.0009	1	0.0011	0.3933939	E
<input type="radio"/>	GO:0045143	10,8,7,5,9,6,4	<a href="#">homologous chromosome segregation</a>	6	0.0009	1	0.0011	0.3933939	E
<input type="radio"/>	GO:0006627	10,9,8,7	<a href="#">mitochondrial protein processing</a>	6	0.0009	1	0.0011	0.3933939	E
<input type="radio"/>	GO:0046578	7,8,6	<a href="#">regulation of Ras protein signal transduction</a>	6	0.0009	1	0.0011	0.3933939	E
<input type="radio"/>	GO:0007029	5	<a href="#">endoplasmic reticulum organization and biogenesis</a>	6	0.0009	1	0.0011	0.3933939	E
<input type="radio"/>	GO:0043254	6,7,5	<a href="#">regulation of protein complex assembly</a>	6	0.0009	1	0.0011	0.3933939	E
<input type="radio"/>	GO:0051347	6	<a href="#">positive regulation of transferase activity</a>	6	0.0009	1	0.0011	0.3933939	E
<input type="radio"/>	GO:0045860	7,8	<a href="#">positive regulation of protein kinase activity</a>	6	0.0009	1	0.0011	0.3933939	E
<input type="radio"/>	GO:0031938	12,8,5,9,13,11	<a href="#">regulation of chromatin silencing at telomere</a>	6	0.0009	1	0.0011	0.3933939	E
<input type="radio"/>	GO:0046580	8,9,7	<a href="#">negative regulation of Ras protein signal transduction</a>	6	0.0009	1	0.0011	0.3933939	E
<input type="radio"/>	GO:0016054	5	<a href="#">organic acid catabolic process</a>	6	0.0009	1	0.0011	0.3933939	E
<input type="radio"/>	GO:0006800	4	<a href="#">oxygen and reactive oxygen species metabolic process</a>	6	0.0009	1	0.0011	0.3933939	E
<input type="radio"/>	GO:0051056	6,7,5	<a href="#">regulation of small GTPase mediated signal transduction</a>	6	0.0009	1	0.0011	0.3933939	E
<input type="radio"/>	GO:0006358	10,9	<a href="#">regulation of global transcription from RNA polymerase II promoter</a>	6	0.0009	1	0.0011	0.3933939	E
<input type="radio"/>	GO:0031344	4,6,8,7,5,9	<a href="#">regulation of cell projection organization and biogenesis</a>	6	0.0009	1	0.0011	0.3933939	E
<input type="radio"/>	GO:0006110	6,10,11,5	<a href="#">regulation of glycolysis</a>	6	0.0009	1	0.0011	0.3933939	E
<input type="radio"/>	GO:0043174	5	<a href="#">nucleoside salvage</a>	6	0.0009	1	0.0011	0.3933939	E
<input type="radio"/>	GO:0048285	5	<a href="#">organelle fission</a>	6	0.0009	1	0.0011	0.3933939	E
<input type="radio"/>	GO:0051058	7,8,6	<a href="#">negative regulation of small GTPase mediated signal transduction</a>	6	0.0009	1	0.0011	0.3933939	E
<input type="radio"/>	GO:0005979	8,7,9,10,6	<a href="#">regulation of glycogen biosynthetic process</a>	6	0.0009	1	0.0011	0.3933939	E
<input type="radio"/>	GO:0031935	11,7,4,8,12,10	<a href="#">regulation of chromatin silencing</a>	6	0.0009	1	0.0011	0.3933939	E
<input type="radio"/>	GO:0006083	7	<a href="#">acetate metabolic process</a>	6	0.0009	1	0.0011	0.3933939	E
<input type="radio"/>	GO:0007019	9,7	<a href="#">microtubule depolymerization</a>	6	0.0009	1	0.0011	0.3933939	E
<input type="radio"/>	GO:0006166	6,8	<a href="#">purine ribonucleoside salvage</a>	6	0.0009	1	0.0011	0.3933939	E
<input type="radio"/>	GO:0031383	5,7,10,9,8,6,11	<a href="#">regulation of mating projection biogenesis</a>	6	0.0009	1	0.0011	0.3933939	E
<input type="radio"/>	GO:0006544	7,8	<a href="#">glycine metabolic process</a>	6	0.0009	1	0.0011	0.3933939	E
<input type="radio"/>	GO:0009743	5,4	<a href="#">response to carbohydrate stimulus</a>	6	0.0009	1	0.0011	0.3933939	E
<input type="radio"/>	GO:0046839	6,7	<a href="#">phospholipid dephosphorylation</a>	7	0.0011	1	0.0011	0.3963226	E
<input type="radio"/>	GO:0006998	5,6	<a href="#">nuclear membrane organization and biogenesis</a>	7	0.0011	1	0.0011	0.3963226	E

<input type="radio"/>	GO:0006621	7,6,5,4	<a href="#">protein retention in ER</a>	7	0.0011	1	0.0011	0.3963226	E
<input type="radio"/>	GO:0009166	5,6	<a href="#">nucleotide catabolic process</a>	7	0.0011	1	0.0011	0.3963226	E
<input type="radio"/>	GO:0046856	7,9,8,10	<a href="#">phosphoinositide dephosphorylation</a>	7	0.0011	1	0.0011	0.3963226	E
<input type="radio"/>	GO:0031382	9,8,10,7	<a href="#">mating projection biogenesis</a>	7	0.0011	1	0.0011	0.3963226	E
<input type="radio"/>	GO:0007008	6,7	<a href="#">outer mitochondrial membrane organization and biogenesis</a>	7	0.0011	1	0.0011	0.3963226	E
<input type="radio"/>	GO:0009102	6,7,8	<a href="#">biotin biosynthetic process</a>	7	0.0011	1	0.0011	0.3963226	E
<input type="radio"/>	GO:0051129	6,5	<a href="#">negative regulation of cell organization and biogenesis</a>	7	0.0011	1	0.0011	0.3963226	E
<input type="radio"/>	GO:0046351	6,7	<a href="#">disaccharide biosynthetic process</a>	7	0.0011	1	0.0011	0.3963226	E
<input type="radio"/>	GO:0009410	4	<a href="#">response to xenobiotic stimulus</a>	7	0.0011	1	0.0011	0.3963226	E
<input type="radio"/>	GO:0005992	7,8	<a href="#">trehalose biosynthetic process</a>	7	0.0011	1	0.0011	0.3963226	E
<input type="radio"/>	GO:0000372	10	<a href="#">Group I intron splicing</a>	7	0.0011	1	0.0011	0.3963226	E
<input type="radio"/>	GO:0006768	5,7,6	<a href="#">biotin metabolic process</a>	7	0.0011	1	0.0011	0.3963226	E
<input type="radio"/>	GO:0000376	9	<a href="#">RNA splicing, via transesterification reactions with guanosine as nucleophile</a>	7	0.0011	1	0.0011	0.3963226	E
<input type="radio"/>	GO:0006551	7,8	<a href="#">leucine metabolic process</a>	7	0.0011	1	0.0011	0.3963226	E
<input type="radio"/>	GO:0008150	1	<a href="#">biological process</a>	6476	1.0000	884	1.0000	1.0000000	D
<input type="radio"/>	GO:0000903	6,4,8,7,9	<a href="#">cellular morphogenesis during vegetative growth</a>	8	0.0012	1	0.0011	0.3911151	D
<input type="radio"/>	GO:0030031	8,7,9	<a href="#">cell projection biogenesis</a>	8	0.0012	1	0.0011	0.3911151	D
<input type="radio"/>	GO:0006672	8,9	<a href="#">ceramide metabolic process</a>	8	0.0012	1	0.0011	0.3911151	D
<input type="radio"/>	GO:0006808	6,5	<a href="#">regulation of nitrogen utilization</a>	8	0.0012	1	0.0011	0.3911151	D
<input type="radio"/>	GO:0051171	5,4	<a href="#">regulation of nitrogen metabolic process</a>	8	0.0012	1	0.0011	0.3911151	D
<input type="radio"/>	GO:0048858	6,7	<a href="#">cell projection morphogenesis</a>	8	0.0012	1	0.0011	0.3911151	D
<input type="radio"/>	GO:0007323	9	<a href="#">peptide pheromone maturation</a>	8	0.0012	1	0.0011	0.3911151	D
<input type="radio"/>	GO:0030011	7,4,8	<a href="#">maintenance of cell polarity</a>	8	0.0012	1	0.0011	0.3911151	D
<input type="radio"/>	GO:0030030	7,6,8	<a href="#">cell projection organization and biogenesis</a>	8	0.0012	1	0.0011	0.3911151	D
<input type="radio"/>	GO:0000751	8,9,7,6	<a href="#">cell cycle arrest in response to pheromone</a>	8	0.0012	1	0.0011	0.3911151	D
<input type="radio"/>	GO:0006855	5,6	<a href="#">multidrug transport</a>	8	0.0012	1	0.0011	0.3911151	D
<input type="radio"/>	GO:0009306	7,5,4,6	<a href="#">protein secretion</a>	8	0.0012	1	0.0011	0.3911151	D
<input type="radio"/>	GO:0032990	5,6	<a href="#">cell part morphogenesis</a>	8	0.0012	1	0.0011	0.3911151	D
<input type="radio"/>	GO:0006528	7,8	<a href="#">asparagine metabolic process</a>	9	0.0014	1	0.0011	0.3799358	D
<input type="radio"/>	GO:0000290	11,8,9,10	<a href="#">deadenylation-dependent decapping</a>	9	0.0014	1	0.0011	0.3799358	D
<input type="radio"/>	GO:0015891	4,5	<a href="#">siderophore transport</a>	9	0.0014	1	0.0011	0.3799358	D
<input type="radio"/>	GO:0022610	2	<a href="#">biological adhesion</a>	9	0.0014	1	0.0011	0.3799358	D
<input type="radio"/>	GO:0006122	10,7,5	<a href="#">mitochondrial electron transport, ubiquinol to cytochrome c</a>	9	0.0014	1	0.0011	0.3799358	D
<input type="radio"/>	GO:0043486	11	<a href="#">histone exchange</a>	9	0.0014	1	0.0011	0.3799358	D
<input type="radio"/>	GO:0007155	3	<a href="#">cell adhesion</a>	9	0.0014	1	0.0011	0.3799358	D
<input type="radio"/>	GO:0030847	10,9	<a href="#">transcription termination from Pol II promoter, RNA polymerase(A)-independent</a>	9	0.0014	1	0.0011	0.3799358	D
<input type="radio"/>	GO:0000162	9,8,7,10	<a href="#">tryptophan biosynthetic process</a>	10	0.0015	1	0.0011	0.3645107	D
<input type="radio"/>	GO:0010033	4	<a href="#">response to organic substance</a>	10	0.0015	1	0.0011	0.3645107	D
<input type="radio"/>	GO:0005991	6,7	<a href="#">trehalose metabolic process</a>	10	0.0015	1	0.0011	0.3645107	D
<input type="radio"/>	GO:0009096	8,7,9	<a href="#">aromatic amino acid family biosynthetic process, anthranilate pathway</a>	10	0.0015	1	0.0011	0.3645107	D
<input type="radio"/>	GO:0006568	7,8,6	<a href="#">tryptophan metabolic process</a>	10	0.0015	1	0.0011	0.3645107	D
<input type="radio"/>	GO:0006012	7,8	<a href="#">galactose metabolic process</a>	10	0.0015	1	0.0011	0.3645107	D
<input type="radio"/>	GO:0006616	9,12,11,7,10,8	<a href="#">SRP-dependent cotranslational protein</a>	10	0.0015	1	0.0011	0.3645107	D

<input type="radio"/>	GO:0000010	9,12,11,7,10,0	<a href="#">targeting to membrane, translocation</a>	10	0.0015	1	0.0011	0.3645107	<input type="checkbox"/>
<input type="radio"/>	GO:0046519	7,8	<a href="#">sphingoid metabolic process</a>	10	0.0015	1	0.0011	0.3645107	<input type="checkbox"/>
<input type="radio"/>	GO:0051261	6	<a href="#">protein depolymerization</a>	10	0.0015	1	0.0011	0.3645107	<input type="checkbox"/>
<input type="radio"/>	GO:0009373	9,8,5	<a href="#">regulation of transcription by pheromones</a>	10	0.0015	1	0.0011	0.3645107	<input type="checkbox"/>
<input type="radio"/>	GO:0051181	4,5	<a href="#">cofactor transport</a>	10	0.0015	1	0.0011	0.3645107	<input type="checkbox"/>
<input type="radio"/>	GO:0046219	7,8,6	<a href="#">indolalkylamine biosynthetic process</a>	10	0.0015	1	0.0011	0.3645107	<input type="checkbox"/>
<input type="radio"/>	GO:0006123	10,7,5	<a href="#">mitochondrial electron transport, cytochrome c to oxygen</a>	10	0.0015	1	0.0011	0.3645107	<input type="checkbox"/>
<input type="radio"/>	GO:0006268	8	<a href="#">DNA unwinding during replication</a>	10	0.0015	1	0.0011	0.3645107	<input type="checkbox"/>
<input type="radio"/>	GO:0042430	5	<a href="#">indole and derivative metabolic process</a>	10	0.0015	1	0.0011	0.3645107	<input type="checkbox"/>
<input type="radio"/>	GO:0046019	10,9,6	<a href="#">regulation of transcription from RNA polymerase II promoter by pheromones</a>	10	0.0015	1	0.0011	0.3645107	<input type="checkbox"/>
<input type="radio"/>	GO:0042435	7,5	<a href="#">indole derivative biosynthetic process</a>	10	0.0015	1	0.0011	0.3645107	<input type="checkbox"/>
<input type="radio"/>	GO:0006586	6,7	<a href="#">indolalkylamine metabolic process</a>	10	0.0015	1	0.0011	0.3645107	<input type="checkbox"/>
<input type="radio"/>	GO:0006446	8,7,6	<a href="#">regulation of translational initiation</a>	10	0.0015	1	0.0011	0.3645107	<input type="checkbox"/>
<input type="radio"/>	GO:0042434	6	<a href="#">indole derivative metabolic process</a>	10	0.0015	1	0.0011	0.3645107	<input type="checkbox"/>
<input type="radio"/>	GO:0006276	3	<a href="#">plasmid maintenance</a>	11	0.0017	1	0.0011	0.3462063	<input type="checkbox"/>
<input type="radio"/>	GO:0046128	7	<a href="#">purine ribonucleoside metabolic process</a>	11	0.0017	1	0.0011	0.3462063	<input type="checkbox"/>
<input type="radio"/>	GO:0016226	6	<a href="#">iron-sulfur cluster assembly</a>	11	0.0017	1	0.0011	0.3462063	<input type="checkbox"/>
<input type="radio"/>	GO:0031163	5	<a href="#">metallo-sulfur cluster assembly</a>	11	0.0017	1	0.0011	0.3462063	<input type="checkbox"/>
<input type="radio"/>	GO:0043086	5	<a href="#">negative regulation of enzyme activity</a>	11	0.0017	1	0.0011	0.3462063	<input type="checkbox"/>
<input type="radio"/>	GO:0016237	4,6	<a href="#">microautophagy</a>	11	0.0017	1	0.0011	0.3462063	<input type="checkbox"/>
<input type="radio"/>	GO:0065002	8,6,7	<a href="#">intracellular protein transport across a membrane</a>	11	0.0017	1	0.0011	0.3462063	<input type="checkbox"/>
<input type="radio"/>	GO:0006488	10,9,8	<a href="#">dolichol-linked oligosaccharide biosynthetic process</a>	11	0.0017	1	0.0011	0.3462063	<input type="checkbox"/>
<input type="radio"/>	GO:0051049	5,4	<a href="#">regulation of transport</a>	11	0.0017	1	0.0011	0.3462063	<input type="checkbox"/>
<input type="radio"/>	GO:0051274	8,9	<a href="#">beta-glucan biosynthetic process</a>	11	0.0017	1	0.0011	0.3462063	<input type="checkbox"/>
<input type="radio"/>	GO:0007050	7,8,6	<a href="#">cell cycle arrest</a>	11	0.0017	1	0.0011	0.3462063	<input type="checkbox"/>
<input type="radio"/>	GO:0015914	5,6	<a href="#">phospholipid transport</a>	12	0.0019	1	0.0011	0.3260955	<input type="checkbox"/>
<input type="radio"/>	GO:0000302	5	<a href="#">response to reactive oxygen species</a>	12	0.0019	1	0.0011	0.3260955	<input type="checkbox"/>
<input type="radio"/>	GO:0051273	7,8	<a href="#">beta-glucan metabolic process</a>	12	0.0019	1	0.0011	0.3260955	<input type="checkbox"/>
<input type="radio"/>	GO:0009070	7,8	<a href="#">serine family amino acid biosynthetic process</a>	12	0.0019	1	0.0011	0.3260955	<input type="checkbox"/>
<input type="radio"/>	GO:0042278	6	<a href="#">purine nucleoside metabolic process</a>	12	0.0019	1	0.0011	0.3260955	<input type="checkbox"/>
<input type="radio"/>	GO:0006067	5	<a href="#">ethanol metabolic process</a>	12	0.0019	1	0.0011	0.3260955	<input type="checkbox"/>
<input type="radio"/>	GO:0009119	6	<a href="#">ribonucleoside metabolic process</a>	13	0.0020	1	0.0011	0.3050124	<input type="checkbox"/>
<input type="radio"/>	GO:0045786	6,7,5	<a href="#">negative regulation of progression through cell cycle</a>	13	0.0020	1	0.0011	0.3050124	<input type="checkbox"/>
<input type="radio"/>	GO:0015893	4,5	<a href="#">drug transport</a>	13	0.0020	1	0.0011	0.3050124	<input type="checkbox"/>
<input type="radio"/>	GO:0006111	8,7,9,10,6	<a href="#">regulation of gluconeogenesis</a>	13	0.0020	1	0.0011	0.3050124	<input type="checkbox"/>
<input type="radio"/>	GO:0001300	5	<a href="#">chronological cell aging</a>	13	0.0020	1	0.0011	0.3050124	<input type="checkbox"/>
<input type="radio"/>	GO:0006031	9,7,8,10	<a href="#">chitin biosynthetic process</a>	15	0.0023	2	0.0023	0.2906413	<input type="checkbox"/>
<input type="radio"/>	GO:0009651	5	<a href="#">response to salt stress</a>	15	0.0023	2	0.0023	0.2906413	<input type="checkbox"/>
<input type="radio"/>	GO:0006374	9,11	<a href="#">nuclear mRNA splicing via U2-type spliceosome</a>	15	0.0023	2	0.0023	0.2906413	<input type="checkbox"/>
<input type="radio"/>	GO:0031023	5	<a href="#">microtubule organizing center organization and biogenesis</a>	16	0.0025	2	0.0023	0.2868176	<input type="checkbox"/>
<input type="radio"/>	GO:0006493	9,8,7	<a href="#">protein amino acid O-linked glycosylation</a>	16	0.0025	2	0.0023	0.2868176	<input type="checkbox"/>
<input type="radio"/>	GO:0043162	10,9,11	<a href="#">ubiquitin-dependent protein catabolic process via the multivesicular body pathway</a>	16	0.0025	2	0.0023	0.2868176	<input type="checkbox"/>

<input type="checkbox"/>	GO:0010383	7,5,6	<a href="#">cell wall polysaccharide metabolic process</a>	16	0.0025	2	0.0023	0.2868176	D
<input type="checkbox"/>	GO:0006536	7,8	<a href="#">glutamate metabolic process</a>	16	0.0025	2	0.0023	0.2868176	D
<input type="checkbox"/>	GO:0051300	5,4,6	<a href="#">spindle pole body organization and biogenesis</a>	16	0.0025	2	0.0023	0.2868176	D
<input type="checkbox"/>	GO:0048278	4,5,6	<a href="#">vesicle docking</a>	14	0.0022	1	0.0011	0.2835974	D
<input type="checkbox"/>	GO:0000394	8	<a href="#">RNA splicing, via endonucleolytic cleavage and ligation</a>	14	0.0022	1	0.0011	0.2835974	D
<input type="checkbox"/>	GO:0006272	9,8	<a href="#">leading strand elongation</a>	14	0.0022	1	0.0011	0.2835974	D
<input type="checkbox"/>	GO:0007118	7,6,5	<a href="#">budding cell apical bud growth</a>	14	0.0022	1	0.0011	0.2835974	D
<input type="checkbox"/>	GO:0006749	6,5	<a href="#">glutathione metabolic process</a>	14	0.0022	1	0.0011	0.2835974	D
<input type="checkbox"/>	GO:0000028	9,7,8,6	<a href="#">ribosomal small subunit assembly and maintenance</a>	14	0.0022	1	0.0011	0.2835974	D
<input type="checkbox"/>	GO:0006388	9,8	<a href="#">tRNA splicing</a>	14	0.0022	1	0.0011	0.2835974	D
<input type="checkbox"/>	GO:0022406	3	<a href="#">membrane docking</a>	14	0.0022	1	0.0011	0.2835974	D
<input type="checkbox"/>	GO:0045002	8,7	<a href="#">double-strand break repair via single-strand annealing</a>	14	0.0022	1	0.0011	0.2835974	D
<input type="checkbox"/>	GO:0019740	4	<a href="#">nitrogen utilization</a>	17	0.0026	2	0.0023	0.2806787	D
<input type="checkbox"/>	GO:0016558	10,9,7,8,6	<a href="#">protein import into peroxisome matrix</a>	17	0.0026	2	0.0023	0.2806787	D
<input type="checkbox"/>	GO:0006042	7,8	<a href="#">glucosamine biosynthetic process</a>	17	0.0026	2	0.0023	0.2806787	D
<input type="checkbox"/>	GO:0046349	6,7	<a href="#">amino sugar biosynthetic process</a>	17	0.0026	2	0.0023	0.2806787	D
<input type="checkbox"/>	GO:0006030	8,6,7,9	<a href="#">chitin metabolic process</a>	17	0.0026	2	0.0023	0.2806787	D
<input type="checkbox"/>	GO:0006113	5	<a href="#">fermentation</a>	17	0.0026	2	0.0023	0.2806787	D
<input type="checkbox"/>	GO:0006045	8,9	<a href="#">N-acetylglucosamine biosynthetic process</a>	17	0.0026	2	0.0023	0.2806787	D
<input type="checkbox"/>	GO:0051789	4	<a href="#">response to protein stimulus</a>	18	0.0028	2	0.0023	0.2726449	D
<input type="checkbox"/>	GO:0031570	8,7	<a href="#">DNA integrity checkpoint</a>	18	0.0028	2	0.0023	0.2726449	D
<input type="checkbox"/>	GO:0042401	6,7	<a href="#">biogenic amine biosynthetic process</a>	18	0.0028	2	0.0023	0.2726449	D
<input type="checkbox"/>	GO:0000018	8,7	<a href="#">regulation of DNA recombination</a>	18	0.0028	2	0.0023	0.2726449	D
<input type="checkbox"/>	GO:0010038	5	<a href="#">response to metal ion</a>	18	0.0028	2	0.0023	0.2726449	D
<input type="checkbox"/>	GO:0006986	4,5	<a href="#">response to unfolded protein</a>	18	0.0028	2	0.0023	0.2726449	D
<input type="checkbox"/>	GO:0006378	9	<a href="#">mRNA polyadenylation</a>	18	0.0028	2	0.0023	0.2726449	D
<input type="checkbox"/>	GO:0009267	7,6,5	<a href="#">cellular response to starvation</a>	19	0.0029	2	0.0023	0.2631036	D
<input type="checkbox"/>	GO:0006275	8,7	<a href="#">regulation of DNA replication</a>	19	0.0029	2	0.0023	0.2631036	D
<input type="checkbox"/>	GO:0043255	7,6,5	<a href="#">regulation of carbohydrate biosynthetic process</a>	19	0.0029	2	0.0023	0.2631036	D
<input type="checkbox"/>	GO:0006040	5,6	<a href="#">amino sugar metabolic process</a>	19	0.0029	2	0.0023	0.2631036	D
<input type="checkbox"/>	GO:0006044	7,8	<a href="#">N-acetylglucosamine metabolic process</a>	19	0.0029	2	0.0023	0.2631036	D
<input type="checkbox"/>	GO:0006041	6,7	<a href="#">glucosamine metabolic process</a>	19	0.0029	2	0.0023	0.2631036	D
<input type="checkbox"/>	GO:0031668	5,4	<a href="#">cellular response to extracellular stimulus</a>	19	0.0029	2	0.0023	0.2631036	D
<input type="checkbox"/>	GO:0042594	6,4	<a href="#">response to starvation</a>	19	0.0029	2	0.0023	0.2631036	D
<input type="checkbox"/>	GO:0031669	6,5	<a href="#">cellular response to nutrient levels</a>	19	0.0029	2	0.0023	0.2631036	D
<input type="checkbox"/>	GO:0000051	4,3	<a href="#">urea cycle intermediate metabolic process</a>	15	0.0023	1	0.0011	0.2623342	D
<input type="checkbox"/>	GO:0009894	5,4	<a href="#">regulation of catabolic process</a>	15	0.0023	1	0.0011	0.2623342	D
<input type="checkbox"/>	GO:0000079	8,7,6	<a href="#">regulation of cyclin-dependent protein kinase activity</a>	15	0.0023	1	0.0011	0.2623342	D
<input type="checkbox"/>	GO:0005978	8,7,9	<a href="#">glycogen biosynthetic process</a>	15	0.0023	1	0.0011	0.2623342	D
<input type="checkbox"/>	GO:0006525	7,8,5,4	<a href="#">arginine metabolic process</a>	15	0.0023	1	0.0011	0.2623342	D
<input type="checkbox"/>	GO:0006625	9,8,6,7	<a href="#">protein targeting to peroxisome</a>	20	0.0031	2	0.0023	0.2524052	D
<input type="checkbox"/>	GO:0043574	7,5,6	<a href="#">peroxisomal transport</a>	20	0.0031	2	0.0023	0.2524052	D
<input type="checkbox"/>	GO:0007094	9,11,10,8	<a href="#">mitotic cell cycle spindle assembly checkpoint</a>	20	0.0031	2	0.0023	0.2524052	D

<input type="radio"/>	GO:0016050	5	<a href="#">vesicle organization and biogenesis</a>	16	0.0025	1	0.0011	0.2415808	D
<input type="radio"/>	GO:0009206	8,9	<a href="#">purine ribonucleoside triphosphate biosynthetic process</a>	22	0.0034	3	0.0034	0.2413467	D
<input type="radio"/>	GO:0009145	7,8	<a href="#">purine nucleoside triphosphate biosynthetic process</a>	22	0.0034	3	0.0034	0.2413467	D
<input type="radio"/>	GO:0045324	8,6,7	<a href="#">late endosome to vacuole transport</a>	21	0.0032	2	0.0023	0.2408616	D
<input type="radio"/>	GO:0051716	3	<a href="#">cellular response to stimulus</a>	21	0.0032	2	0.0023	0.2408616	D
<input type="radio"/>	GO:0033554	4	<a href="#">cellular response to stress</a>	21	0.0032	2	0.0023	0.2408616	D
<input type="radio"/>	GO:0009144	7	<a href="#">purine nucleoside triphosphate metabolic process</a>	23	0.0036	3	0.0034	0.2396620	D
<input type="radio"/>	GO:0009205	8	<a href="#">purine ribonucleoside triphosphate metabolic process</a>	23	0.0036	3	0.0034	0.2396620	D
<input type="radio"/>	GO:0006576	5,6	<a href="#">biogenic amine metabolic process</a>	24	0.0037	3	0.0034	0.2365051	D
<input type="radio"/>	GO:0031577	8,7	<a href="#">spindle checkpoint</a>	24	0.0037	3	0.0034	0.2365051	D
<input type="radio"/>	GO:0007096	8,10,9,7	<a href="#">regulation of exit from mitosis</a>	24	0.0037	3	0.0034	0.2365051	D
<input type="radio"/>	GO:0006890	8,6,5,7	<a href="#">retrograde vesicle-mediated transport, Golgi to ER</a>	24	0.0037	3	0.0034	0.2365051	D
<input type="radio"/>	GO:0051278	8,7	<a href="#">chitin- and beta-glucan-containing cell wall polysaccharide biosynthetic process</a>	24	0.0037	3	0.0034	0.2365051	D
<input type="radio"/>	GO:0000724	8,7	<a href="#">double-strand break repair via homologous recombination</a>	25	0.0039	3	0.0034	0.2320581	D
<input type="radio"/>	GO:0007231	6,5	<a href="#">osmosensory signaling pathway</a>	22	0.0034	2	0.0023	0.2287457	D
<input type="radio"/>	GO:0007120	8,6,10,7,11,5	<a href="#">axial cellular bud site selection</a>	22	0.0034	2	0.0023	0.2287457	D
<input type="radio"/>	GO:0006311	10,8,7,5,9,6,4	<a href="#">meiotic gene conversion</a>	22	0.0034	2	0.0023	0.2287457	D
<input type="radio"/>	GO:0006476	8	<a href="#">protein amino acid deacetylation</a>	26	0.0040	3	0.0034	0.2265011	D
<input type="radio"/>	GO:0006506	10,9,8,7,11	<a href="#">GPI anchor biosynthetic process</a>	26	0.0040	3	0.0034	0.2265011	D
<input type="radio"/>	GO:0045003	9,8	<a href="#">double-strand break repair via synthesis-dependent strand annealing</a>	17	0.0026	1	0.0011	0.2215948	D
<input type="radio"/>	GO:0042147	8,6,7	<a href="#">retrograde transport, endosome to Golgi</a>	17	0.0026	1	0.0011	0.2215948	D
<input type="radio"/>	GO:0007093	8,10,9,7	<a href="#">mitotic cell cycle checkpoint</a>	27	0.0042	3	0.0034	0.2200090	D
<input type="radio"/>	GO:0009084	7,8	<a href="#">glutamine family amino acid biosynthetic process</a>	27	0.0042	3	0.0034	0.2200090	D
<input type="radio"/>	GO:0006505	9,10	<a href="#">GPI anchor metabolic process</a>	27	0.0042	3	0.0034	0.2200090	D
<input type="radio"/>	GO:0043044	10	<a href="#">ATP-dependent chromatin remodeling</a>	23	0.0036	2	0.0023	0.2162936	D
<input type="radio"/>	GO:0006613	10,9,8,7,6	<a href="#">cotranslational protein targeting to membrane</a>	23	0.0036	2	0.0023	0.2162936	D
<input type="radio"/>	GO:0007020	8	<a href="#">microtubule nucleation</a>	23	0.0036	2	0.0023	0.2162936	D
<input type="radio"/>	GO:0046489	9,8,10	<a href="#">phosphoinositide biosynthetic process</a>	28	0.0043	3	0.0034	0.2127479	D
<input type="radio"/>	GO:0031137	6,5	<a href="#">regulation of conjugation with cellular fusion</a>	30	0.0046	4	0.0045	0.2099741	D
<input type="radio"/>	GO:0046999	5,4	<a href="#">regulation of conjugation</a>	30	0.0046	4	0.0045	0.2099741	D
<input type="radio"/>	GO:0009141	6	<a href="#">nucleoside triphosphate metabolic process</a>	30	0.0046	4	0.0045	0.2099741	D
<input type="radio"/>	GO:0006271	8,7	<a href="#">DNA strand elongation during DNA replication</a>	32	0.0049	4	0.0045	0.2054237	D
<input type="radio"/>	GO:0022616	6	<a href="#">DNA strand elongation</a>	32	0.0049	4	0.0045	0.2054237	D
<input type="radio"/>	GO:0016575	11,9	<a href="#">histone deacetylation</a>	24	0.0037	2	0.0023	0.2037060	D
<input type="radio"/>	GO:0010035	4	<a href="#">response to inorganic substance</a>	24	0.0037	2	0.0023	0.2037060	D
<input type="radio"/>	GO:0009116	5	<a href="#">nucleoside metabolic process</a>	18	0.0028	1	0.0011	0.2025539	D
<input type="radio"/>	GO:0006007	8,9	<a href="#">glucose catabolic process</a>	34	0.0053	4	0.0045	0.1975044	D
<input type="radio"/>	GO:0006869	4,5	<a href="#">lipid transport</a>	34	0.0053	4	0.0045	0.1975044	D
<input type="radio"/>	GO:0006893	9,7,6,8	<a href="#">Golgi to plasma membrane transport</a>	30	0.0046	3	0.0034	0.1965301	D
<input type="radio"/>	GO:0043488	9,8,7	<a href="#">regulation of mRNA stability</a>	30	0.0046	3	0.0034	0.1965301	D
<input type="radio"/>	GO:0043487	8,7	<a href="#">regulation of RNA stability</a>	30	0.0046	3	0.0034	0.1965301	D
<input type="radio"/>	GO:0007530	4,5	<a href="#">sex determination</a>	35	0.0054	4	0.0045	0.1925278	D

<input type="checkbox"/>	GO:0003006	3,4	<a href="#">reproductive developmental process</a>	35	0.0054	4	0.0045	0.1925278	D
<input type="checkbox"/>	GO:0007531	4,6,5	<a href="#">mating type determination</a>	35	0.0054	4	0.0045	0.1925278	D
<input type="checkbox"/>	GO:0030433	9,11,10,12	<a href="#">ER-associated protein catabolic process</a>	35	0.0054	4	0.0045	0.1925278	D
<input type="checkbox"/>	GO:0009250	7,8	<a href="#">glucan biosynthetic process</a>	25	0.0039	2	0.0023	0.1911511	D
<input type="checkbox"/>	GO:0043549	6	<a href="#">regulation of kinase activity</a>	25	0.0039	2	0.0023	0.1911511	D
<input type="checkbox"/>	GO:0042773	8,5	<a href="#">ATP synthesis coupled electron transport</a>	25	0.0039	2	0.0023	0.1911511	D
<input type="checkbox"/>	GO:0045859	7	<a href="#">regulation of protein kinase activity</a>	25	0.0039	2	0.0023	0.1911511	D
<input type="checkbox"/>	GO:0042775	9,6	<a href="#">organelle ATP synthesis coupled electron transport</a>	25	0.0039	2	0.0023	0.1911511	D
<input type="checkbox"/>	GO:0051252	7,6	<a href="#">regulation of RNA metabolic process</a>	36	0.0056	4	0.0045	0.1870017	D
<input type="checkbox"/>	GO:0019320	7,8	<a href="#">hexose catabolic process</a>	39	0.0060	5	0.0057	0.1862222	D
<input type="checkbox"/>	GO:0051052	7,6	<a href="#">regulation of DNA metabolic process</a>	41	0.0063	5	0.0057	0.1807025	D
<input type="checkbox"/>	GO:0005977	7,6,8	<a href="#">glycogen metabolic process</a>	32	0.0049	3	0.0034	0.1789468	D
<input type="checkbox"/>	GO:0015672	6,7	<a href="#">monovalent inorganic cation transport</a>	32	0.0049	3	0.0034	0.1789468	D
<input type="checkbox"/>	GO:0007121	8,6,10,7,11,5	<a href="#">bipolar cellular bud site selection</a>	32	0.0049	3	0.0034	0.1789468	D
<input type="checkbox"/>	GO:0051338	5	<a href="#">regulation of transferase activity</a>	26	0.0040	2	0.0023	0.1787677	D
<input type="checkbox"/>	GO:0010382	6,4	<a href="#">cell wall metabolic process</a>	26	0.0040	2	0.0023	0.1787677	D
<input type="checkbox"/>	GO:0006515	8,9	<a href="#">misfolded or incompletely synthesized protein catabolic process</a>	38	0.0059	4	0.0045	0.1746647	D
<input type="checkbox"/>	GO:0016485	8	<a href="#">protein processing</a>	38	0.0059	4	0.0045	0.1746647	D
<input type="checkbox"/>	GO:0007052	5,4,9	<a href="#">mitotic spindle organization and biogenesis</a>	44	0.0068	6	0.0068	0.1733764	D
<input type="checkbox"/>	GO:0006914	3	<a href="#">autophagy</a>	45	0.0069	6	0.0068	0.1727419	D
<input type="checkbox"/>	GO:0007051	8	<a href="#">spindle organization and biogenesis</a>	47	0.0073	6	0.0068	0.1697842	D
<input type="checkbox"/>	GO:0031505	6	<a href="#">chitin- and beta-glucan-containing cell wall organization and biogenesis</a>	44	0.0068	5	0.0057	0.1685364	D
<input type="checkbox"/>	GO:0046365	6,7	<a href="#">monosaccharide catabolic process</a>	44	0.0068	5	0.0057	0.1685364	D
<input type="checkbox"/>	GO:0006112	5	<a href="#">energy reserve metabolic process</a>	39	0.0060	4	0.0045	0.1680232	D
<input type="checkbox"/>	GO:0006308	5,6	<a href="#">DNA catabolic process</a>	20	0.0031	1	0.0011	0.1677185	D
<input type="checkbox"/>	GO:0006754	7,9,6,8,10	<a href="#">ATP biosynthetic process</a>	20	0.0031	1	0.0011	0.1677185	D
<input type="checkbox"/>	GO:0015985	6,8,7,9	<a href="#">energy coupled proton transport, down electrochemical gradient</a>	20	0.0031	1	0.0011	0.1677185	D
<input type="checkbox"/>	GO:0015986	8,10,7,9,11,5	<a href="#">ATP synthesis coupled proton transport</a>	20	0.0031	1	0.0011	0.1677185	D
<input type="checkbox"/>	GO:0006614	11,10,9,8,7	<a href="#">SRP-dependent cotranslational protein targeting to membrane</a>	20	0.0031	1	0.0011	0.1677185	D
<input type="checkbox"/>	GO:0006753	7	<a href="#">nucleoside phosphate metabolic process</a>	20	0.0031	1	0.0011	0.1677185	D
<input type="checkbox"/>	GO:0007568	3	<a href="#">aging</a>	49	0.0076	6	0.0068	0.1648397	D
<input type="checkbox"/>	GO:0007569	4	<a href="#">cell aging</a>	49	0.0076	6	0.0068	0.1648397	D
<input type="checkbox"/>	GO:0048308	5	<a href="#">organelle inheritance</a>	40	0.0062	4	0.0045	0.1611698	D
<input type="checkbox"/>	GO:0006626	9,8,7,6	<a href="#">protein targeting to mitochondrion</a>	52	0.0080	7	0.0079	0.1606444	D
<input type="checkbox"/>	GO:0007166	5	<a href="#">cell surface receptor linked signal transduction</a>	52	0.0080	7	0.0079	0.1606444	D
<input type="checkbox"/>	GO:0000082	8,5,6,7,4	<a href="#">G1/S transition of mitotic cell cycle</a>	52	0.0080	7	0.0079	0.1606444	D
<input type="checkbox"/>	GO:0000075	7,6	<a href="#">cell cycle checkpoint</a>	53	0.0082	7	0.0079	0.1598219	D
<input type="checkbox"/>	GO:0006368	9,7,8	<a href="#">RNA elongation from RNA polymerase II promoter</a>	53	0.0082	7	0.0079	0.1598219	D
<input type="checkbox"/>	GO:0006094	8,9	<a href="#">gluconeogenesis</a>	28	0.0043	2	0.0023	0.1549408	D
<input type="checkbox"/>	GO:0000271	6,7	<a href="#">polysaccharide biosynthetic process</a>	41	0.0063	4	0.0045	0.1541743	D
<input type="checkbox"/>	GO:0016311	6	<a href="#">dephosphorylation</a>	41	0.0063	4	0.0045	0.1541743	D
<input type="checkbox"/>	GO:0046164	5	<a href="#">alcohol catabolic process</a>	47	0.0073	5	0.0057	0.1531728	D
<input type="checkbox"/>	GO:0046034	5,9	<a href="#">ATP metabolic process</a>	21	0.0032	1	0.0011	0.1520183	D

<input type="radio"/>	GO:0001510	7	<a href="#">RNA methylation</a>	60	0.0093	8	0.0090	0.1502024	D
<input type="radio"/>	GO:0006650	7,8	<a href="#">glycerophospholipid metabolic process</a>	60	0.0093	8	0.0090	0.1502024	D
<input type="radio"/>	GO:0008654	7,6,8	<a href="#">phospholipid biosynthetic process</a>	58	0.0090	7	0.0079	0.1495929	D
<input type="radio"/>	GO:0007124	6,4,8,9	<a href="#">pseudohyphal growth</a>	61	0.0094	8	0.0090	0.1492713	D
<input type="radio"/>	GO:0007015	8	<a href="#">actin filament organization</a>	61	0.0094	8	0.0090	0.1492713	D
<input type="radio"/>	GO:0042158	7,5	<a href="#">lipoprotein biosynthetic process</a>	48	0.0074	5	0.0057	0.1476060	D
<input type="radio"/>	GO:0006497	8,7,6	<a href="#">protein amino acid lipidation</a>	48	0.0074	5	0.0057	0.1476060	D
<input type="radio"/>	GO:0042157	6	<a href="#">lipoprotein metabolic process</a>	48	0.0074	5	0.0057	0.1476060	D
<input type="radio"/>	GO:0006354	8,6,7	<a href="#">RNA elongation</a>	59	0.0091	7	0.0079	0.1465373	D
<input type="radio"/>	GO:0007533	5,7,6	<a href="#">mating type switching</a>	29	0.0045	2	0.0023	0.1436542	D
<input type="radio"/>	GO:0006470	8,7	<a href="#">protein amino acid dephosphorylation</a>	29	0.0045	2	0.0023	0.1436542	D
<input type="radio"/>	GO:0000282	7,9,5,6,10	<a href="#">cellular bud site selection</a>	66	0.0102	9	0.0102	0.1424744	D
<input type="radio"/>	GO:0030467	7,4,8	<a href="#">establishment and/or maintenance of cell polarity (sensu Fungi)</a>	66	0.0102	9	0.0102	0.1424744	D
<input type="radio"/>	GO:0030468	8,5,9	<a href="#">establishment of cell polarity (sensu Fungi)</a>	66	0.0102	9	0.0102	0.1424744	D
<input type="radio"/>	GO:0007105	6,4	<a href="#">cytokinesis, site selection</a>	66	0.0102	9	0.0102	0.1424744	D
<input type="radio"/>	GO:0007033	5	<a href="#">vacuole organization and biogenesis</a>	67	0.0103	9	0.0102	0.1421161	D
<input type="radio"/>	GO:0016197	7,5,6	<a href="#">endosome transport</a>	49	0.0076	5	0.0057	0.1419012	D
<input type="radio"/>	GO:0007088	7,9,8,6	<a href="#">regulation of mitosis</a>	55	0.0085	6	0.0068	0.1415003	D
<input type="radio"/>	GO:0006979	4	<a href="#">response to oxidative stress</a>	71	0.0110	9	0.0102	0.1375828	D
<input type="radio"/>	GO:0030150	10,9,8,7	<a href="#">protein import into mitochondrial matrix</a>	22	0.0034	1	0.0011	0.1374720	D
<input type="radio"/>	GO:0006752	6	<a href="#">group transfer coenzyme metabolic process</a>	44	0.0068	4	0.0045	0.1329379	D
<input type="radio"/>	GO:0046364	6,7	<a href="#">monosaccharide biosynthetic process</a>	30	0.0046	2	0.0023	0.1328584	D
<input type="radio"/>	GO:0019319	7,8	<a href="#">hexose biosynthetic process</a>	30	0.0046	2	0.0023	0.1328584	D
<input type="radio"/>	GO:0043161	10,9,11	<a href="#">proteasomal ubiquitin-dependent protein catabolic process</a>	63	0.0097	7	0.0079	0.1320042	D
<input type="radio"/>	GO:0051188	5	<a href="#">cofactor biosynthetic process</a>	79	0.0122	10	0.0113	0.1301092	D
<input type="radio"/>	GO:0006457	6	<a href="#">protein folding</a>	84	0.0130	11	0.0124	0.1274051	D
<input type="radio"/>	GO:0006090	7	<a href="#">pyruvate metabolic process</a>	38	0.0059	3	0.0034	0.1259331	D
<input type="radio"/>	GO:0006897	6,5	<a href="#">endocytosis</a>	86	0.0133	11	0.0124	0.1250973	D
<input type="radio"/>	GO:0009408	5,4	<a href="#">response to heat</a>	23	0.0036	1	0.0011	0.1240576	D
<input type="radio"/>	GO:0007534	6,8,7	<a href="#">gene conversion at mating-type locus</a>	23	0.0036	1	0.0011	0.1240576	D
<input type="radio"/>	GO:0032506	5,3	<a href="#">cytokinetic process</a>	88	0.0136	12	0.0136	0.1238906	D
<input type="radio"/>	GO:0006006	7,8	<a href="#">glucose metabolic process</a>	65	0.0100	7	0.0079	0.1237762	D
<input type="radio"/>	GO:0000002	6	<a href="#">mitochondrial genome maintenance</a>	31	0.0048	2	0.0023	0.1225884	D
<input type="radio"/>	GO:0006970	4	<a href="#">response to osmotic stress</a>	89	0.0137	11	0.0124	0.1201752	D
<input type="radio"/>	GO:0009108	6	<a href="#">coenzyme biosynthetic process</a>	66	0.0102	7	0.0079	0.1195205	D
<input type="radio"/>	GO:0006073	6,7	<a href="#">glucan metabolic process</a>	46	0.0071	4	0.0045	0.1190644	D
<input type="radio"/>	GO:0006644	6,7	<a href="#">phospholipid metabolic process</a>	97	0.0150	13	0.0147	0.1186984	D
<input type="radio"/>	GO:0001522	7	<a href="#">pseudouridine synthesis</a>	39	0.0060	3	0.0034	0.1177582	D
<input type="radio"/>	GO:0046474	8,7,9	<a href="#">glycerophospholipid biosynthetic process</a>	39	0.0060	3	0.0034	0.1177582	D
<input type="radio"/>	GO:0010324	5	<a href="#">membrane invagination</a>	96	0.0148	12	0.0136	0.1163913	D
<input type="radio"/>	GO:0006096	9,10	<a href="#">glycolysis</a>	24	0.0037	1	0.0011	0.1117379	D
<input type="radio"/>	GO:0000288	10,8,9	<a href="#">mRNA catabolic process, deadenylation-dependent decay</a>	24	0.0037	1	0.0011	0.1117379	D
<input type="radio"/>	GO:0006896	9,8,7,6	<a href="#">Golgi to vacuole transport</a>	24	0.0037	1	0.0011	0.1117379	D
<input type="radio"/>	GO:0006818	4,5	<a href="#">hydrogen transport</a>	24	0.0037	1	0.0011	0.1117379	D

<input type="checkbox"/>	GO:0015992	5,7,6,8	<a href="#">proton transport</a>	24	0.0037	1	0.0011	0.1117379	D
<input type="checkbox"/>	GO:0007031	5	<a href="#">peroxisome organization and biogenesis</a>	40	0.0062	3	0.0034	0.1098824	D
<input type="checkbox"/>	GO:0006892	8,6,5,7	<a href="#">post-Golgi vesicle-mediated transport</a>	69	0.0107	7	0.0079	0.1064825	D
<input type="checkbox"/>	GO:0006487	9,8,7	<a href="#">protein amino acid N-linked glycosylation</a>	48	0.0074	4	0.0045	0.1057678	D
<input type="checkbox"/>	GO:0042493	4	<a href="#">response to drug</a>	121	0.0187	15	0.0170	0.1014549	D
<input type="checkbox"/>	GO:0009628	3	<a href="#">response to abiotic stimulus</a>	117	0.0181	14	0.0158	0.0981479	D
<input type="checkbox"/>	GO:0007114	5,4	<a href="#">cell budding</a>	85	0.0131	9	0.0102	0.0970690	D
<input type="checkbox"/>	GO:0019954	3	<a href="#">asexual reproduction</a>	85	0.0131	9	0.0102	0.0970690	D
<input type="checkbox"/>	GO:0044264	5,6	<a href="#">cellular polysaccharide metabolic process</a>	65	0.0100	6	0.0068	0.0925609	D
<input type="checkbox"/>	GO:0005976	5	<a href="#">polysaccharide metabolic process</a>	65	0.0100	6	0.0068	0.0925609	D
<input type="checkbox"/>	GO:0009966	5,4	<a href="#">regulation of signal transduction</a>	26	0.0040	1	0.0011	0.0901815	D
<input type="checkbox"/>	GO:0006486	8,7,6	<a href="#">protein amino acid glycosylation</a>	73	0.0113	7	0.0079	0.0892337	D
<input type="checkbox"/>	GO:0043413	6	<a href="#">biopolymer glycosylation</a>	73	0.0113	7	0.0079	0.0892337	D
<input type="checkbox"/>	GO:0046165	5	<a href="#">alcohol biosynthetic process</a>	35	0.0054	2	0.0023	0.0870550	D
<input type="checkbox"/>	GO:0000086	8,5,6,7,4	<a href="#">G2/M transition of mitotic cell cycle</a>	35	0.0054	2	0.0023	0.0870550	D
<input type="checkbox"/>	GO:0051726	5,4	<a href="#">regulation of cell cycle</a>	167	0.0258	21	0.0238	0.0861325	D
<input type="checkbox"/>	GO:0000074	6,5	<a href="#">regulation of progression through cell cycle</a>	167	0.0258	21	0.0238	0.0861325	D
<input type="checkbox"/>	GO:0048468	3,5	<a href="#">cell development</a>	52	0.0080	4	0.0045	0.0816510	D
<input type="checkbox"/>	GO:0016051	5	<a href="#">carbohydrate biosynthetic process</a>	77	0.0119	7	0.0079	0.0730534	D
<input type="checkbox"/>	GO:0051186	4	<a href="#">cofactor metabolic process</a>	170	0.0263	20	0.0226	0.0727475	D
<input type="checkbox"/>	GO:0009266	4	<a href="#">response to temperature stimulus</a>	28	0.0043	1	0.0011	0.0723460	D
<input type="checkbox"/>	GO:0042144	6	<a href="#">vacuole fusion, non-autophagic</a>	28	0.0043	1	0.0011	0.0723460	D
<input type="checkbox"/>	GO:0006906	6,5	<a href="#">vesicle fusion</a>	28	0.0043	1	0.0011	0.0723460	D
<input type="checkbox"/>	GO:0019318	6,7	<a href="#">hexose metabolic process</a>	85	0.0131	8	0.0090	0.0714419	D
<input type="checkbox"/>	GO:0006732	5	<a href="#">coenzyme metabolic process</a>	136	0.0210	15	0.0170	0.0713737	D
<input type="checkbox"/>	GO:0006119	7,4	<a href="#">oxidative phosphorylation</a>	46	0.0071	3	0.0034	0.0697735	D
<input type="checkbox"/>	GO:0009101	7,5	<a href="#">glycoprotein biosynthetic process</a>	78	0.0120	7	0.0079	0.0692566	D
<input type="checkbox"/>	GO:0043285	5	<a href="#">biopolymer catabolic process</a>	277	0.0428	36	0.0407	0.0688593	D
<input type="checkbox"/>	GO:0009100	6	<a href="#">glycoprotein metabolic process</a>	79	0.0122	7	0.0079	0.0655736	D
<input type="checkbox"/>	GO:0032507	6,5,4	<a href="#">maintenance of cellular protein localization</a>	29	0.0045	1	0.0011	0.0646688	D
<input type="checkbox"/>	GO:0051651	5,4,3	<a href="#">maintenance of cellular localization</a>	29	0.0045	1	0.0011	0.0646688	D
<input type="checkbox"/>	GO:0043632	6	<a href="#">modification-dependent macromolecule catabolic process</a>	155	0.0239	17	0.0192	0.0616549	D
<input type="checkbox"/>	GO:0045185	5,4,3	<a href="#">maintenance of protein localization</a>	30	0.0046	1	0.0011	0.0577361	D
<input type="checkbox"/>	GO:0044265	5	<a href="#">cellular macromolecule catabolic process</a>	314	0.0485	39	0.0441	0.0560907	D
<input type="checkbox"/>	GO:0006950	3	<a href="#">response to stress</a>	488	0.0754	64	0.0724	0.0520010	D
<input type="checkbox"/>	GO:0031118	8,9	<a href="#">rRNA pseudouridine synthesis</a>	31	0.0048	1	0.0011	0.0514881	D
<input type="checkbox"/>	GO:0005984	6	<a href="#">disaccharide metabolic process</a>	31	0.0048	1	0.0011	0.0514881	D
<input type="checkbox"/>	GO:0005996	5,6	<a href="#">monosaccharide metabolic process</a>	92	0.0142	8	0.0090	0.0492104	D
<input type="checkbox"/>	GO:0006066	4	<a href="#">alcohol metabolic process</a>	163	0.0252	17	0.0192	0.0466395	D
<input type="checkbox"/>	GO:0000154	7,8	<a href="#">rRNA modification</a>	85	0.0131	7	0.0079	0.0460780	D
<input type="checkbox"/>	GO:0016044	4	<a href="#">membrane organization and biogenesis</a>	188	0.0290	20	0.0226	0.0429105	D
<input type="checkbox"/>	GO:0009057	4	<a href="#">macromolecule catabolic process</a>	345	0.0533	41	0.0464	0.0411623	D
<input type="checkbox"/>	GO:0051235	3,2	<a href="#">maintenance of localization</a>	33	0.0051	1	0.0011	0.0408192	D
<input type="checkbox"/>	GO:0006091	3	<a href="#">generation of precursor metabolites and energy</a>	183	0.0283	19	0.0215	0.0389235	D



<input type="radio"/>	GO:0006887	8,6,5,7	<a href="#">exocytosis</a>	44	0.0068	2	0.0023	0.0367429	D
<input type="radio"/>	GO:0045333	5	<a href="#">cellular respiration</a>	89	0.0137	7	0.0079	0.0356365	D
<input type="radio"/>	GO:0006511	9,8,10	<a href="#">ubiquitin-dependent protein catabolic process</a>	148	0.0229	14	0.0158	0.0324464	D
<input type="radio"/>	GO:0019941	8,7,9	<a href="#">modification-dependent protein catabolic process</a>	148	0.0229	14	0.0158	0.0324464	D
<input type="radio"/>	GO:0032940	6,4,5	<a href="#">secretion by cell</a>	250	0.0386	27	0.0305	0.0317610	D
<input type="radio"/>	GO:0046903	3,4	<a href="#">secretion</a>	250	0.0386	27	0.0305	0.0317610	D
<input type="radio"/>	GO:0045045	7,5,4,6	<a href="#">secretory pathway</a>	243	0.0375	26	0.0294	0.0310258	D
<input type="radio"/>	GO:0044248	4	<a href="#">cellular catabolic process</a>	425	0.0656	50	0.0566	0.0302903	D
<input type="radio"/>	GO:0048193	7,5,6	<a href="#">Golgi vesicle transport</a>	166	0.0256	16	0.0181	0.0294845	D
<input type="radio"/>	GO:0051603	7,8	<a href="#">proteolysis involved in cellular protein catabolic process</a>	151	0.0233	14	0.0158	0.0279316	D
<input type="radio"/>	GO:0009056	3	<a href="#">catabolic process</a>	438	0.0676	51	0.0577	0.0265250	D
<input type="radio"/>	GO:0015980	4	<a href="#">energy derivation by oxidation of organic compounds</a>	145	0.0224	13	0.0147	0.0249004	D
<input type="radio"/>	GO:0006944	5	<a href="#">membrane fusion</a>	59	0.0091	3	0.0034	0.0219601	D
<input type="radio"/>	GO:0044275	6	<a href="#">cellular carbohydrate catabolic process</a>	80	0.0124	5	0.0057	0.0185171	D
<input type="radio"/>	GO:0016052	5	<a href="#">carbohydrate catabolic process</a>	80	0.0124	5	0.0057	0.0185171	D
<input type="radio"/>	GO:0044257	6,7	<a href="#">cellular protein catabolic process</a>	160	0.0247	14	0.0158	0.0171770	D
<input type="radio"/>	GO:0006888	8,6,5,7	<a href="#">ER to Golgi vesicle-mediated transport</a>	81	0.0125	5	0.0057	0.0170232	D
<input type="radio"/>	GO:0009058	3	<a href="#">biosynthetic process</a>	1249	0.1929	155	0.1753	0.0134660	D
<input type="radio"/>	GO:0030163	6,5	<a href="#">protein catabolic process</a>	173	0.0267	15	0.0170	0.0132328	D
<input type="radio"/>	GO:0009060	6	<a href="#">aerobic respiration</a>	84	0.0130	5	0.0057	0.0131619	D
<input type="radio"/>	GO:0031167	8,9	<a href="#">rRNA methylation</a>	44	0.0068	1	0.0011	0.0107415	D
<input type="radio"/>	GO:0006312	7	<a href="#">mitotic recombination</a>	45	0.0069	1	0.0011	0.0094775	D
<input type="radio"/>	GO:0016192	4,5	<a href="#">vesicle-mediated transport</a>	328	0.0506	32	0.0362	0.0067068	D
<input type="radio"/>	GO:0006508	6	<a href="#">proteolysis</a>	178	0.0275	14	0.0158	0.0056144	D
<input type="radio"/>	GO:0044262	5	<a href="#">cellular carbohydrate metabolic process</a>	213	0.0329	16	0.0181	0.0017484	D
<input type="radio"/>	GO:0019538	4	<a href="#">protein metabolic process</a>	1547	0.2389	182	0.2059	0.0015114	D
<input type="radio"/>	GO:0044267	5	<a href="#">cellular protein metabolic process</a>	1498	0.2313	175	0.1980	0.0013241	D
<input type="radio"/>	GO:0044260	4	<a href="#">cellular macromolecule metabolic process</a>	1552	0.2397	181	0.2048	0.0010433	D
<input type="radio"/>	GO:0005975	4	<a href="#">carbohydrate metabolic process</a>	233	0.0360	17	0.0192	0.0008025	D
<input type="radio"/>	GO:0006412	6,5	<a href="#">translation</a>	688	0.1062	63	0.0713	3.910534E-05	D
<input type="radio"/>	GO:0032196	3	<a href="#">transposition</a>	105	0.0162	2	0.0023	2.508810E-05	D
<input type="radio"/>	GO:0009059	4	<a href="#">macromolecule biosynthetic process</a>	886	0.1368	82	0.0928	4.984603E-06	D
<input type="radio"/>	GO:0043284	5	<a href="#">biopolymer biosynthetic process</a>	354	0.0547	6	0.0068	3.306246E-16	D
<input type="radio"/>	GO:0006414	7,6	<a href="#">translational elongation</a>	313	0.0483	2	0.0023	4.455186E-18	D