

GO-Stats Results

Your dataset contains **468** annotated gene products.

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

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

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

GO ID	Level	GO Term	RO	RF	DO	DF	P-value	E/D
<input type="radio"/> GO:0009987	2	cellular process	4654	0.7187	411	0.8782	5.589253E-15	E
<input type="radio"/> GO:0009101	7,5	glycoprotein biosynthetic process	78	0.0120	25	0.0534	6.837219E-08	E
<input type="radio"/> GO:0009100	6	glycoprotein metabolic process	79	0.0122	25	0.0534	9.310014E-08	E
<input type="radio"/> GO:0043413	6	biopolymer glycosylation	73	0.0113	23	0.0491	5.856006E-07	E
<input type="radio"/> GO:0006486	8,7,6	protein amino acid glycosylation	73	0.0113	23	0.0491	5.856006E-07	E
<input type="radio"/> GO:0016043	3	cellular component organization and biogenesis	2264	0.3496	223	0.4765	1.454407E-06	E
<input type="radio"/> GO:0006464	6	protein modification process	520	0.0803	73	0.1560	6.694529E-06	E
<input type="radio"/> GO:0006487	9,8,7	protein amino acid N-linked glycosylation	48	0.0074	17	0.0363	1.482425E-05	E
<input type="radio"/> GO:0044237	3	cellular metabolic process	3403	0.5255	302	0.6453	1.674464E-05	E
<input type="radio"/> GO:0008152	2	metabolic process	3516	0.5429	308	0.6581	4.562874E-05	E
<input type="radio"/> GO:0043412	5	biopolymer modification	664	0.1025	84	0.1795	5.639801E-05	E
<input type="radio"/> GO:0007049	3	cell cycle	458	0.0707	62	0.1325	0.0003610	E
<input type="radio"/> GO:0044238	3	primary metabolic process	3247	0.5014	283	0.6047	0.0008308	E
<input type="radio"/> GO:0022402	4,3	cell cycle process	439	0.0678	58	0.1239	0.0018774	E
<input type="radio"/> GO:0051234	2,3	establishment of localization	1004	0.1550	108	0.2308	0.0023713	E
<input type="radio"/> GO:0006810	3,4	transport	981	0.1515	105	0.2244	0.0041721	E
<input type="radio"/> GO:0016125	5,6,7	sterol metabolic process	42	0.0065	13	0.0278	0.0041725	E
<input type="radio"/> GO:0051726	5,4	regulation of cell cycle	167	0.0258	29	0.0620	0.0050729	E
<input type="radio"/> GO:0000074	6,5	regulation of progression through cell cycle	167	0.0258	29	0.0620	0.0050729	E
<input type="radio"/> GO:0008202	5,6	steroid metabolic process	43	0.0066	13	0.0278	0.0055577	E
<input type="radio"/> GO:0065007	2	biological regulation	948	0.1464	101	0.2158	0.0078890	E
<input type="radio"/> GO:0000278	4	mitotic cell cycle	266	0.0411	39	0.0833	0.0087014	E
<input type="radio"/> GO:0051649	5,3,4	establishment of cellular localization	606	0.0936	71	0.1517	0.0095977	E
<input type="radio"/> GO:0051179	2	localization	1051	0.1623	109	0.2329	0.0108299	E
<input type="radio"/> GO:0046907	6,4,5	intracellular transport	545	0.0842	65	0.1389	0.0131677	E

<input type="radio"/>	GO:0050789	3	regulation of biological process	761	0.1175	84	0.1795	0.0136994	E
<input type="radio"/>	GO:0050794	4,3	regulation of cellular process	738	0.1140	82	0.1752	0.0137658	E
<input type="radio"/>	GO:0022403	5,4	cell cycle phase	353	0.0545	47	0.1004	0.0142094	E
<input type="radio"/>	GO:0045045	7,5,4,6	secretory pathway	243	0.0375	36	0.0769	0.0150962	E
<input type="radio"/>	GO:0051641	4,3	cellular localization	642	0.0991	73	0.1560	0.0194458	E
<input type="radio"/>	GO:0032940	6,4,5	secretion by cell	250	0.0386	36	0.0769	0.0275003	E
<input type="radio"/>	GO:0046903	3,4	secretion	250	0.0386	36	0.0769	0.0275003	E
<input type="radio"/>	GO:0008610	5,4,6	lipid biosynthetic process	129	0.0199	23	0.0491	0.0300691	E
<input type="radio"/>	GO:0006696	7,8,9	ergosterol biosynthetic process	26	0.0040	9	0.0192	0.0485772	E
<input type="radio"/>	GO:0008204	6,7,8	ergosterol metabolic process	26	0.0040	9	0.0192	0.0485772	E
<input type="radio"/>	GO:0016126	6,7,8	sterol biosynthetic process	32	0.0049	10	0.0214	0.0493768	E
<input type="radio"/>	GO:0006694	6,5,7	steroid biosynthetic process	32	0.0049	10	0.0214	0.0493768	E
<input type="radio"/>	GO:0043283	4	biopolymer metabolic process	2230	0.3443	197	0.4209	0.0721320	E
<input type="radio"/>	GO:0051329	7,5,6	interphase of mitotic cell cycle	112	0.0173	20	0.0427	0.0931577	E
<input type="radio"/>	GO:0051325	6,5	interphase	112	0.0173	20	0.0427	0.0931577	E
<input type="radio"/>	GO:0019219	6,5	regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	440	0.0679	52	0.1111	0.1132415	E
<input type="radio"/>	GO:0006888	8,6,5,7	ER to Golgi vesicle-mediated transport	81	0.0125	16	0.0342	0.1390273	E
<input type="radio"/>	GO:0007346	7,5,6	regulation of progression through mitotic cell cycle	13	0.0020	6	0.0128	0.1536325	E
<input type="radio"/>	GO:0006139	4	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	1532	0.2366	141	0.3013	0.1766547	E
<input type="radio"/>	GO:0044255	4,5	cellular lipid metabolic process	229	0.0354	31	0.0662	0.2719688	E
<input type="radio"/>	GO:0006629	4	lipid metabolic process	242	0.0374	32	0.0684	0.3283169	E
<input type="radio"/>	GO:0006886	7,5,6	intracellular protein transport	274	0.0423	35	0.0748	0.3385847	E
<input type="radio"/>	GO:0045184	3,4,5	establishment of protein localization	296	0.0457	37	0.0791	0.3525380	E
<input type="radio"/>	GO:0045047	9,8,7,6,5	protein targeting to ER	33	0.0051	9	0.0192	0.3575451	E
<input type="radio"/>	GO:0043170	3	macromolecule metabolic process	2841	0.4387	237	0.5064	0.3940332	E
<input type="radio"/>	GO:0006260	6	DNA replication	117	0.0181	19	0.0406	0.4516722	E
<input type="radio"/>	GO:0006605	8,6,7	protein targeting	258	0.0398	33	0.0705	0.4729821	E
<input type="radio"/>	GO:0015031	4,5,6	protein transport	280	0.0432	35	0.0748	0.4924066	E
<input type="radio"/>	GO:0017038	5,6,7	protein import	109	0.0168	18	0.0385	0.5139207	E
<input type="radio"/>	GO:0033036	3	macromolecule localization	382	0.0590	44	0.0940	0.5789022	E
<input type="radio"/>	GO:0000087	7,5,6	M phase of mitotic cell cycle	129	0.0199	20	0.0427	0.5835955	E
<input type="radio"/>	GO:0006350	5	transcription	567	0.0876	60	0.1282	0.5933773	E
<input type="radio"/>	GO:0048519	4	negative regulation of biological process	242	0.0374	31	0.0662	0.6606289	E
<input type="radio"/>	GO:0006259	5	DNA metabolic process	523	0.0808	56	0.1197	0.6693674	E
<input type="radio"/>	GO:0008104	4	protein localization	330	0.0510	39	0.0833	0.7052902	E
<input type="radio"/>	GO:0045449	7,6	regulation of transcription	386	0.0596	44	0.0940	0.7053661	E
<input type="radio"/>	GO:0006996	4	organelle organization and biogenesis	1388	0.2143	125	0.2671	0.8959171	E
<input type="radio"/>	GO:0031323	5,4	regulation of cellular metabolic process	507	0.0783	54	0.1154	0.9080211	E
<input type="radio"/>	GO:0019932	6	second-messenger-mediated signaling	32	0.0049	3	0.0064	1.0000000	E
<input type="radio"/>	GO:0000715	7,8	nucleotide-excision repair, DNA damage recognition	7	0.0011	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0046020	11,10,7	negative regulation of transcription from RNA polymerase II promoter by pheromones	6	0.0009	2	0.0043	1.0000000	E
<input type="radio"/>	GO:0019236	4	response to pheromone	94	0.0145	13	0.0278	1.0000000	E
<input type="radio"/>	GO:0000371	10,6,6	positive regulation of transcription by	5	0.0008	2	0.0021	0.0000000	E

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<input type="radio"/>	GO:0006379	8	mRNA cleavage	26	0.0040	3	0.0064	1.0000000	E
<input type="radio"/>	GO:0006493	9,8,7	protein amino acid O-linked glycosylation	16	0.0025	4	0.0085	1.0000000	E
<input type="radio"/>	GO:0006666	5,8,9	3-keto-sphinganine metabolic process	2	0.0003	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0016094	8,7,9	polyprenol biosynthetic process	3	0.0005	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0015833	4,5	peptide transport	7	0.0011	3	0.0064	1.0000000	E
<input type="radio"/>	GO:0031509	7,11	telomeric heterochromatin formation	60	0.0093	7	0.0150	1.0000000	E
<input type="radio"/>	GO:0001300	5	chronological cell aging	13	0.0020	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0006261	7	DNA-dependent DNA replication	97	0.0150	14	0.0299	1.0000000	E
<input type="radio"/>	GO:0015940	7,8	pantothenate biosynthetic process	8	0.0012	2	0.0043	1.0000000	E
<input type="radio"/>	GO:0000722	9,8	telomere maintenance via recombination	19	0.0029	2	0.0043	1.0000000	E
<input type="radio"/>	GO:0018196	8	peptidyl-asparagine modification	2	0.0003	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0001304	10,6	progressive alteration of chromatin during replicative cell aging	9	0.0014	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0000819	7,4	sister chromatid segregation	62	0.0096	9	0.0192	1.0000000	E
<input type="radio"/>	GO:0006592	8,9,6,5	ornithine biosynthetic process	4	0.0006	2	0.0043	1.0000000	E
<input type="radio"/>	GO:0065008	3	regulation of biological quality	260	0.0401	24	0.0513	1.0000000	E
<input type="radio"/>	GO:0007031	5	peroxisome organization and biogenesis	40	0.0062	3	0.0064	1.0000000	E
<input type="radio"/>	GO:0043681	6,7,8	protein import into mitochondrion	40	0.0062	8	0.0171	1.0000000	E
<input type="radio"/>	GO:0006360	8,7	transcription from RNA polymerase I promoter	34	0.0053	3	0.0064	1.0000000	E
<input type="radio"/>	GO:0007076	10,8,5,6,9,7,4	mitotic chromosome condensation	9	0.0014	2	0.0043	1.0000000	E
<input type="radio"/>	GO:0007569	4	cell aging	49	0.0076	4	0.0085	1.0000000	E
<input type="radio"/>	GO:0007006	5,6	mitochondrial membrane organization and biogenesis	24	0.0037	4	0.0085	1.0000000	E
<input type="radio"/>	GO:0006617	8,12,11,7,10,9	SRP-dependent cotranslational protein targeting to membrane, signal sequence recognition	7	0.0011	3	0.0064	1.0000000	E
<input type="radio"/>	GO:0016071	6	mRNA metabolic process	210	0.0324	24	0.0513	1.0000000	E
<input type="radio"/>	GO:0030011	7,4,8	maintenance of cell polarity	8	0.0012	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0043086	5	negative regulation of enzyme activity	11	0.0017	2	0.0043	1.0000000	E
<input type="radio"/>	GO:0000076	11,9,8,10	DNA replication checkpoint	5	0.0008	2	0.0043	1.0000000	E
<input type="radio"/>	GO:0031023	5	microtubule organizing center organization and biogenesis	16	0.0025	4	0.0085	1.0000000	E
<input type="radio"/>	GO:0009968	6,5	negative regulation of signal transduction	17	0.0026	4	0.0085	1.0000000	E
<input type="radio"/>	GO:0048284	5	organelle fusion	22	0.0034	3	0.0064	1.0000000	E
<input type="radio"/>	GO:0007186	6	G-protein coupled receptor protein signaling pathway	34	0.0053	5	0.0107	1.0000000	E
<input type="radio"/>	GO:0030005	9,7	cellular di-, tri-valent inorganic cation homeostasis	64	0.0099	5	0.0107	1.0000000	E
<input type="radio"/>	GO:0018319	10,9,8	protein amino acid myristoylation	5	0.0008	2	0.0043	1.0000000	E
<input type="radio"/>	GO:0000245	7,6,9,11	spliceosome assembly	19	0.0029	3	0.0064	1.0000000	E
<input type="radio"/>	GO:0046474	8,7,9	glycerophospholipid biosynthetic process	39	0.0060	6	0.0128	1.0000000	E
<input type="radio"/>	GO:0006041	6,7	glucosamine metabolic process	19	0.0029	3	0.0064	1.0000000	E
<input type="radio"/>	GO:0050790	4	regulation of catalytic activity	45	0.0069	5	0.0107	1.0000000	E
<input type="radio"/>	GO:0043044	10	ATP-dependent chromatin remodeling	23	0.0036	2	0.0043	1.0000000	E
<input type="radio"/>	GO:0051052	7,6	regulation of DNA metabolic process	41	0.0063	8	0.0171	1.0000000	E
<input type="radio"/>	GO:0009116	5	nucleoside metabolic process	18	0.0028	4	0.0085	1.0000000	E
<input type="radio"/>	GO:0000375	8	RNA splicing, via transesterification reactions	110	0.0170	10	0.0214	1.0000000	E
<input type="radio"/>	GO:0019740	4	nitrogen utilization	17	0.0026	3	0.0064	1.0000000	E
<input type="radio"/>	GO:0000724	8,7	double-strand break repair via homologous	25	0.0038	2	0.0043	1.0000000	E

<input type="radio"/>	GO:0000724	9,7	recombination	23	0.0039	2	0.0043	1.0000000	E
<input type="radio"/>	GO:0018193	7	peptidyl-amino acid modification	28	0.0043	7	0.0150	1.0000000	E
<input type="radio"/>	GO:0015802	6,7,8	basic amino acid transport	9	0.0014	3	0.0064	1.0000000	E
<input type="radio"/>	GO:0006609	10,11,8,9,7	mRNA-binding (hnRNP) protein import into nucleus	25	0.0039	5	0.0107	1.0000000	E
<input type="radio"/>	GO:0009075	6,7	histidine family amino acid metabolic process	14	0.0022	2	0.0043	1.0000000	E
<input type="radio"/>	GO:0009615	4,5	response to virus	7	0.0011	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0006357	9,8	regulation of transcription from RNA polymerase II promoter	221	0.0341	25	0.0534	1.0000000	E
<input type="radio"/>	GO:0006597	8,9	spermine biosynthetic process	2	0.0003	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0030261	6	chromosome condensation	11	0.0017	2	0.0043	1.0000000	E
<input type="radio"/>	GO:0006338	9	chromatin remodeling	155	0.0239	16	0.0342	1.0000000	E
<input type="radio"/>	GO:0006887	8,6,5,7	exocytosis	44	0.0068	5	0.0107	1.0000000	E
<input type="radio"/>	GO:0007535	6,8,4,7	donor selection	5	0.0008	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0005976	5	polysaccharide metabolic process	65	0.0100	5	0.0107	1.0000000	E
<input type="radio"/>	GO:0015849	4,5	organic acid transport	55	0.0085	6	0.0128	1.0000000	E
<input type="radio"/>	GO:0006085	7	acetyl-CoA biosynthetic process	4	0.0006	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0046021	10,8,5,6,9,7,4	regulation of transcription from RNA polymerase II promoter, mitotic	6	0.0009	1	0.0021	1.0000000	E
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<input type="radio"/>	GO:0018342	9,8,7	protein prenylation	5	0.0008	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0006265	6	DNA topological change	7	0.0011	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0006270	8,6	DNA replication initiation	33	0.0051	4	0.0085	1.0000000	E
<input type="radio"/>	GO:0006596	7,8	polyamine biosynthetic process	4	0.0006	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0042308	8,9,11,12,10,7	negative regulation of protein import into nucleus	2	0.0003	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0007242	5	intracellular signaling cascade	137	0.0212	14	0.0299	1.0000000	E
<input type="radio"/>	GO:0006048	9,7,10	UDP-N-acetylglucosamine biosynthetic process	2	0.0003	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0042176	6,7,5	regulation of protein catabolic process	5	0.0008	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0006826	7,8,9	iron ion transport	20	0.0031	2	0.0043	1.0000000	E
<input type="radio"/>	GO:0016044	4	membrane organization and biogenesis	188	0.0290	14	0.0299	1.0000000	E
<input type="radio"/>	GO:0042435	7,5	indole derivative biosynthetic process	10	0.0015	2	0.0043	1.0000000	E
<input type="radio"/>	GO:0009228	7,8	thiamin biosynthetic process	19	0.0029	3	0.0064	1.0000000	E
<input type="radio"/>	GO:0000742	7,5	karyogamy during conjugation with cellular fusion	17	0.0026	2	0.0043	1.0000000	E
<input type="radio"/>	GO:0007062	7,4	sister chromatid cohesion	31	0.0048	8	0.0171	1.0000000	E
<input type="radio"/>	GO:0006612	9,7,8	protein targeting to membrane	39	0.0060	6	0.0128	1.0000000	E
<input type="radio"/>	GO:0043433	9,8	negative regulation of transcription factor activity	1	0.0002	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0006505	9,10	GPI anchor metabolic process	27	0.0042	6	0.0128	1.0000000	E
<input type="radio"/>	GO:0033013	5	tetrapyrrole metabolic process	14	0.0022	2	0.0043	1.0000000	E
<input type="radio"/>	GO:0051051	6,5	negative regulation of transport	4	0.0006	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0016584	6,10	nucleosome positioning	3	0.0005	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0006368	9,7,8	RNA elongation from RNA polymerase II promoter	53	0.0082	9	0.0192	1.0000000	E
<input type="radio"/>	GO:0031570	8,7	DNA integrity checkpoint	18	0.0028	2	0.0043	1.0000000	E
<input type="radio"/>	GO:0046112	6,5	nucleobase biosynthetic process	21	0.0032	2	0.0043	1.0000000	E
<input type="radio"/>	GO:0006406	11,9,6,8,10,7	mRNA export from nucleus	66	0.0102	10	0.0214	1.0000000	E
<input type="radio"/>	GO:0006397	7	mRNA processing	157	0.0242	16	0.0342	1.0000000	E

<input type="radio"/>	GO:0006465	9,5	signal peptide processing	7	0.0011	3	0.0064	1.0000000	E
<input type="radio"/>	GO:0051647	6,5	nucleus localization	20	0.0031	2	0.0043	1.0000000	E
<input type="radio"/>	GO:0009073	7,6,8	aromatic amino acid family biosynthetic process	16	0.0025	4	0.0085	1.0000000	E
<input type="radio"/>	GO:0031929	6	TOR signaling pathway	13	0.0020	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0043631	8	RNA polyadenylation	24	0.0037	2	0.0043	1.0000000	E
<input type="radio"/>	GO:0000046	5,6	autophagic vacuole fusion	1	0.0002	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0015959	9	diadenosine polyphosphate metabolic process	1	0.0002	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0000409	10,8,9,6	regulation of transcription by galactose	5	0.0008	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0043330	5,6	response to exogenous dsRNA	7	0.0011	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0031119	8,9	tRNA pseudouridine synthesis	4	0.0006	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0031565	8,7	cytokinesis checkpoint	4	0.0006	2	0.0043	1.0000000	E
<input type="radio"/>	GO:0046999	5,4	regulation of conjugation	30	0.0046	5	0.0107	1.0000000	E
<input type="radio"/>	GO:0006348	11,7,8,12,10	chromatin silencing at telomere	60	0.0093	7	0.0150	1.0000000	E
<input type="radio"/>	GO:0006606	9,10,7,8,6	protein import into nucleus	50	0.0077	9	0.0192	1.0000000	E
<input type="radio"/>	GO:0009305	8	protein amino acid biotinylation	1	0.0002	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0006272	9,8	leading strand elongation	14	0.0022	4	0.0085	1.0000000	E
<input type="radio"/>	GO:0019985	7,6	bypass DNA synthesis	1	0.0002	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0000373	10	Group II intron splicing	1	0.0002	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0031577	8,7	spindle checkpoint	24	0.0037	2	0.0043	1.0000000	E
<input type="radio"/>	GO:0000173	10,11,8,9,7	inactivation of MAPK activity during osmolarity sensing	5	0.0008	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0000725	7,6	recombinational repair	29	0.0045	3	0.0064	1.0000000	E
<input type="radio"/>	GO:0006449	8,7,9,6	regulation of translational termination	3	0.0005	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0032297	10,8,9	negative regulation of DNA replication initiation	6	0.0009	2	0.0043	1.0000000	E
<input type="radio"/>	GO:0017157	6,9,5,7,8	regulation of exocytosis	3	0.0005	2	0.0043	1.0000000	E
<input type="radio"/>	GO:0006568	7,8,6	tryptophan metabolic process	10	0.0015	2	0.0043	1.0000000	E
<input type="radio"/>	GO:0019438	5	aromatic compound biosynthetic process	18	0.0028	4	0.0085	1.0000000	E
<input type="radio"/>	GO:0016236	4	macroautophagy	6	0.0009	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0043085	5	positive regulation of enzyme activity	11	0.0017	2	0.0043	1.0000000	E
<input type="radio"/>	GO:0031506	7,5,8,6	cell wall glycoprotein biosynthetic process	12	0.0019	3	0.0064	1.0000000	E
<input type="radio"/>	GO:0007323	9	peptide pheromone maturation	8	0.0012	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0055075	9	potassium ion homeostasis	5	0.0008	2	0.0043	1.0000000	E
<input type="radio"/>	GO:0030258	5,6	lipid modification	13	0.0020	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0018377	9,8,7	protein myristoylation	5	0.0008	2	0.0043	1.0000000	E
<input type="radio"/>	GO:0042981	6,7,9,5	regulation of apoptosis	4	0.0006	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0006374	9,11	nuclear mRNA splicing via U2-type spliceosome	15	0.0023	2	0.0043	1.0000000	E
<input type="radio"/>	GO:0019954	3	asexual reproduction	85	0.0131	11	0.0235	1.0000000	E
<input type="radio"/>	GO:0015781	6,7	pyrimidine nucleotide-sugar transport	2	0.0003	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0006532	8,9	aspartate biosynthetic process	2	0.0003	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0006811	4,5	ion transport	115	0.0178	11	0.0235	1.0000000	E
<input type="radio"/>	GO:0016573	11,9	histone acetylation	40	0.0062	3	0.0064	1.0000000	E
<input type="radio"/>	GO:0006399	6	tRNA metabolic process	121	0.0187	10	0.0214	1.0000000	E
<input type="radio"/>	GO:0009126	7	purine nucleoside monophosphate metabolic process	18	0.0028	2	0.0043	1.0000000	E
<input type="radio"/>	GO:0006402	7	mRNA catabolic process	60	0.0093	10	0.0214	1.0000000	E
<input type="radio"/>	GO:0007047	5	cell wall organization and biogenesis	200	0.0309	23	0.0491	1.0000000	E

<input type="checkbox"/>	GO:0007068	10,8,6,9,7,5	negative regulation of transcription, mitotic	7	0.0011	1	0.0021	1.0000000	E
<input type="checkbox"/>	GO:0009105	7,6	lipoic acid biosynthetic process	1	0.0002	1	0.0021	1.0000000	E
<input type="checkbox"/>	GO:0042138	11,9,8,5,6,10,7,4	meiotic DNA double-strand break formation	9	0.0014	2	0.0043	1.0000000	E
<input type="checkbox"/>	GO:0006829	8,9	zinc ion transport	7	0.0011	1	0.0021	1.0000000	E
<input type="checkbox"/>	GO:0044264	5,6	cellular polysaccharide metabolic process	65	0.0100	5	0.0107	1.0000000	E
<input type="checkbox"/>	GO:0006828	8,9	manganese ion transport	8	0.0012	1	0.0021	1.0000000	E
<input type="checkbox"/>	GO:0006531	7,8	aspartate metabolic process	2	0.0003	1	0.0021	1.0000000	E
<input type="checkbox"/>	GO:0007050	7,8,6	cell cycle arrest	11	0.0017	2	0.0043	1.0000000	E
<input type="checkbox"/>	GO:0043633	7	modification-dependent RNA catabolic process	7	0.0011	2	0.0043	1.0000000	E
<input type="checkbox"/>	GO:0000256	6	allantoin catabolic process	7	0.0011	1	0.0021	1.0000000	E
<input type="checkbox"/>	GO:0009123	6	nucleoside monophosphate metabolic process	19	0.0029	2	0.0043	1.0000000	E
<input type="checkbox"/>	GO:0042727	7	riboflavin and derivative biosynthetic process	8	0.0012	1	0.0021	1.0000000	E
<input type="checkbox"/>	GO:0042398	6,5	amino acid derivative biosynthetic process	20	0.0031	3	0.0064	1.0000000	E
<input type="checkbox"/>	GO:0051053	8,7	negative regulation of DNA metabolic process	20	0.0031	4	0.0085	1.0000000	E
<input type="checkbox"/>	GO:0000079	8,7,6	regulation of cyclin-dependent protein kinase activity	15	0.0023	2	0.0043	1.0000000	E
<input type="checkbox"/>	GO:0006356	9,8	regulation of transcription from RNA polymerase I promoter	8	0.0012	1	0.0021	1.0000000	E
<input type="checkbox"/>	GO:0001308	11,7,10	loss of chromatin silencing during replicative cell aging	8	0.0012	1	0.0021	1.0000000	E
<input type="checkbox"/>	GO:0030100	6,7,5	regulation of endocytosis	3	0.0005	1	0.0021	1.0000000	E
<input type="checkbox"/>	GO:0032377	7,8,6	regulation of intracellular lipid transport	1	0.0002	1	0.0021	1.0000000	E
<input type="checkbox"/>	GO:0015698	6,7	inorganic anion transport	16	0.0025	2	0.0043	1.0000000	E
<input type="checkbox"/>	GO:0009096	8,7,9	aromatic amino acid family biosynthetic process, anthranilate pathway	10	0.0015	2	0.0043	1.0000000	E
<input type="checkbox"/>	GO:0016050	5	vesicle organization and biogenesis	16	0.0025	2	0.0043	1.0000000	E
<input type="checkbox"/>	GO:0030969	8,6,7	UFP-specific transcription factor mRNA processing during unfolded protein response	2	0.0003	1	0.0021	1.0000000	E
<input type="checkbox"/>	GO:0006333	8	chromatin assembly or disassembly	119	0.0184	15	0.0321	1.0000000	E
<input type="checkbox"/>	GO:0006284	7,6	base-excision repair	12	0.0019	2	0.0043	1.0000000	E
<input type="checkbox"/>	GO:0006030	8,6,7,9	chitin metabolic process	17	0.0026	2	0.0043	1.0000000	E
<input type="checkbox"/>	GO:0000185	9,10,8	activation of MAPKKK activity	1	0.0002	1	0.0021	1.0000000	E
<input type="checkbox"/>	GO:0051180	4,5	vitamin transport	9	0.0014	2	0.0043	1.0000000	E
<input type="checkbox"/>	GO:0006591	7,8,5,4	ornithine metabolic process	6	0.0009	2	0.0043	1.0000000	E
<input type="checkbox"/>	GO:0006461	6,5	protein complex assembly	116	0.0179	10	0.0214	1.0000000	E
<input type="checkbox"/>	GO:0009311	5	oligosaccharide metabolic process	7	0.0011	1	0.0021	1.0000000	E
<input type="checkbox"/>	GO:0006744	8,7	ubiquinone biosynthetic process	9	0.0014	1	0.0021	1.0000000	E
<input type="checkbox"/>	GO:0006310	6	DNA recombination	122	0.0188	10	0.0214	1.0000000	E
<input type="checkbox"/>	GO:0006906	6,5	vesicle fusion	28	0.0043	3	0.0064	1.0000000	E
<input type="checkbox"/>	GO:0032365	7,5,6	intracellular lipid transport	1	0.0002	1	0.0021	1.0000000	E
<input type="checkbox"/>	GO:0015914	5,6	phospholipid transport	12	0.0019	2	0.0043	1.0000000	E
<input type="checkbox"/>	GO:0045039	10,9,7,8	protein import into mitochondrial inner membrane	8	0.0012	1	0.0021	1.0000000	E
<input type="checkbox"/>	GO:0000115	10,9,8,5,7,4	S-phase-specific transcription in mitotic cell cycle	1	0.0002	1	0.0021	1.0000000	E
<input type="checkbox"/>	GO:0042992	9,10,12,13,11,8	negative regulation of transcription factor import into nucleus	2	0.0003	1	0.0021	1.0000000	E
<input type="checkbox"/>	GO:0051383	6	kinetochore organization and biogenesis	3	0.0005	1	0.0021	1.0000000	E
<input type="checkbox"/>	GO:0043549	6	regulation of kinase activity	25	0.0039	5	0.0107	1.0000000	E

<input type="checkbox"/>	GO:0015837	4,5	amine transport	50	0.0077	6	0.0128	1.0000000	E
<input type="checkbox"/>	GO:0042542	6	response to hydrogen peroxide	4	0.0006	1	0.0021	1.0000000	E
<input type="checkbox"/>	GO:0008033	7	tRNA processing	84	0.0130	9	0.0192	1.0000000	E
<input type="checkbox"/>	GO:0015867	8,9	ATP transport	3	0.0005	2	0.0043	1.0000000	E
<input type="checkbox"/>	GO:0046686	6	response to cadmium ion	4	0.0006	1	0.0021	1.0000000	E
<input type="checkbox"/>	GO:0007093	8,10,9,7	mitotic cell cycle checkpoint	27	0.0042	4	0.0085	1.0000000	E
<input type="checkbox"/>	GO:0006457	6	protein folding	84	0.0130	7	0.0150	1.0000000	E
<input type="checkbox"/>	GO:0051382	8,7	kinetochore assembly	3	0.0005	1	0.0021	1.0000000	E
<input type="checkbox"/>	GO:0043241	6,5	protein complex disassembly	28	0.0043	3	0.0064	1.0000000	E
<input type="checkbox"/>	GO:0006470	8,7	protein amino acid dephosphorylation	29	0.0045	6	0.0128	1.0000000	E
<input type="checkbox"/>	GO:0045143	10,8,7,5,9,6,4	homologous chromosome segregation	6	0.0009	1	0.0021	1.0000000	E
<input type="checkbox"/>	GO:0055069	9	zinc ion homeostasis	10	0.0015	2	0.0043	1.0000000	E
<input type="checkbox"/>	GO:0051254	8,7	positive regulation of RNA metabolic process	5	0.0008	1	0.0021	1.0000000	E
<input type="checkbox"/>	GO:0006409	11,9,6,8,10,7	tRNA export from nucleus	29	0.0045	4	0.0085	1.0000000	E
<input type="checkbox"/>	GO:0006056	7	mannoprotein metabolic process	12	0.0019	3	0.0064	1.0000000	E
<input type="checkbox"/>	GO:0006336	7,8,11	DNA replication-independent nucleosome assembly	5	0.0008	1	0.0021	1.0000000	E
<input type="checkbox"/>	GO:0006950	3	response to stress	488	0.0754	42	0.0897	1.0000000	E
<input type="checkbox"/>	GO:0043171	5	peptide catabolic process	1	0.0002	1	0.0021	1.0000000	E
<input type="checkbox"/>	GO:0016090	6,7	prenol metabolic process	3	0.0005	1	0.0021	1.0000000	E
<input type="checkbox"/>	GO:0008655	5	pyrimidine salvage	5	0.0008	1	0.0021	1.0000000	E
<input type="checkbox"/>	GO:0044267	5	cellular protein metabolic process	1498	0.2313	122	0.2607	1.0000000	E
<input type="checkbox"/>	GO:0007117	6,5,4	budding cell bud growth	35	0.0054	4	0.0085	1.0000000	E
<input type="checkbox"/>	GO:0015718	6,7	monocarboxylic acid transport	10	0.0015	1	0.0021	1.0000000	E
<input type="checkbox"/>	GO:0019935	7	cyclic-nucleotide-mediated signaling	9	0.0014	1	0.0021	1.0000000	E
<input type="checkbox"/>	GO:0009231	7,8	riboflavin biosynthetic process	6	0.0009	1	0.0021	1.0000000	E
<input type="checkbox"/>	GO:0000105	8,9	histidine biosynthetic process	14	0.0022	2	0.0043	1.0000000	E
<input type="checkbox"/>	GO:0019395	6,8,7	fatty acid oxidation	11	0.0017	1	0.0021	1.0000000	E
<input type="checkbox"/>	GO:0009309	5,6	amine biosynthetic process	114	0.0176	15	0.0321	1.0000000	E
<input type="checkbox"/>	GO:0000282	7,9,5,6,10	cellular bud site selection	66	0.0102	10	0.0214	1.0000000	E
<input type="checkbox"/>	GO:0042991	10,11,8,9,7	transcription factor import into nucleus	2	0.0003	1	0.0021	1.0000000	E
<input type="checkbox"/>	GO:0031106	7	septin ring organization	9	0.0014	2	0.0043	1.0000000	E
<input type="checkbox"/>	GO:0009124	6,7	nucleoside monophosphate biosynthetic process	17	0.0026	2	0.0043	1.0000000	E
<input type="checkbox"/>	GO:0045740	9,8	positive regulation of DNA replication	2	0.0003	1	0.0021	1.0000000	E
<input type="checkbox"/>	GO:0042364	6	water-soluble vitamin biosynthetic process	46	0.0071	4	0.0085	1.0000000	E
<input type="checkbox"/>	GO:0006323	6	DNA packaging	253	0.0391	25	0.0534	1.0000000	E
<input type="checkbox"/>	GO:0015865	6,7	purine nucleotide transport	4	0.0006	3	0.0064	1.0000000	E
<input type="checkbox"/>	GO:0000749	5	response to pheromone during conjugation with cellular fusion	57	0.0088	7	0.0150	1.0000000	E
<input type="checkbox"/>	GO:0006042	7,8	glucosamine biosynthetic process	17	0.0026	3	0.0064	1.0000000	E
<input type="checkbox"/>	GO:0006152	6,7	purine nucleoside catabolic process	1	0.0002	1	0.0021	1.0000000	E
<input type="checkbox"/>	GO:0043624	7,6	cellular protein complex disassembly	28	0.0043	3	0.0064	1.0000000	E
<input type="checkbox"/>	GO:0043111	10,9	replication fork blocking	1	0.0002	1	0.0021	1.0000000	E
<input type="checkbox"/>	GO:0006405	10,8,5,7,9,6	RNA export from nucleus	79	0.0122	11	0.0235	1.0000000	E
<input type="checkbox"/>	GO:0010383	7,5,6	cell wall polysaccharide metabolic process	16	0.0025	2	0.0043	1.0000000	E
<input type="checkbox"/>	GO:0030474	5,6,4,7	spindle pole body duplication	14	0.0022	3	0.0064	1.0000000	E

<input type="checkbox"/>	GO:0007114	5,4	cell budding	85	0.0131	11	0.0235	1.0000000	E
<input type="checkbox"/>	GO:0000165	7	MAPKKK cascade	20	0.0031	4	0.0085	1.0000000	E
<input type="checkbox"/>	GO:0016311	6	dephosphorylation	41	0.0063	8	0.0171	1.0000000	E
<input type="checkbox"/>	GO:0001402	5,4	signal transduction during filamentous growth	7	0.0011	3	0.0064	1.0000000	E
<input type="checkbox"/>	GO:0006359	9,8	regulation of transcription from RNA polymerase III promoter	7	0.0011	1	0.0021	1.0000000	E
<input type="checkbox"/>	GO:0046219	7,8,6	indolalkylamine biosynthetic process	10	0.0015	2	0.0043	1.0000000	E
<input type="checkbox"/>	GO:0000055	11,12,7,9,10	ribosomal large subunit export from nucleus	11	0.0017	1	0.0021	1.0000000	E
<input type="checkbox"/>	GO:0044247	7,6	cellular polysaccharide catabolic process	12	0.0019	1	0.0021	1.0000000	E
<input type="checkbox"/>	GO:0045786	6,7,5	negative regulation of progression through cell cycle	13	0.0020	4	0.0085	1.0000000	E
<input type="checkbox"/>	GO:0016226	6	iron-sulfur cluster assembly	11	0.0017	2	0.0043	1.0000000	E
<input type="checkbox"/>	GO:0022616	6	DNA strand elongation	32	0.0049	4	0.0085	1.0000000	E
<input type="checkbox"/>	GO:0015780	5,6	nucleotide-sugar transport	4	0.0006	1	0.0021	1.0000000	E
<input type="checkbox"/>	GO:0006586	6,7	indolalkylamine metabolic process	10	0.0015	2	0.0043	1.0000000	E
<input type="checkbox"/>	GO:0006298	7,9,6	mismatch repair	25	0.0039	5	0.0107	1.0000000	E
<input type="checkbox"/>	GO:0000903	6,4,8,7,9	cellular morphogenesis during vegetative growth	8	0.0012	2	0.0043	1.0000000	E
<input type="checkbox"/>	GO:0043407	8,9	negative regulation of MAPK activity	5	0.0008	1	0.0021	1.0000000	E
<input type="checkbox"/>	GO:0018344	10,9,8	protein geranylgeranylation	4	0.0006	1	0.0021	1.0000000	E
<input type="checkbox"/>	GO:0009059	4	macromolecule biosynthetic process	886	0.1368	65	0.1389	1.0000000	E
<input type="checkbox"/>	GO:0046839	6,7	phospholipid dephosphorylation	7	0.0011	1	0.0021	1.0000000	E
<input type="checkbox"/>	GO:0000750	8,7,6	pheromone-dependent signal transduction during conjugation with cellular fusion	28	0.0043	5	0.0107	1.0000000	E
<input type="checkbox"/>	GO:0051707	3,4	response to other organism	7	0.0011	1	0.0021	1.0000000	E
<input type="checkbox"/>	GO:0006506	10,9,8,7,11	GPI anchor biosynthetic process	26	0.0040	5	0.0107	1.0000000	E
<input type="checkbox"/>	GO:0000337	9,8,5	regulation of DNA transposition	10	0.0015	2	0.0043	1.0000000	E
<input type="checkbox"/>	GO:0046823	7,10,6,8,9	negative regulation of nucleocytoplasmic transport	2	0.0003	1	0.0021	1.0000000	E
<input type="checkbox"/>	GO:0000041	7,8	transition metal ion transport	46	0.0071	4	0.0085	1.0000000	E
<input type="checkbox"/>	GO:0008654	7,6,8	phospholipid biosynthetic process	58	0.0090	8	0.0171	1.0000000	E
<input type="checkbox"/>	GO:0009085	8,9	lysine biosynthetic process	9	0.0014	1	0.0021	1.0000000	E
<input type="checkbox"/>	GO:0043570	6	maintenance of DNA repeat elements	1	0.0002	1	0.0021	1.0000000	E
<input type="checkbox"/>	GO:0006752	6	group transfer coenzyme metabolic process	44	0.0068	4	0.0085	1.0000000	E
<input type="checkbox"/>	GO:0009067	7,8	aspartate family amino acid biosynthetic process	20	0.0031	2	0.0043	1.0000000	E
<input type="checkbox"/>	GO:0009084	7,8	glutamine family amino acid biosynthetic process	27	0.0042	3	0.0064	1.0000000	E
<input type="checkbox"/>	GO:0000255	5	allantoin metabolic process	7	0.0011	1	0.0021	1.0000000	E
<input type="checkbox"/>	GO:0046148	5	pigment biosynthetic process	19	0.0029	3	0.0064	1.0000000	E
<input type="checkbox"/>	GO:0009113	7,6	purine base biosynthetic process	6	0.0009	1	0.0021	1.0000000	E
<input type="checkbox"/>	GO:0019933	8	cAMP-mediated signaling	9	0.0014	1	0.0021	1.0000000	E
<input type="checkbox"/>	GO:0007004	9	telomere maintenance via telomerase	17	0.0026	2	0.0043	1.0000000	E
<input type="checkbox"/>	GO:0051691	6	cellular oligosaccharide metabolic process	6	0.0009	1	0.0021	1.0000000	E
<input type="checkbox"/>	GO:0000188	9,10,8	inactivation of MAPK activity	5	0.0008	1	0.0021	1.0000000	E
<input type="checkbox"/>	GO:0006616	9,12,11,7,10,8	SRP-dependent cotranslational protein targeting to membrane, translocation	10	0.0015	1	0.0021	1.0000000	E
<input type="checkbox"/>	GO:0045892	9,8	negative regulation of transcription, DNA-dependent	156	0.0241	18	0.0385	1.0000000	E
<input type="checkbox"/>	GO:0018348	11,10,9	protein amino acid geranylgeranylation	4	0.0006	1	0.0021	1.0000000	E
<input type="checkbox"/>	GO:0048280	7,6	vesicle fusion with Golgi apparatus	1	0.0002	1	0.0021	1.0000000	E

<input type="checkbox"/>	GO:0006378	9	mRNA polyadenylation	18	0.0028	2	0.0043	1.0000000	E
<input type="checkbox"/>	GO:0043112	6	receptor metabolic process	5	0.0008	1	0.0021	1.0000000	E
<input type="checkbox"/>	GO:0031507	6,10	heterochromatin formation	95	0.0147	11	0.0235	1.0000000	E
<input type="checkbox"/>	GO:0009108	6	coenzyme biosynthetic process	66	0.0102	5	0.0107	1.0000000	E
<input type="checkbox"/>	GO:0042401	6,7	biogenic amine biosynthetic process	18	0.0028	3	0.0064	1.0000000	E
<input type="checkbox"/>	GO:0045117	5,6	azole transport	1	0.0002	1	0.0021	1.0000000	E
<input type="checkbox"/>	GO:0015936	7	coenzyme A metabolic process	7	0.0011	1	0.0021	1.0000000	E
<input type="checkbox"/>	GO:0006366	8,7	transcription from RNA polymerase II promoter	343	0.0530	37	0.0791	1.0000000	E
<input type="checkbox"/>	GO:0007096	8,10,9,7	regulation of exit from mitosis	24	0.0037	4	0.0085	1.0000000	E
<input type="checkbox"/>	GO:0009127	7,8	purine nucleoside monophosphate biosynthetic process	16	0.0025	2	0.0043	1.0000000	E
<input type="checkbox"/>	GO:0043161	10,9,11	proteasomal ubiquitin-dependent protein catabolic process	63	0.0097	6	0.0128	1.0000000	E
<input type="checkbox"/>	GO:0045814	5	negative regulation of gene expression, epigenetic	95	0.0147	11	0.0235	1.0000000	E
<input type="checkbox"/>	GO:0000767	6,7	cellular morphogenesis during conjugation	20	0.0031	2	0.0043	1.0000000	E
<input type="checkbox"/>	GO:0006528	7,8	asparagine metabolic process	9	0.0014	1	0.0021	1.0000000	E
<input type="checkbox"/>	GO:0043543	7	protein amino acid acylation	62	0.0096	9	0.0192	1.0000000	E
<input type="checkbox"/>	GO:0051090	8,7	regulation of transcription factor activity	1	0.0002	1	0.0021	1.0000000	E
<input type="checkbox"/>	GO:0042440	4	pigment metabolic process	20	0.0031	3	0.0064	1.0000000	E
<input type="checkbox"/>	GO:0000917	6,4	barrier septum formation	3	0.0005	1	0.0021	1.0000000	E
<input type="checkbox"/>	GO:0043285	5	biopolymer catabolic process	277	0.0428	23	0.0491	1.0000000	E
<input type="checkbox"/>	GO:0007124	6,4,8,9	pseudohyphal growth	61	0.0094	11	0.0235	1.0000000	E
<input type="checkbox"/>	GO:0006650	7,8	glycerophospholipid metabolic process	60	0.0093	8	0.0171	1.0000000	E
<input type="checkbox"/>	GO:0045896	9,7,5,8,6,4	regulation of transcription, mitotic	7	0.0011	1	0.0021	1.0000000	E
<input type="checkbox"/>	GO:0006613	10,9,8,7,6	cotranslational protein targeting to membrane	23	0.0036	6	0.0128	1.0000000	E
<input type="checkbox"/>	GO:0006553	7,8	lysine metabolic process	9	0.0014	1	0.0021	1.0000000	E
<input type="checkbox"/>	GO:0030026	10,8	cellular manganese ion homeostasis	5	0.0008	1	0.0021	1.0000000	E
<input type="checkbox"/>	GO:0048856	3	anatomical structure development	248	0.0383	28	0.0598	1.0000000	E
<input type="checkbox"/>	GO:0006986	4,5	response to unfolded protein	18	0.0028	2	0.0043	1.0000000	E
<input type="checkbox"/>	GO:0006396	6	RNA processing	491	0.0758	41	0.0876	1.0000000	E
<input type="checkbox"/>	GO:0007070	11,9,6,7,10,8,5	negative regulation of transcription from RNA polymerase II promoter, mitotic	6	0.0009	1	0.0021	1.0000000	E
<input type="checkbox"/>	GO:0006308	5,6	DNA catabolic process	20	0.0031	2	0.0043	1.0000000	E
<input type="checkbox"/>	GO:0043065	7,8,10,6	positive regulation of apoptosis	3	0.0005	1	0.0021	1.0000000	E
<input type="checkbox"/>	GO:0006797	6	polyphosphate metabolic process	5	0.0008	1	0.0021	1.0000000	E
<input type="checkbox"/>	GO:0010035	4	response to inorganic substance	24	0.0037	2	0.0043	1.0000000	E
<input type="checkbox"/>	GO:0016093	7,8	polyprenol metabolic process	3	0.0005	1	0.0021	1.0000000	E
<input type="checkbox"/>	GO:0006089	7	lactate metabolic process	5	0.0008	1	0.0021	1.0000000	E
<input type="checkbox"/>	GO:0032784	8,7,9	regulation of RNA elongation	3	0.0005	1	0.0021	1.0000000	E
<input type="checkbox"/>	GO:0051224	7,6,8	negative regulation of protein transport	3	0.0005	1	0.0021	1.0000000	E
<input type="checkbox"/>	GO:0019953	3	sexual reproduction	118	0.0182	15	0.0321	1.0000000	E
<input type="checkbox"/>	GO:0015937	7,8	coenzyme A biosynthetic process	7	0.0011	1	0.0021	1.0000000	E
<input type="checkbox"/>	GO:0006206	6	pyrimidine base metabolic process	17	0.0026	2	0.0043	1.0000000	E
<input type="checkbox"/>	GO:0006273	9,8	lagging strand elongation	18	0.0028	2	0.0043	1.0000000	E
<input type="checkbox"/>	GO:0051049	5,4	regulation of transport	11	0.0017	4	0.0085	1.0000000	E
<input type="checkbox"/>	GO:0045996	10,9,6	negative regulation of transcription by pheromones	6	0.0009	2	0.0043	1.0000000	E
<input type="checkbox"/>			negative regulation of cyclin dependent						

<input type="radio"/>	GO:0045736	8,9,7,6	negative regulation of cyclin-dependent protein kinase activity	1	0.0002	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0006643	5,6	membrane lipid metabolic process	125	0.0193	15	0.0321	1.0000000	E
<input type="radio"/>	GO:0016458	5	gene silencing	95	0.0147	11	0.0235	1.0000000	E
<input type="radio"/>	GO:0030384	8,9	phosphoinositide metabolic process	43	0.0066	7	0.0150	1.0000000	E
<input type="radio"/>	GO:0018279	10,9,8	protein amino acid N-linked glycosylation via asparagine	2	0.0003	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0006869	4,5	lipid transport	34	0.0053	5	0.0107	1.0000000	E
<input type="radio"/>	GO:0051276	5	chromosome organization and biogenesis	572	0.0883	59	0.1261	1.0000000	E
<input type="radio"/>	GO:0006047	8,6,9	UDP-N-acetylglucosamine metabolic process	2	0.0003	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0017196	11,9,10	N-terminal peptidyl-methionine acetylation	3	0.0005	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0009653	4,3	anatomical structure morphogenesis	248	0.0383	28	0.0598	1.0000000	E
<input type="radio"/>	GO:0008156	9,8	negative regulation of DNA replication	8	0.0012	2	0.0043	1.0000000	E
<input type="radio"/>	GO:0000086	8,5,6,7,4	G2/M transition of mitotic cell cycle	35	0.0054	8	0.0171	1.0000000	E
<input type="radio"/>	GO:0042990	9,8,11,12,10,7	regulation of transcription factor import into nucleus	2	0.0003	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0000117	10,9,6,5,7,8,4	G2/M-specific transcription in mitotic cell cycle	3	0.0005	2	0.0043	1.0000000	E
<input type="radio"/>	GO:0022401	7,6	adaptation of signaling pathway	15	0.0023	3	0.0064	1.0000000	E
<input type="radio"/>	GO:0007243	6	protein kinase cascade	23	0.0036	5	0.0107	1.0000000	E
<input type="radio"/>	GO:0051301	3	cell division	246	0.0380	24	0.0513	1.0000000	E
<input type="radio"/>	GO:0009895	6,5	negative regulation of catabolic process	2	0.0003	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0045859	7	regulation of protein kinase activity	25	0.0039	5	0.0107	1.0000000	E
<input type="radio"/>	GO:0000070	9,7,5,8,6,4	mitotic sister chromatid segregation	59	0.0091	8	0.0171	1.0000000	E
<input type="radio"/>	GO:0042306	8,7,10,11,9,6	regulation of protein import into nucleus	3	0.0005	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0043331	4	response to dsRNA	7	0.0011	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0006725	4	aromatic compound metabolic process	60	0.0093	7	0.0150	1.0000000	E
<input type="radio"/>	GO:0045910	9,8	negative regulation of DNA recombination	12	0.0019	2	0.0043	1.0000000	E
<input type="radio"/>	GO:0000910	4	cytokinesis	109	0.0168	17	0.0363	1.0000000	E
<input type="radio"/>	GO:0030466	11,7,8,12,10	chromatin silencing at silent mating-type cassette	30	0.0046	5	0.0107	1.0000000	E
<input type="radio"/>	GO:0000272	6	polysaccharide catabolic process	12	0.0019	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0008219	4,6	cell death	13	0.0020	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0007105	6,4	cytokinesis, site selection	66	0.0102	10	0.0214	1.0000000	E
<input type="radio"/>	GO:0009069	6,7	serine family amino acid metabolic process	24	0.0037	2	0.0043	1.0000000	E
<input type="radio"/>	GO:0012501	5,7	programmed cell death	13	0.0020	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0006997	5	nuclear organization and biogenesis	57	0.0088	6	0.0128	1.0000000	E
<input type="radio"/>	GO:0009847	5	spore germination	2	0.0003	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0006491	10,9,8	N-glycan processing	4	0.0006	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0000271	6,7	polysaccharide biosynthetic process	41	0.0063	3	0.0064	1.0000000	E
<input type="radio"/>	GO:0045041	10,9,8,7	protein import into mitochondrial intermembrane space	6	0.0009	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0043094	4	metabolic compound salvage	19	0.0029	2	0.0043	1.0000000	E
<input type="radio"/>	GO:0006469	7,8	negative regulation of protein kinase activity	7	0.0011	2	0.0043	1.0000000	E
<input type="radio"/>	GO:0019321	6,7	pentose metabolic process	11	0.0017	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0007109	7,6,5,4	cytokinesis, completion of separation	11	0.0017	3	0.0064	1.0000000	E
<input type="radio"/>	GO:0043001	10,8,7,9	Golgi to plasma membrane protein transport	5	0.0008	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0006345	10,6,9	loss of chromatin silencing	9	0.0014	2	0.0043	1.0000000	E
<input type="radio"/>	GO:0006038	9,10,7,8,11	cell wall chitin biosynthetic process	13	0.0020	2	0.0043	1.0000000	E

<input type="radio"/>	GO:0006450	8,7,6	regulation of translational fidelity	13	0.0020	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0051789	4	response to protein stimulus	18	0.0028	2	0.0043	1.0000000	E
<input type="radio"/>	GO:0006551	7,8	leucine metabolic process	7	0.0011	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0006518	4	peptide metabolic process	11	0.0017	4	0.0085	1.0000000	E
<input type="radio"/>	GO:0009051	10,7,11,12,8	pentose-phosphate shunt, oxidative branch	5	0.0008	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0006400	7,8	tRNA modification	52	0.0080	8	0.0171	1.0000000	E
<input type="radio"/>	GO:0008361	4,6,7	regulation of cell size	129	0.0199	16	0.0342	1.0000000	E
<input type="radio"/>	GO:0000501	4	flocculation via cell wall protein-carbohydrate interaction	9	0.0014	2	0.0043	1.0000000	E
<input type="radio"/>	GO:0000032	8,6,9,7	cell wall mannoprotein biosynthetic process	12	0.0019	3	0.0064	1.0000000	E
<input type="radio"/>	GO:0043067	5,6,8,4	regulation of programmed cell death	4	0.0006	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0007067	8,6,7,5	mitosis	127	0.0196	18	0.0385	1.0000000	E
<input type="radio"/>	GO:0044260	4	cellular macromolecule metabolic process	1552	0.2397	126	0.2692	1.0000000	E
<input type="radio"/>	GO:0000411	11,9,10,7	positive regulation of transcription by galactose	5	0.0008	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0006525	7,8,5,4	arginine metabolic process	15	0.0023	2	0.0043	1.0000000	E
<input type="radio"/>	GO:0001306	4,5	age-dependent response to oxidative stress	6	0.0009	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0046019	10,9,6	regulation of transcription from RNA polymerase II promoter by pheromones	10	0.0015	3	0.0064	1.0000000	E
<input type="radio"/>	GO:0007008	6,7	outer mitochondrial membrane organization and biogenesis	7	0.0011	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0051668	5,4	localization within membrane	3	0.0005	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0022411	4	cellular component disassembly	36	0.0056	3	0.0064	1.0000000	E
<input type="radio"/>	GO:0051321	4	meiotic cell cycle	148	0.0229	13	0.0278	1.0000000	E
<input type="radio"/>	GO:0015674	6,7	di-, tri-valent inorganic cation transport	34	0.0053	5	0.0107	1.0000000	E
<input type="radio"/>	GO:0042177	7,8,6	negative regulation of protein catabolic process	2	0.0003	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0016562	6,11,10,8,9,7	protein import into peroxisome matrix, receptor recycling	5	0.0008	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0006280	6	mutagenesis	9	0.0014	2	0.0043	1.0000000	E
<input type="radio"/>	GO:0000161	7,8,6	MAPKKK cascade during osmolarity sensing	11	0.0017	2	0.0043	1.0000000	E
<input type="radio"/>	GO:0007266	8	Rho protein signal transduction	17	0.0026	2	0.0043	1.0000000	E
<input type="radio"/>	GO:0031935	11,7,4,8,12,10	regulation of chromatin silencing	6	0.0009	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0000746	3	conjugation	118	0.0182	15	0.0321	1.0000000	E
<input type="radio"/>	GO:0046128	7	purine ribonucleoside metabolic process	11	0.0017	2	0.0043	1.0000000	E
<input type="radio"/>	GO:0065003	5,4	macromolecular complex assembly	328	0.0506	26	0.0556	1.0000000	E
<input type="radio"/>	GO:0000921	8,7	septin ring assembly	9	0.0014	2	0.0043	1.0000000	E
<input type="radio"/>	GO:0031204	9,11,10,7,8	posttranslational protein targeting to membrane, translocation	4	0.0006	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0008215	7,8	spermine metabolic process	2	0.0003	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0007234	7,6	osmosensory signaling pathway via two-component system	3	0.0005	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0006281	6,5	DNA repair	193	0.0298	21	0.0449	1.0000000	E
<input type="radio"/>	GO:0006635	7,9,8	fatty acid beta-oxidation	9	0.0014	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0006082	4	organic acid metabolic process	314	0.0485	23	0.0491	1.0000000	E
<input type="radio"/>	GO:0009068	7,8	aspartate family amino acid catabolic process	10	0.0015	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0045935	7,6	positive regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	108	0.0167	10	0.0214	1.0000000	E
<input type="radio"/>	GO:0031938	12,8,5,9,13,11	regulation of chromatin silencing at telomere	6	0.0009	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0009719	3	response to endogenous stimulus	243	0.0375	22	0.0470	1.0000000	E

<input type="radio"/>	GO:0043687	7	post-translational protein modification	388	0.0599	38	0.0812	1.0000000	E
<input type="radio"/>	GO:0046519	7,8	sphingoid metabolic process	10	0.0015	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0051274	8,9	beta-glucan biosynthetic process	11	0.0017	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0006808	6,5	regulation of nitrogen utilization	8	0.0012	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0031325	6,5	positive regulation of cellular metabolic process	116	0.0179	10	0.0214	1.0000000	E
<input type="radio"/>	GO:0018201	8	peptidyl-glycine modification	1	0.0002	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0007131	10,8,7,5,9,6,4	meiotic recombination	55	0.0085	6	0.0128	1.0000000	E
<input type="radio"/>	GO:0065002	8,6,7	intracellular protein transport across a membrane	11	0.0017	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0050657	5,6	nucleic acid transport	80	0.0124	11	0.0235	1.0000000	E
<input type="radio"/>	GO:0000162	9,8,7,10	tryptophan biosynthetic process	10	0.0015	2	0.0043	1.0000000	E
<input type="radio"/>	GO:0032786	9,8,10	positive regulation of RNA elongation	3	0.0005	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0042434	6	indole derivative metabolic process	10	0.0015	2	0.0043	1.0000000	E
<input type="radio"/>	GO:0043174	5	nucleoside salvage	6	0.0009	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0006560	7,8	proline metabolic process	7	0.0011	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0043144	7	snoRNA processing	8	0.0012	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0009072	6,5,7	aromatic amino acid family metabolic process	21	0.0032	5	0.0107	1.0000000	E
<input type="radio"/>	GO:0051171	5,4	regulation of nitrogen metabolic process	8	0.0012	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0010382	6,4	cell wall metabolic process	26	0.0040	5	0.0107	1.0000000	E
<input type="radio"/>	GO:0000754	8,7,5	adaptation to pheromone during conjugation with cellular fusion	15	0.0023	3	0.0064	1.0000000	E
<input type="radio"/>	GO:0032979	8,7,6	protein insertion into mitochondrial membrane from inner side	1	0.0002	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0007265	7	Ras protein signal transduction	39	0.0060	3	0.0064	1.0000000	E
<input type="radio"/>	GO:0000289	11,9,10	poly(A) tail shortening	7	0.0011	2	0.0043	1.0000000	E
<input type="radio"/>	GO:0000273	6,5	lipic acid metabolic process	1	0.0002	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0009058	3	biosynthetic process	1249	0.1929	109	0.2329	1.0000000	E
<input type="radio"/>	GO:0006576	5,6	biogenic amine metabolic process	24	0.0037	3	0.0064	1.0000000	E
<input type="radio"/>	GO:0046942	5,6	carboxylic acid transport	54	0.0083	6	0.0128	1.0000000	E
<input type="radio"/>	GO:0032368	6,5	regulation of lipid transport	1	0.0002	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0009082	7,8	branched chain family amino acid biosynthetic process	13	0.0020	3	0.0064	1.0000000	E
<input type="radio"/>	GO:0006817	7,8	phosphate transport	10	0.0015	2	0.0043	1.0000000	E
<input type="radio"/>	GO:0015931	4,5	nucleobase, nucleoside, nucleotide and nucleic acid transport	90	0.0139	15	0.0321	1.0000000	E
<input type="radio"/>	GO:0006283	8,7	transcription-coupled nucleotide-excision repair	9	0.0014	2	0.0043	1.0000000	E
<input type="radio"/>	GO:0000747	4	conjugation with cellular fusion	118	0.0182	15	0.0321	1.0000000	E
<input type="radio"/>	GO:0030433	9,11,10,12	ER-associated protein catabolic process	35	0.0054	5	0.0107	1.0000000	E
<input type="radio"/>	GO:0042726	6	riboflavin and derivative metabolic process	8	0.0012	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0006488	10,9,8	dolichol-linked oligosaccharide biosynthetic process	11	0.0017	3	0.0064	1.0000000	E
<input type="radio"/>	GO:0046483	4	heterocycle metabolic process	76	0.0117	8	0.0171	1.0000000	E
<input type="radio"/>	GO:0000168	10,11,8,9,7	activation of MAPKK activity during osmolarity sensing	2	0.0003	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0006793	4	phosphorus metabolic process	212	0.0327	25	0.0534	1.0000000	E
<input type="radio"/>	GO:0030001	6,7	metal ion transport	62	0.0096	7	0.0150	1.0000000	E
<input type="radio"/>	GO:0018318	10,9,8	protein amino acid palmitoylation	8	0.0012	2	0.0043	1.0000000	E
<input type="radio"/>	GO:0051030	5,7,6,8	snRNA transport	23	0.0036	4	0.0085	1.0000000	E
<input type="radio"/>	GO:0046489	9,8,10	phosphoinositide biosynthetic process	28	0.0043	5	0.0107	1.0000000	E

<input type="radio"/>	GO:0007020	8	microtubule nucleation	23	0.0036	5	0.0107	1.0000000	E
<input type="radio"/>	GO:0030007	10,8	cellular potassium ion homeostasis	5	0.0008	2	0.0043	1.0000000	E
<input type="radio"/>	GO:0033157	7,8,6	regulation of intracellular protein transport	3	0.0005	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0009070	7,8	serine family amino acid biosynthetic process	12	0.0019	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0007064	10,8,5,6,9,7,4	mitotic sister chromatid cohesion	22	0.0034	6	0.0128	1.0000000	E
<input type="radio"/>	GO:0006037	8,9,6,7,10	cell wall chitin metabolic process	14	0.0022	2	0.0043	1.0000000	E
<input type="radio"/>	GO:0009607	3	response to biotic stimulus	25	0.0039	3	0.0064	1.0000000	E
<input type="radio"/>	GO:0006407	11,9,6,8,10,7	rRNA export from nucleus	26	0.0040	4	0.0085	1.0000000	E
<input type="radio"/>	GO:0030148	7,6,8	sphingolipid biosynthetic process	20	0.0031	3	0.0064	1.0000000	E
<input type="radio"/>	GO:0006166	6,8	purine ribonucleoside salvage	6	0.0009	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0006289	7,6	nucleotide-excision repair	44	0.0068	6	0.0128	1.0000000	E
<input type="radio"/>	GO:0000078	9,11,10,8,6,7	cell morphogenesis checkpoint	2	0.0003	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0043488	9,8,7	regulation of mRNA stability	30	0.0046	3	0.0064	1.0000000	E
<input type="radio"/>	GO:0040007	2	growth	141	0.0218	20	0.0427	1.0000000	E
<input type="radio"/>	GO:0018346	10,9,8	protein amino acid prenylation	5	0.0008	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0031578	9,11,10,8	mitotic cell cycle spindle orientation checkpoint	4	0.0006	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0006862	5,6	nucleotide transport	5	0.0008	3	0.0064	1.0000000	E
<input type="radio"/>	GO:0032200	7	telomere organization and biogenesis	274	0.0423	27	0.0577	1.0000000	E
<input type="radio"/>	GO:0046467	6,5,7	membrane lipid biosynthetic process	78	0.0120	11	0.0235	1.0000000	E
<input type="radio"/>	GO:0032978	7,6,5	protein insertion into membrane from inner side	1	0.0002	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0015696	7,8	ammonium transport	6	0.0009	2	0.0043	1.0000000	E
<input type="radio"/>	GO:0009373	9,8,5	regulation of transcription by pheromones	10	0.0015	3	0.0064	1.0000000	E
<input type="radio"/>	GO:0032774	6	RNA biosynthetic process	524	0.0809	54	0.1154	1.0000000	E
<input type="radio"/>	GO:0000160	5	two-component signal transduction system (phosphorelay)	3	0.0005	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0045488	6,7	pectin metabolic process	1	0.0002	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0016049	5,3,7,8	cell growth	102	0.0158	15	0.0321	1.0000000	E
<input type="radio"/>	GO:0032989	4,5	cellular structure morphogenesis	248	0.0383	28	0.0598	1.0000000	E
<input type="radio"/>	GO:0051347	6	positive regulation of transferase activity	6	0.0009	2	0.0043	1.0000000	E
<input type="radio"/>	GO:0055071	9	manganese ion homeostasis	5	0.0008	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0006772	7	thiamin metabolic process	20	0.0031	3	0.0064	1.0000000	E
<input type="radio"/>	GO:0006077	8,9	1,6-beta-glucan metabolic process	8	0.0012	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0017182	9	peptidyl-diphthamide metabolic process	5	0.0008	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0007135	9,7,6,8,5	meiosis II	4	0.0006	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0030468	8,5,9	establishment of cell polarity (sensu Fungi)	66	0.0102	10	0.0214	1.0000000	E
<input type="radio"/>	GO:0006301	7,6	postreplication repair	13	0.0020	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0042157	6	lipoprotein metabolic process	48	0.0074	10	0.0214	1.0000000	E
<input type="radio"/>	GO:0042221	3	response to chemical stimulus	382	0.0590	36	0.0769	1.0000000	E
<input type="radio"/>	GO:0030150	10,9,8,7	protein import into mitochondrial matrix	22	0.0034	6	0.0128	1.0000000	E
<input type="radio"/>	GO:0006352	7,8,6	transcription initiation	55	0.0085	4	0.0085	1.0000000	E
<input type="radio"/>	GO:0043623	7,6	cellular protein complex assembly	69	0.0107	8	0.0171	1.0000000	E
<input type="radio"/>	GO:0001323	4,5,6	age-dependent general metabolic decline during chronological cell aging	6	0.0009	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0006515	8,9	misfolded or incompletely synthesized protein catabolic process	38	0.0059	5	0.0107	1.0000000	E
<input type="radio"/>	GO:0051273	7,8	beta-glucan metabolic process	12	0.0019	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0006620	10,9,8,7,6	posttranslational protein targeting to	8	0.0012	1	0.0021	1.0000000	E

<input type="radio"/>	GO:0000020	10,9,0,1,0	membrane	0	0.0012	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0019752	5	carboxylic acid metabolic process	314	0.0485	23	0.0491	1.0000000	E
<input type="radio"/>	GO:0042816	6	vitamin B6 metabolic process	8	0.0012	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0000770	5,6	peptide pheromone export	1	0.0002	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0042546	6	cell wall biogenesis	33	0.0051	4	0.0085	1.0000000	E
<input type="radio"/>	GO:0006760	5,7	folic acid and derivative metabolic process	9	0.0014	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0019878	9,10	lysine biosynthetic process via aminoadipic acid	8	0.0012	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0032185	6	septin cytoskeleton organization and biogenesis	9	0.0014	2	0.0043	1.0000000	E
<input type="radio"/>	GO:0000753	7,8,6	cellular morphogenesis during conjugation with cellular fusion	18	0.0028	2	0.0043	1.0000000	E
<input type="radio"/>	GO:0019408	9,8,10	dolichol biosynthetic process	1	0.0002	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0045941	8,7	positive regulation of transcription	101	0.0156	8	0.0171	1.0000000	E
<input type="radio"/>	GO:0015939	7	pantothenate metabolic process	8	0.0012	2	0.0043	1.0000000	E
<input type="radio"/>	GO:0016192	4,5	vesicle-mediated transport	328	0.0506	32	0.0684	1.0000000	E
<input type="radio"/>	GO:0000266	6	mitochondrial fission	5	0.0008	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0051320	7,6,5	S phase	20	0.0031	4	0.0085	1.0000000	E
<input type="radio"/>	GO:0009628	3	response to abiotic stimulus	117	0.0181	12	0.0256	1.0000000	E
<input type="radio"/>	GO:0051186	4	cofactor metabolic process	170	0.0263	14	0.0299	1.0000000	E
<input type="radio"/>	GO:0006855	5,6	multidrug transport	8	0.0012	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0006890	8,6,5,7	retrograde vesicle-mediated transport, Golgi to ER	24	0.0037	2	0.0043	1.0000000	E
<input type="radio"/>	GO:0018008	11,12,9,10	N-terminal peptidyl-glycine N-myristoylation	1	0.0002	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0009308	4	amine metabolic process	228	0.0352	22	0.0470	1.0000000	E
<input type="radio"/>	GO:0006610	10,11,8,9,7	ribosomal protein import into nucleus	23	0.0036	4	0.0085	1.0000000	E
<input type="radio"/>	GO:0015893	4,5	drug transport	13	0.0020	3	0.0064	1.0000000	E
<input type="radio"/>	GO:0031137	6,5	regulation of conjugation with cellular fusion	30	0.0046	5	0.0107	1.0000000	E
<input type="radio"/>	GO:0006044	7,8	N-acetylglucosamine metabolic process	19	0.0029	3	0.0064	1.0000000	E
<input type="radio"/>	GO:0007103	6,7,5,8	spindle pole body duplication in nuclear envelope	13	0.0020	3	0.0064	1.0000000	E
<input type="radio"/>	GO:0032506	5,3	cytokinetic process	88	0.0136	14	0.0299	1.0000000	E
<input type="radio"/>	GO:0016070	5	RNA metabolic process	1058	0.1634	91	0.1944	1.0000000	E
<input type="radio"/>	GO:0006066	4	alcohol metabolic process	163	0.0252	16	0.0342	1.0000000	E
<input type="radio"/>	GO:0006796	5	phosphate metabolic process	212	0.0327	25	0.0534	1.0000000	E
<input type="radio"/>	GO:0045490	8,7	pectin catabolic process	1	0.0002	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0043648	6	dicarboxylic acid metabolic process	9	0.0014	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0042375	5	quinone cofactor metabolic process	9	0.0014	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0055065	8	metal ion homeostasis	19	0.0029	2	0.0043	1.0000000	E
<input type="radio"/>	GO:0000114	10,8,9,5,7,4	G1-specific transcription in mitotic cell cycle	15	0.0023	3	0.0064	1.0000000	E
<input type="radio"/>	GO:0008299	6,5,7	isoprenoid biosynthetic process	6	0.0009	2	0.0043	1.0000000	E
<input type="radio"/>	GO:0065004	6,5	protein-DNA complex assembly	74	0.0114	8	0.0171	1.0000000	E
<input type="radio"/>	GO:0009112	5	nucleobase metabolic process	31	0.0048	3	0.0064	1.0000000	E
<input type="radio"/>	GO:0048285	5	organelle fission	6	0.0009	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0006778	5,6	porphyrin metabolic process	14	0.0022	2	0.0043	1.0000000	E
<input type="radio"/>	GO:0031324	6,5	negative regulation of cellular metabolic process	198	0.0306	24	0.0513	1.0000000	E
<input type="radio"/>	GO:0015918	5,6	sterol transport	15	0.0023	2	0.0043	1.0000000	E
<input type="radio"/>	GO:0040023	6,7,4,5	establishment of nucleus localization	20	0.0031	2	0.0043	1.0000000	E

<input type="radio"/>	GO:0065009	3	regulation of a molecular function	46	0.0071	5	0.0107	1.0000000	E
<input type="radio"/>	GO:0006658	8,9	phosphatidylserine metabolic process	3	0.0005	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0030488	8,9	tRNA methylation	15	0.0023	2	0.0043	1.0000000	E
<input type="radio"/>	GO:0055066	8	di-, tri-valent inorganic cation homeostasis	64	0.0099	5	0.0107	1.0000000	E
<input type="radio"/>	GO:0007232	7,6	osmosensory signaling pathway via Sho1 osmosensor	5	0.0008	2	0.0043	1.0000000	E
<input type="radio"/>	GO:0019348	8,9	dolichol metabolic process	1	0.0002	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0008614	7	pyridoxine metabolic process	8	0.0012	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0006611	9,10,7,8	protein export from nucleus	56	0.0086	6	0.0128	1.0000000	E
<input type="radio"/>	GO:0051338	5	regulation of transferase activity	26	0.0040	5	0.0107	1.0000000	E
<input type="radio"/>	GO:0006974	4	response to DNA damage stimulus	234	0.0361	22	0.0470	1.0000000	E
<input type="radio"/>	GO:0051302	5,4	regulation of cell division	3	0.0005	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0018345	9,8,7	protein palmitoylation	8	0.0012	2	0.0043	1.0000000	E
<input type="radio"/>	GO:0048193	7,5,6	Golgi vesicle transport	166	0.0256	22	0.0470	1.0000000	E
<input type="radio"/>	GO:0010032	7	meiotic chromosome condensation	2	0.0003	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0000335	10,9,6	negative regulation of DNA transposition	8	0.0012	2	0.0043	1.0000000	E
<input type="radio"/>	GO:0022607	4	cellular component assembly	471	0.0727	38	0.0812	1.0000000	E
<input type="radio"/>	GO:0042723	6	thiamin and derivative metabolic process	22	0.0034	3	0.0064	1.0000000	E
<input type="radio"/>	GO:0051318	6,7,5	G1 phase	27	0.0042	6	0.0128	1.0000000	E
<input type="radio"/>	GO:0033261	7,8,6	regulation of progression through S phase	5	0.0008	3	0.0064	1.0000000	E
<input type="radio"/>	GO:0006779	6,7	porphyrin biosynthetic process	13	0.0020	2	0.0043	1.0000000	E
<input type="radio"/>	GO:0031497	5,9	chromatin assembly	104	0.0161	15	0.0321	1.0000000	E
<input type="radio"/>	GO:0006282	8,7,6	regulation of DNA repair	2	0.0003	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0045860	7,8	positive regulation of protein kinase activity	6	0.0009	2	0.0043	1.0000000	E
<input type="radio"/>	GO:0006519	4	amino acid and derivative metabolic process	202	0.0312	17	0.0363	1.0000000	E
<input type="radio"/>	GO:0000051	4,3	urea cycle intermediate metabolic process	15	0.0023	2	0.0043	1.0000000	E
<input type="radio"/>	GO:0019722	7	calcium-mediated signaling	7	0.0011	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0031163	5	metallo-sulfur cluster assembly	11	0.0017	2	0.0043	1.0000000	E
<input type="radio"/>	GO:0015720	6,7	allantoin transport	1	0.0002	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0006534	7,8,6	cysteine metabolic process	4	0.0006	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0006415	8,7,6	translational termination	7	0.0011	2	0.0043	1.0000000	E
<input type="radio"/>	GO:0006999	6	nuclear pore organization and biogenesis	29	0.0045	4	0.0085	1.0000000	E
<input type="radio"/>	GO:0006040	5,6	amino sugar metabolic process	19	0.0029	3	0.0064	1.0000000	E
<input type="radio"/>	GO:0016078	7	tRNA catabolic process	5	0.0008	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0006575	5	amino acid derivative metabolic process	31	0.0048	3	0.0064	1.0000000	E
<input type="radio"/>	GO:0000723	8	telomere maintenance	274	0.0423	27	0.0577	1.0000000	E
<input type="radio"/>	GO:0006720	5,6	isoprenoid metabolic process	6	0.0009	2	0.0043	1.0000000	E
<input type="radio"/>	GO:0050896	2	response to stimulus	763	0.1178	68	0.1453	1.0000000	E
<input type="radio"/>	GO:0006474	10,9	N-terminal protein amino acid acetylation	9	0.0014	2	0.0043	1.0000000	E
<input type="radio"/>	GO:0045144	10,8,7,5,9,6,4	meiotic sister chromatid segregation	4	0.0006	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0006891	8,6,5,7	intra-Golgi vesicle-mediated transport	21	0.0032	6	0.0128	1.0000000	E
<input type="radio"/>	GO:0045229	4	external encapsulating structure organization and biogenesis	200	0.0309	23	0.0491	1.0000000	E
<input type="radio"/>	GO:0009119	6	ribonucleoside metabolic process	13	0.0020	2	0.0043	1.0000000	E
<input type="radio"/>	GO:0019538	4	protein metabolic process	1547	0.2389	125	0.2671	1.0000000	E
<input type="radio"/>	GO:0030491	7,9,10,6,8	heteroduplex formation	9	0.0014	1	0.0021	1.0000000	E

<input type="radio"/>	GO:0045815	5	positive regulation of gene expression, epigenetic	9	0.0014	2	0.0043	1.0000000	E
<input type="radio"/>	GO:0007005	5	mitochondrion organization and biogenesis	110	0.0170	13	0.0278	1.0000000	E
<input type="radio"/>	GO:0006570	7,6,8	tyrosine metabolic process	1	0.0002	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0007166	5	cell surface receptor linked signal transduction	52	0.0080	9	0.0192	1.0000000	E
<input type="radio"/>	GO:0051223	6,5,7	regulation of protein transport	4	0.0006	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0006839	7,5,6	mitochondrial transport	65	0.0100	10	0.0214	1.0000000	E
<input type="radio"/>	GO:0007568	3	aging	49	0.0076	4	0.0085	1.0000000	E
<input type="radio"/>	GO:0009225	5	nucleotide-sugar metabolic process	7	0.0011	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0000184	8	mRNA catabolic process, nonsense-mediated decay	9	0.0014	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0030968	7,5,6	unfolded protein response	9	0.0014	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0006857	5,6	oligopeptide transport	3	0.0005	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0051327	7,5,6	M phase of meiotic cell cycle	148	0.0229	13	0.0278	1.0000000	E
<input type="radio"/>	GO:0000186	9,10,8	activation of MAPKK activity	3	0.0005	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0007120	8,6,10,7,11,5	axial cellular bud site selection	22	0.0034	5	0.0107	1.0000000	E
<input type="radio"/>	GO:0009110	5	vitamin biosynthetic process	46	0.0071	4	0.0085	1.0000000	E
<input type="radio"/>	GO:0006271	8,7	DNA strand elongation during DNA replication	32	0.0049	4	0.0085	1.0000000	E
<input type="radio"/>	GO:0001301	9,5	progressive alteration of chromatin during cell aging	10	0.0015	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0007163	6,3,7	establishment and/or maintenance of cell polarity	115	0.0178	14	0.0299	1.0000000	E
<input type="radio"/>	GO:0000370	8,9,7,10,11,12,13	U2-type nuclear mRNA branch site recognition	3	0.0005	2	0.0043	1.0000000	E
<input type="radio"/>	GO:0051225	5,9	spindle assembly	3	0.0005	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0045332	5,7,6,8	phospholipid translocation	7	0.0011	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0009092	7,8	homoserine metabolic process	7	0.0011	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0007264	6	small GTPase mediated signal transduction	61	0.0094	5	0.0107	1.0000000	E
<input type="radio"/>	GO:0051704	2	multi-organism process	139	0.0215	18	0.0385	1.0000000	E
<input type="radio"/>	GO:0000902	5,6	cell morphogenesis	248	0.0383	28	0.0598	1.0000000	E
<input type="radio"/>	GO:0031055	10	chromatin remodeling at centromere	2	0.0003	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0030970	8,6,7	retrograde protein transport, ER to cytosol	1	0.0002	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0000083	10,9,6,5,7,8,4	G1/S-specific transcription in mitotic cell cycle	12	0.0019	3	0.0064	1.0000000	E
<input type="radio"/>	GO:0000398	8,10	nuclear mRNA splicing, via spliceosome	102	0.0158	9	0.0192	1.0000000	E
<input type="radio"/>	GO:0009892	5,4	negative regulation of metabolic process	208	0.0321	25	0.0534	1.0000000	E
<input type="radio"/>	GO:0007126	8,6,7,5	meiosis	148	0.0229	13	0.0278	1.0000000	E
<input type="radio"/>	GO:0046822	6,9,5,7,8	regulation of nucleocytoplasmic transport	3	0.0005	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0000084	8,7,6	S phase of mitotic cell cycle	18	0.0028	3	0.0064	1.0000000	E
<input type="radio"/>	GO:0042158	7,5	lipoprotein biosynthetic process	48	0.0074	10	0.0214	1.0000000	E
<input type="radio"/>	GO:0006490	5,11,10,9,7,6	oligosaccharide-lipid intermediate assembly	6	0.0009	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0006875	9,7	cellular metal ion homeostasis	19	0.0029	2	0.0043	1.0000000	E
<input type="radio"/>	GO:0051204	7,6,5	protein insertion into mitochondrial membrane	3	0.0005	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0030010	7,4,8	establishment of cell polarity	103	0.0159	12	0.0256	1.0000000	E
<input type="radio"/>	GO:0000279	6,5	M phase	258	0.0398	31	0.0662	1.0000000	E
<input type="radio"/>	GO:0016255	11,10,8,9,12	attachment of GPI anchor to protein	5	0.0008	2	0.0043	1.0000000	E
<input type="radio"/>	GO:0048522	5,4	positive regulation of cellular process	124	0.0191	13	0.0278	1.0000000	E
<input type="radio"/>	GO:0006526	8,9,6,5	arginine biosynthetic process	10	0.0015	2	0.0043	1.0000000	E
<input type="radio"/>	GO:0044271	5,4	nitrogen compound biosynthetic process	115	0.0178	15	0.0321	1.0000000	E

<input type="radio"/>	GO:0006970	4	response to osmotic stress	89	0.0137	10	0.0214	1.0000000	E
<input type="radio"/>	GO:0042168	6,7,5	heme metabolic process	14	0.0022	2	0.0043	1.0000000	E
<input type="radio"/>	GO:0043007	7	maintenance of rDNA	1	0.0002	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0051028	5,7,6,8	mRNA transport	66	0.0102	10	0.0214	1.0000000	E
<input type="radio"/>	GO:0006979	4	response to oxidative stress	71	0.0110	6	0.0128	1.0000000	E
<input type="radio"/>	GO:0006561	8,9	proline biosynthetic process	3	0.0005	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0006972	5	hyperosmotic response	11	0.0017	3	0.0064	1.0000000	E
<input type="radio"/>	GO:0006621	7,6,5,4	protein retention in ER	7	0.0011	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0032502	2	developmental process	436	0.0673	38	0.0812	1.0000000	E
<input type="radio"/>	GO:0015693	7,8	magnesium ion transport	5	0.0008	2	0.0043	1.0000000	E
<input type="radio"/>	GO:0001408	7,8	guanine nucleotide transport	1	0.0002	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0009081	6,7	branched chain family amino acid metabolic process	16	0.0025	3	0.0064	1.0000000	E
<input type="radio"/>	GO:0040031	7	snRNA modification	7	0.0011	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0006655	9,8,10	phosphatidylglycerol biosynthetic process	1	0.0002	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0032005	7,6	signal transduction during conjugation with cellular fusion	28	0.0043	5	0.0107	1.0000000	E
<input type="radio"/>	GO:0016973	12,10,7,9,11,8	poly(A)+ mRNA export from nucleus	8	0.0012	2	0.0043	1.0000000	E
<input type="radio"/>	GO:0009893	5,4	positive regulation of metabolic process	116	0.0179	10	0.0214	1.0000000	E
<input type="radio"/>	GO:0016054	5	organic acid catabolic process	6	0.0009	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0051252	7,6	regulation of RNA metabolic process	36	0.0056	4	0.0085	1.0000000	E
<input type="radio"/>	GO:0033262	8,9,7	regulation of DNA replication during S phase	2	0.0003	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0000080	7,8,6	G1 phase of mitotic cell cycle	27	0.0042	6	0.0128	1.0000000	E
<input type="radio"/>	GO:0007007	6,7	inner mitochondrial membrane organization and biogenesis	12	0.0019	2	0.0043	1.0000000	E
<input type="radio"/>	GO:0051170	9,7,8	nuclear import	50	0.0077	9	0.0192	1.0000000	E
<input type="radio"/>	GO:0006644	6,7	phospholipid metabolic process	97	0.0150	11	0.0235	1.0000000	E
<input type="radio"/>	GO:0045040	10,9,7,8	protein import into mitochondrial outer membrane	6	0.0009	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0007571	3,4	age-dependent general metabolic decline	7	0.0011	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0006498	9,10,8,7	N-terminal protein lipidation	5	0.0008	2	0.0043	1.0000000	E
<input type="radio"/>	GO:0000226	7	microtubule cytoskeleton organization and biogenesis	81	0.0125	6	0.0128	1.0000000	E
<input type="radio"/>	GO:0046700	5	heterocycle catabolic process	7	0.0011	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0001403	6,4,8,9	invasive growth (sensu Saccharomyces)	42	0.0065	6	0.0128	1.0000000	E
<input type="radio"/>	GO:0006401	6	RNA catabolic process	74	0.0114	11	0.0235	1.0000000	E
<input type="radio"/>	GO:0007097	7,8,5,6	nuclear migration	20	0.0031	2	0.0043	1.0000000	E
<input type="radio"/>	GO:0043068	6,7,9,5	positive regulation of programmed cell death	3	0.0005	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0045787	6,7,5	positive regulation of progression through cell cycle	3	0.0005	2	0.0043	1.0000000	E
<input type="radio"/>	GO:0006367	8,9,7	transcription initiation from RNA polymerase II promoter	44	0.0068	4	0.0085	1.0000000	E
<input type="radio"/>	GO:0007127	9,7,6,8,5	meiosis I	75	0.0116	7	0.0150	1.0000000	E
<input type="radio"/>	GO:0006984	6	ER-nuclear signaling pathway	9	0.0014	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0006325	7	establishment and/or maintenance of chromatin architecture	253	0.0391	25	0.0534	1.0000000	E
<input type="radio"/>	GO:0019795	7,8	nonprotein amino acid biosynthetic process	6	0.0009	2	0.0043	1.0000000	E
<input type="radio"/>	GO:0000288	10,8,9	mRNA catabolic process, deadenylation-dependent decay	24	0.0037	3	0.0064	1.0000000	E
<input type="radio"/>	GO:0040020	7,9,8,6	regulation of meiosis	22	0.0034	2	0.0043	1.0000000	E
<input type="radio"/>	GO:0006403	4	RNA localization	90	0.0139	11	0.0235	1.0000000	E

<input type="checkbox"/>	GO:0006351	7,6	transcription, DNA-dependent	522	0.0806	54	0.1154	1.0000000	E
<input type="checkbox"/>	GO:0015888	5,6	thiamin transport	3	0.0005	1	0.0021	1.0000000	E
<input type="checkbox"/>	GO:0032386	6,7,5	regulation of intracellular transport	3	0.0005	1	0.0021	1.0000000	E
<input type="checkbox"/>	GO:0006468	8,7	protein amino acid phosphorylation	101	0.0156	15	0.0321	1.0000000	E
<input type="checkbox"/>	GO:0007154	3	cell communication	240	0.0371	25	0.0534	1.0000000	E
<input type="checkbox"/>	GO:0051188	5	cofactor biosynthetic process	79	0.0122	7	0.0150	1.0000000	E
<input type="checkbox"/>	GO:0006311	10,8,7,5,9,6,4	meiotic gene conversion	22	0.0034	2	0.0043	1.0000000	E
<input type="checkbox"/>	GO:0048518	4	positive regulation of biological process	124	0.0191	13	0.0278	1.0000000	E
<input type="checkbox"/>	GO:0046471	8,9	phosphatidylglycerol metabolic process	1	0.0002	1	0.0021	1.0000000	E
<input type="checkbox"/>	GO:0051300	5,4,6	spindle pole body organization and biogenesis	16	0.0025	4	0.0085	1.0000000	E
<input type="checkbox"/>	GO:0030447	3	filamentous growth	94	0.0145	15	0.0321	1.0000000	E
<input type="checkbox"/>	GO:0045005	8,6	maintenance of fidelity during DNA-dependent DNA replication	25	0.0039	5	0.0107	1.0000000	E
<input type="checkbox"/>	GO:0016091	7,6,8	prenol biosynthetic process	3	0.0005	1	0.0021	1.0000000	E
<input type="checkbox"/>	GO:0042278	6	purine nucleoside metabolic process	12	0.0019	3	0.0064	1.0000000	E
<input type="checkbox"/>	GO:0043408	6,8,5	regulation of MAPKKK cascade	3	0.0005	1	0.0021	1.0000000	E
<input type="checkbox"/>	GO:0042493	4	response to drug	121	0.0187	10	0.0214	1.0000000	E
<input type="checkbox"/>	GO:0007165	4	signal transduction	209	0.0323	24	0.0513	1.0000000	E
<input type="checkbox"/>	GO:0045893	9,8	positive regulation of transcription, DNA-dependent	95	0.0147	8	0.0171	1.0000000	E
<input type="checkbox"/>	GO:0051278	8,7	chitin- and beta-glucan-containing cell wall polysaccharide biosynthetic process	24	0.0037	3	0.0064	1.0000000	E
<input type="checkbox"/>	GO:0019266	9,10,7,8	asparagine biosynthetic process from oxaloacetate	2	0.0003	1	0.0021	1.0000000	E
<input type="checkbox"/>	GO:0006816	7,8	calcium ion transport	5	0.0008	1	0.0021	1.0000000	E
<input type="checkbox"/>	GO:0007121	8,6,10,7,11,5	bipolar cellular bud site selection	32	0.0049	3	0.0064	1.0000000	E
<input type="checkbox"/>	GO:0009076	7,8	histidine family amino acid biosynthetic process	14	0.0022	2	0.0043	1.0000000	E
<input type="checkbox"/>	GO:0007089	8,9,7,6	traversing start control point of mitotic cell cycle	6	0.0009	1	0.0021	1.0000000	E
<input type="checkbox"/>	GO:0030174	9,7,8	regulation of DNA replication initiation	10	0.0015	3	0.0064	1.0000000	E
<input type="checkbox"/>	GO:0033260	8,7,6	DNA replication during S phase	2	0.0003	1	0.0021	1.0000000	E
<input type="checkbox"/>	GO:0015851	5,6	nucleobase transport	3	0.0005	1	0.0021	1.0000000	E
<input type="checkbox"/>	GO:0032147	8,9	activation of protein kinase activity	4	0.0006	2	0.0043	1.0000000	E
<input type="checkbox"/>	GO:0006408	11,9,6,8,10,7	snRNA export from nucleus	23	0.0036	4	0.0085	1.0000000	E
<input type="checkbox"/>	GO:0000002	6	mitochondrial genome maintenance	31	0.0048	6	0.0128	1.0000000	E
<input type="checkbox"/>	GO:0044249	4	cellular biosynthetic process	366	0.0565	30	0.0641	1.0000000	E
<input type="checkbox"/>	GO:0009966	5,4	regulation of signal transduction	26	0.0040	4	0.0085	1.0000000	E
<input type="checkbox"/>	GO:0006732	5	coenzyme metabolic process	136	0.0210	10	0.0214	1.0000000	E
<input type="checkbox"/>	GO:0006614	11,10,9,8,7	SRP-dependent cotranslational protein targeting to membrane	20	0.0031	6	0.0128	1.0000000	E
<input type="checkbox"/>	GO:0019222	4,3	regulation of metabolic process	538	0.0831	56	0.1197	1.0000000	E
<input type="checkbox"/>	GO:0006452	8,7,6	translational frameshifting	3	0.0005	1	0.0021	1.0000000	E
<input type="checkbox"/>	GO:0031365	8	N-terminal protein amino acid modification	15	0.0023	4	0.0085	1.0000000	E
<input type="checkbox"/>	GO:0006268	8	DNA unwinding during replication	10	0.0015	1	0.0021	1.0000000	E
<input type="checkbox"/>	GO:0045426	7,6	quinone cofactor biosynthetic process	9	0.0014	1	0.0021	1.0000000	E
<input type="checkbox"/>	GO:0007088	7,9,8,6	regulation of mitosis	55	0.0085	9	0.0192	1.0000000	E
<input type="checkbox"/>	GO:0006743	7,6	ubiquinone metabolic process	9	0.0014	1	0.0021	1.0000000	E
<input type="checkbox"/>	GO:0051348	6	negative regulation of transferase activity	7	0.0011	2	0.0043	1.0000000	E
<input type="checkbox"/>	GO:0000920	6,4	cell separation during cytokinesis	13	0.0020	3	0.0064	1.0000000	E

<input type="radio"/>	GO:0046685	5	response to arsenic	9	0.0014	2	0.0043	1.0000000	E
<input type="radio"/>	GO:0051503	7,8	adenine nucleotide transport	3	0.0005	2	0.0043	1.0000000	E
<input type="radio"/>	GO:0042430	5	indole and derivative metabolic process	10	0.0015	2	0.0043	1.0000000	E
<input type="radio"/>	GO:0016568	8	chromatin modification	223	0.0344	20	0.0427	1.0000000	E
<input type="radio"/>	GO:0009164	5,6	nucleoside catabolic process	4	0.0006	2	0.0043	1.0000000	E
<input type="radio"/>	GO:0006533	8,9	aspartate catabolic process	2	0.0003	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0050658	4,6,5,7	RNA transport	80	0.0124	11	0.0235	1.0000000	E
<input type="radio"/>	GO:0007090	8,9,7,6	regulation of S phase of mitotic cell cycle	3	0.0005	2	0.0043	1.0000000	E
<input type="radio"/>	GO:0008652	6,7	amino acid biosynthetic process	106	0.0164	14	0.0299	1.0000000	E
<input type="radio"/>	GO:0050000	6,5	chromosome localization	4	0.0006	2	0.0043	1.0000000	E
<input type="radio"/>	GO:0006529	8,9	asparagine biosynthetic process	4	0.0006	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0045991	10,8,9,6	positive regulation of transcription by carbon catabolites	5	0.0008	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0006915	6,8	apoptosis	13	0.0020	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0006499	10,11,9,8	N-terminal protein myristoylation	5	0.0008	2	0.0043	1.0000000	E
<input type="radio"/>	GO:0000302	5	response to reactive oxygen species	12	0.0019	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0006078	9,8,10	1,6-beta-glucan biosynthetic process	7	0.0011	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0030467	7,4,8	establishment and/or maintenance of cell polarity (sensu Fungi)	66	0.0102	10	0.0214	1.0000000	E
<input type="radio"/>	GO:0018206	8	peptidyl-methionine modification	3	0.0005	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0000135	9,8	septin checkpoint	4	0.0006	2	0.0043	1.0000000	E
<input type="radio"/>	GO:0051169	7,5,6	nuclear transport	129	0.0199	17	0.0363	1.0000000	E
<input type="radio"/>	GO:0006771	7	riboflavin metabolic process	6	0.0009	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0006865	5,6,7	amino acid transport	39	0.0060	5	0.0107	1.0000000	E
<input type="radio"/>	GO:0006275	8,7	regulation of DNA replication	19	0.0029	5	0.0107	1.0000000	E
<input type="radio"/>	GO:0007059	3	chromosome segregation	119	0.0184	16	0.0342	1.0000000	E
<input type="radio"/>	GO:0040029	4	regulation of gene expression, epigenetic	100	0.0154	13	0.0278	1.0000000	E
<input type="radio"/>	GO:0000059	8,10,11,7,9	protein import into nucleus, docking	4	0.0006	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0016485	8	protein processing	38	0.0059	5	0.0107	1.0000000	E
<input type="radio"/>	GO:0006595	6,7	polyamine metabolic process	7	0.0011	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0046856	7,9,8,10	phosphoinositide dephosphorylation	7	0.0011	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0015677	9,10	copper ion import	8	0.0012	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0000741	6	karyogamy	17	0.0026	2	0.0043	1.0000000	E
<input type="radio"/>	GO:0006107	7	oxaloacetate metabolic process	2	0.0003	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0006812	5,6	cation transport	97	0.0150	10	0.0214	1.0000000	E
<input type="radio"/>	GO:0006354	8,6,7	RNA elongation	59	0.0091	10	0.0214	1.0000000	E
<input type="radio"/>	GO:0018195	8	peptidyl-arginine modification	2	0.0003	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0001881	5,7	receptor recycling	5	0.0008	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0006608	10,11,8,9,7	snRNP protein import into nucleus	23	0.0036	4	0.0085	1.0000000	E
<input type="radio"/>	GO:0048523	5,4	negative regulation of cellular process	239	0.0369	30	0.0641	1.0000000	E
<input type="radio"/>	GO:0016481	8,7	negative regulation of transcription	162	0.0250	20	0.0427	1.0000000	E
<input type="radio"/>	GO:0009098	8,9	leucine biosynthetic process	5	0.0008	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0051029	5,7,6,8	rRNA transport	26	0.0040	4	0.0085	1.0000000	E
<input type="radio"/>	GO:0033014	6	tetrapyrrole biosynthetic process	13	0.0020	2	0.0043	1.0000000	E
<input type="radio"/>	GO:0006913	8,6,7	nucleocytoplasmic transport	129	0.0199	17	0.0363	1.0000000	E
<input type="radio"/>	GO:0006302	7,6	double-strand break repair	57	0.0088	5	0.0107	1.0000000	E
<input type="radio"/>	GO:0008380	7	RNA splicing	132	0.0204	12	0.0256	1.0000000	E

<input type="radio"/>	GO:0051205	6,5,4	protein insertion into membrane	3	0.0005	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0019794	6,7	nonprotein amino acid metabolic process	9	0.0014	2	0.0043	1.0000000	E
<input type="radio"/>	GO:0000128	3	flocculation	9	0.0014	2	0.0043	1.0000000	E
<input type="radio"/>	GO:0000737	6,7	DNA catabolic process, endonucleolytic	15	0.0023	2	0.0043	1.0000000	E
<input type="radio"/>	GO:0006342	10,6,7,11,9	chromatin silencing	95	0.0147	11	0.0235	1.0000000	E
<input type="radio"/>	GO:0001324	5,6,7	age-dependent response to oxidative stress during chronological cell aging	6	0.0009	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0045132	9,7,8,6,4	meiotic chromosome segregation	17	0.0026	3	0.0064	1.0000000	E
<input type="radio"/>	GO:0042180	4	ketone metabolic process	4	0.0006	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0031120	8	snRNA pseudouridine synthesis	7	0.0011	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0045934	7,6	negative regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	179	0.0276	24	0.0513	1.0000000	E
<input type="radio"/>	GO:0015695	6,7	organic cation transport	6	0.0009	2	0.0043	1.0000000	E
<input type="radio"/>	GO:0000348	7,8,6,10,12	nuclear mRNA branch site recognition	4	0.0006	2	0.0043	1.0000000	E
<input type="radio"/>	GO:0006607	10,11,8,9,7	NLS-bearing substrate import into nucleus	23	0.0036	4	0.0085	1.0000000	E
<input type="radio"/>	GO:0043487	8,7	regulation of RNA stability	30	0.0046	3	0.0064	1.0000000	E
<input type="radio"/>	GO:0043101	5	purine salvage	9	0.0014	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0007329	11,10,7	positive regulation of transcription from RNA polymerase II promoter by pheromones	5	0.0008	2	0.0043	1.0000000	E
<input type="radio"/>	GO:0017183	10,4	peptidyl-diphthamide biosynthetic process from peptidyl-histidine	5	0.0008	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0006012	7,8	galactose metabolic process	10	0.0015	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0006031	9,7,8,10	chitin biosynthetic process	15	0.0023	2	0.0043	1.0000000	E
<input type="radio"/>	GO:0006334	6,7,10	nucleosome assembly	13	0.0020	4	0.0085	1.0000000	E
<input type="radio"/>	GO:0001100	9,11,10,8	negative regulation of exit from mitosis	4	0.0006	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0000122	10,9	negative regulation of transcription from RNA polymerase II promoter	63	0.0097	7	0.0150	1.0000000	E
<input type="radio"/>	GO:0006783	7,6,8	heme biosynthetic process	13	0.0020	2	0.0043	1.0000000	E
<input type="radio"/>	GO:0006547	7,8	histidine metabolic process	14	0.0022	2	0.0043	1.0000000	E
<input type="radio"/>	GO:0031146	11,10,12	SCF-dependent proteasomal ubiquitin-dependent protein catabolic process	8	0.0012	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0051236	3,4,5	establishment of RNA localization	80	0.0124	11	0.0235	1.0000000	E
<input type="radio"/>	GO:0007010	5	cytoskeleton organization and biogenesis	227	0.0351	21	0.0449	1.0000000	E
<input type="radio"/>	GO:0006057	8,6	mannoprotein biosynthetic process	12	0.0019	3	0.0064	1.0000000	E
<input type="radio"/>	GO:0045016	8,6,7,9	mitochondrial magnesium ion transport	2	0.0003	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0015785	7,8	UDP-galactose transport	1	0.0002	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0007231	6,5	osmosensory signaling pathway	22	0.0034	6	0.0128	1.0000000	E
<input type="radio"/>	GO:0000377	9	RNA splicing, via transesterification reactions with bulged adenosine as nucleophile	103	0.0159	10	0.0214	1.0000000	E
<input type="radio"/>	GO:0051666	5,4	actin cortical patch localization	2	0.0003	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0000003	2	reproduction	323	0.0499	29	0.0620	1.0000000	E
<input type="radio"/>	GO:0018202	8	peptidyl-histidine modification	5	0.0008	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0051031	5,7,6,8	tRNA transport	30	0.0046	4	0.0085	1.0000000	E
<input type="radio"/>	GO:0016265	3	death	13	0.0020	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0006098	9,10,11	pentose-phosphate shunt	11	0.0017	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0051054	8,7	positive regulation of DNA metabolic process	3	0.0005	1	0.0021	1.0000000	E
<input type="radio"/>	GO:0051168	9,7,8	nuclear export	102	0.0158	12	0.0256	1.0000000	E
<input type="radio"/>	GO:0000731	7,6	DNA synthesis during DNA repair	4	0.0006	1	0.0021	1.0000000	E

<input type="checkbox"/>	GO:0000018	8,7	regulation of DNA recombination	18	0.0028	2	0.0043	1.0000000	E
<input type="checkbox"/>	GO:0006497	8,7,6	protein amino acid lipidation	48	0.0074	10	0.0214	1.0000000	E
<input type="checkbox"/>	GO:0006355	8,7	regulation of transcription, DNA-dependent	359	0.0554	40	0.0855	1.0000000	E
<input type="checkbox"/>	GO:0006627	10,9,8,7	mitochondrial protein processing	6	0.0009	1	0.0021	1.0000000	E
<input type="checkbox"/>	GO:0001302	5	replicative cell aging	39	0.0060	4	0.0085	1.0000000	E
<input type="checkbox"/>	GO:0000082	8,5,6,7,4	G1/S transition of mitotic cell cycle	52	0.0080	8	0.0171	1.0000000	E
<input type="checkbox"/>	GO:0006520	5,6	amino acid metabolic process	187	0.0289	16	0.0342	1.0000000	E
<input type="checkbox"/>	GO:0006020	7,8	inositol metabolic process	6	0.0009	1	0.0021	1.0000000	E
<input type="checkbox"/>	GO:0006807	3	nitrogen compound metabolic process	251	0.0388	26	0.0556	1.0000000	E
<input type="checkbox"/>	GO:0006882	10,8	cellular zinc ion homeostasis	10	0.0015	2	0.0043	1.0000000	E
<input type="checkbox"/>	GO:0006626	9,8,7,6	protein targeting to mitochondrion	52	0.0080	9	0.0192	1.0000000	E
<input type="checkbox"/>	GO:0006633	7,6,8,5	fatty acid biosynthetic process	13	0.0020	1	0.0021	1.0000000	E
<input type="checkbox"/>	GO:0048590	3	non-developmental growth	35	0.0054	4	0.0085	1.0000000	E
<input type="checkbox"/>	GO:0032984	5	macromolecular complex disassembly	32	0.0049	3	0.0064	1.0000000	E
<input type="checkbox"/>	GO:0006279	7	premeiotic DNA synthesis	5	0.0008	1	0.0021	1.0000000	E
<input type="checkbox"/>	GO:0031505	6	chitin- and beta-glucan-containing cell wall organization and biogenesis	44	0.0068	5	0.0107	1.0000000	E
<input type="checkbox"/>	GO:0019346	8,9,7	transsulfuration	1	0.0002	1	0.0021	1.0000000	E
<input type="checkbox"/>	GO:0006665	6,7	sphingolipid metabolic process	30	0.0046	4	0.0085	1.0000000	E
<input type="checkbox"/>	GO:0009272	7	chitin- and beta-glucan-containing cell wall biogenesis	33	0.0051	4	0.0085	1.0000000	E
<input type="checkbox"/>	GO:0046349	6,7	amino sugar biosynthetic process	17	0.0026	3	0.0064	1.0000000	E
<input type="checkbox"/>	GO:0032465	6,5	regulation of cytokinesis	2	0.0003	1	0.0021	1.0000000	E
<input type="checkbox"/>	GO:0015871	5,6	choline transport	1	0.0002	1	0.0021	1.0000000	E
<input type="checkbox"/>	GO:0051083	8	cotranslational protein folding	5	0.0008	1	0.0021	1.0000000	E
<input type="checkbox"/>	GO:0043634	8	polyadenylation-dependent ncRNA catabolic process	7	0.0011	2	0.0043	1.0000000	E
<input type="checkbox"/>	GO:0043649	6,7	dicarboxylic acid catabolic process	2	0.0003	1	0.0021	1.0000000	E
<input type="checkbox"/>	GO:0042724	7	thiamin and derivative biosynthetic process	20	0.0031	3	0.0064	1.0000000	E
<input type="checkbox"/>	GO:0018409	9	peptide or protein amino-terminal blocking	15	0.0023	4	0.0085	1.0000000	E
<input type="checkbox"/>	GO:0016310	6	phosphorylation	155	0.0239	15	0.0321	1.0000000	E
<input type="checkbox"/>	GO:0006473	8	protein amino acid acetylation	48	0.0074	5	0.0107	1.0000000	E
<input type="checkbox"/>	GO:0043405	8	regulation of MAPK activity	6	0.0009	1	0.0021	1.0000000	E
<input type="checkbox"/>	GO:0006045	8,9	N-acetylglucosamine biosynthetic process	17	0.0026	3	0.0064	1.0000000	E
<input type="checkbox"/>	GO:0006313	7,4	transposition, DNA-mediated	10	0.0015	2	0.0043	1.0000000	E
<input type="checkbox"/>	GO:0006820	5,6	anion transport	17	0.0026	2	0.0043	1.0000000	E
<input type="checkbox"/>	GO:0019748	3	secondary metabolic process	23	0.0036	3	0.0064	1.0000000	E
<input type="checkbox"/>	GO:0043409	7,9,6	negative regulation of MAPKKK cascade	2	0.0003	1	0.0021	1.0000000	E
<input type="checkbox"/>	GO:0000075	7,6	cell cycle checkpoint	53	0.0082	8	0.0171	1.0000000	E
<input type="checkbox"/>	GO:0007001	6	chromosome organization and biogenesis (sensu Eukaryota)	567	0.0876	58	0.1239	1.0000000	E
<input type="checkbox"/>	GO:0009894	5,4	regulation of catabolic process	15	0.0023	1	0.0021	1.0000000	D
<input type="checkbox"/>	GO:0030435	5	sporulation	123	0.0190	6	0.0128	1.0000000	D
<input type="checkbox"/>	GO:0048878	5	chemical homeostasis	121	0.0187	8	0.0171	1.0000000	D
<input type="checkbox"/>	GO:0019941	8,7,9	modification-dependent protein catabolic process	148	0.0229	9	0.0192	1.0000000	D
<input type="checkbox"/>	GO:0001522	7	pseudouridine synthesis	39	0.0060	1	0.0021	1.0000000	D
<input type="checkbox"/>	GO:0006091	3	generation of precursor metabolites and energy	183	0.0283	7	0.0150	1.0000000	D
<input type="checkbox"/>	GO:0003006	3,4	reproductive developmental process	35	0.0054	2	0.0043	1.0000000	D

<input type="radio"/>	GO:0042787	10,9,11	protein ubiquitination during ubiquitin-dependent protein catabolic process	14	0.0022	1	0.0021	1.0000000	D
<input type="radio"/>	GO:0006749	6,5	glutathione metabolic process	14	0.0022	1	0.0021	1.0000000	D
<input type="radio"/>	GO:0030705	7,5,6	cytoskeleton-dependent intracellular transport	17	0.0026	1	0.0021	1.0000000	D
<input type="radio"/>	GO:0032446	8	protein modification by small protein conjugation	84	0.0130	4	0.0085	1.0000000	D
<input type="radio"/>	GO:0051640	5,4	organelle localization	56	0.0086	4	0.0085	1.0000000	D
<input type="radio"/>	GO:0000478	7,8	endonucleolytic cleavages during rRNA processing	20	0.0031	1	0.0021	1.0000000	D
<input type="radio"/>	GO:0009991	4	response to extracellular stimulus	37	0.0057	1	0.0021	1.0000000	D
<input type="radio"/>	GO:0032507	6,5,4	maintenance of cellular protein localization	29	0.0045	1	0.0021	1.0000000	D
<input type="radio"/>	GO:0032196	3	transposition	105	0.0162	2	0.0043	1.0000000	D
<input type="radio"/>	GO:0007034	7,5,6	vacuolar transport	114	0.0176	5	0.0107	1.0000000	D
<input type="radio"/>	GO:0006739	9,8	NADP metabolic process	17	0.0026	1	0.0021	1.0000000	D
<input type="radio"/>	GO:0045185	5,4,3	maintenance of protein localization	30	0.0046	1	0.0021	1.0000000	D
<input type="radio"/>	GO:0051248	6,5	negative regulation of protein metabolic process	18	0.0028	1	0.0021	1.0000000	D
<input type="radio"/>	GO:0030437	7,6	sporulation (sensu Fungi)	108	0.0167	4	0.0085	1.0000000	D
<input type="radio"/>	GO:0000154	7,8	rRNA modification	85	0.0131	2	0.0043	1.0000000	D
<input type="radio"/>	GO:0009889	5,4	regulation of biosynthetic process	69	0.0107	3	0.0064	1.0000000	D
<input type="radio"/>	GO:0046040	9	IMP metabolic process	14	0.0022	1	0.0021	1.0000000	D
<input type="radio"/>	GO:0001510	7	RNA methylation	60	0.0093	2	0.0043	1.0000000	D
<input type="radio"/>	GO:0042273	6,5	ribosomal large subunit biogenesis and assembly	64	0.0099	2	0.0043	1.0000000	D
<input type="radio"/>	GO:0030473	8,9,6,7	nuclear migration, microtubule-mediated	15	0.0023	1	0.0021	1.0000000	D
<input type="radio"/>	GO:0009451	6	RNA modification	139	0.0215	10	0.0214	1.0000000	D
<input type="radio"/>	GO:0009117	5	nucleotide metabolic process	111	0.0171	4	0.0085	1.0000000	D
<input type="radio"/>	GO:0007094	9,11,10,8	mitotic cell cycle spindle assembly checkpoint	20	0.0031	1	0.0021	1.0000000	D
<input type="radio"/>	GO:0000011	6	vacuole inheritance	14	0.0022	1	0.0021	1.0000000	D
<input type="radio"/>	GO:0016051	5	carbohydrate biosynthetic process	77	0.0119	4	0.0085	1.0000000	D
<input type="radio"/>	GO:0030154	4	cell differentiation	173	0.0267	10	0.0214	1.0000000	D
<input type="radio"/>	GO:0031667	5	response to nutrient levels	37	0.0057	1	0.0021	1.0000000	D
<input type="radio"/>	GO:0048308	5	organelle inheritance	40	0.0062	2	0.0043	1.0000000	D
<input type="radio"/>	GO:0006511	9,8,10	ubiquitin-dependent protein catabolic process	148	0.0229	9	0.0192	1.0000000	D
<input type="radio"/>	GO:0000001	8,7,6	mitochondrion inheritance	26	0.0040	1	0.0021	1.0000000	D
<input type="radio"/>	GO:0007052	5,4,9	mitotic spindle organization and biogenesis	44	0.0068	1	0.0021	1.0000000	D
<input type="radio"/>	GO:0030003	8,6	cellular cation homeostasis	102	0.0158	7	0.0150	1.0000000	D
<input type="radio"/>	GO:0009259	6	ribonucleotide metabolic process	43	0.0066	1	0.0021	1.0000000	D
<input type="radio"/>	GO:0055072	9	iron ion homeostasis	38	0.0059	2	0.0043	1.0000000	D
<input type="radio"/>	GO:0042254	5	ribosome biogenesis and assembly	410	0.0633	19	0.0406	1.0000000	D
<input type="radio"/>	GO:0042592	4	homeostatic process	134	0.0207	8	0.0171	1.0000000	D
<input type="radio"/>	GO:0000027	9,7,8,6	ribosomal large subunit assembly and maintenance	41	0.0063	1	0.0021	1.0000000	D
<input type="radio"/>	GO:0000096	6,7,5	sulfur amino acid metabolic process	33	0.0051	1	0.0021	1.0000000	D
<input type="radio"/>	GO:0019318	6,7	hexose metabolic process	85	0.0131	3	0.0064	1.0000000	D
<input type="radio"/>	GO:0006825	8,9	copper ion transport	14	0.0022	1	0.0021	1.0000000	D
<input type="radio"/>	GO:0055067	8	monovalent inorganic cation homeostasis	34	0.0053	2	0.0043	1.0000000	D
<input type="radio"/>	GO:0051656	6,3,5,4	establishment of organelle localization	29	0.0045	2	0.0043	1.0000000	D
<input type="radio"/>	GO:0032259	5	methylation	83	0.0128	3	0.0064	1.0000000	D

<input type="radio"/>	GO:0048015	7	phosphoinositide-mediated signaling	16	0.0025	1	0.0021	1.0000000	D
<input type="radio"/>	GO:0006118	4	electron transport	33	0.0051	2	0.0043	1.0000000	D
<input type="radio"/>	GO:0046164	5	alcohol catabolic process	47	0.0073	1	0.0021	1.0000000	D
<input type="radio"/>	GO:0032392	6	DNA geometric change	16	0.0025	1	0.0021	1.0000000	D
<input type="radio"/>	GO:0015980	4	energy derivation by oxidation of organic compounds	145	0.0224	5	0.0107	1.0000000	D
<input type="radio"/>	GO:0007584	6,4	response to nutrient	18	0.0028	1	0.0021	1.0000000	D
<input type="radio"/>	GO:0009250	7,8	glucan biosynthetic process	25	0.0039	1	0.0021	1.0000000	D
<input type="radio"/>	GO:0007530	4,5	sex determination	35	0.0054	2	0.0043	1.0000000	D
<input type="radio"/>	GO:0006769	8,7	nicotinamide metabolic process	42	0.0065	2	0.0043	1.0000000	D
<input type="radio"/>	GO:0051235	3,2	maintenance of localization	33	0.0051	1	0.0021	1.0000000	D
<input type="radio"/>	GO:0055082	6,4	cellular chemical homeostasis	115	0.0178	8	0.0171	1.0000000	D
<input type="radio"/>	GO:0016570	10,8	histone modification	91	0.0141	4	0.0085	1.0000000	D
<input type="radio"/>	GO:0006766	4	vitamin metabolic process	89	0.0137	6	0.0128	1.0000000	D
<input type="radio"/>	GO:0000466	8,9	maturation of 5.8S rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	34	0.0053	1	0.0021	1.0000000	D
<input type="radio"/>	GO:0006081	4	aldehyde metabolic process	21	0.0032	1	0.0021	1.0000000	D
<input type="radio"/>	GO:0000479	8,9	endonucleolytic cleavage of tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	20	0.0031	1	0.0021	1.0000000	D
<input type="radio"/>	GO:0032508	7	DNA duplex unwinding	16	0.0025	1	0.0021	1.0000000	D
<input type="radio"/>	GO:0044270	5,4	nitrogen compound catabolic process	32	0.0049	1	0.0021	1.0000000	D
<input type="radio"/>	GO:0006508	6	proteolysis	178	0.0275	11	0.0235	1.0000000	D
<input type="radio"/>	GO:0006790	4	sulfur metabolic process	67	0.0103	2	0.0043	1.0000000	D
<input type="radio"/>	GO:0006007	8,9	glucose catabolic process	34	0.0053	1	0.0021	1.0000000	D
<input type="radio"/>	GO:0006413	7,6	translational initiation	49	0.0076	3	0.0064	1.0000000	D
<input type="radio"/>	GO:0042255	7,6	ribosome assembly	66	0.0102	2	0.0043	1.0000000	D
<input type="radio"/>	GO:0006631	5,7,6	fatty acid metabolic process	47	0.0073	2	0.0043	1.0000000	D
<input type="radio"/>	GO:0000460	7,8	maturation of 5.8S rRNA	36	0.0056	1	0.0021	1.0000000	D
<input type="radio"/>	GO:0008213	8	protein amino acid alkylation	23	0.0036	1	0.0021	1.0000000	D
<input type="radio"/>	GO:0045990	9,7,8,5	regulation of transcription by carbon catabolites	14	0.0022	1	0.0021	1.0000000	D
<input type="radio"/>	GO:0006513	10	protein monoubiquitination	22	0.0034	1	0.0021	1.0000000	D
<input type="radio"/>	GO:0000028	9,7,8,6	ribosomal small subunit assembly and maintenance	14	0.0022	1	0.0021	1.0000000	D
<input type="radio"/>	GO:0019856	7,6	pyrimidine base biosynthetic process	15	0.0023	1	0.0021	1.0000000	D
<input type="radio"/>	GO:0051603	7,8	proteolysis involved in cellular protein catabolic process	151	0.0233	9	0.0192	1.0000000	D
<input type="radio"/>	GO:0016074	6	snoRNA metabolic process	17	0.0026	1	0.0021	1.0000000	D
<input type="radio"/>	GO:0006369	9,8	transcription termination from RNA polymerase II promoter	18	0.0028	1	0.0021	1.0000000	D
<input type="radio"/>	GO:0006733	6	oxidoreduction coenzyme metabolic process	56	0.0086	3	0.0064	1.0000000	D
<input type="radio"/>	GO:0005996	5,6	monosaccharide metabolic process	92	0.0142	3	0.0064	1.0000000	D
<input type="radio"/>	GO:0048468	3,5	cell development	52	0.0080	3	0.0064	1.0000000	D
<input type="radio"/>	GO:0009167	8	purine ribonucleoside monophosphate metabolic process	17	0.0026	1	0.0021	1.0000000	D
<input type="radio"/>	GO:0006090	7	pyruvate metabolic process	38	0.0059	2	0.0043	1.0000000	D
<input type="radio"/>	GO:0046365	6,7	monosaccharide catabolic process	44	0.0068	1	0.0021	1.0000000	D
<input type="radio"/>	GO:0030036	7	actin cytoskeleton organization and biogenesis	107	0.0165	7	0.0150	1.0000000	D
<input type="radio"/>	GO:0042147	8,6,7	retrograde transport, endosome to Golgi	17	0.0026	1	0.0021	1.0000000	D

<input type="radio"/>	GO:0006383	8,7	transcription from RNA polymerase III promoter	38	0.0059	2	0.0043	1.0000000	D
<input type="radio"/>	GO:0009063	6,7	amino acid catabolic process	29	0.0045	1	0.0021	1.0000000	D
<input type="radio"/>	GO:0006893	9,7,6,8	Golgi to plasma membrane transport	30	0.0046	2	0.0043	1.0000000	D
<input type="radio"/>	GO:0050801	6	ion homeostasis	119	0.0184	8	0.0171	1.0000000	D
<input type="radio"/>	GO:0006163	6	purine nucleotide metabolic process	47	0.0073	2	0.0043	1.0000000	D
<input type="radio"/>	GO:0006897	6,5	endocytosis	86	0.0133	5	0.0107	1.0000000	D
<input type="radio"/>	GO:0006879	10,8	cellular iron ion homeostasis	38	0.0059	2	0.0043	1.0000000	D
<input type="radio"/>	GO:0022406	3	membrane docking	14	0.0022	1	0.0021	1.0000000	D
<input type="radio"/>	GO:0009651	5	response to salt stress	15	0.0023	1	0.0021	1.0000000	D
<input type="radio"/>	GO:0007015	8	actin filament organization	61	0.0094	2	0.0043	1.0000000	D
<input type="radio"/>	GO:0045944	10,9	positive regulation of transcription from RNA polymerase II promoter	76	0.0117	5	0.0107	1.0000000	D
<input type="radio"/>	GO:0045333	5	cellular respiration	89	0.0137	5	0.0107	1.0000000	D
<input type="radio"/>	GO:0000462	8,9	maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	45	0.0069	1	0.0021	1.0000000	D
<input type="radio"/>	GO:0016579	9	protein deubiquitination	20	0.0031	1	0.0021	1.0000000	D
<input type="radio"/>	GO:0006914	3	autophagy	45	0.0069	3	0.0064	1.0000000	D
<input type="radio"/>	GO:0048017	8	inositol lipid-mediated signaling	16	0.0025	1	0.0021	1.0000000	D
<input type="radio"/>	GO:0006073	6,7	glucan metabolic process	46	0.0071	2	0.0043	1.0000000	D
<input type="radio"/>	GO:0006625	9,8,6,7	protein targeting to peroxisome	20	0.0031	1	0.0021	1.0000000	D
<input type="radio"/>	GO:0010324	5	membrane invagination	96	0.0148	5	0.0107	1.0000000	D
<input type="radio"/>	GO:0044265	5	cellular macromolecule catabolic process	314	0.0485	22	0.0470	1.0000000	D
<input type="radio"/>	GO:0051651	5,4,3	maintenance of cellular localization	29	0.0045	1	0.0021	1.0000000	D
<input type="radio"/>	GO:0042144	6	vacuole fusion, non-autophagic	28	0.0043	1	0.0021	1.0000000	D
<input type="radio"/>	GO:0006312	7	mitotic recombination	45	0.0069	2	0.0043	1.0000000	D
<input type="radio"/>	GO:0030163	6,5	protein catabolic process	173	0.0267	10	0.0214	1.0000000	D
<input type="radio"/>	GO:0009060	6	aerobic respiration	84	0.0130	5	0.0107	1.0000000	D
<input type="radio"/>	GO:0048869	3	cellular developmental process	173	0.0267	10	0.0214	1.0000000	D
<input type="radio"/>	GO:0042257	8,7	ribosomal subunit assembly	55	0.0085	2	0.0043	1.0000000	D
<input type="radio"/>	GO:0044262	5	cellular carbohydrate metabolic process	213	0.0329	11	0.0235	1.0000000	D
<input type="radio"/>	GO:0009168	8,9	purine ribonucleoside monophosphate biosynthetic process	15	0.0023	1	0.0021	1.0000000	D
<input type="radio"/>	GO:0009310	5,6	amine catabolic process	32	0.0049	1	0.0021	1.0000000	D
<input type="radio"/>	GO:0006734	9,8	NADH metabolic process	14	0.0022	1	0.0021	1.0000000	D
<input type="radio"/>	GO:0007533	5,7,6	mating type switching	29	0.0045	2	0.0043	1.0000000	D
<input type="radio"/>	GO:0044248	4	cellular catabolic process	425	0.0656	28	0.0598	1.0000000	D
<input type="radio"/>	GO:0051646	6,5	mitochondrion localization	27	0.0042	1	0.0021	1.0000000	D
<input type="radio"/>	GO:0051246	5,4	regulation of protein metabolic process	72	0.0111	4	0.0085	1.0000000	D
<input type="radio"/>	GO:0009057	4	macromolecule catabolic process	345	0.0533	24	0.0513	1.0000000	D
<input type="radio"/>	GO:0006417	7,6,5	regulation of translation	47	0.0073	3	0.0064	1.0000000	D
<input type="radio"/>	GO:0005975	4	carbohydrate metabolic process	233	0.0360	12	0.0256	1.0000000	D
<input type="radio"/>	GO:0030004	9,7	cellular monovalent inorganic cation homeostasis	34	0.0053	2	0.0043	1.0000000	D
<input type="radio"/>	GO:0019725	5,3	cellular homeostasis	128	0.0198	8	0.0171	1.0000000	D
<input type="radio"/>	GO:0007051	8	spindle organization and biogenesis	47	0.0073	2	0.0043	1.0000000	D
<input type="radio"/>	GO:0048311	7,6	mitochondrion distribution	26	0.0040	1	0.0021	1.0000000	D
<input type="radio"/>	GO:0006740	10,9	NADPH regeneration	14	0.0022	1	0.0021	1.0000000	D

<input type="radio"/>	GO:0031326	6,5	regulation of cellular biosynthetic process	67	0.0103	3	0.0064	1.0000000	D
<input type="radio"/>	GO:0045003	9,8	double-strand break repair via synthesis-dependent strand annealing	17	0.0026	1	0.0021	1.0000000	D
<input type="radio"/>	GO:0006944	5	membrane fusion	59	0.0091	4	0.0085	1.0000000	D
<input type="radio"/>	GO:0030029	6	actin filament-based process	112	0.0173	7	0.0150	1.0000000	D
<input type="radio"/>	GO:0044257	6,7	cellular protein catabolic process	160	0.0247	9	0.0192	1.0000000	D
<input type="radio"/>	GO:0043574	7,5,6	peroxisomal transport	20	0.0031	1	0.0021	1.0000000	D
<input type="radio"/>	GO:0022414	3,2	reproductive process	183	0.0283	10	0.0214	1.0000000	D
<input type="radio"/>	GO:0006896	9,8,7,6	Golgi to vacuole transport	24	0.0037	1	0.0021	1.0000000	D
<input type="radio"/>	GO:0006144	6	purine base metabolic process	14	0.0022	1	0.0021	1.0000000	D
<input type="radio"/>	GO:0009150	7	purine ribonucleotide metabolic process	41	0.0063	1	0.0021	1.0000000	D
<input type="radio"/>	GO:0006100	6	tricarboxylic acid cycle intermediate metabolic process	20	0.0031	1	0.0021	1.0000000	D
<input type="radio"/>	GO:0042244	5,6	spore wall assembly	42	0.0065	2	0.0043	1.0000000	D
<input type="radio"/>	GO:0009266	4	response to temperature stimulus	28	0.0043	2	0.0043	1.0000000	D
<input type="radio"/>	GO:0016052	5	carbohydrate catabolic process	80	0.0124	2	0.0043	1.0000000	D
<input type="radio"/>	GO:0009161	7	ribonucleoside monophosphate metabolic process	17	0.0026	1	0.0021	1.0000000	D
<input type="radio"/>	GO:0006623	9,8,7,6	protein targeting to vacuole	67	0.0103	3	0.0064	1.0000000	D
<input type="radio"/>	GO:0006188	9,10	IMP biosynthetic process	14	0.0022	1	0.0021	1.0000000	D
<input type="radio"/>	GO:0009066	6,7	aspartate family amino acid metabolic process	46	0.0071	2	0.0043	1.0000000	D
<input type="radio"/>	GO:0009260	6,7	ribonucleotide biosynthetic process	40	0.0062	1	0.0021	1.0000000	D
<input type="radio"/>	GO:0046394	6	carboxylic acid biosynthetic process	17	0.0026	1	0.0021	1.0000000	D
<input type="radio"/>	GO:0000054	10,11,6,8,9	ribosome export from nucleus	28	0.0043	2	0.0043	1.0000000	D
<input type="radio"/>	GO:0030476	8,6,7	spore wall assembly (sensu Fungi)	42	0.0065	2	0.0043	1.0000000	D
<input type="radio"/>	GO:0032787	6	monocarboxylic acid metabolic process	126	0.0195	6	0.0128	1.0000000	D
<input type="radio"/>	GO:0016569	9	covalent chromatin modification	91	0.0141	4	0.0085	1.0000000	D
<input type="radio"/>	GO:0030472	6,5,10	mitotic spindle organization and biogenesis in nucleus	22	0.0034	1	0.0021	1.0000000	D
<input type="radio"/>	GO:0022413	5,4	reproductive process in single-celled organism	149	0.0230	8	0.0171	1.0000000	D
<input type="radio"/>	GO:0048278	4,5,6	vesicle docking	14	0.0022	1	0.0021	1.0000000	D
<input type="radio"/>	GO:0016073	6	snRNA metabolic process	15	0.0023	1	0.0021	1.0000000	D
<input type="radio"/>	GO:0006267	8,7	pre-replicative complex assembly	15	0.0023	1	0.0021	1.0000000	D
<input type="radio"/>	GO:0000394	8	RNA splicing, via endonucleolytic cleavage and ligation	14	0.0022	1	0.0021	1.0000000	D
<input type="radio"/>	GO:0009605	3	response to external stimulus	37	0.0057	1	0.0021	1.0000000	D
<input type="radio"/>	GO:0008643	4,5	carbohydrate transport	38	0.0059	2	0.0043	1.0000000	D
<input type="radio"/>	GO:0009064	6,7	glutamine family amino acid metabolic process	43	0.0066	3	0.0064	1.0000000	D
<input type="radio"/>	GO:0007531	4,6,5	mating type determination	35	0.0054	2	0.0043	1.0000000	D
<input type="radio"/>	GO:0016571	11,9,10,8	histone methylation	18	0.0028	1	0.0021	1.0000000	D
<input type="radio"/>	GO:0016072	6	rRNA metabolic process	256	0.0395	13	0.0278	1.0000000	D
<input type="radio"/>	GO:0000447	9,10	endonucleolytic cleavage between SSU-rRNA and 5.8S rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	20	0.0031	1	0.0021	1.0000000	D
<input type="radio"/>	GO:0019362	7,6	pyridine nucleotide metabolic process	45	0.0069	2	0.0043	1.0000000	D
<input type="radio"/>	GO:0042274	6,5	ribosomal small subunit biogenesis and assembly	26	0.0040	1	0.0021	1.0000000	D
<input type="radio"/>	GO:0048622	6,5	reproductive sporulation	108	0.0167	4	0.0085	1.0000000	D
<input type="radio"/>	GO:0009165	5,6	nucleotide biosynthetic process	59	0.0091	2	0.0043	1.0000000	D

<input type="radio"/>	GO:0016558	10,9,7,8,6	protein import into peroxisome matrix	17	0.0026	1	0.0021	1.0000000	D
<input type="radio"/>	GO:0009156	7,8	ribonucleoside monophosphate biosynthetic process	15	0.0023	1	0.0021	1.0000000	D
<input type="radio"/>	GO:0016053	5	organic acid biosynthetic process	17	0.0026	1	0.0021	1.0000000	D
<input type="radio"/>	GO:0008150	1	biological process	6476	1.0000	468	1.0000	1.0000000	D
<input type="radio"/>	GO:0006730	4	one-carbon compound metabolic process	97	0.0150	4	0.0085	1.0000000	D
<input type="radio"/>	GO:0000209	10	protein polyubiquitination	20	0.0031	1	0.0021	1.0000000	D
<input type="radio"/>	GO:0007534	6,8,7	gene conversion at mating-type locus	23	0.0036	1	0.0021	1.0000000	D
<input type="radio"/>	GO:0016567	9	protein ubiquitination	66	0.0102	4	0.0085	1.0000000	D
<input type="radio"/>	GO:0006353	8,7	transcription termination	20	0.0031	1	0.0021	1.0000000	D
<input type="radio"/>	GO:0006512	8	ubiquitin cycle	88	0.0136	5	0.0107	1.0000000	D
<input type="radio"/>	GO:0006364	6,7	rRNA processing	249	0.0384	13	0.0278	1.0000000	D
<input type="radio"/>	GO:0030490	7,8	maturation of SSU-rRNA	45	0.0069	1	0.0021	1.0000000	D
<input type="radio"/>	GO:0006892	8,6,5,7	post-Golgi vesicle-mediated transport	69	0.0107	3	0.0064	1.0000000	D
<input type="radio"/>	GO:0006109	5,4	regulation of carbohydrate metabolic process	29	0.0045	1	0.0021	1.0000000	D
<input type="radio"/>	GO:0032505	4,3	reproduction of a single-celled organism	194	0.0300	14	0.0299	1.0000000	D
<input type="radio"/>	GO:0006084	6	acetyl-CoA metabolic process	20	0.0031	1	0.0021	1.0000000	D
<input type="radio"/>	GO:0009636	4	response to toxin	28	0.0043	2	0.0043	1.0000000	D
<input type="radio"/>	GO:0007017	6	microtubule-based process	101	0.0156	7	0.0150	1.0000000	D
<input type="radio"/>	GO:0010038	5	response to metal ion	18	0.0028	1	0.0021	1.0000000	D
<input type="radio"/>	GO:0043632	6	modification-dependent macromolecule catabolic process	155	0.0239	11	0.0235	1.0000000	D
<input type="radio"/>	GO:0006873	7,5	cellular ion homeostasis	115	0.0178	8	0.0171	1.0000000	D
<input type="radio"/>	GO:0019320	7,8	hexose catabolic process	39	0.0060	1	0.0021	1.0000000	D
<input type="radio"/>	GO:0007018	8,7,6	microtubule-based movement	15	0.0023	1	0.0021	1.0000000	D
<input type="radio"/>	GO:0006164	6,7	purine nucleotide biosynthetic process	41	0.0063	2	0.0043	1.0000000	D
<input type="radio"/>	GO:0009408	5,4	response to heat	23	0.0036	1	0.0021	1.0000000	D
<input type="radio"/>	GO:0006388	9,8	tRNA splicing	14	0.0022	1	0.0021	1.0000000	D
<input type="radio"/>	GO:0009152	7,8	purine ribonucleotide biosynthetic process	38	0.0059	1	0.0021	1.0000000	D
<input type="radio"/>	GO:0006006	7,8	glucose metabolic process	65	0.0100	1	0.0021	1.0000000	D
<input type="radio"/>	GO:0007033	5	vacuole organization and biogenesis	67	0.0103	3	0.0064	1.0000000	D
<input type="radio"/>	GO:0043414	6	biopolymer methylation	83	0.0128	3	0.0064	1.0000000	D
<input type="radio"/>	GO:0016197	7,5,6	endosome transport	49	0.0076	1	0.0021	1.0000000	D
<input type="radio"/>	GO:0044275	6	cellular carbohydrate catabolic process	80	0.0124	2	0.0043	1.0000000	D
<input type="radio"/>	GO:0048610	3,4	reproductive cellular process	149	0.0230	8	0.0171	1.0000000	D
<input type="radio"/>	GO:0022613	4	ribonucleoprotein complex biogenesis and assembly	483	0.0746	25	0.0534	1.0000000	D
<input type="radio"/>	GO:0006479	9,7	protein amino acid methylation	23	0.0036	1	0.0021	1.0000000	D
<input type="radio"/>	GO:0055080	7	cation homeostasis	102	0.0158	7	0.0150	1.0000000	D
<input type="radio"/>	GO:0009056	3	catabolic process	438	0.0676	29	0.0620	1.0000000	D
<input type="radio"/>	GO:0006767	5	water-soluble vitamin metabolic process	89	0.0137	6	0.0128	1.0000000	D
<input type="radio"/>	GO:0022618	6,5	protein-RNA complex assembly	144	0.0222	8	0.0171	1.0000000	D
<input type="radio"/>	GO:0006412	6,5	translation	688	0.1062	27	0.0577	0.0599444	D
<input type="radio"/>	GO:0043284	5	biopolymer biosynthetic process	354	0.0547	3	0.0064	6.035407E-06	D