

GO-Stats Results

Your dataset contains **604** 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:0005975	4	carbohydrate metabolic process	233	0.0360	58	0.0960	6.861717E-13	E
<input type="radio"/> GO:0050896	2	response to stimulus	763	0.1178	128	0.2119	1.387054E-12	E
<input type="radio"/> GO:0006091	3	generation of precursor metabolites and energy	183	0.0283	49	0.0811	2.586479E-12	E
<input type="radio"/> GO:0006950	3	response to stress	488	0.0754	92	0.1523	5.215846E-12	E
<input type="radio"/> GO:0044262	5	cellular carbohydrate metabolic process	213	0.0329	52	0.0861	2.424247E-11	E
<input type="radio"/> GO:0009056	3	catabolic process	438	0.0676	82	0.1358	1.200586E-10	E
<input type="radio"/> GO:0044248	4	cellular catabolic process	425	0.0656	79	0.1308	3.822978E-10	E
<input type="radio"/> GO:0015980	4	energy derivation by oxidation of organic compounds	145	0.0224	39	0.0646	3.943660E-10	E
<input type="radio"/> GO:0009987	2	cellular process	4654	0.7187	493	0.8162	1.904787E-09	E
<input type="radio"/> GO:0051179	2	localization	1051	0.1623	150	0.2483	3.293481E-09	E
<input type="radio"/> GO:0016310	6	phosphorylation	155	0.0239	37	0.0613	3.446941E-08	E
<input type="radio"/> GO:0030029	6	actin filament-based process	112	0.0173	30	0.0497	4.513118E-08	E
<input type="radio"/> GO:0030036	7	actin cytoskeleton organization and biogenesis	107	0.0165	29	0.0480	5.706530E-08	E
<input type="radio"/> GO:0006810	3,4	transport	981	0.1515	137	0.2268	7.134189E-08	E
<input type="radio"/> GO:0051234	2,3	establishment of localization	1004	0.1550	139	0.2301	9.519341E-08	E
<input type="radio"/> GO:0007154	3	cell communication	240	0.0371	48	0.0795	1.234415E-07	E
<input type="radio"/> GO:0009060	6	aerobic respiration	84	0.0130	24	0.0397	2.704810E-07	E
<input type="radio"/> GO:0006119	7,4	oxidative phosphorylation	46	0.0071	17	0.0281	2.729455E-07	E
<input type="radio"/> GO:0046164	5	alcohol catabolic process	47	0.0073	17	0.0281	3.885773E-07	E
<input type="radio"/> GO:0006118	4	electron transport	33	0.0051	14	0.0232	4.349025E-07	E
<input type="radio"/> GO:0009628	3	response to abiotic stimulus	117	0.0181	29	0.0480	4.374778E-07	E

<input type="radio"/>	GO:0009057	4	macromolecule catabolic process	345	0.0533	60	0.0993	5.475139E-07	E
<input type="radio"/>	GO:0042775	9,6	organelle ATP synthesis coupled electron transport	25	0.0039	12	0.0199	5.842924E-07	E
<input type="radio"/>	GO:0042773	8,5	ATP synthesis coupled electron transport	25	0.0039	12	0.0199	5.842924E-07	E
<input type="radio"/>	GO:0007165	4	signal transduction	209	0.0323	42	0.0695	6.457117E-07	E
<input type="radio"/>	GO:0046365	6,7	monosaccharide catabolic process	44	0.0068	16	0.0265	7.825094E-07	E
<input type="radio"/>	GO:0045333	5	cellular respiration	89	0.0137	24	0.0397	8.446309E-07	E
<input type="radio"/>	GO:0006796	5	phosphate metabolic process	212	0.0327	42	0.0695	9.479791E-07	E
<input type="radio"/>	GO:0006793	4	phosphorus metabolic process	212	0.0327	42	0.0695	9.479791E-07	E
<input type="radio"/>	GO:0006066	4	alcohol metabolic process	163	0.0252	35	0.0579	1.123695E-06	E
<input type="radio"/>	GO:0006732	5	coenzyme metabolic process	136	0.0210	31	0.0513	1.215953E-06	E
<input type="radio"/>	GO:0044265	5	cellular macromolecule catabolic process	314	0.0485	55	0.0911	1.276099E-06	E
<input type="radio"/>	GO:0046356	7	acetyl-CoA catabolic process	15	0.0023	9	0.0149	1.418338E-06	E
<input type="radio"/>	GO:0006099	8,7,6	tricarboxylic acid cycle	15	0.0023	9	0.0149	1.418338E-06	E
<input type="radio"/>	GO:0007242	5	intracellular signaling cascade	137	0.0212	31	0.0513	1.429526E-06	E
<input type="radio"/>	GO:0005996	5,6	monosaccharide metabolic process	92	0.0142	24	0.0397	1.590580E-06	E
<input type="radio"/>	GO:0051186	4	cofactor metabolic process	170	0.0263	35	0.0579	3.009431E-06	E
<input type="radio"/>	GO:0006084	6	acetyl-CoA metabolic process	20	0.0031	10	0.0166	3.277848E-06	E
<input type="radio"/>	GO:0006112	5	energy reserve metabolic process	39	0.0060	14	0.0232	4.501742E-06	E
<input type="radio"/>	GO:0051187	5	cofactor catabolic process	21	0.0032	10	0.0166	5.681955E-06	E
<input type="radio"/>	GO:0048308	5	organelle inheritance	40	0.0062	14	0.0232	6.290959E-06	E
<input type="radio"/>	GO:0000001	8,7,6	mitochondrion inheritance	26	0.0040	11	0.0182	7.788551E-06	E
<input type="radio"/>	GO:0048311	7,6	mitochondrion distribution	26	0.0040	11	0.0182	7.788551E-06	E
<input type="radio"/>	GO:0010324	5	membrane invagination	96	0.0148	23	0.0381	1.151491E-05	E
<input type="radio"/>	GO:0016044	4	membrane organization and biogenesis	188	0.0290	36	0.0596	1.152429E-05	E
<input type="radio"/>	GO:0051646	6,5	mitochondrion localization	27	0.0042	11	0.0182	1.193482E-05	E
<input type="radio"/>	GO:0019752	5	carboxylic acid metabolic process	314	0.0485	52	0.0861	1.193716E-05	E
<input type="radio"/>	GO:0006082	4	organic acid metabolic process	314	0.0485	52	0.0861	1.193716E-05	E
<input type="radio"/>	GO:0032787	6	monocarboxylic acid metabolic process	126	0.0195	27	0.0447	1.802666E-05	E
<input type="radio"/>	GO:0006897	6,5	endocytosis	86	0.0133	21	0.0348	1.991443E-05	E
<input type="radio"/>	GO:0044275	6	cellular carbohydrate catabolic process	80	0.0124	20	0.0331	2.163253E-05	E
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<input type="radio"/>	GO:0019320	7,8	hexose catabolic process	39	0.0060	13	0.0215	2.398175E-05	E
<input type="radio"/>	GO:0007010	5	cytoskeleton organization and biogenesis	227	0.0351	40	0.0662	2.798960E-05	E
<input type="radio"/>	GO:0009109	6	coenzyme catabolic process	20	0.0031	9	0.0149	2.935790E-05	E

<input type="radio"/>	GO:0006970	4	response to osmotic stress	89	0.0137	21	0.0348	3.386605E-05	E
<input type="radio"/>	GO:0016192	4,5	vesicle-mediated transport	328	0.0506	52	0.0861	3.789297E-05	E
<input type="radio"/>	GO:0006122	10,7,5	mitochondrial electron transport, ubiquinol to cytochrome c	9	0.0014	6	0.0099	4.040848E-05	E
<input type="radio"/>	GO:0042026	7	protein refolding	9	0.0014	6	0.0099	4.040848E-05	E
<input type="radio"/>	GO:0006006	7,8	glucose metabolic process	65	0.0100	17	0.0281	4.713866E-05	E
<input type="radio"/>	GO:0019318	6,7	hexose metabolic process	85	0.0131	20	0.0331	5.321629E-05	E
<input type="radio"/>	GO:0030163	6,5	protein catabolic process	173	0.0267	32	0.0530	6.495707E-05	E
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<input type="radio"/>	GO:0007015	8	actin filament organization	61	0.0094	16	0.0265	7.447134E-05	E
<input type="radio"/>	GO:0005991	6,7	trehalose metabolic process	10	0.0015	6	0.0099	9.167983E-05	E
<input type="radio"/>	GO:0007243	6	protein kinase cascade	23	0.0036	9	0.0149	0.0001069	E
<input type="radio"/>	GO:0006508	6	proteolysis	178	0.0275	32	0.0530	0.0001101	E
<input type="radio"/>	GO:0006007	8,9	glucose catabolic process	34	0.0053	11	0.0182	0.0001333	E
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<input type="radio"/>	GO:0051603	7,8	proteolysis involved in cellular protein catabolic process	151	0.0233	28	0.0464	0.0001661	E
<input type="radio"/>	GO:0007034	7,5,6	vacuolar transport	114	0.0176	23	0.0381	0.0001747	E
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<input type="radio"/>	GO:0000165	7	MAPKKK cascade	20	0.0031	8	0.0132	0.0002165	E
<input type="radio"/>	GO:0006100	6	tricarboxylic acid cycle intermediate metabolic process	20	0.0031	8	0.0132	0.0002165	E
<input type="radio"/>	GO:0006629	4	lipid metabolic process	242	0.0374	39	0.0646	0.0002199	E
<input type="radio"/>	GO:0043687	7	post-translational protein modification	388	0.0599	56	0.0927	0.0002246	E
<input type="radio"/>	GO:0042221	3	response to chemical stimulus	382	0.0590	55	0.0911	0.0002667	E
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<input type="radio"/>	GO:0019941	8,7,9	modification-dependent protein catabolic process	148	0.0229	27	0.0447	0.0002744	E
<input type="radio"/>	GO:0030865	6	cortical cytoskeleton organization and biogenesis	16	0.0025	7	0.0116	0.0002845	E
<input type="radio"/>	GO:0030866	8,7	cortical actin cytoskeleton organization and biogenesis	16	0.0025	7	0.0116	0.0002845	E
<input type="radio"/>	GO:0006733	6	oxidoreduction coenzyme metabolic process	56	0.0086	14	0.0232	0.0003372	E
<input type="radio"/>	GO:0044270	5,4	nitrogen compound catabolic process	32	0.0049	10	0.0166	0.0003591	E
<input type="radio"/>	GO:0009310	5,6	amine catabolic process	32	0.0049	10	0.0166	0.0003591	E
<input type="radio"/>	GO:0005977	7,6,8	glycogen metabolic process	32	0.0049	10	0.0166	0.0003591	E
<input type="radio"/>	GO:0006457	6	protein folding	84	0.0130	18	0.0298	0.0003903	E
<input type="radio"/>	GO:0016051	5	carbohydrate biosynthetic process	77	0.0119	17	0.0281	0.0003907	E
<input type="radio"/>	GO:0007047	5	cell wall organization and biogenesis	200	0.0309	33	0.0546	0.0004055	E
<input type="radio"/>	GO:0045229	4	external encapsulating structure organization and biogenesis	200	0.0309	33	0.0546	0.0004055	E
<input type="radio"/>	GO:0006979	4	response to oxidative stress	71	0.0110	16	0.0265	0.0004492	E
<input type="radio"/>	GO:0043285	5	biopolymer catabolic process	277	0.0428	42	0.0695	0.0004526	E
<input type="radio"/>	GO:0030435	5	sporulation	123	0.0190	23	0.0381	0.0005101	E
<input type="radio"/>	GO:0043632	6	modification-dependent macromolecule catabolic process	155	0.0239	27	0.0447	0.0005525	E

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<input type="radio"/>	GO:0044255	4,5	cellular lipid metabolic process	229	0.0354	36	0.0596	0.0005617	E
<input type="radio"/>	GO:0044237	3	cellular metabolic process	3403	0.5255	350	0.5795	0.0006889	E
<input type="radio"/>	GO:0006096	9,10	glycolysis	24	0.0037	8	0.0132	0.0008580	E
<input type="radio"/>	GO:0006769	8,7	nicotinamide metabolic process	42	0.0065	11	0.0182	0.0009205	E
<input type="radio"/>	GO:0045040	10,9,7,8	protein import into mitochondrial outer membrane	6	0.0009	4	0.0066	0.0009259	E
<input type="radio"/>	GO:0051056	6,7,5	regulation of small GTPase mediated signal transduction	6	0.0009	4	0.0066	0.0009259	E
<input type="radio"/>	GO:0051058	7,8,6	negative regulation of small GTPase mediated signal transduction	6	0.0009	4	0.0066	0.0009259	E
<input type="radio"/>	GO:0046580	8,9,7	negative regulation of Ras protein signal transduction	6	0.0009	4	0.0066	0.0009259	E
<input type="radio"/>	GO:0046578	7,8,6	regulation of Ras protein signal transduction	6	0.0009	4	0.0066	0.0009259	E
<input type="radio"/>	GO:0051641	4,3	cellular localization	642	0.0991	80	0.1325	0.0011164	E
<input type="radio"/>	GO:0065008	3	regulation of biological quality	260	0.0401	38	0.0629	0.0014465	E
<input type="radio"/>	GO:0005976	5	polysaccharide metabolic process	65	0.0100	14	0.0232	0.0014873	E
<input type="radio"/>	GO:0044264	5,6	cellular polysaccharide metabolic process	65	0.0100	14	0.0232	0.0014873	E
<input type="radio"/>	GO:0009966	5,4	regulation of signal transduction	26	0.0040	8	0.0132	0.0015014	E
<input type="radio"/>	GO:0019362	7,6	pyridine nucleotide metabolic process	45	0.0069	11	0.0182	0.0016331	E
<input type="radio"/>	GO:0009117	5	nucleotide metabolic process	111	0.0171	20	0.0331	0.0016733	E
<input type="radio"/>	GO:0006464	6	protein modification process	520	0.0803	66	0.1093	0.0017274	E
<input type="radio"/>	GO:0032502	2	developmental process	436	0.0673	57	0.0944	0.0017595	E
<input type="radio"/>	GO:0019321	6,7	pentose metabolic process	11	0.0017	5	0.0083	0.0017928	E
<input type="radio"/>	GO:0000161	7,8,6	MAPKKK cascade during osmolarity sensing	11	0.0017	5	0.0083	0.0017928	E
<input type="radio"/>	GO:0019395	6,8,7	fatty acid oxidation	11	0.0017	5	0.0083	0.0017928	E
<input type="radio"/>	GO:0065002	8,6,7	intracellular protein transport across a membrane	11	0.0017	5	0.0083	0.0017928	E
<input type="radio"/>	GO:0005992	7,8	trehalose biosynthetic process	7	0.0011	4	0.0066	0.0019602	E
<input type="radio"/>	GO:0046351	6,7	disaccharide biosynthetic process	7	0.0011	4	0.0066	0.0019602	E
<input type="radio"/>	GO:0007008	6,7	outer mitochondrial membrane organization and biogenesis	7	0.0011	4	0.0066	0.0019602	E
<input type="radio"/>	GO:0006623	9,8,7,6	protein targeting to vacuole	67	0.0103	14	0.0232	0.0019673	E
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<input type="radio"/>	GO:0048622	6,5	reproductive sporulation	108	0.0167	19	0.0315	0.0027174	E
<input type="radio"/>	GO:0030437	7,6	sporulation (sensu Fungi)	108	0.0167	19	0.0315	0.0027174	E
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<input type="radio"/>	GO:0000196	8,6	MAPKKK cascade during cell wall biogenesis	4	0.0006	3	0.0050	0.0029307	E
<input type="radio"/>	GO:0019439	5	aromatic compound catabolic process	4	0.0006	3	0.0050	0.0029307	E
<input type="radio"/>	GO:0006121	10,7,5	mitochondrial electron transport, succinate to ubiquinone	4	0.0006	3	0.0050	0.0029307	E
<input type="radio"/>	GO:0006468	8,7	protein amino acid phosphorylation	101	0.0156	18	0.0298	0.0029803	E
<input type="radio"/>	GO:0009063	6,7	amino acid catabolic process	29	0.0045	8	0.0132	0.0030838	E
<input type="radio"/>	GO:0065007	2	biological regulation	948	0.1464	108	0.1788	0.0031274	E
<input type="radio"/>	GO:0007568	3	aging	49	0.0076	11	0.0182	0.0031831	E
<input type="radio"/>	GO:0007569	4	cell aging	49	0.0076	11	0.0182	0.0031831	E
<input type="radio"/>	GO:0007005	5	mitochondrion organization and biogenesis	110	0.0170	19	0.0315	0.0032808	E
<input type="radio"/>	GO:0044238	3	primary metabolic process	3247	0.5014	328	0.5430	0.0033799	E
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<input type="radio"/>	GO:0042493	4	response to drug	121	0.0187	20	0.0331	0.0042062	E
<input type="radio"/>	GO:0006767	5	water-soluble vitamin metabolic process	89	0.0137	16	0.0265	0.0043655	E
<input type="radio"/>	GO:0006766	4	vitamin metabolic process	89	0.0137	16	0.0265	0.0043655	E
<input type="radio"/>	GO:0009108	6	coenzyme biosynthetic process	66	0.0102	13	0.0215	0.0044586	E
<input type="radio"/>	GO:0009165	5,6	nucleotide biosynthetic process	59	0.0091	12	0.0199	0.0047257	E
<input type="radio"/>	GO:0007166	5	cell surface receptor linked signal transduction	52	0.0080	11	0.0182	0.0049356	E
<input type="radio"/>	GO:0006515	8,9	misfolded or incompletely synthesized protein catabolic process	38	0.0059	9	0.0149	0.0049870	E
<input type="radio"/>	GO:0009250	7,8	glucan biosynthetic process	25	0.0039	7	0.0116	0.0049920	E
<input type="radio"/>	GO:0048610	3,4	reproductive cellular process	149	0.0230	23	0.0381	0.0051717	E
<input type="radio"/>	GO:0022413	5,4	reproductive process in single-celled organism	149	0.0230	23	0.0381	0.0051717	E
<input type="radio"/>	GO:0032505	4,3	reproduction of a single-celled organism	194	0.0300	28	0.0464	0.0056056	E
<input type="radio"/>	GO:0043038	6,7	amino acid activation	32	0.0049	8	0.0132	0.0056487	E
<input type="radio"/>	GO:0043039	7,8	tRNA aminoacylation	32	0.0049	8	0.0132	0.0056487	E
<input type="radio"/>	GO:0006418	8,7,9,6	tRNA aminoacylation for protein translation	32	0.0049	8	0.0132	0.0056487	E
<input type="radio"/>	GO:0006643	5,6	membrane lipid metabolic process	125	0.0193	20	0.0331	0.0057987	E
<input type="radio"/>	GO:0000147	5,9,8	actin cortical patch assembly	14	0.0022	5	0.0083	0.0058031	E
<input type="radio"/>	GO:0019935	7	cyclic-nucleotide-mediated signaling	9	0.0014	4	0.0066	0.0058082	E
<input type="radio"/>	GO:0000290	11,8,9,10	deadenylation-dependent decapping	9	0.0014	4	0.0066	0.0058082	E
<input type="radio"/>	GO:0019933	8	cAMP-mediated signaling	9	0.0014	4	0.0066	0.0058082	E
<input type="radio"/>	GO:0006635	7,9,8	fatty acid beta-oxidation	9	0.0014	4	0.0066	0.0058082	E
<input type="radio"/>	GO:0008154	8,5	actin polymerization and/or depolymerization	9	0.0014	4	0.0066	0.0058082	E
<input type="radio"/>	GO:0043648	6	dicarboxylic acid metabolic process	9	0.0014	4	0.0066	0.0058082	E
<input type="radio"/>	GO:0000003	2	reproduction	323	0.0499	42	0.0695	0.0058132	E
<input type="radio"/>	GO:0042592	4	homeostatic process	134	0.0207	21	0.0348	0.0060265	E
<input type="radio"/>	GO:0051649	5,3,4	establishment of cellular localization	606	0.0936	71	0.1175	0.0064259	E
<input type="radio"/>	GO:0046942	5,6	carboxylic acid transport	54	0.0083	11	0.0182	0.0064440	E
<input type="radio"/>	GO:0000266	6	mitochondrial fission	5	0.0008	3	0.0050	0.0066464	E
<input type="radio"/>	GO:0009268	4	response to pH	5	0.0008	3	0.0050	0.0066464	E
<input type="radio"/>	GO:0019323	7,8	pentose catabolic process	5	0.0008	3	0.0050	0.0066464	E
<input type="radio"/>	GO:0042219	6,5	amino acid derivative catabolic process	5	0.0008	3	0.0050	0.0066464	E
<input type="radio"/>	GO:0015849	4,5	organic acid transport	55	0.0085	11	0.0182	0.0073113	E
<input type="radio"/>	GO:0051188	5	cofactor biosynthetic process	79	0.0122	14	0.0232	0.0078415	E
<input type="radio"/>	GO:0048869	3	cellular developmental process	173	0.0267	25	0.0414	0.0078695	E
<input type="radio"/>	GO:0030154	4	cell differentiation	173	0.0267	25	0.0414	0.0078695	E
<input type="radio"/>	GO:0005978	8,7,9	glycogen biosynthetic process	15	0.0023	5	0.0083	0.0078978	E
<input type="radio"/>	GO:0000271	6,7	polysaccharide biosynthetic process	41	0.0063	9	0.0149	0.0080121	E
<input type="radio"/>	GO:0051640	5,4	organelle localization	56	0.0086	11	0.0182	0.0082582	E
<input type="radio"/>	GO:0032889	6,7,5	regulation of vacuole fusion, non-autophagic	2	0.0003	2	0.0033	0.0086858	E
<input type="radio"/>	GO:0019482	7,8	beta-alanine metabolic process	2	0.0003	2	0.0033	0.0086858	E
<input type="radio"/>	GO:0051339	5	regulation of lyase activity	2	0.0003	2	0.0033	0.0086858	E
<input type="radio"/>	GO:0015804	6,7,8	neutral amino acid transport	2	0.0003	2	0.0033	0.0086858	E
<input type="radio"/>	GO:0031279	5	regulation of cyclase activity	2	0.0003	2	0.0033	0.0086858	E

<input type="radio"/>	GO:0009074	7,6,8	aromatic amino acid family catabolic process	2	0.0003	2	0.0033	0.0086858	E
<input type="radio"/>	GO:0019483	8,9	beta-alanine biosynthetic process	2	0.0003	2	0.0033	0.0086858	E
<input type="radio"/>	GO:0001315	6	age-dependent response to reactive oxygen species	2	0.0003	2	0.0033	0.0086858	E
<input type="radio"/>	GO:0015824	7,8,9	proline transport	2	0.0003	2	0.0033	0.0086858	E
<input type="radio"/>	GO:0000060	9,10,11,7,8	protein import into nucleus, translocation	2	0.0003	2	0.0033	0.0086858	E
<input type="radio"/>	GO:0001320	6,7,8	age-dependent response to reactive oxygen species during chronological cell aging	2	0.0003	2	0.0033	0.0086858	E
<input type="radio"/>	GO:0006103	5,7	2-oxoglutarate metabolic process	2	0.0003	2	0.0033	0.0086858	E
<input type="radio"/>	GO:0045761	6,9,10	regulation of adenylate cyclase activity	2	0.0003	2	0.0033	0.0086858	E
<input type="radio"/>	GO:0006538	8,9	glutamate catabolic process	2	0.0003	2	0.0033	0.0086858	E
<input type="radio"/>	GO:0019363	7,6,8	pyridine nucleotide biosynthetic process	10	0.0015	4	0.0066	0.0087822	E
<input type="radio"/>	GO:0006616	9,12,11,7,10,8	SRP-dependent cotranslational protein targeting to membrane, translocation	10	0.0015	4	0.0066	0.0087822	E
<input type="radio"/>	GO:0016197	7,5,6	endosome transport	49	0.0076	10	0.0166	0.0088177	E
<input type="radio"/>	GO:0006812	5,6	cation transport	97	0.0150	16	0.0265	0.0090541	E
<input type="radio"/>	GO:0006906	6,5	vesicle fusion	28	0.0043	7	0.0116	0.0091880	E
<input type="radio"/>	GO:0030433	9,11,10,12	ER-associated protein catabolic process	35	0.0054	8	0.0132	0.0094464	E
<input type="radio"/>	GO:0015837	4,5	amine transport	50	0.0077	10	0.0166	0.0100035	E
<input type="radio"/>	GO:0007231	6,5	osmosensory signaling pathway	22	0.0034	6	0.0099	0.0101548	E
<input type="radio"/>	GO:0006536	7,8	glutamate metabolic process	16	0.0025	5	0.0083	0.0104227	E
<input type="radio"/>	GO:0048015	7	phosphoinositide-mediated signaling	16	0.0025	5	0.0083	0.0104227	E
<input type="radio"/>	GO:0048017	8	inositol lipid-mediated signaling	16	0.0025	5	0.0083	0.0104227	E
<input type="radio"/>	GO:0006944	5	membrane fusion	59	0.0091	11	0.0182	0.0116052	E
<input type="radio"/>	GO:0006000	7,8	fructose metabolic process	6	0.0009	3	0.0050	0.0120582	E
<input type="radio"/>	GO:0006800	4	oxygen and reactive oxygen species metabolic process	6	0.0009	3	0.0050	0.0120582	E
<input type="radio"/>	GO:0051347	6	positive regulation of transferase activity	6	0.0009	3	0.0050	0.0120582	E
<input type="radio"/>	GO:0045860	7,8	positive regulation of protein kinase activity	6	0.0009	3	0.0050	0.0120582	E
<input type="radio"/>	GO:0048285	5	organelle fission	6	0.0009	3	0.0050	0.0120582	E
<input type="radio"/>	GO:0015758	7,8	glucose transport	6	0.0009	3	0.0050	0.0120582	E
<input type="radio"/>	GO:0031505	6	chitin- and beta-glucan-containing cell wall organization and biogenesis	44	0.0068	9	0.0149	0.0121180	E
<input type="radio"/>	GO:0043085	5	positive regulation of enzyme activity	11	0.0017	4	0.0066	0.0125200	E
<input type="radio"/>	GO:0031667	5	response to nutrient levels	37	0.0057	8	0.0132	0.0127606	E
<input type="radio"/>	GO:0009605	3	response to external stimulus	37	0.0057	8	0.0132	0.0127606	E
<input type="radio"/>	GO:0009991	4	response to extracellular stimulus	37	0.0057	8	0.0132	0.0127606	E
<input type="radio"/>	GO:0032940	6,4,5	secretion by cell	250	0.0386	32	0.0530	0.0143117	E
<input type="radio"/>	GO:0046903	3,4	secretion	250	0.0386	32	0.0530	0.0143117	E
<input type="radio"/>	GO:0000288	10,8,9	mRNA catabolic process, deadenylation-dependent decay	24	0.0037	6	0.0099	0.0150808	E
<input type="radio"/>	GO:0006865	5,6,7	amino acid transport	39	0.0060	8	0.0132	0.0167441	E
<input type="radio"/>	GO:0001302	5	replicative cell aging	39	0.0060	8	0.0132	0.0167441	E
<input type="radio"/>	GO:0007265	7	Ras protein signal transduction	39	0.0060	8	0.0132	0.0167441	E
<input type="radio"/>	GO:0006067	5	ethanol metabolic process	12	0.0019	4	0.0066	0.0170370	E
<input type="radio"/>	GO:0051273	7,8	beta-glucan metabolic process	12	0.0019	4	0.0066	0.0170370	E
<input type="radio"/>	GO:0043161	10,9,11	proteasomal ubiquitin-dependent protein catabolic process	63	0.0097	11	0.0182	0.0173237	E
<input type="radio"/>	GO:0015672	6,7	monovalent inorganic cation transport	32	0.0049	7	0.0116	0.0177064	E

<input type="radio"/>	GO:0006811	4,5	ion transport	115	0.0178	17	0.0281	0.0177459	E
<input type="radio"/>	GO:0045184	3,4,5	establishment of protein localization	296	0.0457	36	0.0596	0.0186543	E
<input type="radio"/>	GO:0007571	3,4	age-dependent general metabolic decline	7	0.0011	3	0.0050	0.0191417	E
<input type="radio"/>	GO:0006078	9,8,10	1,6-beta-glucan biosynthetic process	7	0.0011	3	0.0050	0.0191417	E
<input type="radio"/>	GO:0043248	8,7	proteasome assembly	7	0.0011	3	0.0050	0.0191417	E
<input type="radio"/>	GO:0009653	4,3	anatomical structure morphogenesis	248	0.0383	31	0.0513	0.0191954	E
<input type="radio"/>	GO:0032989	4,5	cellular structure morphogenesis	248	0.0383	31	0.0513	0.0191954	E
<input type="radio"/>	GO:0048856	3	anatomical structure development	248	0.0383	31	0.0513	0.0191954	E
<input type="radio"/>	GO:0000902	5,6	cell morphogenesis	248	0.0383	31	0.0513	0.0191954	E
<input type="radio"/>	GO:0006605	8,6,7	protein targeting	258	0.0398	32	0.0530	0.0193897	E
<input type="radio"/>	GO:0022414	3,2	reproductive process	183	0.0283	24	0.0397	0.0210237	E
<input type="radio"/>	GO:0050789	3	regulation of biological process	761	0.1175	81	0.1341	0.0214028	E
<input type="radio"/>	GO:0046907	6,4,5	intracellular transport	545	0.0842	60	0.0993	0.0221722	E
<input type="radio"/>	GO:0040008	4,3	regulation of growth	13	0.0020	4	0.0066	0.0223248	E
<input type="radio"/>	GO:0001300	5	chronological cell aging	13	0.0020	4	0.0066	0.0223248	E
<input type="radio"/>	GO:0006869	4,5	lipid transport	34	0.0053	7	0.0116	0.0232988	E
<input type="radio"/>	GO:0007186	6	G-protein coupled receptor protein signaling pathway	34	0.0053	7	0.0116	0.0232988	E
<input type="radio"/>	GO:0008361	4,6,7	regulation of cell size	129	0.0199	18	0.0298	0.0235174	E
<input type="radio"/>	GO:0042402	6,7	biogenic amine catabolic process	3	0.0005	2	0.0033	0.0236343	E
<input type="radio"/>	GO:0006011	8,6,9	UDP-glucose metabolic process	3	0.0005	2	0.0033	0.0236343	E
<input type="radio"/>	GO:0006741	8,7,10,9	NADP biosynthetic process	3	0.0005	2	0.0033	0.0236343	E
<input type="radio"/>	GO:0009437	6,7	carnitine metabolic process	3	0.0005	2	0.0033	0.0236343	E
<input type="radio"/>	GO:0006598	7,8	polyamine catabolic process	3	0.0005	2	0.0033	0.0236343	E
<input type="radio"/>	GO:0006003	8,9	fructose 2,6-bisphosphate metabolic process	3	0.0005	2	0.0033	0.0236343	E
<input type="radio"/>	GO:0045010	8	actin nucleation	3	0.0005	2	0.0033	0.0236343	E
<input type="radio"/>	GO:0005993	8,7	trehalose catabolic process	3	0.0005	2	0.0033	0.0236343	E
<input type="radio"/>	GO:0046459	6,8,7	short-chain fatty acid metabolic process	3	0.0005	2	0.0033	0.0236343	E
<input type="radio"/>	GO:0000186	9,10,8	activation of MAPKK activity	3	0.0005	2	0.0033	0.0236343	E
<input type="radio"/>	GO:0006886	7,5,6	intracellular protein transport	274	0.0423	33	0.0546	0.0238478	E
<input type="radio"/>	GO:0006754	7,9,6,8,10	ATP biosynthetic process	20	0.0031	5	0.0083	0.0250644	E
<input type="radio"/>	GO:0015986	8,10,7,9,11,5	ATP synthesis coupled proton transport	20	0.0031	5	0.0083	0.0250644	E
<input type="radio"/>	GO:0016579	9	protein deubiquitination	20	0.0031	5	0.0083	0.0250644	E
<input type="radio"/>	GO:0006753	7	nucleoside phosphate metabolic process	20	0.0031	5	0.0083	0.0250644	E
<input type="radio"/>	GO:0000209	10	protein polyubiquitination	20	0.0031	5	0.0083	0.0250644	E
<input type="radio"/>	GO:0015985	6,8,7,9	energy coupled proton transport, down electrochemical gradient	20	0.0031	5	0.0083	0.0250644	E
<input type="radio"/>	GO:0016043	3	cellular component organization and biogenesis	2264	0.3496	220	0.3642	0.0259397	E
<input type="radio"/>	GO:0009064	6,7	glutamine family amino acid metabolic process	43	0.0066	8	0.0132	0.0267539	E
<input type="radio"/>	GO:0040007	2	growth	141	0.0218	19	0.0315	0.0268435	E
<input type="radio"/>	GO:0009306	7,5,4,6	protein secretion	8	0.0012	3	0.0050	0.0277813	E
<input type="radio"/>	GO:0008104	4	protein localization	330	0.0510	38	0.0629	0.0280720	E
<input type="radio"/>	GO:0006740	10,9	NADPH regeneration	14	0.0022	4	0.0066	0.0283531	E
<input type="radio"/>	GO:0015031	4,5,6	protein transport	280	0.0432	33	0.0546	0.0285485	E
<input type="radio"/>	GO:0009266	4	response to temperature stimulus	28	0.0043	6	0.0099	0.0286040	E
<input type="radio"/>	GO:0006094	8,9	gluconeogenesis	28	0.0043	6	0.0099	0.0286040	E

<input type="checkbox"/>	GO:0043412	5	biopolymer modification	664	0.1025	70	0.1159	0.0286340	E
<input type="checkbox"/>	GO:0006887	8,6,5,7	exocytosis	44	0.0068	8	0.0132	0.0296697	E
<input type="checkbox"/>	GO:0033554	4	cellular response to stress	21	0.0032	5	0.0083	0.0298447	E
<input type="checkbox"/>	GO:0046034	5,9	ATP metabolic process	21	0.0032	5	0.0083	0.0298447	E
<input type="checkbox"/>	GO:0051716	3	cellular response to stimulus	21	0.0032	5	0.0083	0.0298447	E
<input type="checkbox"/>	GO:0045324	8,6,7	late endosome to vacuole transport	21	0.0032	5	0.0083	0.0298447	E
<input type="checkbox"/>	GO:0019674	9,8	NAD metabolic process	21	0.0032	5	0.0083	0.0298447	E
<input type="checkbox"/>	GO:0055082	6,4	cellular chemical homeostasis	115	0.0178	16	0.0265	0.0299234	E
<input type="checkbox"/>	GO:0006873	7,5	cellular ion homeostasis	115	0.0178	16	0.0265	0.0299234	E
<input type="checkbox"/>	GO:0007264	6	small GTPase mediated signal transduction	61	0.0094	10	0.0166	0.0301889	E
<input type="checkbox"/>	GO:0006644	6,7	phospholipid metabolic process	97	0.0150	14	0.0232	0.0308056	E
<input type="checkbox"/>	GO:0045045	7,5,4,6	secretory pathway	243	0.0375	29	0.0480	0.0313938	E
<input type="checkbox"/>	GO:0009719	3	response to endogenous stimulus	243	0.0375	29	0.0480	0.0313938	E
<input type="checkbox"/>	GO:0043170	3	macromolecule metabolic process	2841	0.4387	269	0.4454	0.0322917	E
<input type="checkbox"/>	GO:0006974	4	response to DNA damage stimulus	234	0.0361	28	0.0464	0.0324056	E
<input type="checkbox"/>	GO:0050790	4	regulation of catalytic activity	45	0.0069	8	0.0132	0.0327411	E
<input type="checkbox"/>	GO:0051301	3	cell division	246	0.0380	29	0.0480	0.0342656	E
<input type="checkbox"/>	GO:0006513	10	protein monoubiquitination	22	0.0034	5	0.0083	0.0350385	E
<input type="checkbox"/>	GO:0009145	7,8	purine nucleoside triphosphate biosynthetic process	22	0.0034	5	0.0083	0.0350385	E
<input type="checkbox"/>	GO:0009206	8,9	purine ribonucleoside triphosphate biosynthetic process	22	0.0034	5	0.0083	0.0350385	E
<input type="checkbox"/>	GO:0015918	5,6	sterol transport	15	0.0023	4	0.0066	0.0350734	E
<input type="checkbox"/>	GO:0065009	3	regulation of a molecular function	46	0.0071	8	0.0132	0.0359609	E
<input type="checkbox"/>	GO:0050801	6	ion homeostasis	119	0.0184	16	0.0265	0.0364575	E
<input type="checkbox"/>	GO:0006090	7	pyruvate metabolic process	38	0.0059	7	0.0116	0.0370395	E
<input type="checkbox"/>	GO:0009152	7,8	purine ribonucleotide biosynthetic process	38	0.0059	7	0.0116	0.0370395	E
<input type="checkbox"/>	GO:0043488	9,8,7	regulation of mRNA stability	30	0.0046	6	0.0099	0.0371075	E
<input type="checkbox"/>	GO:0006665	6,7	sphingolipid metabolic process	30	0.0046	6	0.0099	0.0371075	E
<input type="checkbox"/>	GO:0043487	8,7	regulation of RNA stability	30	0.0046	6	0.0099	0.0371075	E
<input type="checkbox"/>	GO:0046364	6,7	monosaccharide biosynthetic process	30	0.0046	6	0.0099	0.0371075	E
<input type="checkbox"/>	GO:0019319	7,8	hexose biosynthetic process	30	0.0046	6	0.0099	0.0371075	E
<input type="checkbox"/>	GO:0006744	8,7	ubiquinone biosynthetic process	9	0.0014	3	0.0050	0.0377999	E
<input type="checkbox"/>	GO:0015891	4,5	siderophore transport	9	0.0014	3	0.0050	0.0377999	E
<input type="checkbox"/>	GO:0030952	6	establishment and/or maintenance of cytoskeleton polarity	9	0.0014	3	0.0050	0.0377999	E
<input type="checkbox"/>	GO:0006874	10,8	cellular calcium ion homeostasis	9	0.0014	3	0.0050	0.0377999	E
<input type="checkbox"/>	GO:0045426	7,6	quinone cofactor biosynthetic process	9	0.0014	3	0.0050	0.0377999	E
<input type="checkbox"/>	GO:0055074	9	calcium ion homeostasis	9	0.0014	3	0.0050	0.0377999	E
<input type="checkbox"/>	GO:0030950	8,7	establishment and/or maintenance of actin cytoskeleton polarity	9	0.0014	3	0.0050	0.0377999	E
<input type="checkbox"/>	GO:0006743	7,6	ubiquinone metabolic process	9	0.0014	3	0.0050	0.0377999	E
<input type="checkbox"/>	GO:0042375	5	quinone cofactor metabolic process	9	0.0014	3	0.0050	0.0377999	E
<input type="checkbox"/>	GO:0044260	4	cellular macromolecule metabolic process	1552	0.2397	147	0.2434	0.0387322	E
<input type="checkbox"/>	GO:0048878	5	chemical homeostasis	121	0.0187	16	0.0265	0.0399228	E
<input type="checkbox"/>	GO:0016049	5,3,7,8	cell growth	102	0.0158	14	0.0232	0.0403088	E
<input type="checkbox"/>	GO:0009144	7	purine nucleoside triphosphate metabolic process	23	0.0036	5	0.0083	0.0406162	E
<input type="checkbox"/>	GO:0009408	5,4	response to heat	23	0.0036	5	0.0083	0.0406162	E

<input type="radio"/>	GO:0009205	8	purine ribonucleoside triphosphate metabolic process	23	0.0036	5	0.0083	0.0406162	E
<input type="radio"/>	GO:0006519	4	amino acid and derivative metabolic process	202	0.0312	24	0.0397	0.0417239	E
<input type="radio"/>	GO:0005984	6	disaccharide metabolic process	31	0.0048	6	0.0099	0.0417446	E
<input type="radio"/>	GO:0032446	8	protein modification by small protein conjugation	84	0.0130	12	0.0199	0.0422212	E
<input type="radio"/>	GO:0043162	10,9,11	ubiquitin-dependent protein catabolic process via the multivesicular body pathway	16	0.0025	4	0.0066	0.0424218	E
<input type="radio"/>	GO:0046323	8,9	glucose import	4	0.0006	2	0.0033	0.0428725	E
<input type="radio"/>	GO:0030162	6,7,5	regulation of proteolysis	4	0.0006	2	0.0033	0.0428725	E
<input type="radio"/>	GO:0019566	7,8	arabinose metabolic process	4	0.0006	2	0.0033	0.0428725	E
<input type="radio"/>	GO:0042732	7,8	D-xylose metabolic process	4	0.0006	2	0.0033	0.0428725	E
<input type="radio"/>	GO:0042843	8,9	D-xylose catabolic process	4	0.0006	2	0.0033	0.0428725	E
<input type="radio"/>	GO:0030042	9,6,7	actin filament depolymerization	4	0.0006	2	0.0033	0.0428725	E
<input type="radio"/>	GO:0006101	6,7	citrate metabolic process	4	0.0006	2	0.0033	0.0428725	E
<input type="radio"/>	GO:0042542	6	response to hydrogen peroxide	4	0.0006	2	0.0033	0.0428725	E
<input type="radio"/>	GO:0042180	4	ketone metabolic process	4	0.0006	2	0.0033	0.0428725	E
<input type="radio"/>	GO:0000045	5	autophagic vacuole formation	4	0.0006	2	0.0033	0.0428725	E
<input type="radio"/>	GO:0016577	11,9,10	histone demethylation	4	0.0006	2	0.0033	0.0428725	E
<input type="radio"/>	GO:0019568	8,9	arabinose catabolic process	4	0.0006	2	0.0033	0.0428725	E
<input type="radio"/>	GO:0032147	8,9	activation of protein kinase activity	4	0.0006	2	0.0033	0.0428725	E
<input type="radio"/>	GO:0006482	9	protein amino acid demethylation	4	0.0006	2	0.0033	0.0428725	E
<input type="radio"/>	GO:0006814	7,8	sodium ion transport	4	0.0006	2	0.0033	0.0428725	E
<input type="radio"/>	GO:0006562	8,9	proline catabolic process	4	0.0006	2	0.0033	0.0428725	E
<input type="radio"/>	GO:0046395	6	carboxylic acid catabolic process	4	0.0006	2	0.0033	0.0428725	E
<input type="radio"/>	GO:0008214	8	protein amino acid dealkylation	4	0.0006	2	0.0033	0.0428725	E
<input type="radio"/>	GO:0006281	6,5	DNA repair	193	0.0298	23	0.0381	0.0432275	E
<input type="radio"/>	GO:0016567	9	protein ubiquitination	66	0.0102	10	0.0166	0.0434438	E
<input type="radio"/>	GO:0050794	4,3	regulation of cellular process	738	0.1140	73	0.1209	0.0448705	E
<input type="radio"/>	GO:0009260	6,7	ribonucleotide biosynthetic process	40	0.0062	7	0.0116	0.0450393	E
<input type="radio"/>	GO:0009201	7,8	ribonucleoside triphosphate biosynthetic process	24	0.0037	5	0.0083	0.0465423	E
<input type="radio"/>	GO:0015992	5,7,6,8	proton transport	24	0.0037	5	0.0083	0.0465423	E
<input type="radio"/>	GO:0051278	8,7	chitin- and beta-glucan-containing cell wall polysaccharide biosynthetic process	24	0.0037	5	0.0083	0.0465423	E
<input type="radio"/>	GO:0006818	4,5	hydrogen transport	24	0.0037	5	0.0083	0.0465423	E
<input type="radio"/>	GO:0008654	7,6,8	phospholipid biosynthetic process	58	0.0090	9	0.0149	0.0466997	E
<input type="radio"/>	GO:0009308	4	amine metabolic process	228	0.0352	26	0.0430	0.0479822	E
<input type="radio"/>	GO:0006520	5,6	amino acid metabolic process	187	0.0289	22	0.0364	0.0488590	E
<input type="radio"/>	GO:0051261	6	protein depolymerization	10	0.0015	3	0.0050	0.0489814	E
<input type="radio"/>	GO:0015718	6,7	monocarboxylic acid transport	10	0.0015	3	0.0050	0.0489814	E
<input type="radio"/>	GO:0006123	10,7,5	mitochondrial electron transport, cytochrome c to oxygen	10	0.0015	3	0.0050	0.0489814	E
<input type="radio"/>	GO:0006164	6,7	purine nucleotide biosynthetic process	41	0.0063	7	0.0116	0.0492741	E
<input type="radio"/>	GO:0009150	7	purine ribonucleotide metabolic process	41	0.0063	7	0.0116	0.0492741	E
<input type="radio"/>	GO:0006807	3	nitrogen compound metabolic process	251	0.0388	28	0.0464	0.0500176	E
<input type="radio"/>	GO:0016053	5	organic acid biosynthetic process	17	0.0026	4	0.0066	0.0503222	E
<input type="radio"/>	GO:0046394	6	carboxylic acid biosynthetic process	17	0.0026	4	0.0066	0.0503222	E
<input type="radio"/>	GO:0033036	3	macromolecule localization	382	0.0590	40	0.0662	0.0507672	E

<input type="radio"/>	GO:0046467	6,5,7	membrane lipid biosynthetic process	78	0.0120	11	0.0182	0.0509700	E
<input type="radio"/>	GO:0009272	7	chitin- and beta-glucan-containing cell wall biogenesis	33	0.0051	6	0.0099	0.0516821	E
<input type="radio"/>	GO:0042546	6	cell wall biogenesis	33	0.0051	6	0.0099	0.0516821	E
<input type="radio"/>	GO:0007126	8,6,7,5	meiosis	148	0.0229	18	0.0298	0.0521517	E
<input type="radio"/>	GO:0051327	7,5,6	M phase of meiotic cell cycle	148	0.0229	18	0.0298	0.0521517	E
<input type="radio"/>	GO:0051321	4	meiotic cell cycle	148	0.0229	18	0.0298	0.0521517	E
<input type="radio"/>	GO:0006892	8,6,5,7	post-Golgi vesicle-mediated transport	69	0.0107	10	0.0166	0.0522979	E
<input type="radio"/>	GO:0009199	7	ribonucleoside triphosphate metabolic process	25	0.0039	5	0.0083	0.0527767	E
<input type="radio"/>	GO:0001403	6,4,8,9	invasive growth (sensu Saccharomyces)	42	0.0065	7	0.0116	0.0536433	E
<input type="radio"/>	GO:0022402	4,3	cell cycle process	439	0.0678	44	0.0728	0.0575667	E
<input type="radio"/>	GO:0000082	8,5,6,7,4	G1/S transition of mitotic cell cycle	52	0.0080	8	0.0132	0.0578441	E
<input type="radio"/>	GO:0009259	6	ribonucleotide metabolic process	43	0.0066	7	0.0116	0.0581286	E
<input type="radio"/>	GO:0007584	6,4	response to nutrient	18	0.0028	4	0.0066	0.0586898	E
<input type="radio"/>	GO:0007049	3	cell cycle	458	0.0707	45	0.0745	0.0604866	E
<input type="radio"/>	GO:0006098	9,10,11	pentose-phosphate shunt	11	0.0017	3	0.0050	0.0610895	E
<input type="radio"/>	GO:0045454	6,4	cell redox homeostasis	11	0.0017	3	0.0050	0.0610895	E
<input type="radio"/>	GO:0006116	10,9	NADH oxidation	11	0.0017	3	0.0050	0.0610895	E
<input type="radio"/>	GO:0030503	5,7,4	regulation of cell redox homeostasis	11	0.0017	3	0.0050	0.0610895	E
<input type="radio"/>	GO:0006488	10,9,8	dolichol-linked oligosaccharide biosynthetic process	11	0.0017	3	0.0050	0.0610895	E
<input type="radio"/>	GO:0051274	8,9	beta-glucan biosynthetic process	11	0.0017	3	0.0050	0.0610895	E
<input type="radio"/>	GO:0001558	5,6,4,8,9	regulation of cell growth	11	0.0017	3	0.0050	0.0610895	E
<input type="radio"/>	GO:0006972	5	hyperosmotic response	11	0.0017	3	0.0050	0.0610895	E
<input type="radio"/>	GO:0022403	5,4	cell cycle phase	353	0.0545	36	0.0596	0.0612817	E
<input type="radio"/>	GO:0055080	7	cation homeostasis	102	0.0158	13	0.0215	0.0620553	E
<input type="radio"/>	GO:0030003	8,6	cellular cation homeostasis	102	0.0158	13	0.0215	0.0620553	E
<input type="radio"/>	GO:0044249	4	cellular biosynthetic process	366	0.0565	37	0.0613	0.0620807	E
<input type="radio"/>	GO:0046165	5	alcohol biosynthetic process	35	0.0054	6	0.0099	0.0623329	E
<input type="radio"/>	GO:0006357	9,8	regulation of transcription from RNA polymerase II promoter	221	0.0341	24	0.0397	0.0646985	E
<input type="radio"/>	GO:0042149	8,7,6	cellular response to glucose starvation	5	0.0008	2	0.0033	0.0648078	E
<input type="radio"/>	GO:0019388	8,9	galactose catabolic process	5	0.0008	2	0.0033	0.0648078	E
<input type="radio"/>	GO:0006499	10,11,9,8	N-terminal protein myristoylation	5	0.0008	2	0.0033	0.0648078	E
<input type="radio"/>	GO:0006498	9,10,8,7	N-terminal protein lipidation	5	0.0008	2	0.0033	0.0648078	E
<input type="radio"/>	GO:0042946	5,6	glucoside transport	5	0.0008	2	0.0033	0.0648078	E
<input type="radio"/>	GO:0000017	6,7	alpha-glucoside transport	5	0.0008	2	0.0033	0.0648078	E
<input type="radio"/>	GO:0019541	7	propionate metabolic process	5	0.0008	2	0.0033	0.0648078	E
<input type="radio"/>	GO:0007187	7,8	G-protein signaling, coupled to cyclic nucleotide second messenger	5	0.0008	2	0.0033	0.0648078	E
<input type="radio"/>	GO:0007188	8,9	G-protein signaling, coupled to cAMP nucleotide second messenger	5	0.0008	2	0.0033	0.0648078	E
<input type="radio"/>	GO:0009051	10,7,11,12,8	pentose-phosphate shunt, oxidative branch	5	0.0008	2	0.0033	0.0648078	E
<input type="radio"/>	GO:0018319	10,9,8	protein amino acid myristoylation	5	0.0008	2	0.0033	0.0648078	E
<input type="radio"/>	GO:0018377	9,8,7	protein myristoylation	5	0.0008	2	0.0033	0.0648078	E
<input type="radio"/>	GO:0009142	6,7	nucleoside triphosphate biosynthetic process	27	0.0042	5	0.0083	0.0659911	E
<input type="radio"/>	GO:0055066	8	di-, tri-valent inorganic cation homeostasis	64	0.0099	9	0.0149	0.0673538	E
<input type="radio"/>	GO:0030005	9,7	cellular di-, tri-valent inorganic cation homeostasis	64	0.0099	9	0.0149	0.0673538	E

<input type="radio"/>	GO:0031668	5,4	cellular response to extracellular stimulus	19	0.0029	4	0.0066	0.0674336	E
<input type="radio"/>	GO:0031669	6,5	cellular response to nutrient levels	19	0.0029	4	0.0066	0.0674336	E
<input type="radio"/>	GO:0006875	9,7	cellular metal ion homeostasis	19	0.0029	4	0.0066	0.0674336	E
<input type="radio"/>	GO:0055065	8	metal ion homeostasis	19	0.0029	4	0.0066	0.0674336	E
<input type="radio"/>	GO:0042594	6,4	response to starvation	19	0.0029	4	0.0066	0.0674336	E
<input type="radio"/>	GO:0009267	7,6,5	cellular response to starvation	19	0.0029	4	0.0066	0.0674336	E
<input type="radio"/>	GO:0019236	4	response to pheromone	94	0.0145	12	0.0199	0.0674670	E
<input type="radio"/>	GO:0051252	7,6	regulation of RNA metabolic process	36	0.0056	6	0.0099	0.0678548	E
<input type="radio"/>	GO:0006461	6,5	protein complex assembly	116	0.0179	14	0.0232	0.0703468	E
<input type="radio"/>	GO:0006839	7,5,6	mitochondrial transport	65	0.0100	9	0.0149	0.0709240	E
<input type="radio"/>	GO:0032005	7,6	signal transduction during conjugation with cellular fusion	28	0.0043	5	0.0083	0.0728750	E
<input type="radio"/>	GO:0000750	8,7,6	pheromone-dependent signal transduction during conjugation with cellular fusion	28	0.0043	5	0.0083	0.0728750	E
<input type="radio"/>	GO:0015846	5,6	polyamine transport	12	0.0019	3	0.0050	0.0738806	E
<input type="radio"/>	GO:0008054	7,6,11,10,12	cyclin catabolic process	12	0.0019	3	0.0050	0.0738806	E
<input type="radio"/>	GO:0019953	3	sexual reproduction	118	0.0182	14	0.0232	0.0746229	E
<input type="radio"/>	GO:0000747	4	conjugation with cellular fusion	118	0.0182	14	0.0232	0.0746229	E
<input type="radio"/>	GO:0000746	3	conjugation	118	0.0182	14	0.0232	0.0746229	E
<input type="radio"/>	GO:0008610	5,4,6	lipid biosynthetic process	129	0.0199	15	0.0248	0.0750181	E
<input type="radio"/>	GO:0006614	11,10,9,8,7	SRP-dependent cotranslational protein targeting to membrane	20	0.0031	4	0.0066	0.0764593	E
<input type="radio"/>	GO:0006163	6	purine nucleotide metabolic process	47	0.0073	7	0.0116	0.0768363	E
<input type="radio"/>	GO:0008643	4,5	carbohydrate transport	38	0.0059	6	0.0099	0.0791405	E
<input type="radio"/>	GO:0016485	8	protein processing	38	0.0059	6	0.0099	0.0791405	E
<input type="radio"/>	GO:0006399	6	tRNA metabolic process	121	0.0187	14	0.0232	0.0808351	E
<input type="radio"/>	GO:0051726	5,4	regulation of cell cycle	167	0.0258	18	0.0298	0.0819631	E
<input type="radio"/>	GO:0000074	6,5	regulation of progression through cell cycle	167	0.0258	18	0.0298	0.0819631	E
<input type="radio"/>	GO:0046474	8,7,9	glycerophospholipid biosynthetic process	39	0.0060	6	0.0099	0.0848421	E
<input type="radio"/>	GO:0051329	7,5,6	interphase of mitotic cell cycle	112	0.0173	13	0.0215	0.0851333	E
<input type="radio"/>	GO:0051325	6,5	interphase	112	0.0173	13	0.0215	0.0851333	E
<input type="radio"/>	GO:0043623	7,6	cellular protein complex assembly	69	0.0107	9	0.0149	0.0851562	E
<input type="radio"/>	GO:0009141	6	nucleoside triphosphate metabolic process	30	0.0046	5	0.0083	0.0869467	E
<input type="radio"/>	GO:0046999	5,4	regulation of conjugation	30	0.0046	5	0.0083	0.0869467	E
<input type="radio"/>	GO:0031137	6,5	regulation of conjugation with cellular fusion	30	0.0046	5	0.0083	0.0869467	E
<input type="radio"/>	GO:0031929	6	TOR signaling pathway	13	0.0020	3	0.0050	0.0871149	E
<input type="radio"/>	GO:0006537	8,9	glutamate biosynthetic process	13	0.0020	3	0.0050	0.0871149	E
<input type="radio"/>	GO:0006083	7	acetate metabolic process	6	0.0009	2	0.0033	0.0881680	E
<input type="radio"/>	GO:0015695	6,7	organic cation transport	6	0.0009	2	0.0033	0.0881680	E
<input type="radio"/>	GO:0006013	7,8	mannose metabolic process	6	0.0009	2	0.0033	0.0881680	E
<input type="radio"/>	GO:0015696	7,8	ammonium transport	6	0.0009	2	0.0033	0.0881680	E
<input type="radio"/>	GO:0006358	10,9	regulation of global transcription from RNA polymerase II promoter	6	0.0009	2	0.0033	0.0881680	E
<input type="radio"/>	GO:0001306	4,5	age-dependent response to oxidative stress	6	0.0009	2	0.0033	0.0881680	E
<input type="radio"/>	GO:0043405	8	regulation of MAPK activity	6	0.0009	2	0.0033	0.0881680	E
<input type="radio"/>	GO:0001323	4,5,6	age-dependent general metabolic decline during chronological cell aging	6	0.0009	2	0.0033	0.0881680	E
<input type="radio"/>	GO:0016054	5	organic acid catabolic process	6	0.0009	2	0.0033	0.0881680	E

<input type="checkbox"/>	GO:0006110	6,10,11,5	regulation of glycolysis	6	0.0009	2	0.0033	0.0881680	E
<input type="checkbox"/>	GO:0016236	4	macroautophagy	6	0.0009	2	0.0033	0.0881680	E
<input type="checkbox"/>	GO:0019795	7,8	nonprotein amino acid biosynthetic process	6	0.0009	2	0.0033	0.0881680	E
<input type="checkbox"/>	GO:0001324	5,6,7	age-dependent response to oxidative stress during chronological cell aging	6	0.0009	2	0.0033	0.0881680	E
<input type="checkbox"/>	GO:0006650	7,8	glycerophospholipid metabolic process	60	0.0093	8	0.0132	0.0902100	E
<input type="checkbox"/>	GO:0051704	2	multi-organism process	139	0.0215	15	0.0248	0.0924040	E
<input type="checkbox"/>	GO:0019629	8,9	propionate catabolic process, 2-methylcitrate cycle	1	0.0002	1	0.0017	0.0932674	E
<input type="checkbox"/>	GO:0006801	5	superoxide metabolic process	1	0.0002	1	0.0017	0.0932674	E
<input type="checkbox"/>	GO:0048228	6,9,8,5	actin cortical patch distribution	1	0.0002	1	0.0017	0.0932674	E
<input type="checkbox"/>	GO:0006105	7	succinate metabolic process	1	0.0002	1	0.0017	0.0932674	E
<input type="checkbox"/>	GO:0043406	8,9	positive regulation of MAPK activity	1	0.0002	1	0.0017	0.0932674	E
<input type="checkbox"/>	GO:0005998	8,9	xylulose catabolic process	1	0.0002	1	0.0017	0.0932674	E
<input type="checkbox"/>	GO:0007190	8,10,11,12	adenylate cyclase activation	1	0.0002	1	0.0017	0.0932674	E
<input type="checkbox"/>	GO:0031098	6	stress-activated protein kinase signaling pathway	1	0.0002	1	0.0017	0.0932674	E
<input type="checkbox"/>	GO:0000187	9,10,8	activation of MAPK activity	1	0.0002	1	0.0017	0.0932674	E
<input type="checkbox"/>	GO:0051403	8,7	stress-activated MAPK cascade	1	0.0002	1	0.0017	0.0932674	E
<input type="checkbox"/>	GO:0042391	6,4	regulation of membrane potential	1	0.0002	1	0.0017	0.0932674	E
<input type="checkbox"/>	GO:0006559	8,7,9	L-phenylalanine catabolic process	1	0.0002	1	0.0017	0.0932674	E
<input type="checkbox"/>	GO:0000208	8,9,11,12,13,10,7	nuclear translocation of MAPK during osmolarity sensing	1	0.0002	1	0.0017	0.0932674	E
<input type="checkbox"/>	GO:0015879	5,6	carnitine transport	1	0.0002	1	0.0017	0.0932674	E
<input type="checkbox"/>	GO:0032872	7,9,8,6	regulation of stress-activated MAPK cascade	1	0.0002	1	0.0017	0.0932674	E
<input type="checkbox"/>	GO:0005997	7,8	xylulose metabolic process	1	0.0002	1	0.0017	0.0932674	E
<input type="checkbox"/>	GO:0045762	7,10,11	positive regulation of adenylate cyclase activity	1	0.0002	1	0.0017	0.0932674	E
<input type="checkbox"/>	GO:0006850	8,6,7,9	mitochondrial pyruvate transport	1	0.0002	1	0.0017	0.0932674	E
<input type="checkbox"/>	GO:0000169	10,11,8,9,7	activation of MAPK activity during osmolarity sensing	1	0.0002	1	0.0017	0.0932674	E
<input type="checkbox"/>	GO:0015727	7,8	lactate transport	1	0.0002	1	0.0017	0.0932674	E
<input type="checkbox"/>	GO:0006540	9,10,8	glutamate decarboxylation to succinate	1	0.0002	1	0.0017	0.0932674	E
<input type="checkbox"/>	GO:0015771	6,7,8	trehalose transport	1	0.0002	1	0.0017	0.0932674	E
<input type="checkbox"/>	GO:0009249	9	protein lipoylation	1	0.0002	1	0.0017	0.0932674	E
<input type="checkbox"/>	GO:0046098	7	guanine metabolic process	1	0.0002	1	0.0017	0.0932674	E
<input type="checkbox"/>	GO:0006787	6,7	porphyrin catabolic process	1	0.0002	1	0.0017	0.0932674	E
<input type="checkbox"/>	GO:0019626	7,8,9	short-chain fatty acid catabolic process	1	0.0002	1	0.0017	0.0932674	E
<input type="checkbox"/>	GO:0006659	9,8,10	phosphatidylserine biosynthetic process	1	0.0002	1	0.0017	0.0932674	E
<input type="checkbox"/>	GO:0042167	7,6,8	heme catabolic process	1	0.0002	1	0.0017	0.0932674	E
<input type="checkbox"/>	GO:0001321	4,5,6	age-dependent general metabolic decline during replicative cell aging	1	0.0002	1	0.0017	0.0932674	E
<input type="checkbox"/>	GO:0008277	6,7,5	regulation of G-protein coupled receptor protein signaling pathway	1	0.0002	1	0.0017	0.0932674	E
<input type="checkbox"/>	GO:0006848	7,8	pyruvate transport	1	0.0002	1	0.0017	0.0932674	E
<input type="checkbox"/>	GO:0006973	6,4	intracellular accumulation of glycerol	1	0.0002	1	0.0017	0.0932674	E
<input type="checkbox"/>	GO:0019265	9,10	glycine biosynthetic process, by transamination of glyoxylate	1	0.0002	1	0.0017	0.0932674	E
<input type="checkbox"/>	GO:0019543	7,8	propionate catabolic process	1	0.0002	1	0.0017	0.0932674	E
<input type="checkbox"/>	GO:0033015	6	tetrapyrrole catabolic process	1	0.0002	1	0.0017	0.0932674	E
<input type="checkbox"/>	GO:0007624	3	ultradian rhythm	1	0.0002	1	0.0017	0.0932674	E

<input type="checkbox"/>	GO:0019605	7,9,8	butyrate metabolic process	1	0.0002	1	0.0017	0.0932674	E
<input type="checkbox"/>	GO:0031281	6	positive regulation of cyclase activity	1	0.0002	1	0.0017	0.0932674	E
<input type="checkbox"/>	GO:0046149	5	pigment catabolic process	1	0.0002	1	0.0017	0.0932674	E
<input type="checkbox"/>	GO:0009450	6,7,9,10,11	gamma-aminobutyric acid catabolic process	1	0.0002	1	0.0017	0.0932674	E
<input type="checkbox"/>	GO:0006654	7,9,8,10	phosphatidic acid biosynthetic process	1	0.0002	1	0.0017	0.0932674	E
<input type="checkbox"/>	GO:0017062	9,8	cytochrome bc(1) complex assembly	1	0.0002	1	0.0017	0.0932674	E
<input type="checkbox"/>	GO:0006435	9,8,10,7	threonyl-tRNA aminoacylation	1	0.0002	1	0.0017	0.0932674	E
<input type="checkbox"/>	GO:0046473	8,6,9	phosphatidic acid metabolic process	1	0.0002	1	0.0017	0.0932674	E
<input type="checkbox"/>	GO:0009448	5,6,8,10,9	gamma-aminobutyric acid metabolic process	1	0.0002	1	0.0017	0.0932674	E
<input type="checkbox"/>	GO:0015700	7,8	arsenite transport	1	0.0002	1	0.0017	0.0932674	E
<input type="checkbox"/>	GO:0000189	8,10,11,12,9	nuclear translocation of MAPK	1	0.0002	1	0.0017	0.0932674	E
<input type="checkbox"/>	GO:0051349	6	positive regulation of lyase activity	1	0.0002	1	0.0017	0.0932674	E
<input type="checkbox"/>	GO:0046359	8,9,10	butyrate catabolic process	1	0.0002	1	0.0017	0.0932674	E
<input type="checkbox"/>	GO:0048511	2	rhythmic process	1	0.0002	1	0.0017	0.0932674	E
<input type="checkbox"/>	GO:0006575	5	amino acid derivative metabolic process	31	0.0048	5	0.0083	0.0940338	E
<input type="checkbox"/>	GO:0048193	7,5,6	Golgi vesicle transport	166	0.0256	17	0.0281	0.0949654	E
<input type="checkbox"/>	GO:0040020	7,9,8,6	regulation of meiosis	22	0.0034	4	0.0066	0.0949772	E
<input type="checkbox"/>	GO:0030447	3	filamentous growth	94	0.0145	11	0.0182	0.0952399	E
<input type="checkbox"/>	GO:0030001	6,7	metal ion transport	62	0.0096	8	0.0132	0.0980882	E
<input type="checkbox"/>	GO:0006626	9,8,7,6	protein targeting to mitochondrion	52	0.0080	7	0.0116	0.1003880	E
<input type="checkbox"/>	GO:0007118	7,6,5	budding cell apical bud growth	14	0.0022	3	0.0050	0.1005633	E
<input type="checkbox"/>	GO:0045990	9,7,8,5	regulation of transcription by carbon catabolites	14	0.0022	3	0.0050	0.1005633	E
<input type="checkbox"/>	GO:0006734	9,8	NADH metabolic process	14	0.0022	3	0.0050	0.1005633	E
<input type="checkbox"/>	GO:0007121	8,6,10,7,11,5	bipolar cellular bud site selection	32	0.0049	5	0.0083	0.1010896	E
<input type="checkbox"/>	GO:0019954	3	asexual reproduction	85	0.0131	10	0.0166	0.1012719	E
<input type="checkbox"/>	GO:0007114	5,4	cell budding	85	0.0131	10	0.0166	0.1012719	E
<input type="checkbox"/>	GO:0006613	10,9,8,7,6	cotranslational protein targeting to membrane	23	0.0036	4	0.0066	0.1042839	E
<input type="checkbox"/>	GO:0051129	6,5	negative regulation of cell organization and biogenesis	7	0.0011	2	0.0033	0.1119502	E
<input type="checkbox"/>	GO:0009225	5	nucleotide-sugar metabolic process	7	0.0011	2	0.0033	0.1119502	E
<input type="checkbox"/>	GO:0005980	9,8,7	glycogen catabolic process	7	0.0011	2	0.0033	0.1119502	E
<input type="checkbox"/>	GO:0009435	8,7,10,9	NAD biosynthetic process	7	0.0011	2	0.0033	0.1119502	E
<input type="checkbox"/>	GO:0019722	7	calcium-mediated signaling	7	0.0011	2	0.0033	0.1119502	E
<input type="checkbox"/>	GO:0001402	5,4	signal transduction during filamentous growth	7	0.0011	2	0.0033	0.1119502	E
<input type="checkbox"/>	GO:0006595	6,7	polyamine metabolic process	7	0.0011	2	0.0033	0.1119502	E
<input type="checkbox"/>	GO:0006560	7,8	proline metabolic process	7	0.0011	2	0.0033	0.1119502	E
<input type="checkbox"/>	GO:0006752	6	group transfer coenzyme metabolic process	44	0.0068	6	0.0099	0.1127189	E
<input type="checkbox"/>	GO:0007006	5,6	mitochondrial membrane organization and biogenesis	24	0.0037	4	0.0066	0.1135051	E
<input type="checkbox"/>	GO:0006576	5,6	biogenic amine metabolic process	24	0.0037	4	0.0066	0.1135051	E
<input type="checkbox"/>	GO:0006896	9,8,7,6	Golgi to vacuole transport	24	0.0037	4	0.0066	0.1135051	E
<input type="checkbox"/>	GO:0009651	5	response to salt stress	15	0.0023	3	0.0050	0.1140130	E
<input type="checkbox"/>	GO:0031145	11,10,12	anaphase-promoting complex-dependent proteasomal ubiquitin-dependent protein catabolic process	15	0.0023	3	0.0050	0.1140130	E
<input type="checkbox"/>	GO:0009894	5,4	regulation of catabolic process	15	0.0023	3	0.0050	0.1140130	E
<input type="checkbox"/>	GO:0007091	9,7,5,8,6,4	mitotic metaphase/anaphase transition	15	0.0023	3	0.0050	0.1140130	E

<input type="radio"/>	GO:0006914	3	autophagy	45	0.0069	6	0.0099	0.1179682	E
<input type="radio"/>	GO:0000749	5	response to pheromone during conjugation with cellular fusion	57	0.0088	7	0.0116	0.1217985	E
<input type="radio"/>	GO:0043549	6	regulation of kinase activity	25	0.0039	4	0.0066	0.1225592	E
<input type="radio"/>	GO:0045859	7	regulation of protein kinase activity	25	0.0039	4	0.0066	0.1225592	E
<input type="radio"/>	GO:0009110	5	vitamin biosynthetic process	46	0.0071	6	0.0099	0.1230485	E
<input type="radio"/>	GO:0042364	6	water-soluble vitamin biosynthetic process	46	0.0071	6	0.0099	0.1230485	E
<input type="radio"/>	GO:0008645	6,7	hexose transport	26	0.0040	4	0.0066	0.1313711	E
<input type="radio"/>	GO:0015749	5,6	monosaccharide transport	26	0.0040	4	0.0066	0.1313711	E
<input type="radio"/>	GO:0051338	5	regulation of transferase activity	26	0.0040	4	0.0066	0.1313711	E
<input type="radio"/>	GO:0042158	7,5	lipoprotein biosynthetic process	48	0.0074	6	0.0099	0.1326137	E
<input type="radio"/>	GO:0042157	6	lipoprotein metabolic process	48	0.0074	6	0.0099	0.1326137	E
<input type="radio"/>	GO:0006497	8,7,6	protein amino acid lipidation	48	0.0074	6	0.0099	0.1326137	E
<input type="radio"/>	GO:0006725	4	aromatic compound metabolic process	60	0.0093	7	0.0116	0.1327448	E
<input type="radio"/>	GO:0030011	7,4,8	maintenance of cell polarity	8	0.0012	2	0.0033	0.1353763	E
<input type="radio"/>	GO:0006855	5,6	multidrug transport	8	0.0012	2	0.0033	0.1353763	E
<input type="radio"/>	GO:0045013	10,8,9,6	negative regulation of transcription by carbon catabolites	8	0.0012	2	0.0033	0.1353763	E
<input type="radio"/>	GO:0006672	8,9	ceramide metabolic process	8	0.0012	2	0.0033	0.1353763	E
<input type="radio"/>	GO:0000751	8,9,7,6	cell cycle arrest in response to pheromone	8	0.0012	2	0.0033	0.1353763	E
<input type="radio"/>	GO:0045893	9,8	positive regulation of transcription, DNA-dependent	95	0.0147	9	0.0149	0.1393361	E
<input type="radio"/>	GO:0042147	8,6,7	retrograde transport, endosome to Golgi	17	0.0026	3	0.0050	0.1401654	E
<input type="radio"/>	GO:0000122	10,9	negative regulation of transcription from RNA polymerase II promoter	63	0.0097	7	0.0116	0.1418621	E
<input type="radio"/>	GO:0000226	7	microtubule cytoskeleton organization and biogenesis	81	0.0125	8	0.0132	0.1458796	E
<input type="radio"/>	GO:0006612	9,7,8	protein targeting to membrane	39	0.0060	5	0.0083	0.1459471	E
<input type="radio"/>	GO:0042144	6	vacuole fusion, non-autophagic	28	0.0043	4	0.0066	0.1480021	E
<input type="radio"/>	GO:0043681	6,7,8	protein import into mitochondrion	40	0.0062	5	0.0083	0.1512753	E
<input type="radio"/>	GO:0006109	5,4	regulation of carbohydrate metabolic process	29	0.0045	4	0.0066	0.1557070	E
<input type="radio"/>	GO:0006470	8,7	protein amino acid dephosphorylation	29	0.0045	4	0.0066	0.1557070	E
<input type="radio"/>	GO:0016311	6	dephosphorylation	41	0.0063	5	0.0083	0.1562511	E
<input type="radio"/>	GO:0007127	9,7,6,8,5	meiosis I	75	0.0116	7	0.0116	0.1573803	E
<input type="radio"/>	GO:0006071	6	glycerol metabolic process	9	0.0014	2	0.0033	0.1578553	E
<input type="radio"/>	GO:0019751	5	polyol metabolic process	9	0.0014	2	0.0033	0.1578553	E
<input type="radio"/>	GO:0019794	6,7	nonprotein amino acid metabolic process	9	0.0014	2	0.0033	0.1578553	E
<input type="radio"/>	GO:0009251	8,7	glucan catabolic process	9	0.0014	2	0.0033	0.1578553	E
<input type="radio"/>	GO:0007131	10,8,7,5,9,6,4	meiotic recombination	55	0.0085	6	0.0099	0.1581018	E
<input type="radio"/>	GO:0051128	5,4	regulation of cellular component organization and biogenesis	30	0.0046	4	0.0066	0.1629414	E
<input type="radio"/>	GO:0006893	9,7,6,8	Golgi to plasma membrane transport	30	0.0046	4	0.0066	0.1629414	E
<input type="radio"/>	GO:0043255	7,6,5	regulation of carbohydrate biosynthetic process	19	0.0029	3	0.0050	0.1642922	E
<input type="radio"/>	GO:0030384	8,9	phosphoinositide metabolic process	43	0.0066	5	0.0083	0.1650753	E
<input type="radio"/>	GO:0006402	7	mRNA catabolic process	60	0.0093	6	0.0099	0.1674438	E
<input type="radio"/>	GO:0007124	6,4,8,9	pseudohyphal growth	61	0.0094	6	0.0099	0.1684013	E
<input type="radio"/>	GO:0051259	7,6	protein oligomerization	2	0.0003	1	0.0017	0.1691634	E
<input type="radio"/>	GO:0045016	8,6,7,9	mitochondrial magnesium ion transport	2	0.0003	1	0.0017	0.1691634	E
<input type="radio"/>	GO:0030810	11,9,10,8	negative regulation of cAMP biosynthetic	2	0.0003	1	0.0017	0.1691634	E

<input type="radio"/>	GO:0030610	11,9,10,0	process	2	0.0003	1	0.0017	0.1691634	E
<input type="radio"/>	GO:0030799	8,7	regulation of cyclic nucleotide metabolic process	2	0.0003	1	0.0017	0.1691634	E
<input type="radio"/>	GO:0030809	9,7,8,6	negative regulation of nucleotide biosynthetic process	2	0.0003	1	0.0017	0.1691634	E
<input type="radio"/>	GO:0006824	7,8,9	cobalt ion transport	2	0.0003	1	0.0017	0.1691634	E
<input type="radio"/>	GO:0006545	8,9	glycine biosynthetic process	2	0.0003	1	0.0017	0.1691634	E
<input type="radio"/>	GO:0009062	6,7,8	fatty acid catabolic process	2	0.0003	1	0.0017	0.1691634	E
<input type="radio"/>	GO:0051693	8,9,12,7,10	actin filament capping	2	0.0003	1	0.0017	0.1691634	E
<input type="radio"/>	GO:0006008	9,10	glucose 1-phosphate utilization	2	0.0003	1	0.0017	0.1691634	E
<input type="radio"/>	GO:0006426	9,8,10,7	glycyl-tRNA aminoacylation	2	0.0003	1	0.0017	0.1691634	E
<input type="radio"/>	GO:0009187	6	cyclic nucleotide metabolic process	2	0.0003	1	0.0017	0.1691634	E
<input type="radio"/>	GO:0043619	10,11,9,7,5	regulation of transcription from RNA polymerase II promoter in response to oxidative stress	2	0.0003	1	0.0017	0.1691634	E
<input type="radio"/>	GO:0032445	8,9	fructose import	2	0.0003	1	0.0017	0.1691634	E
<input type="radio"/>	GO:0006171	7,8	cAMP biosynthetic process	2	0.0003	1	0.0017	0.1691634	E
<input type="radio"/>	GO:0030817	10,8,9,7	regulation of cAMP biosynthetic process	2	0.0003	1	0.0017	0.1691634	E
<input type="radio"/>	GO:0042886	4,5	amide transport	2	0.0003	1	0.0017	0.1691634	E
<input type="radio"/>	GO:0006558	7,6,8	L-phenylalanine metabolic process	2	0.0003	1	0.0017	0.1691634	E
<input type="radio"/>	GO:0006437	9,8,10,7	tyrosyl-tRNA aminoacylation	2	0.0003	1	0.0017	0.1691634	E
<input type="radio"/>	GO:0030808	8,6,7,5	regulation of nucleotide biosynthetic process	2	0.0003	1	0.0017	0.1691634	E
<input type="radio"/>	GO:0051156	8,9	glucose 6-phosphate metabolic process	2	0.0003	1	0.0017	0.1691634	E
<input type="radio"/>	GO:0032318	7,8,9	regulation of Ras GTPase activity	2	0.0003	1	0.0017	0.1691634	E
<input type="radio"/>	GO:0009190	6,7	cyclic nucleotide biosynthetic process	2	0.0003	1	0.0017	0.1691634	E
<input type="radio"/>	GO:0006104	6,7	succinyl-CoA metabolic process	2	0.0003	1	0.0017	0.1691634	E
<input type="radio"/>	GO:0006552	8,9	leucine catabolic process	2	0.0003	1	0.0017	0.1691634	E
<input type="radio"/>	GO:0051666	5,4	actin cortical patch localization	2	0.0003	1	0.0017	0.1691634	E
<input type="radio"/>	GO:0015805	7,8,9	S-adenosylmethionine transport	2	0.0003	1	0.0017	0.1691634	E
<input type="radio"/>	GO:0006846	7,8	acetate transport	2	0.0003	1	0.0017	0.1691634	E
<input type="radio"/>	GO:0032320	8,9,10	positive regulation of Ras GTPase activity	2	0.0003	1	0.0017	0.1691634	E
<input type="radio"/>	GO:0006430	9,8,10,7	lysyl-tRNA aminoacylation	2	0.0003	1	0.0017	0.1691634	E
<input type="radio"/>	GO:0030834	7,10,6,8	regulation of actin filament depolymerization	2	0.0003	1	0.0017	0.1691634	E
<input type="radio"/>	GO:0007189	9,10	G-protein signaling, adenylate cyclase activating pathway	2	0.0003	1	0.0017	0.1691634	E
<input type="radio"/>	GO:0010133	9,8,10	proline catabolic process to glutamate	2	0.0003	1	0.0017	0.1691634	E
<input type="radio"/>	GO:0048309	6	endoplasmic reticulum inheritance	2	0.0003	1	0.0017	0.1691634	E
<input type="radio"/>	GO:0015766	5,6	disaccharide transport	2	0.0003	1	0.0017	0.1691634	E
<input type="radio"/>	GO:0030835	7,8,11,6,9	negative regulation of actin filament depolymerization	2	0.0003	1	0.0017	0.1691634	E
<input type="radio"/>	GO:0006420	9,8,10,7	arginyl-tRNA aminoacylation	2	0.0003	1	0.0017	0.1691634	E
<input type="radio"/>	GO:0030800	9,8	negative regulation of cyclic nucleotide metabolic process	2	0.0003	1	0.0017	0.1691634	E
<input type="radio"/>	GO:0006140	7,6	regulation of nucleotide metabolic process	2	0.0003	1	0.0017	0.1691634	E
<input type="radio"/>	GO:0051260	8,7	protein homooligomerization	2	0.0003	1	0.0017	0.1691634	E
<input type="radio"/>	GO:0044419	3	interspecies interaction between organisms	2	0.0003	1	0.0017	0.1691634	E
<input type="radio"/>	GO:0006429	9,8,10,7	leucyl-tRNA aminoacylation	2	0.0003	1	0.0017	0.1691634	E
<input type="radio"/>	GO:0015840	5,6	urea transport	2	0.0003	1	0.0017	0.1691634	E
<input type="radio"/>	GO:0030815	10,9	negative regulation of cAMP metabolic process	2	0.0003	1	0.0017	0.1691634	E

<input type="radio"/>	GO:0033108	8,7	mitochondrial respiratory chain complex assembly	2	0.0003	1	0.0017	0.1691634	E
<input type="radio"/>	GO:0000168	10,11,8,9,7	activation of MAPKK activity during osmolarity sensing	2	0.0003	1	0.0017	0.1691634	E
<input type="radio"/>	GO:0030814	9,8	regulation of cAMP metabolic process	2	0.0003	1	0.0017	0.1691634	E
<input type="radio"/>	GO:0043132	5,6	NAD transport	2	0.0003	1	0.0017	0.1691634	E
<input type="radio"/>	GO:0006010	9,10	glucose 6-phosphate utilization	2	0.0003	1	0.0017	0.1691634	E
<input type="radio"/>	GO:0045980	8,7	negative regulation of nucleotide metabolic process	2	0.0003	1	0.0017	0.1691634	E
<input type="radio"/>	GO:0000358	9,8,10,11,12,13	formation of catalytic U2-type spliceosome for second transesterification step	2	0.0003	1	0.0017	0.1691634	E
<input type="radio"/>	GO:0015755	7,8	fructose transport	2	0.0003	1	0.0017	0.1691634	E
<input type="radio"/>	GO:0046058	7	cAMP metabolic process	2	0.0003	1	0.0017	0.1691634	E
<input type="radio"/>	GO:0030803	10,8,9,7	negative regulation of cyclic nucleotide biosynthetic process	2	0.0003	1	0.0017	0.1691634	E
<input type="radio"/>	GO:0051016	9,10,13,8,11	barbed-end actin filament capping	2	0.0003	1	0.0017	0.1691634	E
<input type="radio"/>	GO:0019255	8,9	glucose 1-phosphate metabolic process	2	0.0003	1	0.0017	0.1691634	E
<input type="radio"/>	GO:0006527	8,9,6,5	arginine catabolic process	2	0.0003	1	0.0017	0.1691634	E
<input type="radio"/>	GO:0030802	9,7,8,6	regulation of cyclic nucleotide biosynthetic process	2	0.0003	1	0.0017	0.1691634	E
<input type="radio"/>	GO:0051231	5,4,9,7	spindle elongation	20	0.0031	3	0.0050	0.1752945	E
<input type="radio"/>	GO:0000022	6,5,10,8	mitotic spindle elongation	20	0.0031	3	0.0050	0.1752945	E
<input type="radio"/>	GO:0051181	4,5	cofactor transport	10	0.0015	2	0.0033	0.1789510	E
<input type="radio"/>	GO:0046519	7,8	sphingoid metabolic process	10	0.0015	2	0.0033	0.1789510	E
<input type="radio"/>	GO:0006012	7,8	galactose metabolic process	10	0.0015	2	0.0033	0.1789510	E
<input type="radio"/>	GO:0006882	10,8	cellular zinc ion homeostasis	10	0.0015	2	0.0033	0.1789510	E
<input type="radio"/>	GO:0051336	5	regulation of hydrolase activity	10	0.0015	2	0.0033	0.1789510	E
<input type="radio"/>	GO:0055069	9	zinc ion homeostasis	10	0.0015	2	0.0033	0.1789510	E
<input type="radio"/>	GO:0045047	9,8,7,6,5	protein targeting to ER	33	0.0051	4	0.0066	0.1814772	E
<input type="radio"/>	GO:0006081	4	aldehyde metabolic process	21	0.0032	3	0.0050	0.1854720	E
<input type="radio"/>	GO:0006891	8,6,5,7	intra-Golgi vesicle-mediated transport	21	0.0032	3	0.0050	0.1854720	E
<input type="radio"/>	GO:0009072	6,5,7	aromatic amino acid family metabolic process	21	0.0032	3	0.0050	0.1854720	E
<input type="radio"/>	GO:0015674	6,7	di-, tri-valent inorganic cation transport	34	0.0053	4	0.0066	0.1865209	E
<input type="radio"/>	GO:0048590	3	non-developmental growth	35	0.0054	4	0.0066	0.1909742	E
<input type="radio"/>	GO:0007117	6,5,4	budding cell bud growth	35	0.0054	4	0.0066	0.1909742	E
<input type="radio"/>	GO:0016237	4,6	microautophagy	11	0.0017	2	0.0033	0.1983548	E
<input type="radio"/>	GO:0043086	5	negative regulation of enzyme activity	11	0.0017	2	0.0033	0.1983548	E
<input type="radio"/>	GO:0007050	7,8,6	cell cycle arrest	11	0.0017	2	0.0033	0.1983548	E
<input type="radio"/>	GO:0006879	10,8	cellular iron ion homeostasis	38	0.0059	4	0.0066	0.2007708	E
<input type="radio"/>	GO:0055072	9	iron ion homeostasis	38	0.0059	4	0.0066	0.2007708	E
<input type="radio"/>	GO:0006303	8,7	double-strand break repair via nonhomologous end joining	23	0.0036	3	0.0050	0.2031194	E
<input type="radio"/>	GO:0007031	5	peroxisome organization and biogenesis	40	0.0062	4	0.0066	0.2043968	E
<input type="radio"/>	GO:0016125	5,6,7	sterol metabolic process	42	0.0065	4	0.0066	0.2058322	E
<input type="radio"/>	GO:0016575	11,9	histone deacetylation	24	0.0037	3	0.0050	0.2105164	E
<input type="radio"/>	GO:0006904	9,5,7,6,8	vesicle docking during exocytosis	12	0.0019	2	0.0033	0.2158616	E
<input type="radio"/>	GO:0000083	10,9,6,5,7,8,4	G1/S-specific transcription in mitotic cell cycle	12	0.0019	2	0.0033	0.2158616	E
<input type="radio"/>	GO:0000272	6	polysaccharide catabolic process	12	0.0019	2	0.0033	0.2158616	E
<input type="radio"/>	GO:0044247	7,6	cellular polysaccharide catabolic process	12	0.0019	2	0.0033	0.2158616	E
<input type="radio"/>	GO:0006506	10,9,8,7,11	GPI anchor biosynthetic process	26	0.0040	3	0.0050	0.2223890	E

<input type="checkbox"/>	GO:0006476	8	protein amino acid deacetylation	26	0.0040	3	0.0050	0.2223890	E
<input type="checkbox"/>	GO:0006505	9,10	GPI anchor metabolic process	27	0.0042	3	0.0050	0.2268756	E
<input type="checkbox"/>	GO:0051318	6,7,5	G1 phase	27	0.0042	3	0.0050	0.2268756	E
<input type="checkbox"/>	GO:0009084	7,8	glutamine family amino acid biosynthetic process	27	0.0042	3	0.0050	0.2268756	E
<input type="checkbox"/>	GO:0000080	7,8,6	G1 phase of mitotic cell cycle	27	0.0042	3	0.0050	0.2268756	E
<input type="checkbox"/>	GO:0006431	9,8,10,7	methionyl-tRNA aminoacylation	3	0.0005	1	0.0017	0.2301108	E
<input type="checkbox"/>	GO:0000321	9,8,7,6	re-entry into mitotic cell cycle after pheromone arrest	3	0.0005	1	0.0017	0.2301108	E
<input type="checkbox"/>	GO:0006108	7	malate metabolic process	3	0.0005	1	0.0017	0.2301108	E
<input type="checkbox"/>	GO:0050821	7	protein stabilization	3	0.0005	1	0.0017	0.2301108	E
<input type="checkbox"/>	GO:0055078	9	sodium ion homeostasis	3	0.0005	1	0.0017	0.2301108	E
<input type="checkbox"/>	GO:0030832	8	regulation of actin filament length	3	0.0005	1	0.0017	0.2301108	E
<input type="checkbox"/>	GO:0046160	7,8,6	heme a metabolic process	3	0.0005	1	0.0017	0.2301108	E
<input type="checkbox"/>	GO:0046174	6	polyol catabolic process	3	0.0005	1	0.0017	0.2301108	E
<input type="checkbox"/>	GO:0042325	8,7	regulation of phosphorylation	3	0.0005	1	0.0017	0.2301108	E
<input type="checkbox"/>	GO:0006432	9,8,10,7	phenylalanyl-tRNA aminoacylation	3	0.0005	1	0.0017	0.2301108	E
<input type="checkbox"/>	GO:0051352	6	negative regulation of ligase activity	3	0.0005	1	0.0017	0.2301108	E
<input type="checkbox"/>	GO:0019413	7,8	acetate biosynthetic process	3	0.0005	1	0.0017	0.2301108	E
<input type="checkbox"/>	GO:0042326	8,9,7	negative regulation of phosphorylation	3	0.0005	1	0.0017	0.2301108	E
<input type="checkbox"/>	GO:0032974	8,6,7,9	amino acid export from vacuole	3	0.0005	1	0.0017	0.2301108	E
<input type="checkbox"/>	GO:0000160	5	two-component signal transduction system (phosphorelay)	3	0.0005	1	0.0017	0.2301108	E
<input type="checkbox"/>	GO:0032973	6,7,8	amino acid export	3	0.0005	1	0.0017	0.2301108	E
<input type="checkbox"/>	GO:0006687	7,8	glycosphingolipid metabolic process	3	0.0005	1	0.0017	0.2301108	E
<input type="checkbox"/>	GO:0019563	7	glycerol catabolic process	3	0.0005	1	0.0017	0.2301108	E
<input type="checkbox"/>	GO:0006883	10,8	cellular sodium ion homeostasis	3	0.0005	1	0.0017	0.2301108	E
<input type="checkbox"/>	GO:0006784	8,7,9	heme a biosynthetic process	3	0.0005	1	0.0017	0.2301108	E
<input type="checkbox"/>	GO:0006688	8,7,9	glycosphingolipid biosynthetic process	3	0.0005	1	0.0017	0.2301108	E
<input type="checkbox"/>	GO:0042044	4,5	fluid transport	3	0.0005	1	0.0017	0.2301108	E
<input type="checkbox"/>	GO:0009303	8,7	rRNA transcription	3	0.0005	1	0.0017	0.2301108	E
<input type="checkbox"/>	GO:0043461	8,7	F-type ATPase complex assembly	3	0.0005	1	0.0017	0.2301108	E
<input type="checkbox"/>	GO:0043328	10,9,11,8,7,12	protein targeting to vacuole during ubiquitin-dependent protein catabolic process via the MVB pathway	3	0.0005	1	0.0017	0.2301108	E
<input type="checkbox"/>	GO:0009438	5	methylglyoxal metabolic process	3	0.0005	1	0.0017	0.2301108	E
<input type="checkbox"/>	GO:0051436	8,6,5	negative regulation of ubiquitin ligase activity during mitotic cell cycle	3	0.0005	1	0.0017	0.2301108	E
<input type="checkbox"/>	GO:0006880	11,9,5,4	intracellular sequestering of iron ion	3	0.0005	1	0.0017	0.2301108	E
<input type="checkbox"/>	GO:0043408	6,8,5	regulation of MAPKKK cascade	3	0.0005	1	0.0017	0.2301108	E
<input type="checkbox"/>	GO:0051238	4,3	sequestering of metal ion	3	0.0005	1	0.0017	0.2301108	E
<input type="checkbox"/>	GO:0000320	7,6	re-entry into mitotic cell cycle	3	0.0005	1	0.0017	0.2301108	E
<input type="checkbox"/>	GO:0000370	8,9,7,10,11,12,13	U2-type nuclear mRNA branch site recognition	3	0.0005	1	0.0017	0.2301108	E
<input type="checkbox"/>	GO:0019243	7,8,6	methylglyoxal catabolic process to D-lactate	3	0.0005	1	0.0017	0.2301108	E
<input type="checkbox"/>	GO:0031647	6	regulation of protein stability	3	0.0005	1	0.0017	0.2301108	E
<input type="checkbox"/>	GO:0051444	7	negative regulation of ubiquitin ligase activity	3	0.0005	1	0.0017	0.2301108	E
<input type="checkbox"/>	GO:0051596	6	methylglyoxal catabolic process	3	0.0005	1	0.0017	0.2301108	E
<input type="checkbox"/>	GO:0043666	6	regulation of phosphoprotein phosphatase activity	3	0.0005	1	0.0017	0.2301108	E

<input type="checkbox"/>	GO:0006664	6,7	glycolipid metabolic process	3	0.0005	1	0.0017	0.2301108	E
<input type="checkbox"/>	GO:0006658	8,9	phosphatidylserine metabolic process	3	0.0005	1	0.0017	0.2301108	E
<input type="checkbox"/>	GO:0018065	8	protein-cofactor linkage	3	0.0005	1	0.0017	0.2301108	E
<input type="checkbox"/>	GO:0009247	7,6,8	glycolipid biosynthetic process	3	0.0005	1	0.0017	0.2301108	E
<input type="checkbox"/>	GO:0051595	5	response to methylglyoxal	3	0.0005	1	0.0017	0.2301108	E
<input type="checkbox"/>	GO:0007234	7,6	osmosensory signaling pathway via two-component system	3	0.0005	1	0.0017	0.2301108	E
<input type="checkbox"/>	GO:0006390	8,7	transcription from mitochondrial promoter	3	0.0005	1	0.0017	0.2301108	E
<input type="checkbox"/>	GO:0006404	10,8,5,7,9,6	RNA import into nucleus	3	0.0005	1	0.0017	0.2301108	E
<input type="checkbox"/>	GO:0045936	7,8,6	negative regulation of phosphate metabolic process	3	0.0005	1	0.0017	0.2301108	E
<input type="checkbox"/>	GO:0006833	5,6	water transport	3	0.0005	1	0.0017	0.2301108	E
<input type="checkbox"/>	GO:0008064	6,9,5	regulation of actin polymerization and/or depolymerization	3	0.0005	1	0.0017	0.2301108	E
<input type="checkbox"/>	GO:0046489	9,8,10	phosphoinositide biosynthetic process	28	0.0043	3	0.0050	0.2304203	E
<input type="checkbox"/>	GO:0009636	4	response to toxin	28	0.0043	3	0.0050	0.2304203	E
<input type="checkbox"/>	GO:0006038	9,10,7,8,11	cell wall chitin biosynthetic process	13	0.0020	2	0.0033	0.2313505	E
<input type="checkbox"/>	GO:0030258	5,6	lipid modification	13	0.0020	2	0.0033	0.2313505	E
<input type="checkbox"/>	GO:0006633	7,6,8,5	fatty acid biosynthetic process	13	0.0020	2	0.0033	0.2313505	E
<input type="checkbox"/>	GO:0006111	8,7,9,10,6	regulation of gluconeogenesis	13	0.0020	2	0.0033	0.2313505	E
<input type="checkbox"/>	GO:0015893	4,5	drug transport	13	0.0020	2	0.0033	0.2313505	E
<input type="checkbox"/>	GO:0045786	6,7,5	negative regulation of progression through cell cycle	13	0.0020	2	0.0033	0.2313505	E
<input type="checkbox"/>	GO:0006301	7,6	postreplication repair	13	0.0020	2	0.0033	0.2313505	E
<input type="checkbox"/>	GO:0006895	8,9,6,7	Golgi to endosome transport	13	0.0020	2	0.0033	0.2313505	E
<input type="checkbox"/>	GO:0000002	6	mitochondrial genome maintenance	31	0.0048	3	0.0050	0.2357273	E
<input type="checkbox"/>	GO:0009112	5	nucleobase metabolic process	31	0.0048	3	0.0050	0.2357273	E
<input type="checkbox"/>	GO:0006037	8,9,6,7,10	cell wall chitin metabolic process	14	0.0022	2	0.0033	0.2447681	E
<input type="checkbox"/>	GO:0022406	3	membrane docking	14	0.0022	2	0.0033	0.2447681	E
<input type="checkbox"/>	GO:0006188	9,10	IMP biosynthetic process	14	0.0022	2	0.0033	0.2447681	E
<input type="checkbox"/>	GO:0006144	6	purine base metabolic process	14	0.0022	2	0.0033	0.2447681	E
<input type="checkbox"/>	GO:0033013	5	tetrapyrrole metabolic process	14	0.0022	2	0.0033	0.2447681	E
<input type="checkbox"/>	GO:0046040	9	IMP metabolic process	14	0.0022	2	0.0033	0.2447681	E
<input type="checkbox"/>	GO:0000011	6	vacuole inheritance	14	0.0022	2	0.0033	0.2447681	E
<input type="checkbox"/>	GO:0048278	4,5,6	vesicle docking	14	0.0022	2	0.0033	0.2447681	E
<input type="checkbox"/>	GO:0006778	5,6	porphyrin metabolic process	14	0.0022	2	0.0033	0.2447681	E
<input type="checkbox"/>	GO:0042168	6,7,5	heme metabolic process	14	0.0022	2	0.0033	0.2447681	E
<input type="checkbox"/>	GO:0006374	9,11	nuclear mRNA splicing via U2-type spliceosome	15	0.0023	2	0.0033	0.2561140	E
<input type="checkbox"/>	GO:0000754	8,7,5	adaptation to pheromone during conjugation with cellular fusion	15	0.0023	2	0.0033	0.2561140	E
<input type="checkbox"/>	GO:0000737	6,7	DNA catabolic process, endonucleolytic	15	0.0023	2	0.0033	0.2561140	E
<input type="checkbox"/>	GO:0006031	9,7,8,10	chitin biosynthetic process	15	0.0023	2	0.0033	0.2561140	E
<input type="checkbox"/>	GO:0009168	8,9	purine ribonucleoside monophosphate biosynthetic process	15	0.0023	2	0.0033	0.2561140	E
<input type="checkbox"/>	GO:0018409	9	peptide or protein amino-terminal blocking	15	0.0023	2	0.0033	0.2561140	E
<input type="checkbox"/>	GO:0022401	7,6	adaptation of signaling pathway	15	0.0023	2	0.0033	0.2561140	E
<input type="checkbox"/>	GO:0031365	8	N-terminal protein amino acid modification	15	0.0023	2	0.0033	0.2561140	E
<input type="checkbox"/>	GO:0009156	7,8	ribonucleoside monophosphate biosynthetic process	15	0.0023	2	0.0033	0.2561140	E
<input type="checkbox"/>	GO:0009127	7,8	purine nucleoside monophosphate	15	0.0023	2	0.0033	0.2561140	E

<input type="radio"/>	GO:0009127	1,0	biosynthetic process	10	0.0023	2	0.0033	0.2654294	E
<input type="radio"/>	GO:0010383	7,5,6	cell wall polysaccharide metabolic process	16	0.0025	2	0.0033	0.2654294	E
<input type="radio"/>	GO:0016050	5	vesicle organization and biogenesis	16	0.0025	2	0.0033	0.2654294	E
<input type="radio"/>	GO:0046349	6,7	amino sugar biosynthetic process	17	0.0026	2	0.0033	0.2727869	E
<input type="radio"/>	GO:0009124	6,7	nucleoside monophosphate biosynthetic process	17	0.0026	2	0.0033	0.2727869	E
<input type="radio"/>	GO:0006045	8,9	N-acetylglucosamine biosynthetic process	17	0.0026	2	0.0033	0.2727869	E
<input type="radio"/>	GO:0009161	7	ribonucleoside monophosphate metabolic process	17	0.0026	2	0.0033	0.2727869	E
<input type="radio"/>	GO:0009167	8	purine ribonucleoside monophosphate metabolic process	17	0.0026	2	0.0033	0.2727869	E
<input type="radio"/>	GO:0019740	4	nitrogen utilization	17	0.0026	2	0.0033	0.2727869	E
<input type="radio"/>	GO:0009968	6,5	negative regulation of signal transduction	17	0.0026	2	0.0033	0.2727869	E
<input type="radio"/>	GO:0006030	8,6,7,9	chitin metabolic process	17	0.0026	2	0.0033	0.2727869	E
<input type="radio"/>	GO:0006042	7,8	glucosamine biosynthetic process	17	0.0026	2	0.0033	0.2727869	E
<input type="radio"/>	GO:0032988	6	protein-RNA complex disassembly	4	0.0006	1	0.0017	0.2782327	E
<input type="radio"/>	GO:0031321	4,8,6,7	prospore formation	4	0.0006	1	0.0017	0.2782327	E
<input type="radio"/>	GO:0000350	8,7,10,12	generation of catalytic spliceosome for second transesterification step	4	0.0006	1	0.0017	0.2782327	E
<input type="radio"/>	GO:0006097	6,8	glyoxylate cycle	4	0.0006	1	0.0017	0.2782327	E
<input type="radio"/>	GO:0008617	8	guanosine metabolic process	4	0.0006	1	0.0017	0.2782327	E
<input type="radio"/>	GO:0000304	6	response to singlet oxygen	4	0.0006	1	0.0017	0.2782327	E
<input type="radio"/>	GO:0031204	9,11,10,7,8	posttranslational protein targeting to membrane, translocation	4	0.0006	1	0.0017	0.2782327	E
<input type="radio"/>	GO:0000348	7,8,6,10,12	nuclear mRNA branch site recognition	4	0.0006	1	0.0017	0.2782327	E
<input type="radio"/>	GO:0015793	5,6	glycerol transport	4	0.0006	1	0.0017	0.2782327	E
<input type="radio"/>	GO:0043620	8,7,5	regulation of transcription in response to stress	4	0.0006	1	0.0017	0.2782327	E
<input type="radio"/>	GO:0031590	9	wybutosine metabolic process	4	0.0006	1	0.0017	0.2782327	E
<input type="radio"/>	GO:0006501	9,8,7	C-terminal protein lipidation	4	0.0006	1	0.0017	0.2782327	E
<input type="radio"/>	GO:0000390	7,9,11	spliceosome disassembly	4	0.0006	1	0.0017	0.2782327	E
<input type="radio"/>	GO:0031591	10,8,9	wybutosine biosynthetic process	4	0.0006	1	0.0017	0.2782327	E
<input type="radio"/>	GO:0045722	7,9,8,10,6,11	positive regulation of gluconeogenesis	4	0.0006	1	0.0017	0.2782327	E
<input type="radio"/>	GO:0043618	9,10,8,6	regulation of transcription from RNA polymerase II promoter in response to stress	4	0.0006	1	0.0017	0.2782327	E
<input type="radio"/>	GO:0015908	5,6	fatty acid transport	4	0.0006	1	0.0017	0.2782327	E
<input type="radio"/>	GO:0000391	8,10,12	U2-dependent spliceosome disassembly	4	0.0006	1	0.0017	0.2782327	E
<input type="radio"/>	GO:0009083	7,8	branched chain family amino acid catabolic process	4	0.0006	1	0.0017	0.2782327	E
<input type="radio"/>	GO:0051789	4	response to protein stimulus	18	0.0028	2	0.0033	0.2782826	E
<input type="radio"/>	GO:0006986	4,5	response to unfolded protein	18	0.0028	2	0.0033	0.2782826	E
<input type="radio"/>	GO:0051248	6,5	negative regulation of protein metabolic process	18	0.0028	2	0.0033	0.2782826	E
<input type="radio"/>	GO:0009126	7	purine nucleoside monophosphate metabolic process	18	0.0028	2	0.0033	0.2782826	E
<input type="radio"/>	GO:0009123	6	nucleoside monophosphate metabolic process	19	0.0029	2	0.0033	0.2820290	E
<input type="radio"/>	GO:0006040	5,6	amino sugar metabolic process	19	0.0029	2	0.0033	0.2820290	E
<input type="radio"/>	GO:0000245	7,6,9,11	spliceosome assembly	19	0.0029	2	0.0033	0.2820290	E
<input type="radio"/>	GO:0006044	7,8	N-acetylglucosamine metabolic process	19	0.0029	2	0.0033	0.2820290	E
<input type="radio"/>	GO:0006041	6,7	glucosamine metabolic process	19	0.0029	2	0.0033	0.2820290	E
<input type="radio"/>	GO:0042440	4	pigment metabolic process	20	0.0031	2	0.0033	0.2841498	E

<input type="checkbox"/>	GO:0030148	7,6,8	sphingolipid biosynthetic process	20	0.0031	2	0.0033	0.2841498	E
<input type="checkbox"/>	GO:0045053	7,6,5,4	protein retention in Golgi	20	0.0031	2	0.0033	0.2841498	E
<input type="checkbox"/>	GO:0006625	9,8,6,7	protein targeting to peroxisome	20	0.0031	2	0.0033	0.2841498	E
<input type="checkbox"/>	GO:0006308	5,6	DNA catabolic process	20	0.0031	2	0.0033	0.2841498	E
<input type="checkbox"/>	GO:0043574	7,5,6	peroxisomal transport	20	0.0031	2	0.0033	0.2841498	E
<input type="checkbox"/>	GO:0007094	9,11,10,8	mitotic cell cycle spindle assembly checkpoint	20	0.0031	2	0.0033	0.2841498	E
<input type="checkbox"/>	GO:0006089	7	lactate metabolic process	5	0.0008	1	0.0017	0.3153871	E
<input type="checkbox"/>	GO:0007026	8,7,11,9,6	negative regulation of microtubule depolymerization	5	0.0008	1	0.0017	0.3153871	E
<input type="checkbox"/>	GO:0006995	8,7,6	cellular response to nitrogen starvation	5	0.0008	1	0.0017	0.3153871	E
<input type="checkbox"/>	GO:0016560	8,11,10,7,9	protein import into peroxisome matrix, docking	5	0.0008	1	0.0017	0.3153871	E
<input type="checkbox"/>	GO:0015693	7,8	magnesium ion transport	5	0.0008	1	0.0017	0.3153871	E
<input type="checkbox"/>	GO:0045991	10,8,9,6	positive regulation of transcription by carbon catabolites	5	0.0008	1	0.0017	0.3153871	E
<input type="checkbox"/>	GO:0031111	7,10,6	negative regulation of microtubule polymerization or depolymerization	5	0.0008	1	0.0017	0.3153871	E
<input type="checkbox"/>	GO:0006530	8,9	asparagine catabolic process	5	0.0008	1	0.0017	0.3153871	E
<input type="checkbox"/>	GO:0018410	8	peptide or protein carboxyl-terminal blocking	5	0.0008	1	0.0017	0.3153871	E
<input type="checkbox"/>	GO:0000101	6,7,8	sulfur amino acid transport	5	0.0008	1	0.0017	0.3153871	E
<input type="checkbox"/>	GO:0006336	7,8,11	DNA replication-independent nucleosome assembly	5	0.0008	1	0.0017	0.3153871	E
<input type="checkbox"/>	GO:0006816	7,8	calcium ion transport	5	0.0008	1	0.0017	0.3153871	E
<input type="checkbox"/>	GO:0000409	10,8,9,6	regulation of transcription by galactose	5	0.0008	1	0.0017	0.3153871	E
<input type="checkbox"/>	GO:0043562	7,6	cellular response to nitrogen levels	5	0.0008	1	0.0017	0.3153871	E
<input type="checkbox"/>	GO:0006813	7,8	potassium ion transport	5	0.0008	1	0.0017	0.3153871	E
<input type="checkbox"/>	GO:0046854	7,9,8,10	phosphoinositide phosphorylation	5	0.0008	1	0.0017	0.3153871	E
<input type="checkbox"/>	GO:0000188	9,10,8	inactivation of MAPK activity	5	0.0008	1	0.0017	0.3153871	E
<input type="checkbox"/>	GO:0006279	7	premeiotic DNA synthesis	5	0.0008	1	0.0017	0.3153871	E
<input type="checkbox"/>	GO:0043087	6	regulation of GTPase activity	5	0.0008	1	0.0017	0.3153871	E
<input type="checkbox"/>	GO:0006102	6,7	isocitrate metabolic process	5	0.0008	1	0.0017	0.3153871	E
<input type="checkbox"/>	GO:0000411	11,9,10,7	positive regulation of transcription by galactose	5	0.0008	1	0.0017	0.3153871	E
<input type="checkbox"/>	GO:0051439	7,5,4	regulation of ubiquitin ligase activity during mitotic cell cycle	5	0.0008	1	0.0017	0.3153871	E
<input type="checkbox"/>	GO:0043407	8,9	negative regulation of MAPK activity	5	0.0008	1	0.0017	0.3153871	E
<input type="checkbox"/>	GO:0046487	5,7	glyoxylate metabolic process	5	0.0008	1	0.0017	0.3153871	E
<input type="checkbox"/>	GO:0046834	6,7	lipid phosphorylation	5	0.0008	1	0.0017	0.3153871	E
<input type="checkbox"/>	GO:0031114	7,10,6,8	regulation of microtubule depolymerization	5	0.0008	1	0.0017	0.3153871	E
<input type="checkbox"/>	GO:0042176	6,7,5	regulation of protein catabolic process	5	0.0008	1	0.0017	0.3153871	E
<input type="checkbox"/>	GO:0007232	7,6	osmosensory signaling pathway via Sho1 osmosensor	5	0.0008	1	0.0017	0.3153871	E
<input type="checkbox"/>	GO:0017004	8,7	cytochrome complex assembly	5	0.0008	1	0.0017	0.3153871	E
<input type="checkbox"/>	GO:0045816	11,10	negative regulation of global transcription from RNA polymerase II promoter	5	0.0008	1	0.0017	0.3153871	E
<input type="checkbox"/>	GO:0000173	10,11,8,9,7	inactivation of MAPK activity during osmolarity sensing	5	0.0008	1	0.0017	0.3153871	E
<input type="checkbox"/>	GO:0051340	5	regulation of ligase activity	6	0.0009	1	0.0017	0.3431973	E
<input type="checkbox"/>	GO:0046185	5	aldehyde catabolic process	6	0.0009	1	0.0017	0.3431973	E
<input type="checkbox"/>	GO:0046021	10,8,5,6,9,7,4	regulation of transcription from RNA polymerase II promoter, mitotic	6	0.0009	1	0.0017	0.3431973	E
<input type="checkbox"/>	GO:0006490	5,11,10,9,7,6	oligosaccharide-lipid intermediate assembly	6	0.0009	1	0.0017	0.3431973	E

<input type="checkbox"/>	GO:0009231	7,8	riboflavin biosynthetic process	6	0.0009	1	0.0017	0.3431973	E
<input type="checkbox"/>	GO:0007019	9,7	microtubule depolymerization	6	0.0009	1	0.0017	0.3431973	E
<input type="checkbox"/>	GO:0045116	9	protein neddylation	6	0.0009	1	0.0017	0.3431973	E
<input type="checkbox"/>	GO:0006020	7,8	inositol metabolic process	6	0.0009	1	0.0017	0.3431973	E
<input type="checkbox"/>	GO:0015791	4,5	polyol transport	6	0.0009	1	0.0017	0.3431973	E
<input type="checkbox"/>	GO:0051438	6	regulation of ubiquitin ligase activity	6	0.0009	1	0.0017	0.3431973	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	0.0017	0.3431973	E
<input type="checkbox"/>	GO:0009743	5,4	response to carbohydrate stimulus	6	0.0009	1	0.0017	0.3431973	E
<input type="checkbox"/>	GO:0043254	6,7,5	regulation of protein complex assembly	6	0.0009	1	0.0017	0.3431973	E
<input type="checkbox"/>	GO:0006544	7,8	glycine metabolic process	6	0.0009	1	0.0017	0.3431973	E
<input type="checkbox"/>	GO:0031930	6	mitochondrial signaling pathway	6	0.0009	1	0.0017	0.3431973	E
<input type="checkbox"/>	GO:0000717	8,7	nucleotide-excision repair, DNA duplex unwinding	6	0.0009	1	0.0017	0.3431973	E
<input type="checkbox"/>	GO:0005979	8,7,9,10,6	regulation of glycogen biosynthetic process	6	0.0009	1	0.0017	0.3431973	E
<input type="checkbox"/>	GO:0051691	6	cellular oligosaccharide metabolic process	6	0.0009	1	0.0017	0.3431973	E
<input type="checkbox"/>	GO:0007029	5	endoplasmic reticulum organization and biogenesis	6	0.0009	1	0.0017	0.3431973	E
<input type="checkbox"/>	GO:0006771	7	riboflavin metabolic process	6	0.0009	1	0.0017	0.3431973	E
<input type="checkbox"/>	GO:0006376	8,7,10,12,3	mRNA splice site selection	6	0.0009	1	0.0017	0.3431973	E
<input type="checkbox"/>	GO:0007089	8,9,7,6	traversing start control point of mitotic cell cycle	6	0.0009	1	0.0017	0.3431973	E
<input type="checkbox"/>	GO:0046839	6,7	phospholipid dephosphorylation	7	0.0011	1	0.0017	0.3630801	E
<input type="checkbox"/>	GO:0009311	5	oligosaccharide metabolic process	7	0.0011	1	0.0017	0.3630801	E
<input type="checkbox"/>	GO:0051174	6,5	regulation of phosphorus metabolic process	7	0.0011	1	0.0017	0.3630801	E
<input type="checkbox"/>	GO:0007068	10,8,6,9,7,5	negative regulation of transcription, mitotic	7	0.0011	1	0.0017	0.3630801	E
<input type="checkbox"/>	GO:0006551	7,8	leucine metabolic process	7	0.0011	1	0.0017	0.3630801	E
<input type="checkbox"/>	GO:0009102	6,7,8	biotin biosynthetic process	7	0.0011	1	0.0017	0.3630801	E
<input type="checkbox"/>	GO:0000372	10	Group I intron splicing	7	0.0011	1	0.0017	0.3630801	E
<input type="checkbox"/>	GO:0019220	7,6	regulation of phosphate metabolic process	7	0.0011	1	0.0017	0.3630801	E
<input type="checkbox"/>	GO:0006768	5,7,6	biotin metabolic process	7	0.0011	1	0.0017	0.3630801	E
<input type="checkbox"/>	GO:0015936	7	coenzyme A metabolic process	7	0.0011	1	0.0017	0.3630801	E
<input type="checkbox"/>	GO:0045835	8,10,9,7	negative regulation of meiosis	7	0.0011	1	0.0017	0.3630801	E
<input type="checkbox"/>	GO:0000727	9,8	double-strand break repair via break-induced replication	7	0.0011	1	0.0017	0.3630801	E
<input type="checkbox"/>	GO:0019655	6,7	glucose catabolic process to ethanol	7	0.0011	1	0.0017	0.3630801	E
<input type="checkbox"/>	GO:0045896	9,7,5,8,6,4	regulation of transcription, mitotic	7	0.0011	1	0.0017	0.3630801	E
<input type="checkbox"/>	GO:0046856	7,9,8,10	phosphoinositide dephosphorylation	7	0.0011	1	0.0017	0.3630801	E
<input type="checkbox"/>	GO:0009409	5,4	response to cold	7	0.0011	1	0.0017	0.3630801	E
<input type="checkbox"/>	GO:0000433	12,10,11,8	negative regulation of transcription from RNA polymerase II promoter by glucose	7	0.0011	1	0.0017	0.3630801	E
<input type="checkbox"/>	GO:0006265	6	DNA topological change	7	0.0011	1	0.0017	0.3630801	E
<input type="checkbox"/>	GO:0000437	11,9,10,7	negative regulation of transcription from RNA polymerase II promoter by carbon catabolites	7	0.0011	1	0.0017	0.3630801	E
<input type="checkbox"/>	GO:0006656	9,8,10	phosphatidylcholine biosynthetic process	7	0.0011	1	0.0017	0.3630801	E
<input type="checkbox"/>	GO:0006469	7,8	negative regulation of protein kinase activity	7	0.0011	1	0.0017	0.3630801	E
<input type="checkbox"/>	GO:0015937	7,8	coenzyme A biosynthetic process	7	0.0011	1	0.0017	0.3630801	E
<input type="checkbox"/>	GO:0033205	5,4	cytokinesis during cell cycle	7	0.0011	1	0.0017	0.3630801	E
<input type="checkbox"/>	GO:0006829	8,9	zinc ion transport	7	0.0011	1	0.0017	0.3630801	E
			DNA replication, via transrepression						

<input type="radio"/>	GO:0000376	9	RNA splicing, via transesterification reactions with guanosine as nucleophile	7	0.0011	1	0.0017	0.3630801	E
<input type="radio"/>	GO:0006878	10,8	cellular copper ion homeostasis	7	0.0011	1	0.0017	0.3630801	E
<input type="radio"/>	GO:0000715	7,8	nucleotide-excision repair, DNA damage recognition	7	0.0011	1	0.0017	0.3630801	E
<input type="radio"/>	GO:0045913	6,5	positive regulation of carbohydrate metabolic process	7	0.0011	1	0.0017	0.3630801	E
<input type="radio"/>	GO:0045014	11,9,10,7	negative regulation of transcription by glucose	7	0.0011	1	0.0017	0.3630801	E
<input type="radio"/>	GO:0051348	6	negative regulation of transferase activity	7	0.0011	1	0.0017	0.3630801	E
<input type="radio"/>	GO:0055070	9	copper ion homeostasis	7	0.0011	1	0.0017	0.3630801	E
<input type="radio"/>	GO:0000429	10,8,9,6	regulation of transcription from RNA polymerase II promoter by carbon catabolites	7	0.0011	1	0.0017	0.3630801	E
<input type="radio"/>	GO:0000430	11,9,10,7	regulation of transcription from RNA polymerase II promoter by glucose	7	0.0011	1	0.0017	0.3630801	E
<input type="radio"/>	GO:0007323	9	peptide pheromone maturation	8	0.0012	1	0.0017	0.3762697	E
<input type="radio"/>	GO:0019660	6	glycolytic fermentation	8	0.0012	1	0.0017	0.3762697	E
<input type="radio"/>	GO:0042726	6	riboflavin and derivative metabolic process	8	0.0012	1	0.0017	0.3762697	E
<input type="radio"/>	GO:0044242	5,6	cellular lipid catabolic process	8	0.0012	1	0.0017	0.3762697	E
<input type="radio"/>	GO:0042816	6	vitamin B6 metabolic process	8	0.0012	1	0.0017	0.3762697	E
<input type="radio"/>	GO:0006620	10,9,8,7,6	posttranslational protein targeting to membrane	8	0.0012	1	0.0017	0.3762697	E
<input type="radio"/>	GO:0007119	7,6,5	budding cell isotropic bud growth	8	0.0012	1	0.0017	0.3762697	E
<input type="radio"/>	GO:0016042	4,5	lipid catabolic process	8	0.0012	1	0.0017	0.3762697	E
<input type="radio"/>	GO:0008614	7	pyridoxine metabolic process	8	0.0012	1	0.0017	0.3762697	E
<input type="radio"/>	GO:0046015	10,8,9,6	regulation of transcription by glucose	8	0.0012	1	0.0017	0.3762697	E
<input type="radio"/>	GO:0042727	7	riboflavin and derivative biosynthetic process	8	0.0012	1	0.0017	0.3762697	E
<input type="radio"/>	GO:0001308	11,7,10	loss of chromatin silencing during replicative cell aging	8	0.0012	1	0.0017	0.3762697	E
<input type="radio"/>	GO:0009890	6,5	negative regulation of biosynthetic process	8	0.0012	1	0.0017	0.3762697	E
<input type="radio"/>	GO:0000903	6,4,8,7,9	cellular morphogenesis during vegetative growth	8	0.0012	1	0.0017	0.3762697	E
<input type="radio"/>	GO:0045815	5	positive regulation of gene expression, epigenetic	9	0.0014	1	0.0017	0.3838396	E
<input type="radio"/>	GO:0001304	10,6	progressive alteration of chromatin during replicative cell aging	9	0.0014	1	0.0017	0.3838396	E
<input type="radio"/>	GO:0000184	8	mRNA catabolic process, nonsense-mediated decay	9	0.0014	1	0.0017	0.3838396	E
<input type="radio"/>	GO:0006345	10,6,9	loss of chromatin silencing	9	0.0014	1	0.0017	0.3838396	E
<input type="radio"/>	GO:0006528	7,8	asparagine metabolic process	9	0.0014	1	0.0017	0.3838396	E
<input type="radio"/>	GO:0051180	4,5	vitamin transport	9	0.0014	1	0.0017	0.3838396	E
<input type="radio"/>	GO:0006280	6	mutagenesis	9	0.0014	1	0.0017	0.3838396	E
<input type="radio"/>	GO:0042138	11,9,8,5,6,10,7,4	meiotic DNA double-strand break formation	9	0.0014	1	0.0017	0.3838396	E
<input type="radio"/>	GO:0046470	8,9	phosphatidylcholine metabolic process	9	0.0014	1	0.0017	0.3838396	E
<input type="radio"/>	GO:0046685	5	response to arsenic	9	0.0014	1	0.0017	0.3838396	E
<input type="radio"/>	GO:0006984	6	ER-nuclear signaling pathway	9	0.0014	1	0.0017	0.3838396	E
<input type="radio"/>	GO:0000393	7,6,9,11	spliceosomal conformational changes to generate catalytic conformation	9	0.0014	1	0.0017	0.3838396	E
<input type="radio"/>	GO:0008535	8,7	cytochrome c oxidase complex assembly	9	0.0014	1	0.0017	0.3838396	E
<input type="radio"/>	GO:0045912	6,5	negative regulation of carbohydrate metabolic process	9	0.0014	1	0.0017	0.3838396	E
<input type="radio"/>	GO:0030968	7,5,6	unfolded protein response	9	0.0014	1	0.0017	0.3838396	E
<input type="radio"/>	GO:0045721	7,9,8,10,6,11	negative regulation of gluconeogenesis	9	0.0014	1	0.0017	0.3838396	E
<input type="radio"/>	GO:0006283	8,7	transcription-coupled nucleotide-excision repair	9	0.0014	1	0.0017	0.3838396	E

<input type="radio"/>	GO:0007129	10,8,7,5,9,6,4	synapsis	10	0.0015	1	0.0017	0.3867216	E
<input type="radio"/>	GO:0010033	4	response to organic substance	10	0.0015	1	0.0017	0.3867216	E
<input type="radio"/>	GO:0001301	9,5	progressive alteration of chromatin during cell aging	10	0.0015	1	0.0017	0.3867216	E
<input type="radio"/>	GO:0008298	5	intracellular mRNA localization	10	0.0015	1	0.0017	0.3867216	E
<input type="radio"/>	GO:0016925	9	protein sumoylation	10	0.0015	1	0.0017	0.3867216	E
<input type="radio"/>	GO:0009068	7,8	aspartate family amino acid catabolic process	10	0.0015	1	0.0017	0.3867216	E
<input type="radio"/>	GO:0008150	1	biological process	6476	1.0000	604	1.0000	1.0000000	D
<input type="radio"/>	GO:0046128	7	purine ribonucleoside metabolic process	11	0.0017	1	0.0017	0.3857228	D
<input type="radio"/>	GO:0007109	7,6,5,4	cytokinesis, completion of separation	11	0.0017	1	0.0017	0.3857228	D
<input type="radio"/>	GO:0031163	5	metallo-sulfur cluster assembly	11	0.0017	1	0.0017	0.3857228	D
<input type="radio"/>	GO:0007039	7,8	vacuolar protein catabolic process	11	0.0017	1	0.0017	0.3857228	D
<input type="radio"/>	GO:0016226	6	iron-sulfur cluster assembly	11	0.0017	1	0.0017	0.3857228	D
<input type="radio"/>	GO:0001101	4	response to acid	11	0.0017	1	0.0017	0.3857228	D
<input type="radio"/>	GO:0009070	7,8	serine family amino acid biosynthetic process	12	0.0019	1	0.0017	0.3815409	D
<input type="radio"/>	GO:0015914	5,6	phospholipid transport	12	0.0019	1	0.0017	0.3815409	D
<input type="radio"/>	GO:0042278	6	purine nucleoside metabolic process	12	0.0019	1	0.0017	0.3815409	D
<input type="radio"/>	GO:0009119	6	ribonucleoside metabolic process	13	0.0020	1	0.0017	0.3747776	D
<input type="radio"/>	GO:0006779	6,7	porphyrin biosynthetic process	13	0.0020	1	0.0017	0.3747776	D
<input type="radio"/>	GO:0033014	6	tetrapyrrole biosynthetic process	13	0.0020	1	0.0017	0.3747776	D
<input type="radio"/>	GO:0007103	6,7,5,8	spindle pole body duplication in nuclear envelope	13	0.0020	1	0.0017	0.3747776	D
<input type="radio"/>	GO:0006334	6,7,10	nucleosome assembly	13	0.0020	1	0.0017	0.3747776	D
<input type="radio"/>	GO:0006783	7,6,8	heme biosynthetic process	13	0.0020	1	0.0017	0.3747776	D
<input type="radio"/>	GO:0006915	6,8	apoptosis	13	0.0020	1	0.0017	0.3747776	D
<input type="radio"/>	GO:0007346	7,5,6	regulation of progression through mitotic cell cycle	13	0.0020	1	0.0017	0.3747776	D
<input type="radio"/>	GO:0008219	4,6	cell death	13	0.0020	1	0.0017	0.3747776	D
<input type="radio"/>	GO:0016265	3	death	13	0.0020	1	0.0017	0.3747776	D
<input type="radio"/>	GO:0012501	5,7	programmed cell death	13	0.0020	1	0.0017	0.3747776	D
<input type="radio"/>	GO:0000920	6,4	cell separation during cytokinesis	13	0.0020	1	0.0017	0.3747776	D
<input type="radio"/>	GO:0042770	5	DNA damage response, signal transduction	14	0.0022	1	0.0017	0.3659500	D
<input type="radio"/>	GO:0042787	10,9,11	protein ubiquitination during ubiquitin-dependent protein catabolic process	14	0.0022	1	0.0017	0.3659500	D
<input type="radio"/>	GO:0006749	6,5	glutathione metabolic process	14	0.0022	1	0.0017	0.3659500	D
<input type="radio"/>	GO:0000077	9,8,6	DNA damage checkpoint	14	0.0022	1	0.0017	0.3659500	D
<input type="radio"/>	GO:0006825	8,9	copper ion transport	14	0.0022	1	0.0017	0.3659500	D
<input type="radio"/>	GO:0030474	5,6,4,7	spindle pole body duplication	14	0.0022	1	0.0017	0.3659500	D
<input type="radio"/>	GO:0006525	7,8,5,4	arginine metabolic process	15	0.0023	1	0.0017	0.3555015	D
<input type="radio"/>	GO:0007018	8,7,6	microtubule-based movement	15	0.0023	1	0.0017	0.3555015	D
<input type="radio"/>	GO:0031110	6,9,5	regulation of microtubule polymerization or depolymerization	15	0.0023	1	0.0017	0.3555015	D
<input type="radio"/>	GO:0030473	8,9,6,7	nuclear migration, microtubule-mediated	15	0.0023	1	0.0017	0.3555015	D
<input type="radio"/>	GO:0006267	8,7	pre-replicative complex assembly	15	0.0023	1	0.0017	0.3555015	D
<input type="radio"/>	GO:0000051	4,3	urea cycle intermediate metabolic process	15	0.0023	1	0.0017	0.3555015	D
<input type="radio"/>	GO:0019856	7,6	pyrimidine base biosynthetic process	15	0.0023	1	0.0017	0.3555015	D
<input type="radio"/>	GO:0030488	8,9	tRNA methylation	15	0.0023	1	0.0017	0.3555015	D
<input type="radio"/>	GO:0000114	10,8,9,5,7,4	G1-specific transcription in mitotic cell cycle	15	0.0023	1	0.0017	0.3555015	D

<input type="radio"/>	GO:0009081	6,7	branched chain family amino acid metabolic process	16	0.0025	1	0.0017	0.3438111	D
<input type="radio"/>	GO:0031109	8	microtubule polymerization or depolymerization	16	0.0025	1	0.0017	0.3438111	D
<input type="radio"/>	GO:0032392	6	DNA geometric change	16	0.0025	1	0.0017	0.3438111	D
<input type="radio"/>	GO:0051300	5,4,6	spindle pole body organization and biogenesis	16	0.0025	1	0.0017	0.3438111	D
<input type="radio"/>	GO:0015698	6,7	inorganic anion transport	16	0.0025	1	0.0017	0.3438111	D
<input type="radio"/>	GO:0032508	7	DNA duplex unwinding	16	0.0025	1	0.0017	0.3438111	D
<input type="radio"/>	GO:0031023	5	microtubule organizing center organization and biogenesis	16	0.0025	1	0.0017	0.3438111	D
<input type="radio"/>	GO:0000742	7,5	karyogamy during conjugation with cellular fusion	17	0.0026	1	0.0017	0.3312009	D
<input type="radio"/>	GO:0006820	5,6	anion transport	17	0.0026	1	0.0017	0.3312009	D
<input type="radio"/>	GO:0030705	7,5,6	cytoskeleton-dependent intracellular transport	17	0.0026	1	0.0017	0.3312009	D
<input type="radio"/>	GO:0007266	8	Rho protein signal transduction	17	0.0026	1	0.0017	0.3312009	D
<input type="radio"/>	GO:0016558	10,9,7,8,6	protein import into peroxisome matrix	17	0.0026	1	0.0017	0.3312009	D
<input type="radio"/>	GO:0006113	5	fermentation	17	0.0026	1	0.0017	0.3312009	D
<input type="radio"/>	GO:0000741	6	karyogamy	17	0.0026	1	0.0017	0.3312009	D
<input type="radio"/>	GO:0007004	9	telomere maintenance via telomerase	17	0.0026	1	0.0017	0.3312009	D
<input type="radio"/>	GO:0006206	6	pyrimidine base metabolic process	17	0.0026	1	0.0017	0.3312009	D
<input type="radio"/>	GO:0031570	8,7	DNA integrity checkpoint	18	0.0028	1	0.0017	0.3179442	D
<input type="radio"/>	GO:0000084	8,7,6	S phase of mitotic cell cycle	18	0.0028	1	0.0017	0.3179442	D
<input type="radio"/>	GO:0010038	5	response to metal ion	18	0.0028	1	0.0017	0.3179442	D
<input type="radio"/>	GO:0009116	5	nucleoside metabolic process	18	0.0028	1	0.0017	0.3179442	D
<input type="radio"/>	GO:0016571	11,9,10,8	histone methylation	18	0.0028	1	0.0017	0.3179442	D
<input type="radio"/>	GO:0046148	5	pigment biosynthetic process	19	0.0029	1	0.0017	0.3042712	D
<input type="radio"/>	GO:0000722	9,8	telomere maintenance via recombination	19	0.0029	1	0.0017	0.3042712	D
<input type="radio"/>	GO:0051647	6,5	nucleus localization	20	0.0031	1	0.0017	0.2903749	D
<input type="radio"/>	GO:0051320	7,6,5	S phase	20	0.0031	1	0.0017	0.2903749	D
<input type="radio"/>	GO:0000767	6,7	cellular morphogenesis during conjugation	20	0.0031	1	0.0017	0.2903749	D
<input type="radio"/>	GO:0040023	6,7,4,5	establishment of nucleus localization	20	0.0031	1	0.0017	0.2903749	D
<input type="radio"/>	GO:0006826	7,8,9	iron ion transport	20	0.0031	1	0.0017	0.2903749	D
<input type="radio"/>	GO:0007097	7,8,5,6	nuclear migration	20	0.0031	1	0.0017	0.2903749	D
<input type="radio"/>	GO:0007120	8,6,10,7,11,5	axial cellular bud site selection	22	0.0034	2	0.0033	0.2840385	D
<input type="radio"/>	GO:0007020	8	microtubule nucleation	23	0.0036	2	0.0033	0.2820727	D
<input type="radio"/>	GO:0019748	3	secondary metabolic process	23	0.0036	2	0.0033	0.2820727	D
<input type="radio"/>	GO:0031577	8,7	spindle checkpoint	24	0.0037	2	0.0033	0.2790089	D
<input type="radio"/>	GO:0046352	7	disaccharide catabolic process	24	0.0037	2	0.0033	0.2790089	D
<input type="radio"/>	GO:0046112	6,5	nucleobase biosynthetic process	21	0.0032	1	0.0017	0.2764162	D
<input type="radio"/>	GO:0009607	3	response to biotic stimulus	25	0.0039	2	0.0033	0.2749741	D
<input type="radio"/>	GO:0010382	6,4	cell wall metabolic process	26	0.0040	2	0.0033	0.2700900	D
<input type="radio"/>	GO:0007093	8,10,9,7	mitotic cell cycle checkpoint	27	0.0042	2	0.0033	0.2644721	D
<input type="radio"/>	GO:0030150	10,9,8,7	protein import into mitochondrial matrix	22	0.0034	1	0.0017	0.2625276	D
<input type="radio"/>	GO:0030472	6,5,10	mitotic spindle organization and biogenesis in nucleus	22	0.0034	1	0.0017	0.2625276	D
<input type="radio"/>	GO:0044272	5	sulfur compound biosynthetic process	22	0.0034	1	0.0017	0.2625276	D
<input type="radio"/>	GO:0048284	5	organelle fusion	22	0.0034	1	0.0017	0.2625276	D
<input type="radio"/>	GO:0006311	10,8,7,5,9,6,4	meiotic gene conversion	22	0.0034	1	0.0017	0.2625276	D

<input type="checkbox"/>	GO:0018193	7	peptidyl-amino acid modification	28	0.0043	2	0.0033	0.2582291	D
<input type="checkbox"/>	GO:0051651	5,4,3	maintenance of cellular localization	29	0.0045	2	0.0033	0.2514625	D
<input type="checkbox"/>	GO:0032507	6,5,4	maintenance of cellular protein localization	29	0.0045	2	0.0033	0.2514625	D
<input type="checkbox"/>	GO:0000725	7,6	recombinational repair	29	0.0045	2	0.0033	0.2514625	D
<input type="checkbox"/>	GO:0043044	10	ATP-dependent chromatin remodeling	23	0.0036	1	0.0017	0.2488177	D
<input type="checkbox"/>	GO:0006479	9,7	protein amino acid methylation	23	0.0036	1	0.0017	0.2488177	D
<input type="checkbox"/>	GO:0007534	6,8,7	gene conversion at mating-type locus	23	0.0036	1	0.0017	0.2488177	D
<input type="checkbox"/>	GO:0008213	8	protein amino acid alkylation	23	0.0036	1	0.0017	0.2488177	D
<input type="checkbox"/>	GO:0045185	5,4,3	maintenance of protein localization	30	0.0046	2	0.0033	0.2442662	D
<input type="checkbox"/>	GO:0051031	5,7,6,8	tRNA transport	30	0.0046	2	0.0033	0.2442662	D
<input type="checkbox"/>	GO:0006890	8,6,5,7	retrograde vesicle-mediated transport, Golgi to ER	24	0.0037	1	0.0017	0.2353742	D
<input type="checkbox"/>	GO:0007035	13,10,6,11	vacuolar acidification	24	0.0037	1	0.0017	0.2353742	D
<input type="checkbox"/>	GO:0010035	4	response to inorganic substance	24	0.0037	1	0.0017	0.2353742	D
<input type="checkbox"/>	GO:0009069	6,7	serine family amino acid metabolic process	24	0.0037	1	0.0017	0.2353742	D
<input type="checkbox"/>	GO:0045851	8	pH reduction	24	0.0037	1	0.0017	0.2353742	D
<input type="checkbox"/>	GO:0051452	12,9,10	cellular pH reduction	24	0.0037	1	0.0017	0.2353742	D
<input type="checkbox"/>	GO:0051235	3,2	maintenance of localization	33	0.0051	3	0.0050	0.2352460	D
<input type="checkbox"/>	GO:0030004	9,7	cellular monovalent inorganic cation homeostasis	34	0.0053	3	0.0050	0.2339445	D
<input type="checkbox"/>	GO:0055067	8	monovalent inorganic cation homeostasis	34	0.0053	3	0.0050	0.2339445	D
<input type="checkbox"/>	GO:0000726	7,6	non-recombinational repair	35	0.0054	3	0.0050	0.2320051	D
<input type="checkbox"/>	GO:0016126	6,7,8	sterol biosynthetic process	32	0.0049	2	0.0033	0.2289226	D
<input type="checkbox"/>	GO:0006694	6,5,7	steroid biosynthetic process	32	0.0049	2	0.0033	0.2289226	D
<input type="checkbox"/>	GO:0051453	11,8,9	regulation of cellular pH	25	0.0039	1	0.0017	0.2222669	D
<input type="checkbox"/>	GO:0045005	8,6	maintenance of fidelity during DNA-dependent DNA replication	25	0.0039	1	0.0017	0.2222669	D
<input type="checkbox"/>	GO:0030641	10,8	cellular hydrogen ion homeostasis	25	0.0039	1	0.0017	0.2222669	D
<input type="checkbox"/>	GO:0006609	10,11,8,9,7	mRNA-binding (hnRNP) protein import into nucleus	25	0.0039	1	0.0017	0.2222669	D
<input type="checkbox"/>	GO:0000724	8,7	double-strand break repair via homologous recombination	25	0.0039	1	0.0017	0.2222669	D
<input type="checkbox"/>	GO:0006298	7,9,6	mismatch repair	25	0.0039	1	0.0017	0.2222669	D
<input type="checkbox"/>	GO:0006379	8	mRNA cleavage	26	0.0040	1	0.0017	0.2095504	D
<input type="checkbox"/>	GO:0008202	5,6	steroid metabolic process	43	0.0066	4	0.0066	0.2057797	D
<input type="checkbox"/>	GO:0007052	5,4,9	mitotic spindle organization and biogenesis	44	0.0068	4	0.0066	0.2052455	D
<input type="checkbox"/>	GO:0006289	7,6	nucleotide-excision repair	44	0.0068	4	0.0066	0.2052455	D
<input type="checkbox"/>	GO:0007051	8	spindle organization and biogenesis	47	0.0073	4	0.0066	0.2010175	D
<input type="checkbox"/>	GO:0006487	9,8,7	protein amino acid N-linked glycosylation	48	0.0074	4	0.0066	0.1988260	D
<input type="checkbox"/>	GO:0006367	8,9,7	transcription initiation from RNA polymerase II promoter	44	0.0068	3	0.0050	0.1943090	D
<input type="checkbox"/>	GO:0051170	9,7,8	nuclear import	50	0.0077	4	0.0066	0.1934413	D
<input type="checkbox"/>	GO:0006606	9,10,7,8,6	protein import into nucleus	50	0.0077	4	0.0066	0.1934413	D
<input type="checkbox"/>	GO:0006312	7	mitotic recombination	45	0.0069	3	0.0050	0.1887353	D
<input type="checkbox"/>	GO:0000075	7,6	cell cycle checkpoint	53	0.0082	4	0.0066	0.1832871	D
<input type="checkbox"/>	GO:0000041	7,8	transition metal ion transport	46	0.0071	3	0.0050	0.1830343	D
<input type="checkbox"/>	GO:0006302	7,6	double-strand break repair	57	0.0088	5	0.0083	0.1824986	D
<input type="checkbox"/>	GO:0051656	6,3,5,4	establishment of organelle localization	29	0.0045	1	0.0017	0.1741055	D
<input type="checkbox"/>	GO:0007533	5,7,6	mating type switching	29	0.0045	1	0.0017	0.1741055	D
<input type="checkbox"/>	GO:0006999	6	nuclear pore organization and biogenesis	29	0.0045	1	0.0017	0.1741055	D

<input type="radio"/>	GO:0006409	11,9,6,8,10,7	tRNA export from nucleus	29	0.0045	1	0.0017	0.1741055	D
<input type="radio"/>	GO:0006885	7	regulation of pH	29	0.0045	1	0.0017	0.1741055	D
<input type="radio"/>	GO:0000282	7,9,5,6,10	cellular bud site selection	66	0.0102	6	0.0099	0.1689131	D
<input type="radio"/>	GO:0030468	8,5,9	establishment of cell polarity (sensu Fungi)	66	0.0102	6	0.0099	0.1689131	D
<input type="radio"/>	GO:0007105	6,4	cytokinesis, site selection	66	0.0102	6	0.0099	0.1689131	D
<input type="radio"/>	GO:0030467	7,4,8	establishment and/or maintenance of cell polarity (sensu Fungi)	66	0.0102	6	0.0099	0.1689131	D
<input type="radio"/>	GO:0007033	5	vacuole organization and biogenesis	67	0.0103	6	0.0099	0.1682193	D
<input type="radio"/>	GO:0006413	7,6	translational initiation	49	0.0076	3	0.0050	0.1654905	D
<input type="radio"/>	GO:0016573	11,9	histone acetylation	40	0.0062	2	0.0033	0.1641932	D
<input type="radio"/>	GO:0051246	5,4	regulation of protein metabolic process	72	0.0111	6	0.0099	0.1613565	D
<input type="radio"/>	GO:0006354	8,6,7	RNA elongation	59	0.0091	4	0.0066	0.1581262	D
<input type="radio"/>	GO:0006401	6	RNA catabolic process	74	0.0114	6	0.0099	0.1572540	D
<input type="radio"/>	GO:0045944	10,9	positive regulation of transcription from RNA polymerase II promoter	76	0.0117	7	0.0116	0.1571790	D
<input type="radio"/>	GO:0046483	4	heterocycle metabolic process	76	0.0117	6	0.0099	0.1525267	D
<input type="radio"/>	GO:0030476	8,6,7	spore wall assembly (sensu Fungi)	42	0.0065	2	0.0033	0.1489215	D
<input type="radio"/>	GO:0042244	5,6	spore wall assembly	42	0.0065	2	0.0033	0.1489215	D
<input type="radio"/>	GO:0048468	3,5	cell development	52	0.0080	3	0.0050	0.1478587	D
<input type="radio"/>	GO:0016569	9	covalent chromatin modification	91	0.0141	8	0.0132	0.1448052	D
<input type="radio"/>	GO:0016570	10,8	histone modification	91	0.0141	8	0.0132	0.1448052	D
<input type="radio"/>	GO:0043543	7	protein amino acid acylation	62	0.0096	4	0.0066	0.1443664	D
<input type="radio"/>	GO:0032984	5	macromolecular complex disassembly	32	0.0049	1	0.0017	0.1430873	D
<input type="radio"/>	GO:0006271	8,7	DNA strand elongation during DNA replication	32	0.0049	1	0.0017	0.1430873	D
<input type="radio"/>	GO:0022616	6	DNA strand elongation	32	0.0049	1	0.0017	0.1430873	D
<input type="radio"/>	GO:0032506	5,3	cytokinetic process	88	0.0136	7	0.0116	0.1407915	D
<input type="radio"/>	GO:0045941	8,7	positive regulation of transcription	101	0.0156	9	0.0149	0.1376128	D
<input type="radio"/>	GO:0000398	8,10	nuclear mRNA splicing, via spliceosome	102	0.0158	9	0.0149	0.1368433	D
<input type="radio"/>	GO:0006486	8,7,6	protein amino acid glycosylation	73	0.0113	5	0.0083	0.1362944	D
<input type="radio"/>	GO:0043413	6	biopolymer glycosylation	73	0.0113	5	0.0083	0.1362944	D
<input type="radio"/>	GO:0000377	9	RNA splicing, via transesterification reactions with bulged adenosine as nucleophile	103	0.0159	9	0.0149	0.1359482	D
<input type="radio"/>	GO:0006270	8,6	DNA replication initiation	33	0.0051	1	0.0017	0.1337509	D
<input type="radio"/>	GO:0017038	5,6,7	protein import	109	0.0168	10	0.0166	0.1321661	D
<input type="radio"/>	GO:0000375	8	RNA splicing, via transesterification reactions	110	0.0170	10	0.0166	0.1318194	D
<input type="radio"/>	GO:0006352	7,8,6	transcription initiation	55	0.0085	3	0.0050	0.1307190	D
<input type="radio"/>	GO:0045935	7,6	positive regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	108	0.0167	9	0.0149	0.1297716	D
<input type="radio"/>	GO:0008033	7	tRNA processing	84	0.0130	6	0.0099	0.1293257	D
<input type="radio"/>	GO:0007017	6	microtubule-based process	101	0.0156	8	0.0132	0.1291516	D
<input type="radio"/>	GO:0007163	6,3,7	establishment and/or maintenance of cell polarity	115	0.0178	10	0.0166	0.1283655	D
<input type="radio"/>	GO:0000910	4	cytokinesis	109	0.0168	9	0.0149	0.1282344	D
<input type="radio"/>	GO:0009893	5,4	positive regulation of metabolic process	116	0.0179	10	0.0166	0.1273577	D
<input type="radio"/>	GO:0031325	6,5	positive regulation of cellular metabolic process	116	0.0179	10	0.0166	0.1273577	D
<input type="radio"/>	GO:0006310	6	DNA recombination	122	0.0188	11	0.0182	0.1254042	D
<input type="radio"/>	GO:0030010	7,4,8	establishment of cell polarity	103	0.0159	8	0.0132	0.1248601	D

<input type="radio"/>	GO:0007059	3	chromosome segregation	119	0.0184	10	0.0166	0.1237763	D
<input type="radio"/>	GO:0006997	5	nuclear organization and biogenesis	57	0.0088	3	0.0050	0.1197748	D
<input type="radio"/>	GO:0009101	7,5	glycoprotein biosynthetic process	78	0.0120	5	0.0083	0.1172083	D
<input type="radio"/>	GO:0007530	4,5	sex determination	35	0.0054	1	0.0017	0.1165449	D
<input type="radio"/>	GO:0003006	3,4	reproductive developmental process	35	0.0054	1	0.0017	0.1165449	D
<input type="radio"/>	GO:0000086	8,5,6,7,4	G2/M transition of mitotic cell cycle	35	0.0054	1	0.0017	0.1165449	D
<input type="radio"/>	GO:0007531	4,6,5	mating type determination	35	0.0054	1	0.0017	0.1165449	D
<input type="radio"/>	GO:0048518	4	positive regulation of biological process	124	0.0191	10	0.0166	0.1162212	D
<input type="radio"/>	GO:0048522	5,4	positive regulation of cellular process	124	0.0191	10	0.0166	0.1162212	D
<input type="radio"/>	GO:0009100	6	glycoprotein metabolic process	79	0.0122	5	0.0083	0.1134130	D
<input type="radio"/>	GO:0009889	5,4	regulation of biosynthetic process	69	0.0107	4	0.0066	0.1124588	D
<input type="radio"/>	GO:0000070	9,7,5,8,6,4	mitotic sister chromatid segregation	59	0.0091	3	0.0050	0.1093202	D
<input type="radio"/>	GO:0022411	4	cellular component disassembly	36	0.0056	1	0.0017	0.1086522	D
<input type="radio"/>	GO:0006473	8	protein amino acid acetylation	48	0.0074	2	0.0033	0.1081876	D
<input type="radio"/>	GO:0008380	7	RNA splicing	132	0.0204	10	0.0166	0.1012867	D
<input type="radio"/>	GO:0000819	7,4	sister chromatid segregation	62	0.0096	3	0.0050	0.0946835	D
<input type="radio"/>	GO:0016071	6	mRNA metabolic process	210	0.0324	18	0.0298	0.0922072	D
<input type="radio"/>	GO:0065004	6,5	protein-DNA complex assembly	74	0.0114	4	0.0066	0.0915330	D
<input type="radio"/>	GO:0006397	7	mRNA processing	157	0.0242	12	0.0199	0.0903918	D
<input type="radio"/>	GO:0000279	6,5	M phase	258	0.0398	24	0.0397	0.0869455	D
<input type="radio"/>	GO:0006400	7,8	tRNA modification	52	0.0080	2	0.0033	0.0858121	D
<input type="radio"/>	GO:0006368	9,7,8	RNA elongation from RNA polymerase II promoter	53	0.0082	2	0.0033	0.0808204	D
<input type="radio"/>	GO:0031326	6,5	regulation of cellular biosynthetic process	67	0.0103	3	0.0050	0.0733197	D
<input type="radio"/>	GO:0006790	4	sulfur metabolic process	67	0.0103	3	0.0050	0.0733197	D
<input type="radio"/>	GO:0007088	7,9,8,6	regulation of mitosis	55	0.0085	2	0.0033	0.0715337	D
<input type="radio"/>	GO:0006355	8,7	regulation of transcription, DNA-dependent	359	0.0554	31	0.0513	0.0687859	D
<input type="radio"/>	GO:0006888	8,6,5,7	ER to Golgi vesicle-mediated transport	81	0.0125	4	0.0066	0.0664379	D
<input type="radio"/>	GO:0019219	6,5	regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	440	0.0679	39	0.0646	0.0649835	D
<input type="radio"/>	GO:0000278	4	mitotic cell cycle	266	0.0411	21	0.0348	0.0646728	D
<input type="radio"/>	GO:0045449	7,6	regulation of transcription	386	0.0596	33	0.0546	0.0641208	D
<input type="radio"/>	GO:0008652	6,7	amino acid biosynthetic process	106	0.0164	6	0.0099	0.0623007	D
<input type="radio"/>	GO:0019222	4,3	regulation of metabolic process	538	0.0831	50	0.0828	0.0617271	D
<input type="radio"/>	GO:0006259	5	DNA metabolic process	523	0.0808	47	0.0778	0.0609701	D
<input type="radio"/>	GO:0048523	5,4	negative regulation of cellular process	239	0.0369	18	0.0298	0.0598371	D
<input type="radio"/>	GO:0006366	8,7	transcription from RNA polymerase II promoter	343	0.0530	28	0.0464	0.0594777	D
<input type="radio"/>	GO:0048519	4	negative regulation of biological process	242	0.0374	18	0.0298	0.0561740	D
<input type="radio"/>	GO:0016568	8	chromatin modification	223	0.0344	16	0.0265	0.0528936	D
<input type="radio"/>	GO:0009066	6,7	aspartate family amino acid metabolic process	46	0.0071	1	0.0017	0.0519061	D
<input type="radio"/>	GO:0032200	7	telomere organization and biogenesis	274	0.0423	20	0.0331	0.0446096	D
<input type="radio"/>	GO:0000723	8	telomere maintenance	274	0.0423	20	0.0331	0.0446096	D
<input type="radio"/>	GO:0009309	5,6	amine biosynthetic process	114	0.0176	6	0.0099	0.0442432	D
<input type="radio"/>	GO:0009892	5,4	negative regulation of metabolic process	208	0.0321	14	0.0232	0.0435310	D
<input type="radio"/>	GO:0044271	5,4	nitrogen compound biosynthetic process	115	0.0178	6	0.0099	0.0422910	D

<input type="radio"/>	GO:0031323	5,4	regulation of cellular metabolic process	507	0.0783	41	0.0679	0.0399773	D
<input type="radio"/>	GO:0019538	4	protein metabolic process	1547	0.2389	140	0.2318	0.0367577	D
<input type="radio"/>	GO:0006338	9	chromatin remodeling	155	0.0239	9	0.0149	0.0364249	D
<input type="radio"/>	GO:0044267	5	cellular protein metabolic process	1498	0.2313	135	0.2235	0.0364083	D
<input type="radio"/>	GO:0065003	5,4	macromolecular complex assembly	328	0.0506	24	0.0397	0.0356406	D
<input type="radio"/>	GO:0045892	9,8	negative regulation of transcription, DNA-dependent	156	0.0241	9	0.0149	0.0350163	D
<input type="radio"/>	GO:0006325	7	establishment and/or maintenance of chromatin architecture	253	0.0391	17	0.0281	0.0317936	D
<input type="radio"/>	GO:0006323	6	DNA packaging	253	0.0391	17	0.0281	0.0317936	D
<input type="radio"/>	GO:0031324	6,5	negative regulation of cellular metabolic process	198	0.0306	12	0.0199	0.0280183	D
<input type="radio"/>	GO:0016481	8,7	negative regulation of transcription	162	0.0250	9	0.0149	0.0274080	D
<input type="radio"/>	GO:0007067	8,6,7,5	mitosis	127	0.0196	6	0.0099	0.0237364	D
<input type="radio"/>	GO:0045934	7,6	negative regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	179	0.0276	10	0.0166	0.0226232	D
<input type="radio"/>	GO:0000087	7,5,6	M phase of mitotic cell cycle	129	0.0199	6	0.0099	0.0214298	D
<input type="radio"/>	GO:0007001	6	chromosome organization and biogenesis (sensu Eukaryota)	567	0.0876	43	0.0712	0.0201850	D
<input type="radio"/>	GO:0006260	6	DNA replication	117	0.0181	5	0.0083	0.0198802	D
<input type="radio"/>	GO:0006403	4	RNA localization	90	0.0139	3	0.0050	0.0185978	D
<input type="radio"/>	GO:0051276	5	chromosome organization and biogenesis	572	0.0883	43	0.0712	0.0181410	D
<input type="radio"/>	GO:0031509	7,11	telomeric heterochromatin formation	60	0.0093	1	0.0017	0.0170314	D
<input type="radio"/>	GO:0006348	11,7,8,12,10	chromatin silencing at telomere	60	0.0093	1	0.0017	0.0170314	D
<input type="radio"/>	GO:0001510	7	RNA methylation	60	0.0093	1	0.0017	0.0170314	D
<input type="radio"/>	GO:0006139	4	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	1532	0.2366	129	0.2136	0.0153096	D
<input type="radio"/>	GO:0050658	4,6,5,7	RNA transport	80	0.0124	2	0.0033	0.0129273	D
<input type="radio"/>	GO:0051236	3,4,5	establishment of RNA localization	80	0.0124	2	0.0033	0.0129273	D
<input type="radio"/>	GO:0050657	5,6	nucleic acid transport	80	0.0124	2	0.0033	0.0129273	D
<input type="radio"/>	GO:0006350	5	transcription	567	0.0876	41	0.0679	0.0119305	D
<input type="radio"/>	GO:0006261	7	DNA-dependent DNA replication	97	0.0150	3	0.0050	0.0116811	D
<input type="radio"/>	GO:0006351	7,6	transcription, DNA-dependent	522	0.0806	37	0.0613	0.0114997	D
<input type="radio"/>	GO:0032774	6	RNA biosynthetic process	524	0.0809	37	0.0613	0.0108999	D
<input type="radio"/>	GO:0032259	5	methylation	83	0.0128	2	0.0033	0.0103484	D
<input type="radio"/>	GO:0043414	6	biopolymer methylation	83	0.0128	2	0.0033	0.0103484	D
<input type="radio"/>	GO:0051169	7,5,6	nuclear transport	129	0.0199	5	0.0083	0.0099521	D
<input type="radio"/>	GO:0006913	8,6,7	nucleocytoplasmic transport	129	0.0199	5	0.0083	0.0099521	D
<input type="radio"/>	GO:0022618	6,5	protein-RNA complex assembly	144	0.0222	6	0.0099	0.0094988	D
<input type="radio"/>	GO:0022607	4	cellular component assembly	471	0.0727	32	0.0530	0.0092292	D
<input type="radio"/>	GO:0015931	4,5	nucleobase, nucleoside, nucleotide and nucleic acid transport	90	0.0139	2	0.0033	0.0060927	D
<input type="radio"/>	GO:0043283	4	biopolymer metabolic process	2230	0.3443	187	0.3096	0.0060246	D
<input type="radio"/>	GO:0006996	4	organelle organization and biogenesis	1388	0.2143	110	0.1821	0.0052401	D
<input type="radio"/>	GO:0006730	4	one-carbon compound metabolic process	97	0.0150	2	0.0033	0.0035405	D
<input type="radio"/>	GO:0006405	10,8,5,7,9,6	RNA export from nucleus	79	0.0122	1	0.0017	0.0034285	D
<input type="radio"/>	GO:0040029	4	regulation of gene expression, epigenetic	100	0.0154	2	0.0033	0.0027957	D
<input type="radio"/>	GO:0031497	5,9	chromatin assembly	104	0.0161	2	0.0033	0.0020342	D
<input type="radio"/>	GO:0045814	5	negative regulation of gene expression, epigenetic	95	0.0147	1	0.0017	0.0008441	D

<input type="checkbox"/>	GO:0031507	6,10	heterochromatin formation	95	0.0147	1	0.0017	0.0008441	D
<input type="checkbox"/>	GO:0006342	10,6,7,11,9	chromatin silencing	95	0.0147	1	0.0017	0.0008441	D
<input type="checkbox"/>	GO:0016458	5	gene silencing	95	0.0147	1	0.0017	0.0008441	D
<input type="checkbox"/>	GO:0006333	8	chromatin assembly or disassembly	119	0.0184	2	0.0033	0.0006008	D
<input type="checkbox"/>	GO:0051168	9,7,8	nuclear export	102	0.0158	1	0.0017	0.0004522	D
<input type="checkbox"/>	GO:0009058	3	biosynthetic process	1249	0.1929	88	0.1457	0.0003013	D
<input type="checkbox"/>	GO:0009451	6	RNA modification	139	0.0215	2	0.0033	0.0001119	D
<input type="checkbox"/>	GO:0016070	5	RNA metabolic process	1058	0.1634	66	0.1093	2.150272E-05	D
<input type="checkbox"/>	GO:0009059	4	macromolecule biosynthetic process	886	0.1368	50	0.0828	5.696235E-06	D
<input type="checkbox"/>	GO:0043284	5	biopolymer biosynthetic process	354	0.0547	9	0.0149	1.445099E-07	D
<input type="checkbox"/>	GO:0006396	6	RNA processing	491	0.0758	17	0.0281	1.156647E-07	D
<input type="checkbox"/>	GO:0006364	6,7	rRNA processing	249	0.0384	1	0.0017	4.174652E-10	D
<input type="checkbox"/>	GO:0016072	6	rRNA metabolic process	256	0.0395	1	0.0017	2.103143E-10	D
<input type="checkbox"/>	GO:0006412	6,5	translation	688	0.1062	23	0.0381	9.836112E-11	D
<input type="checkbox"/>	GO:0022613	4	ribonucleoprotein complex biogenesis and assembly	483	0.0746	8	0.0132	6.742110E-13	D
<input type="checkbox"/>	GO:0042254	5	ribosome biogenesis and assembly	410	0.0633	2	0.0033	9.354221E-16	D