

GO-Stats Results

Your dataset contains **319** annotated gene products.

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

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

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

GO ID	Level	GO Term	RO	RF	DO	DF	P-value	E/D
<input type="radio"/> GO:0009987	2	cellular process	4654	0.7187	268	0.8401	7.466782E-08	E
<input type="radio"/> GO:0009058	3	biosynthetic process	1249	0.1929	93	0.2915	3.897708E-06	E
<input type="radio"/> GO:0008152	2	metabolic process	3516	0.5429	210	0.6583	4.882082E-06	E
<input type="radio"/> GO:0006839	7,5,6	mitochondrial transport	65	0.0100	13	0.0408	1.036304E-05	E
<input type="radio"/> GO:0044237	3	cellular metabolic process	3403	0.5255	203	0.6364	1.069164E-05	E
<input type="radio"/> GO:0008610	5,4,6	lipid biosynthetic process	129	0.0199	19	0.0596	1.120245E-05	E
<input type="radio"/> GO:0006629	4	lipid metabolic process	242	0.0374	27	0.0846	3.155527E-05	E
<input type="radio"/> GO:0044255	4,5	cellular lipid metabolic process	229	0.0354	26	0.0815	3.275948E-05	E
<input type="radio"/> GO:0046474	8,7,9	glycerophospholipid biosynthetic process	39	0.0060	9	0.0282	7.412978E-05	E
<input type="radio"/> GO:0006810	3,4	transport	981	0.1515	72	0.2257	8.676908E-05	E
<input type="radio"/> GO:0006888	8,6,5,7	ER to Golgi vesicle-mediated transport	81	0.0125	13	0.0408	0.0001082	E
<input type="radio"/> GO:0006650	7,8	glycerophospholipid metabolic process	60	0.0093	11	0.0345	0.0001090	E
<input type="radio"/> GO:0006626	9,8,7,6	protein targeting to mitochondrion	52	0.0080	10	0.0313	0.0001476	E
<input type="radio"/> GO:0006486	8,7,6	protein amino acid glycosylation	73	0.0113	12	0.0376	0.0001558	E
<input type="radio"/> GO:0043413	6	biopolymer glycosylation	73	0.0113	12	0.0376	0.0001558	E
<input type="radio"/> GO:0051234	2,3	establishment of localization	1004	0.1550	72	0.2257	0.0001698	E
<input type="radio"/> GO:0009101	7,5	glycoprotein biosynthetic process	78	0.0120	12	0.0376	0.0002878	E
<input type="radio"/> GO:0046467	6,5,7	membrane lipid biosynthetic process	78	0.0120	12	0.0376	0.0002878	E
<input type="radio"/> GO:0009100	6	glycoprotein metabolic process	79	0.0122	12	0.0376	0.0003231	E
<input type="radio"/> GO:0008654	7,6,8	phospholipid biosynthetic process	58	0.0090	10	0.0313	0.0003621	E
<input type="radio"/> GO:0051179	2	localization	1051	0.1623	73	0.2288	0.0003727	E
<input type="radio"/> GO:0006487	9,8,7	protein amino acid N-linked glycosylation	48	0.0074	9	0.0282	0.0003761	E
<input type="radio"/> GO:0006464	6	protein modification process	520	0.0803	42	0.1317	0.0003988	E
<input type="radio"/> GO:0044260	4	cellular macromolecule metabolic process	1552	0.2397	100	0.3135	0.0004362	E
<input type="radio"/> GO:0006546	8,9	glycine catabolic process	4	0.0006	3	0.0094	0.0004507	E

<input type="checkbox"/>	GO:0015865	6,7	purine nucleotide transport	4	0.0006	3	0.0094	0.0004507	E
<input type="checkbox"/>	GO:0030150	10,9,8,7	protein import into mitochondrial matrix	22	0.0034	6	0.0188	0.0004605	E
<input type="checkbox"/>	GO:0043681	6,7,8	protein import into mitochondrion	40	0.0062	8	0.0251	0.0005044	E
<input type="checkbox"/>	GO:0044238	3	primary metabolic process	3247	0.5014	186	0.5831	0.0005169	E
<input type="checkbox"/>	GO:0019538	4	protein metabolic process	1547	0.2389	99	0.3103	0.0005800	E
<input type="checkbox"/>	GO:0044267	5	cellular protein metabolic process	1498	0.2313	96	0.3009	0.0006713	E
<input type="checkbox"/>	GO:0006807	3	nitrogen compound metabolic process	251	0.0388	24	0.0752	0.0007253	E
<input type="checkbox"/>	GO:0044249	4	cellular biosynthetic process	366	0.0565	31	0.0972	0.0009891	E
<input type="checkbox"/>	GO:0009308	4	amine metabolic process	228	0.0352	22	0.0690	0.0010300	E
<input type="checkbox"/>	GO:0009071	7,8	serine family amino acid catabolic process	5	0.0008	3	0.0094	0.0010717	E
<input type="checkbox"/>	GO:0006862	5,6	nucleotide transport	5	0.0008	3	0.0094	0.0010717	E
<input type="checkbox"/>	GO:0019752	5	carboxylic acid metabolic process	314	0.0485	27	0.0846	0.0015805	E
<input type="checkbox"/>	GO:0006082	4	organic acid metabolic process	314	0.0485	27	0.0846	0.0015805	E
<input type="checkbox"/>	GO:0009060	6	aerobic respiration	84	0.0130	11	0.0345	0.0018103	E
<input type="checkbox"/>	GO:0006644	6,7	phospholipid metabolic process	97	0.0150	12	0.0376	0.0018534	E
<input type="checkbox"/>	GO:0006544	7,8	glycine metabolic process	6	0.0009	3	0.0094	0.0020388	E
<input type="checkbox"/>	GO:0006643	5,6	membrane lipid metabolic process	125	0.0193	14	0.0439	0.0020512	E
<input type="checkbox"/>	GO:0045333	5	cellular respiration	89	0.0137	11	0.0345	0.0027804	E
<input type="checkbox"/>	GO:0006656	9,8,10	phosphatidylcholine biosynthetic process	7	0.0011	3	0.0094	0.0033936	E
<input type="checkbox"/>	GO:0000715	7,8	nucleotide-excision repair, DNA damage recognition	7	0.0011	3	0.0094	0.0033936	E
<input type="checkbox"/>	GO:0006749	6,5	glutathione metabolic process	14	0.0022	4	0.0125	0.0035134	E
<input type="checkbox"/>	GO:0030384	8,9	phosphoinositide metabolic process	43	0.0066	7	0.0219	0.0035743	E
<input type="checkbox"/>	GO:0006732	5	coenzyme metabolic process	136	0.0210	14	0.0439	0.0041400	E
<input type="checkbox"/>	GO:0017038	5,6,7	protein import	109	0.0168	12	0.0376	0.0045055	E
<input type="checkbox"/>	GO:0006031	9,7,8,10	chitin biosynthetic process	15	0.0023	4	0.0125	0.0045574	E
<input type="checkbox"/>	GO:0009069	6,7	serine family amino acid metabolic process	24	0.0037	5	0.0157	0.0046431	E
<input type="checkbox"/>	GO:0051186	4	cofactor metabolic process	170	0.0263	16	0.0502	0.0052405	E
<input type="checkbox"/>	GO:0032787	6	monocarboxylic acid metabolic process	126	0.0195	13	0.0408	0.0053767	E
<input type="checkbox"/>	GO:0043412	5	biopolymer modification	664	0.1025	45	0.1411	0.0056223	E
<input type="checkbox"/>	GO:0009081	6,7	branched chain family amino acid metabolic process	16	0.0025	4	0.0125	0.0057803	E
<input type="checkbox"/>	GO:0009309	5,6	amine biosynthetic process	114	0.0176	12	0.0376	0.0062020	E
<input type="checkbox"/>	GO:0050789	3	regulation of biological process	761	0.1175	50	0.1567	0.0063901	E
<input type="checkbox"/>	GO:0046907	6,4,5	intracellular transport	545	0.0842	38	0.1191	0.0064812	E
<input type="checkbox"/>	GO:0010382	6,4	cell wall metabolic process	26	0.0040	5	0.0157	0.0065034	E
<input type="checkbox"/>	GO:0044271	5,4	nitrogen compound biosynthetic process	115	0.0178	12	0.0376	0.0065904	E
<input type="checkbox"/>	GO:0051503	7,8	adenine nucleotide transport	3	0.0005	2	0.0063	0.0069022	E
<input type="checkbox"/>	GO:0015867	8,9	ATP transport	3	0.0005	2	0.0063	0.0069022	E
<input type="checkbox"/>	GO:0017157	6,9,5,7,8	regulation of exocytosis	3	0.0005	2	0.0063	0.0069022	E
<input type="checkbox"/>	GO:0006042	7,8	glucosamine biosynthetic process	17	0.0026	4	0.0125	0.0071903	E
<input type="checkbox"/>	GO:0006030	8,6,7,9	chitin metabolic process	17	0.0026	4	0.0125	0.0071903	E
<input type="checkbox"/>	GO:0046349	6,7	amino sugar biosynthetic process	17	0.0026	4	0.0125	0.0071903	E
<input type="checkbox"/>	GO:0006045	8,9	N-acetylglucosamine biosynthetic process	17	0.0026	4	0.0125	0.0071903	E
<input type="checkbox"/>	GO:0046470	8,9	phosphatidylcholine metabolic process	9	0.0014	3	0.0094	0.0073683	E
<input type="checkbox"/>	GO:0006505	9,10	GPI anchor metabolic process	27	0.0042	5	0.0157	0.0075928	E

<input type="checkbox"/>	GO:0016485	8	protein processing	38	0.0059	6	0.0188	0.0076836	E
<input type="checkbox"/>	GO:0046489	9,8,10	phosphoinositide biosynthetic process	28	0.0043	5	0.0157	0.0087934	E
<input type="checkbox"/>	GO:0051789	4	response to protein stimulus	18	0.0028	4	0.0125	0.0087938	E
<input type="checkbox"/>	GO:0006986	4,5	response to unfolded protein	18	0.0028	4	0.0125	0.0087938	E
<input type="checkbox"/>	GO:0031570	8,7	DNA integrity checkpoint	18	0.0028	4	0.0125	0.0087938	E
<input type="checkbox"/>	GO:0048193	7,5,6	Golgi vesicle transport	166	0.0256	15	0.0470	0.0089635	E
<input type="checkbox"/>	GO:0008652	6,7	amino acid biosynthetic process	106	0.0164	11	0.0345	0.0091251	E
<input type="checkbox"/>	GO:0009063	6,7	amino acid catabolic process	29	0.0045	5	0.0157	0.0101079	E
<input type="checkbox"/>	GO:0006040	5,6	amino sugar metabolic process	19	0.0029	4	0.0125	0.0105955	E
<input type="checkbox"/>	GO:0006044	7,8	N-acetylglucosamine metabolic process	19	0.0029	4	0.0125	0.0105955	E
<input type="checkbox"/>	GO:0006041	6,7	glucosamine metabolic process	19	0.0029	4	0.0125	0.0105955	E
<input type="checkbox"/>	GO:0009228	7,8	thiamin biosynthetic process	19	0.0029	4	0.0125	0.0105955	E
<input type="checkbox"/>	GO:0009059	4	macromolecule biosynthetic process	886	0.1368	55	0.1724	0.0112321	E
<input type="checkbox"/>	GO:0046942	5,6	carboxylic acid transport	54	0.0083	7	0.0219	0.0113642	E
<input type="checkbox"/>	GO:0050794	4,3	regulation of cellular process	738	0.1140	47	0.1473	0.0116224	E
<input type="checkbox"/>	GO:0015849	4,5	organic acid transport	55	0.0085	7	0.0219	0.0123888	E
<input type="checkbox"/>	GO:0051053	8,7	negative regulation of DNA metabolic process	20	0.0031	4	0.0125	0.0125983	E
<input type="checkbox"/>	GO:0006772	7	thiamin metabolic process	20	0.0031	4	0.0125	0.0125983	E
<input type="checkbox"/>	GO:0042724	7	thiamin and derivative biosynthetic process	20	0.0031	4	0.0125	0.0125983	E
<input type="checkbox"/>	GO:0000002	6	mitochondrial genome maintenance	31	0.0048	5	0.0157	0.0130876	E
<input type="checkbox"/>	GO:0045454	6,4	cell redox homeostasis	11	0.0017	3	0.0094	0.0130934	E
<input type="checkbox"/>	GO:0007109	7,6,5,4	cytokinesis, completion of separation	11	0.0017	3	0.0094	0.0130934	E
<input type="checkbox"/>	GO:0006518	4	peptide metabolic process	11	0.0017	3	0.0094	0.0130934	E
<input type="checkbox"/>	GO:0030503	5,7,4	regulation of cell redox homeostasis	11	0.0017	3	0.0094	0.0130934	E
<input type="checkbox"/>	GO:0009083	7,8	branched chain family amino acid catabolic process	4	0.0006	2	0.0063	0.0131284	E
<input type="checkbox"/>	GO:0048519	4	negative regulation of biological process	242	0.0374	19	0.0596	0.0135829	E
<input type="checkbox"/>	GO:0006457	6	protein folding	84	0.0130	9	0.0282	0.0138625	E
<input type="checkbox"/>	GO:0044270	5,4	nitrogen compound catabolic process	32	0.0049	5	0.0157	0.0147555	E
<input type="checkbox"/>	GO:0009310	5,6	amine catabolic process	32	0.0049	5	0.0157	0.0147555	E
<input type="checkbox"/>	GO:0051649	5,3,4	establishment of cellular localization	606	0.0936	39	0.1223	0.0156150	E
<input type="checkbox"/>	GO:0009070	7,8	serine family amino acid biosynthetic process	12	0.0019	3	0.0094	0.0166046	E
<input type="checkbox"/>	GO:0042723	6	thiamin and derivative metabolic process	22	0.0034	4	0.0125	0.0172099	E
<input type="checkbox"/>	GO:0006519	4	amino acid and derivative metabolic process	202	0.0312	16	0.0502	0.0191957	E
<input type="checkbox"/>	GO:0065007	2	biological regulation	948	0.1464	56	0.1755	0.0203478	E
<input type="checkbox"/>	GO:0030433	9,11,10,12	ER-associated protein catabolic process	35	0.0054	5	0.0157	0.0204758	E
<input type="checkbox"/>	GO:0000920	6,4	cell separation during cytokinesis	13	0.0020	3	0.0094	0.0205307	E
<input type="checkbox"/>	GO:0009082	7,8	branched chain family amino acid biosynthetic process	13	0.0020	3	0.0094	0.0205307	E
<input type="checkbox"/>	GO:0006633	7,6,8,5	fatty acid biosynthetic process	13	0.0020	3	0.0094	0.0205307	E
<input type="checkbox"/>	GO:0006038	9,10,7,8,11	cell wall chitin biosynthetic process	13	0.0020	3	0.0094	0.0205307	E
<input type="checkbox"/>	GO:0051641	4,3	cellular localization	642	0.0991	40	0.1254	0.0207147	E
<input type="checkbox"/>	GO:0042158	7,5	lipoprotein biosynthetic process	48	0.0074	6	0.0188	0.0207416	E
<input type="checkbox"/>	GO:0006497	8,7,6	protein amino acid lipidation	48	0.0074	6	0.0188	0.0207416	E
<input type="checkbox"/>	GO:0042157	6	lipoprotein metabolic process	48	0.0074	6	0.0188	0.0207416	E
<input type="checkbox"/>	GO:0015693	7,8	magnesium ion transport	5	0.0008	2	0.0063	0.0208090	E

<input type="radio"/>	GO:0000076	11,9,8,10	DNA replication checkpoint	5	0.0008	2	0.0063	0.0208090	E
<input type="radio"/>	GO:0016192	4,5	vesicle-mediated transport	328	0.0506	23	0.0721	0.0211948	E
<input type="radio"/>	GO:0006890	8,6,5,7	retrograde vesicle-mediated transport, Golgi to ER	24	0.0037	4	0.0125	0.0226187	E
<input type="radio"/>	GO:0009892	5,4	negative regulation of metabolic process	208	0.0321	16	0.0502	0.0231952	E
<input type="radio"/>	GO:0045045	7,5,4,6	secretory pathway	243	0.0375	18	0.0564	0.0233459	E
<input type="radio"/>	GO:0043170	3	macromolecule metabolic process	2841	0.4387	150	0.4702	0.0233814	E
<input type="radio"/>	GO:0043687	7	post-translational protein modification	388	0.0599	26	0.0815	0.0238189	E
<input type="radio"/>	GO:0007165	4	signal transduction	209	0.0323	16	0.0502	0.0239039	E
<input type="radio"/>	GO:0051188	5	cofactor biosynthetic process	79	0.0122	8	0.0251	0.0246507	E
<input type="radio"/>	GO:0006037	8,9,6,7,10	cell wall chitin metabolic process	14	0.0022	3	0.0094	0.0248524	E
<input type="radio"/>	GO:0009607	3	response to biotic stimulus	25	0.0039	4	0.0125	0.0256124	E
<input type="radio"/>	GO:0006515	8,9	misfolded or incompletely synthesized protein catabolic process	38	0.0059	5	0.0157	0.0272507	E
<input type="radio"/>	GO:0015980	4	energy derivation by oxidation of organic compounds	145	0.0224	12	0.0376	0.0272792	E
<input type="radio"/>	GO:0032940	6,4,5	secretion by cell	250	0.0386	18	0.0564	0.0280357	E
<input type="radio"/>	GO:0046903	3,4	secretion	250	0.0386	18	0.0564	0.0280357	E
<input type="radio"/>	GO:0009966	5,4	regulation of signal transduction	26	0.0040	4	0.0125	0.0287912	E
<input type="radio"/>	GO:0006506	10,9,8,7,11	GPI anchor biosynthetic process	26	0.0040	4	0.0125	0.0287912	E
<input type="radio"/>	GO:0022401	7,6	adaptation of signaling pathway	15	0.0023	3	0.0094	0.0295464	E
<input type="radio"/>	GO:0000754	8,7,5	adaptation to pheromone during conjugation with cellular fusion	15	0.0023	3	0.0094	0.0295464	E
<input type="radio"/>	GO:0006490	5,11,10,9,7,6	oligosaccharide-lipid intermediate assembly	6	0.0009	2	0.0063	0.0296844	E
<input type="radio"/>	GO:0032297	10,8,9	negative regulation of DNA replication initiation	6	0.0009	2	0.0063	0.0296844	E
<input type="radio"/>	GO:0051691	6	cellular oligosaccharide metabolic process	6	0.0009	2	0.0063	0.0296844	E
<input type="radio"/>	GO:0045041	10,9,8,7	protein import into mitochondrial intermembrane space	6	0.0009	2	0.0063	0.0296844	E
<input type="radio"/>	GO:0006627	10,9,8,7	mitochondrial protein processing	6	0.0009	2	0.0063	0.0296844	E
<input type="radio"/>	GO:0006591	7,8,5,4	ornithine metabolic process	6	0.0009	2	0.0063	0.0296844	E
<input type="radio"/>	GO:0042221	3	response to chemical stimulus	382	0.0590	25	0.0784	0.0302606	E
<input type="radio"/>	GO:0006811	4,5	ion transport	115	0.0178	10	0.0313	0.0306740	E
<input type="radio"/>	GO:0008104	4	protein localization	330	0.0510	22	0.0690	0.0326433	E
<input type="radio"/>	GO:0048523	5,4	negative regulation of cellular process	239	0.0369	17	0.0533	0.0332663	E
<input type="radio"/>	GO:0006605	8,6,7	protein targeting	258	0.0398	18	0.0564	0.0339095	E
<input type="radio"/>	GO:0007154	3	cell communication	240	0.0371	17	0.0533	0.0340687	E
<input type="radio"/>	GO:0006493	9,8,7	protein amino acid O-linked glycosylation	16	0.0025	3	0.0094	0.0345862	E
<input type="radio"/>	GO:0010383	7,5,6	cell wall polysaccharide metabolic process	16	0.0025	3	0.0094	0.0345862	E
<input type="radio"/>	GO:0006520	5,6	amino acid metabolic process	187	0.0289	14	0.0439	0.0347445	E
<input type="radio"/>	GO:0000271	6,7	polysaccharide biosynthetic process	41	0.0063	5	0.0157	0.0350170	E
<input type="radio"/>	GO:0000725	7,6	recombinational repair	29	0.0045	4	0.0125	0.0393600	E
<input type="radio"/>	GO:0043633	7	modification-dependent RNA catabolic process	7	0.0011	2	0.0063	0.0395219	E
<input type="radio"/>	GO:0009311	5	oligosaccharide metabolic process	7	0.0011	2	0.0063	0.0395219	E
<input type="radio"/>	GO:0006551	7,8	leucine metabolic process	7	0.0011	2	0.0063	0.0395219	E
<input type="radio"/>	GO:0015833	4,5	peptide transport	7	0.0011	2	0.0063	0.0395219	E
<input type="radio"/>	GO:0006465	9,5	signal peptide processing	7	0.0011	2	0.0063	0.0395219	E
<input type="radio"/>	GO:0006621	7,6,5,4	protein retention in ER	7	0.0011	2	0.0063	0.0395219	E
<input type="radio"/>	GO:0043634	8	polyadenylation-dependent ncRNA	7	0.0011	2	0.0063	0.0395219	E

<input type="radio"/>	GO:0043034	0	catabolic process	7	0.0011	2	0.0003	0.0395219	E
<input type="radio"/>	GO:0016053	5	organic acid biosynthetic process	17	0.0026	3	0.0094	0.0399432	E
<input type="radio"/>	GO:0046394	6	carboxylic acid biosynthetic process	17	0.0026	3	0.0094	0.0399432	E
<input type="radio"/>	GO:0009968	6,5	negative regulation of signal transduction	17	0.0026	3	0.0094	0.0399432	E
<input type="radio"/>	GO:0006766	4	vitamin metabolic process	89	0.0137	8	0.0251	0.0405261	E
<input type="radio"/>	GO:0006767	5	water-soluble vitamin metabolic process	89	0.0137	8	0.0251	0.0405261	E
<input type="radio"/>	GO:0019222	4,3	regulation of metabolic process	538	0.0831	32	0.1003	0.0411539	E
<input type="radio"/>	GO:0044248	4	cellular catabolic process	425	0.0656	26	0.0815	0.0440023	E
<input type="radio"/>	GO:0045934	7,6	negative regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	179	0.0276	13	0.0408	0.0452452	E
<input type="radio"/>	GO:0051248	6,5	negative regulation of protein metabolic process	18	0.0028	3	0.0094	0.0455868	E
<input type="radio"/>	GO:0031324	6,5	negative regulation of cellular metabolic process	198	0.0306	14	0.0439	0.0460314	E
<input type="radio"/>	GO:0006886	7,5,6	intracellular protein transport	274	0.0423	18	0.0564	0.0469026	E
<input type="radio"/>	GO:0016043	3	cellular component organization and biogenesis	2264	0.3496	113	0.3542	0.0471108	E
<input type="radio"/>	GO:0007005	5	mitochondrion organization and biogenesis	110	0.0170	9	0.0282	0.0478833	E
<input type="radio"/>	GO:0016051	5	carbohydrate biosynthetic process	77	0.0119	7	0.0219	0.0489839	E
<input type="radio"/>	GO:0045184	3,4,5	establishment of protein localization	296	0.0457	19	0.0596	0.0492102	E
<input type="radio"/>	GO:0009305	8	protein amino acid biotinylation	1	0.0002	1	0.0031	0.0492588	E
<input type="radio"/>	GO:0015866	8,9	ADP transport	1	0.0002	1	0.0031	0.0492588	E
<input type="radio"/>	GO:0000713	11,9,8,6,5,10,7,4	meiotic heteroduplex formation	1	0.0002	1	0.0031	0.0492588	E
<input type="radio"/>	GO:0051037	9,7,8,6	regulation of transcription, meiotic chaperone-mediated protein complex assembly	1	0.0002	1	0.0031	0.0492588	E
<input type="radio"/>	GO:0006573	7,8	valine metabolic process	1	0.0002	1	0.0031	0.0492588	E
<input type="radio"/>	GO:0043171	5	peptide catabolic process	1	0.0002	1	0.0031	0.0492588	E
<input type="radio"/>	GO:0000373	10	Group II intron splicing	1	0.0002	1	0.0031	0.0492588	E
<input type="radio"/>	GO:0006550	8,9	isoleucine catabolic process	1	0.0002	1	0.0031	0.0492588	E
<input type="radio"/>	GO:0019985	7,6	bypass DNA synthesis	1	0.0002	1	0.0031	0.0492588	E
<input type="radio"/>	GO:0046471	8,9	phosphatidylglycerol metabolic process	1	0.0002	1	0.0031	0.0492588	E
<input type="radio"/>	GO:0043111	10,9	replication fork blocking	1	0.0002	1	0.0031	0.0492588	E
<input type="radio"/>	GO:0006106	7	fumarate metabolic process	1	0.0002	1	0.0031	0.0492588	E
<input type="radio"/>	GO:0001408	7,8	guanine nucleotide transport	1	0.0002	1	0.0031	0.0492588	E
<input type="radio"/>	GO:0006655	9,8,10	phosphatidylglycerol biosynthetic process	1	0.0002	1	0.0031	0.0492588	E
<input type="radio"/>	GO:0015807	6,7,8	L-amino acid transport	1	0.0002	1	0.0031	0.0492588	E
<input type="radio"/>	GO:0009230	7,8	thiamin catabolic process	1	0.0002	1	0.0031	0.0492588	E
<input type="radio"/>	GO:0030041	9,6,7	actin filament polymerization	1	0.0002	1	0.0031	0.0492588	E
<input type="radio"/>	GO:0015811	7,8,9	L-cystine transport	1	0.0002	1	0.0031	0.0492588	E
<input type="radio"/>	GO:0006574	8,9	valine catabolic process	1	0.0002	1	0.0031	0.0492588	E
<input type="radio"/>	GO:0042989	8,9,12,10,6,5,4,7	sequestering of actin monomers	1	0.0002	1	0.0031	0.0492588	E
<input type="radio"/>	GO:0042725	7	thiamin and derivative catabolic process	1	0.0002	1	0.0031	0.0492588	E
<input type="radio"/>	GO:0046482	5,6,8	para-aminobenzoic acid metabolic process	1	0.0002	1	0.0031	0.0492588	E
<input type="radio"/>	GO:0051258	6	protein polymerization	1	0.0002	1	0.0031	0.0492588	E
<input type="radio"/>	GO:0030837	7,8,11,9,6	negative regulation of actin filament polymerization	1	0.0002	1	0.0031	0.0492588	E
<input type="radio"/>	GO:0000770	5,6	peptide pheromone export	1	0.0002	1	0.0031	0.0492588	E
<input type="radio"/>	GO:0051014	7	actin filament severing	1	0.0002	1	0.0031	0.0492588	E

<input type="radio"/>	GO:0015719	7,8	allantoate transport	1	0.0002	1	0.0031	0.0492588	E
<input type="radio"/>	GO:0030833	7,10,6,8	regulation of actin filament polymerization	1	0.0002	1	0.0031	0.0492588	E
<input type="radio"/>	GO:0019236	4	response to pheromone	94	0.0145	8	0.0251	0.0497620	E
<input type="radio"/>	GO:0009110	5	vitamin biosynthetic process	46	0.0071	5	0.0157	0.0498724	E
<input type="radio"/>	GO:0042364	6	water-soluble vitamin biosynthetic process	46	0.0071	5	0.0157	0.0498724	E
<input type="radio"/>	GO:0006091	3	generation of precursor metabolites and energy	183	0.0283	13	0.0408	0.0499030	E
<input type="radio"/>	GO:0006808	6,5	regulation of nitrogen utilization	8	0.0012	2	0.0063	0.0501137	E
<input type="radio"/>	GO:0051171	5,4	regulation of nitrogen metabolic process	8	0.0012	2	0.0063	0.0501137	E
<input type="radio"/>	GO:0008156	9,8	negative regulation of DNA replication	8	0.0012	2	0.0063	0.0501137	E
<input type="radio"/>	GO:0019878	9,10	lysine biosynthetic process via amino adipic acid	8	0.0012	2	0.0063	0.0501137	E
<input type="radio"/>	GO:0030001	6,7	metal ion transport	62	0.0096	6	0.0188	0.0516192	E
<input type="radio"/>	GO:0009056	3	catabolic process	438	0.0676	26	0.0815	0.0516948	E
<input type="radio"/>	GO:0015031	4,5,6	protein transport	280	0.0432	18	0.0564	0.0520317	E
<input type="radio"/>	GO:0006631	5,7,6	fatty acid metabolic process	47	0.0073	5	0.0157	0.0530842	E
<input type="radio"/>	GO:0043161	10,9,11	proteasomal ubiquitin-dependent protein catabolic process	63	0.0097	6	0.0188	0.0542687	E
<input type="radio"/>	GO:0033036	3	macromolecule localization	382	0.0590	23	0.0721	0.0544150	E
<input type="radio"/>	GO:0042546	6	cell wall biogenesis	33	0.0051	4	0.0125	0.0554965	E
<input type="radio"/>	GO:0009272	7	chitin- and beta-glucan-containing cell wall biogenesis	33	0.0051	4	0.0125	0.0554965	E
<input type="radio"/>	GO:0006812	5,6	cation transport	97	0.0150	8	0.0251	0.0556125	E
<input type="radio"/>	GO:0009067	7,8	aspartate family amino acid biosynthetic process	20	0.0031	3	0.0094	0.0576068	E
<input type="radio"/>	GO:0006260	6	DNA replication	117	0.0181	9	0.0282	0.0600396	E
<input type="radio"/>	GO:0051180	4,5	vitamin transport	9	0.0014	2	0.0063	0.0612740	E
<input type="radio"/>	GO:0030847	10,9	transcription termination from Pol II promoter, RNA polymerase(A)-independent	9	0.0014	2	0.0063	0.0612740	E
<input type="radio"/>	GO:0019794	6,7	nonprotein amino acid metabolic process	9	0.0014	2	0.0063	0.0612740	E
<input type="radio"/>	GO:0045426	7,6	quinone cofactor biosynthetic process	9	0.0014	2	0.0063	0.0612740	E
<input type="radio"/>	GO:0008154	8,5	actin polymerization and/or depolymerization	9	0.0014	2	0.0063	0.0612740	E
<input type="radio"/>	GO:0015802	6,7,8	basic amino acid transport	9	0.0014	2	0.0063	0.0612740	E
<input type="radio"/>	GO:0006553	7,8	lysine metabolic process	9	0.0014	2	0.0063	0.0612740	E
<input type="radio"/>	GO:0009085	8,9	lysine biosynthetic process	9	0.0014	2	0.0063	0.0612740	E
<input type="radio"/>	GO:0043648	6	dicarboxylic acid metabolic process	9	0.0014	2	0.0063	0.0612740	E
<input type="radio"/>	GO:0006744	8,7	ubiquinone biosynthetic process	9	0.0014	2	0.0063	0.0612740	E
<input type="radio"/>	GO:0006743	7,6	ubiquinone metabolic process	9	0.0014	2	0.0063	0.0612740	E
<input type="radio"/>	GO:0042375	5	quinone cofactor metabolic process	9	0.0014	2	0.0063	0.0612740	E
<input type="radio"/>	GO:0043632	6	modification-dependent macromolecule catabolic process	155	0.0239	11	0.0345	0.0619786	E
<input type="radio"/>	GO:0009108	6	coenzyme biosynthetic process	66	0.0102	6	0.0188	0.0624526	E
<input type="radio"/>	GO:0044262	5	cellular carbohydrate metabolic process	213	0.0329	14	0.0439	0.0626552	E
<input type="radio"/>	GO:0005975	4	carbohydrate metabolic process	233	0.0360	15	0.0470	0.0630743	E
<input type="radio"/>	GO:0050896	2	response to stimulus	763	0.1178	40	0.1254	0.0631158	E
<input type="radio"/>	GO:0006351	7,6	transcription, DNA-dependent	522	0.0806	29	0.0909	0.0631928	E
<input type="radio"/>	GO:0006350	5	transcription	567	0.0876	31	0.0972	0.0640277	E
<input type="radio"/>	GO:0032774	6	RNA biosynthetic process	524	0.0809	29	0.0909	0.0640905	E

<input type="radio"/>	GO:0019219	6,5	regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	440	0.0679	25	0.0784	0.0647025	E
<input type="radio"/>	GO:0006790	4	sulfur metabolic process	67	0.0103	6	0.0188	0.0652460	E
<input type="radio"/>	GO:0031323	5,4	regulation of cellular metabolic process	507	0.0783	28	0.0878	0.0661231	E
<input type="radio"/>	GO:0006508	6	proteolysis	178	0.0275	12	0.0376	0.0674105	E
<input type="radio"/>	GO:0006366	8,7	transcription from RNA polymerase II promoter	343	0.0530	20	0.0627	0.0699721	E
<input type="radio"/>	GO:0006357	9,8	regulation of transcription from RNA polymerase II promoter	221	0.0341	14	0.0439	0.0715465	E
<input type="radio"/>	GO:0006817	7,8	phosphate transport	10	0.0015	2	0.0063	0.0728381	E
<input type="radio"/>	GO:0015718	6,7	monocarboxylic acid transport	10	0.0015	2	0.0063	0.0728381	E
<input type="radio"/>	GO:0030174	9,7,8	regulation of DNA replication initiation	10	0.0015	2	0.0063	0.0728381	E
<input type="radio"/>	GO:0009373	9,8,5	regulation of transcription by pheromones	10	0.0015	2	0.0063	0.0728381	E
<input type="radio"/>	GO:0046019	10,9,6	regulation of transcription from RNA polymerase II promoter by pheromones	10	0.0015	2	0.0063	0.0728381	E
<input type="radio"/>	GO:0006526	8,9,6,5	arginine biosynthetic process	10	0.0015	2	0.0063	0.0728381	E
<input type="radio"/>	GO:0006512	8	ubiquitin cycle	88	0.0136	7	0.0219	0.0745838	E
<input type="radio"/>	GO:0051301	3	cell division	246	0.0380	15	0.0470	0.0762433	E
<input type="radio"/>	GO:0006950	3	response to stress	488	0.0754	26	0.0815	0.0764978	E
<input type="radio"/>	GO:0008213	8	protein amino acid alkylation	23	0.0036	3	0.0094	0.0769824	E
<input type="radio"/>	GO:0006479	9,7	protein amino acid methylation	23	0.0036	3	0.0094	0.0769824	E
<input type="radio"/>	GO:0006090	7	pyruvate metabolic process	38	0.0059	4	0.0125	0.0779100	E
<input type="radio"/>	GO:0015931	4,5	nucleobase, nucleoside, nucleotide and nucleic acid transport	90	0.0139	7	0.0219	0.0794122	E
<input type="radio"/>	GO:0000910	4	cytokinesis	109	0.0168	8	0.0251	0.0802062	E
<input type="radio"/>	GO:0006355	8,7	regulation of transcription, DNA-dependent	359	0.0554	20	0.0627	0.0802282	E
<input type="radio"/>	GO:0000723	8	telomere maintenance	274	0.0423	16	0.0502	0.0823558	E
<input type="radio"/>	GO:0032200	7	telomere organization and biogenesis	274	0.0423	16	0.0502	0.0823558	E
<input type="radio"/>	GO:0045449	7,6	regulation of transcription	386	0.0596	21	0.0658	0.0824173	E
<input type="radio"/>	GO:0006865	5,6,7	amino acid transport	39	0.0060	4	0.0125	0.0825663	E
<input type="radio"/>	GO:0051278	8,7	chitin- and beta-glucan-containing cell wall polysaccharide biosynthetic process	24	0.0037	3	0.0094	0.0836716	E
<input type="radio"/>	GO:0006733	6	oxidoreduction coenzyme metabolic process	56	0.0086	5	0.0157	0.0842077	E
<input type="radio"/>	GO:0006796	5	phosphate metabolic process	212	0.0327	13	0.0408	0.0843016	E
<input type="radio"/>	GO:0006793	4	phosphorus metabolic process	212	0.0327	13	0.0408	0.0843016	E
<input type="radio"/>	GO:0051049	5,4	regulation of transport	11	0.0017	2	0.0063	0.0846599	E
<input type="radio"/>	GO:0006488	10,9,8	dolichol-linked oligosaccharide biosynthetic process	11	0.0017	2	0.0063	0.0846599	E
<input type="radio"/>	GO:0006384	8,9,7	transcription initiation from RNA polymerase III promoter	11	0.0017	2	0.0063	0.0846599	E
<input type="radio"/>	GO:0006974	4	response to DNA damage stimulus	234	0.0361	14	0.0439	0.0851046	E
<input type="radio"/>	GO:0065004	6,5	protein-DNA complex assembly	74	0.0114	6	0.0188	0.0852927	E
<input type="radio"/>	GO:0006281	6,5	DNA repair	193	0.0298	12	0.0376	0.0865989	E
<input type="radio"/>	GO:0000724	8,7	double-strand break repair via homologous recombination	25	0.0039	3	0.0094	0.0904246	E
<input type="radio"/>	GO:0016311	6	dephosphorylation	41	0.0063	4	0.0125	0.0919515	E
<input type="radio"/>	GO:0051052	7,6	regulation of DNA metabolic process	41	0.0063	4	0.0125	0.0919515	E
<input type="radio"/>	GO:0009719	3	response to endogenous stimulus	243	0.0375	14	0.0439	0.0933214	E
<input type="radio"/>	GO:0019915	5	sequestering of lipid	2	0.0003	1	0.0031	0.0936792	E
<input type="radio"/>	GO:0006666	5,8,9	3-keto-sphinganine metabolic process	2	0.0003	1	0.0031	0.0936792	E

<input type="checkbox"/>	GO:0009298	9,6,7,10	GDP-mannose biosynthetic process	2	0.0003	1	0.0031	0.0936792	E
<input type="checkbox"/>	GO:0007092	9,11,7,10,8,6,12,13	anaphase-promoting complex activation during mitotic cell cycle	2	0.0003	1	0.0031	0.0936792	E
<input type="checkbox"/>	GO:0009111	5	vitamin catabolic process	2	0.0003	1	0.0031	0.0936792	E
<input type="checkbox"/>	GO:0006661	10,9,11	phosphatidylinositol biosynthetic process	2	0.0003	1	0.0031	0.0936792	E
<input type="checkbox"/>	GO:0006531	7,8	aspartate metabolic process	2	0.0003	1	0.0031	0.0936792	E
<input type="checkbox"/>	GO:0045016	8,6,7,9	mitochondrial magnesium ion transport	2	0.0003	1	0.0031	0.0936792	E
<input type="checkbox"/>	GO:0006533	8,9	aspartate catabolic process	2	0.0003	1	0.0031	0.0936792	E
<input type="checkbox"/>	GO:0051437	8,6,5	positive regulation of ubiquitin ligase activity during mitotic cell cycle	2	0.0003	1	0.0031	0.0936792	E
<input type="checkbox"/>	GO:0032204	6,9,5	regulation of telomere maintenance	2	0.0003	1	0.0031	0.0936792	E
<input type="checkbox"/>	GO:0006436	9,8,10,7	tryptophanyl-tRNA aminoacylation	2	0.0003	1	0.0031	0.0936792	E
<input type="checkbox"/>	GO:0008215	7,8	spermine metabolic process	2	0.0003	1	0.0031	0.0936792	E
<input type="checkbox"/>	GO:0009895	6,5	negative regulation of catabolic process	2	0.0003	1	0.0031	0.0936792	E
<input type="checkbox"/>	GO:0006563	7,8	L-serine metabolic process	2	0.0003	1	0.0031	0.0936792	E
<input type="checkbox"/>	GO:0032210	7,10,6	regulation of telomere maintenance via telomerase	2	0.0003	1	0.0031	0.0936792	E
<input type="checkbox"/>	GO:0042365	6	water-soluble vitamin catabolic process	2	0.0003	1	0.0031	0.0936792	E
<input type="checkbox"/>	GO:0046504	5	glycerol ether biosynthetic process	2	0.0003	1	0.0031	0.0936792	E
<input type="checkbox"/>	GO:0043649	6,7	dicarboxylic acid catabolic process	2	0.0003	1	0.0031	0.0936792	E
<input type="checkbox"/>	GO:0006086	8	acetyl-CoA biosynthetic process from pyruvate	2	0.0003	1	0.0031	0.0936792	E
<input type="checkbox"/>	GO:0019307	8,9	mannose biosynthetic process	2	0.0003	1	0.0031	0.0936792	E
<input type="checkbox"/>	GO:0009226	5,6	nucleotide-sugar biosynthetic process	2	0.0003	1	0.0031	0.0936792	E
<input type="checkbox"/>	GO:0046463	6,7,8	acylglycerol biosynthetic process	2	0.0003	1	0.0031	0.0936792	E
<input type="checkbox"/>	GO:0042177	7,8,6	negative regulation of protein catabolic process	2	0.0003	1	0.0031	0.0936792	E
<input type="checkbox"/>	GO:0006107	7	oxaloacetate metabolic process	2	0.0003	1	0.0031	0.0936792	E
<input type="checkbox"/>	GO:0042938	5,6	dipeptide transport	2	0.0003	1	0.0031	0.0936792	E
<input type="checkbox"/>	GO:0019266	9,10,7,8	asparagine biosynthetic process from oxaloacetate	2	0.0003	1	0.0031	0.0936792	E
<input type="checkbox"/>	GO:0006750	7,6	glutathione biosynthetic process	2	0.0003	1	0.0031	0.0936792	E
<input type="checkbox"/>	GO:0019673	8,6,9	GDP-mannose metabolic process	2	0.0003	1	0.0031	0.0936792	E
<input type="checkbox"/>	GO:0006597	8,9	spermine biosynthetic process	2	0.0003	1	0.0031	0.0936792	E
<input type="checkbox"/>	GO:0009061	6	anaerobic respiration	2	0.0003	1	0.0031	0.0936792	E
<input type="checkbox"/>	GO:0045017	6,5,7	glycerolipid biosynthetic process	2	0.0003	1	0.0031	0.0936792	E
<input type="checkbox"/>	GO:0045861	7,8,6	negative regulation of proteolysis	2	0.0003	1	0.0031	0.0936792	E
<input type="checkbox"/>	GO:0006552	8,9	leucine catabolic process	2	0.0003	1	0.0031	0.0936792	E
<input type="checkbox"/>	GO:0046460	6,5,7	neutral lipid biosynthetic process	2	0.0003	1	0.0031	0.0936792	E
<input type="checkbox"/>	GO:0019432	7,8,9	triacylglycerol biosynthetic process	2	0.0003	1	0.0031	0.0936792	E
<input type="checkbox"/>	GO:0006532	8,9	aspartate biosynthetic process	2	0.0003	1	0.0031	0.0936792	E
<input type="checkbox"/>	GO:0051488	8	anaphase-promoting complex activation	2	0.0003	1	0.0031	0.0936792	E
<input type="checkbox"/>	GO:0006564	8,9	L-serine biosynthetic process	2	0.0003	1	0.0031	0.0936792	E
<input type="checkbox"/>	GO:0007047	5	cell wall organization and biogenesis	200	0.0309	12	0.0376	0.0946727	E
<input type="checkbox"/>	GO:0045229	4	external encapsulating structure organization and biogenesis	200	0.0309	12	0.0376	0.0946727	E
<input type="checkbox"/>	GO:0007242	5	intracellular signaling cascade	137	0.0212	9	0.0282	0.0956994	E
<input type="checkbox"/>	GO:0000032	8,6,9,7	cell wall mannoprotein biosynthetic process	12	0.0019	2	0.0063	0.0966105	E
<input type="checkbox"/>	GO:0045910	9,8	negative regulation of DNA recombination	12	0.0019	2	0.0063	0.0966105	E
<input type="checkbox"/>	GO:0006056	7	mannoprotein metabolic process	12	0.0019	2	0.0063	0.0966105	E

<input type="checkbox"/>	GO:0031506	7,5,8,6	cell wall glycoprotein biosynthetic process	12	0.0019	2	0.0063	0.0966105	E
<input type="checkbox"/>	GO:0006057	8,6	mannoprotein biosynthetic process	12	0.0019	2	0.0063	0.0966105	E
<input type="checkbox"/>	GO:0016125	5,6,7	sterol metabolic process	42	0.0065	4	0.0125	0.0966556	E
<input type="checkbox"/>	GO:0008204	6,7,8	ergosterol metabolic process	26	0.0040	3	0.0094	0.0972119	E
<input type="checkbox"/>	GO:0006696	7,8,9	ergosterol biosynthetic process	26	0.0040	3	0.0094	0.0972119	E
<input type="checkbox"/>	GO:0000747	4	conjugation with cellular fusion	118	0.0182	8	0.0251	0.0983760	E
<input type="checkbox"/>	GO:0019953	3	sexual reproduction	118	0.0182	8	0.0251	0.0983760	E
<input type="checkbox"/>	GO:0000746	3	conjugation	118	0.0182	8	0.0251	0.0983760	E
<input type="checkbox"/>	GO:0044257	6,7	cellular protein catabolic process	160	0.0247	10	0.0313	0.0987459	E
<input type="checkbox"/>	GO:0051704	2	multi-organism process	139	0.0215	9	0.0282	0.0990183	E
<input type="checkbox"/>	GO:0008202	5,6	steroid metabolic process	43	0.0066	4	0.0125	0.1013516	E
<input type="checkbox"/>	GO:0016481	8,7	negative regulation of transcription	162	0.0250	10	0.0313	0.1015002	E
<input type="checkbox"/>	GO:0007015	8	actin filament organization	61	0.0094	5	0.0157	0.1020559	E
<input type="checkbox"/>	GO:0000003	2	reproduction	323	0.0499	16	0.0502	0.1043900	E
<input type="checkbox"/>	GO:0006289	7,6	nucleotide-excision repair	44	0.0068	4	0.0125	0.1060276	E
<input type="checkbox"/>	GO:0031505	6	chitin- and beta-glucan-containing cell wall organization and biogenesis	44	0.0068	4	0.0125	0.1060276	E
<input type="checkbox"/>	GO:0006783	7,6,8	heme biosynthetic process	13	0.0020	2	0.0063	0.1085767	E
<input type="checkbox"/>	GO:0033014	6	tetrapyrrole biosynthetic process	13	0.0020	2	0.0063	0.1085767	E
<input type="checkbox"/>	GO:0015893	4,5	drug transport	13	0.0020	2	0.0063	0.1085767	E
<input type="checkbox"/>	GO:0006779	6,7	porphyrin biosynthetic process	13	0.0020	2	0.0063	0.1085767	E
<input type="checkbox"/>	GO:0006334	6,7,10	nucleosome assembly	13	0.0020	2	0.0063	0.1085767	E
<input type="checkbox"/>	GO:0048522	5,4	positive regulation of cellular process	124	0.0191	8	0.0251	0.1095653	E
<input type="checkbox"/>	GO:0048518	4	positive regulation of biological process	124	0.0191	8	0.0251	0.1095653	E
<input type="checkbox"/>	GO:0006914	3	autophagy	45	0.0069	4	0.0125	0.1106726	E
<input type="checkbox"/>	GO:0043285	5	biopolymer catabolic process	277	0.0428	14	0.0439	0.1106759	E
<input type="checkbox"/>	GO:0043241	6,5	protein complex disassembly	28	0.0043	3	0.0094	0.1107783	E
<input type="checkbox"/>	GO:0043624	7,6	cellular protein complex disassembly	28	0.0043	3	0.0094	0.1107783	E
<input type="checkbox"/>	GO:0032505	4,3	reproduction of a single-celled organism	194	0.0300	11	0.0345	0.1116872	E
<input type="checkbox"/>	GO:0031497	5,9	chromatin assembly	104	0.0161	7	0.0219	0.1119009	E
<input type="checkbox"/>	GO:0006511	9,8,10	ubiquitin-dependent protein catabolic process	148	0.0229	9	0.0282	0.1126915	E
<input type="checkbox"/>	GO:0019941	8,7,9	modification-dependent protein catabolic process	148	0.0229	9	0.0282	0.1126915	E
<input type="checkbox"/>	GO:0030163	6,5	protein catabolic process	173	0.0267	10	0.0313	0.1147756	E
<input type="checkbox"/>	GO:0009066	6,7	aspartate family amino acid metabolic process	46	0.0071	4	0.0125	0.1152757	E
<input type="checkbox"/>	GO:0044264	5,6	cellular polysaccharide metabolic process	65	0.0100	5	0.0157	0.1159189	E
<input type="checkbox"/>	GO:0005976	5	polysaccharide metabolic process	65	0.0100	5	0.0157	0.1159189	E
<input type="checkbox"/>	GO:0019954	3	asexual reproduction	85	0.0131	6	0.0188	0.1159647	E
<input type="checkbox"/>	GO:0007114	5,4	cell budding	85	0.0131	6	0.0188	0.1159647	E
<input type="checkbox"/>	GO:0007010	5	cytoskeleton organization and biogenesis	227	0.0351	12	0.0376	0.1160147	E
<input type="checkbox"/>	GO:0051603	7,8	proteolysis involved in cellular protein catabolic process	151	0.0233	9	0.0282	0.1166962	E
<input type="checkbox"/>	GO:0006470	8,7	protein amino acid dephosphorylation	29	0.0045	3	0.0094	0.1175050	E
<input type="checkbox"/>	GO:0030036	7	actin cytoskeleton organization and biogenesis	107	0.0165	7	0.0219	0.1181494	E
<input type="checkbox"/>	GO:0016567	9	protein ubiquitination	66	0.0102	5	0.0157	0.1192775	E
<input type="checkbox"/>	GO:0042770	5	DNA damage response, signal transduction	14	0.0022	2	0.0063	0.1204597	E

<input type="checkbox"/>	GO:0006778	5,6	porphyrin metabolic process	14	0.0022	2	0.0063	0.1204597	E
<input type="checkbox"/>	GO:0033013	5	tetrapyrrole metabolic process	14	0.0022	2	0.0063	0.1204597	E
<input type="checkbox"/>	GO:0006388	9,8	tRNA splicing	14	0.0022	2	0.0063	0.1204597	E
<input type="checkbox"/>	GO:0000394	8	RNA splicing, via endonucleolytic cleavage and ligation	14	0.0022	2	0.0063	0.1204597	E
<input type="checkbox"/>	GO:0000077	9,8,6	DNA damage checkpoint	14	0.0022	2	0.0063	0.1204597	E
<input type="checkbox"/>	GO:0042168	6,7,5	heme metabolic process	14	0.0022	2	0.0063	0.1204597	E
<input type="checkbox"/>	GO:0045892	9,8	negative regulation of transcription, DNA-dependent	156	0.0241	9	0.0282	0.1226512	E
<input type="checkbox"/>	GO:0032506	5,3	cytokinetic process	88	0.0136	6	0.0188	0.1235954	E
<input type="checkbox"/>	GO:0030466	11,7,8,12,10	chromatin silencing at silent mating-type cassette	30	0.0046	3	0.0094	0.1241617	E
<input type="checkbox"/>	GO:0045185	5,4,3	maintenance of protein localization	30	0.0046	3	0.0094	0.1241617	E
<input type="checkbox"/>	GO:0030029	6	actin filament-based process	112	0.0173	7	0.0219	0.1276822	E
<input type="checkbox"/>	GO:0006066	4	alcohol metabolic process	163	0.0252	9	0.0282	0.1293390	E
<input type="checkbox"/>	GO:0000114	10,8,9,5,7,4	G1-specific transcription in mitotic cell cycle	15	0.0023	2	0.0063	0.1321736	E
<input type="checkbox"/>	GO:0000051	4,3	urea cycle intermediate metabolic process	15	0.0023	2	0.0063	0.1321736	E
<input type="checkbox"/>	GO:0006525	7,8,5,4	arginine metabolic process	15	0.0023	2	0.0063	0.1321736	E
<input type="checkbox"/>	GO:0051170	9,7,8	nuclear import	50	0.0077	4	0.0125	0.1330676	E
<input type="checkbox"/>	GO:0006606	9,10,7,8,6	protein import into nucleus	50	0.0077	4	0.0125	0.1330676	E
<input type="checkbox"/>	GO:0015837	4,5	amine transport	50	0.0077	4	0.0125	0.1330676	E
<input type="checkbox"/>	GO:0006658	8,9	phosphatidylserine metabolic process	3	0.0005	1	0.0031	0.1336166	E
<input type="checkbox"/>	GO:0030832	8	regulation of actin filament length	3	0.0005	1	0.0031	0.1336166	E
<input type="checkbox"/>	GO:0046160	7,8,6	heme a metabolic process	3	0.0005	1	0.0031	0.1336166	E
<input type="checkbox"/>	GO:0051205	6,5,4	protein insertion into membrane	3	0.0005	1	0.0031	0.1336166	E
<input type="checkbox"/>	GO:0006285	7,8	base-excision repair, AP site formation	3	0.0005	1	0.0031	0.1336166	E
<input type="checkbox"/>	GO:0045950	10,9	negative regulation of mitotic recombination	3	0.0005	1	0.0031	0.1336166	E
<input type="checkbox"/>	GO:0032786	9,8,10	positive regulation of RNA elongation	3	0.0005	1	0.0031	0.1336166	E
<input type="checkbox"/>	GO:0051204	7,6,5	protein insertion into mitochondrial membrane	3	0.0005	1	0.0031	0.1336166	E
<input type="checkbox"/>	GO:0032784	8,7,9	regulation of RNA elongation	3	0.0005	1	0.0031	0.1336166	E
<input type="checkbox"/>	GO:0006835	6,7	dicarboxylic acid transport	3	0.0005	1	0.0031	0.1336166	E
<input type="checkbox"/>	GO:0006549	7,8	isoleucine metabolic process	3	0.0005	1	0.0031	0.1336166	E
<input type="checkbox"/>	GO:0006784	8,7,9	heme a biosynthetic process	3	0.0005	1	0.0031	0.1336166	E
<input type="checkbox"/>	GO:0046488	9,10	phosphatidylinositol metabolic process	3	0.0005	1	0.0031	0.1336166	E
<input type="checkbox"/>	GO:0015888	5,6	thiamin transport	3	0.0005	1	0.0031	0.1336166	E
<input type="checkbox"/>	GO:0051668	5,4	localization within membrane	3	0.0005	1	0.0031	0.1336166	E
<input type="checkbox"/>	GO:0051351	6	positive regulation of ligase activity	3	0.0005	1	0.0031	0.1336166	E
<input type="checkbox"/>	GO:0006370	8	mRNA capping	3	0.0005	1	0.0031	0.1336166	E
<input type="checkbox"/>	GO:0009090	8,9	homoserine biosynthetic process	3	0.0005	1	0.0031	0.1336166	E
<input type="checkbox"/>	GO:0009437	6,7	carnitine metabolic process	3	0.0005	1	0.0031	0.1336166	E
<input type="checkbox"/>	GO:0006901	6,7	vesicle coating	3	0.0005	1	0.0031	0.1336166	E
<input type="checkbox"/>	GO:0051382	8,7	kinetochore assembly	3	0.0005	1	0.0031	0.1336166	E
<input type="checkbox"/>	GO:0051383	6	kinetochore organization and biogenesis	3	0.0005	1	0.0031	0.1336166	E
<input type="checkbox"/>	GO:0043065	7,8,10,6	positive regulation of apoptosis	3	0.0005	1	0.0031	0.1336166	E
<input type="checkbox"/>	GO:0008064	6,9,5	regulation of actin polymerization and/or depolymerization	3	0.0005	1	0.0031	0.1336166	E
<input type="checkbox"/>	GO:0051443	7	positive regulation of ubiquitin ligase activity	3	0.0005	1	0.0031	0.1336166	E

<input type="radio"/>	GO:0000706	11,9,8,5,6,10,7,4	meiotic DNA double-strand break processing	3	0.0005	1	0.0031	0.1336166	E
<input type="radio"/>	GO:0018022	9,10,8	peptidyl-lysine methylation	3	0.0005	1	0.0031	0.1336166	E
<input type="radio"/>	GO:0043068	6,7,9,5	positive regulation of programmed cell death	3	0.0005	1	0.0031	0.1336166	E
<input type="radio"/>	GO:0031325	6,5	positive regulation of cellular metabolic process	116	0.0179	7	0.0219	0.1343951	E
<input type="radio"/>	GO:0009893	5,4	positive regulation of metabolic process	116	0.0179	7	0.0219	0.1343951	E
<input type="radio"/>	GO:0016126	6,7,8	sterol biosynthetic process	32	0.0049	3	0.0094	0.1371766	E
<input type="radio"/>	GO:0006694	6,5,7	steroid biosynthetic process	32	0.0049	3	0.0094	0.1371766	E
<input type="radio"/>	GO:0015672	6,7	monovalent inorganic cation transport	32	0.0049	3	0.0094	0.1371766	E
<input type="radio"/>	GO:0019932	6	second-messenger-mediated signaling	32	0.0049	3	0.0094	0.1371766	E
<input type="radio"/>	GO:0032984	5	macromolecular complex disassembly	32	0.0049	3	0.0094	0.1371766	E
<input type="radio"/>	GO:0006333	8	chromatin assembly or disassembly	119	0.0184	7	0.0219	0.1388411	E
<input type="radio"/>	GO:0045814	5	negative regulation of gene expression, epigenetic	95	0.0147	6	0.0188	0.1394209	E
<input type="radio"/>	GO:0016458	5	gene silencing	95	0.0147	6	0.0188	0.1394209	E
<input type="radio"/>	GO:0006342	10,6,7,11,9	chromatin silencing	95	0.0147	6	0.0188	0.1394209	E
<input type="radio"/>	GO:0031507	6,10	heterochromatin formation	95	0.0147	6	0.0188	0.1394209	E
<input type="radio"/>	GO:0048610	3,4	reproductive cellular process	149	0.0230	8	0.0251	0.1408569	E
<input type="radio"/>	GO:0022413	5,4	reproductive process in single-celled organism	149	0.0230	8	0.0251	0.1408569	E
<input type="radio"/>	GO:0007166	5	cell surface receptor linked signal transduction	52	0.0080	4	0.0125	0.1414642	E
<input type="radio"/>	GO:0006261	7	DNA-dependent DNA replication	97	0.0150	6	0.0188	0.1433498	E
<input type="radio"/>	GO:0006730	4	one-carbon compound metabolic process	97	0.0150	6	0.0188	0.1433498	E
<input type="radio"/>	GO:0051235	3,2	maintenance of localization	33	0.0051	3	0.0094	0.1434947	E
<input type="radio"/>	GO:0006270	8,6	DNA replication initiation	33	0.0051	3	0.0094	0.1434947	E
<input type="radio"/>	GO:0016050	5	vesicle organization and biogenesis	16	0.0025	2	0.0063	0.1436442	E
<input type="radio"/>	GO:0015698	6,7	inorganic anion transport	16	0.0025	2	0.0063	0.1436442	E
<input type="radio"/>	GO:0000075	7,6	cell cycle checkpoint	53	0.0082	4	0.0125	0.1455093	E
<input type="radio"/>	GO:0040029	4	regulation of gene expression, epigenetic	100	0.0154	6	0.0188	0.1486957	E
<input type="radio"/>	GO:0045944	10,9	positive regulation of transcription from RNA polymerase II promoter	76	0.0117	5	0.0157	0.1491637	E
<input type="radio"/>	GO:0015674	6,7	di-, tri-valent inorganic cation transport	34	0.0053	3	0.0094	0.1496625	E
<input type="radio"/>	GO:0042592	4	homeostatic process	134	0.0207	7	0.0219	0.1527916	E
<input type="radio"/>	GO:0006352	7,8,6	transcription initiation	55	0.0085	4	0.0125	0.1532589	E
<input type="radio"/>	GO:0045003	9,8	double-strand break repair via synthesis-dependent strand annealing	17	0.0026	2	0.0063	0.1548081	E
<input type="radio"/>	GO:0006820	5,6	anion transport	17	0.0026	2	0.0063	0.1548081	E
<input type="radio"/>	GO:0019740	4	nitrogen utilization	17	0.0026	2	0.0063	0.1548081	E
<input type="radio"/>	GO:0045935	7,6	positive regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	108	0.0167	6	0.0188	0.1595363	E
<input type="radio"/>	GO:0006302	7,6	double-strand break repair	57	0.0088	4	0.0125	0.1605145	E
<input type="radio"/>	GO:0022411	4	cellular component disassembly	36	0.0056	3	0.0094	0.1614837	E
<input type="radio"/>	GO:0006461	6,5	protein complex assembly	116	0.0179	6	0.0188	0.1652556	E
<input type="radio"/>	GO:0006369	9,8	transcription termination from RNA polymerase II promoter	18	0.0028	2	0.0063	0.1656116	E
<input type="radio"/>	GO:0016571	11,9,10,8	histone methylation	18	0.0028	2	0.0063	0.1656116	E
<input type="radio"/>	GO:0000018	8,7	regulation of DNA recombination	18	0.0028	2	0.0063	0.1656116	E
<input type="radio"/>	GO:0006399	6	tRNA metabolic process	121	0.0187	6	0.0188	0.1663008	E

<input type="radio"/>	GO:0042493	4	response to drug	121	0.0187	6	0.0188	0.1663008	E
<input type="radio"/>	GO:0032446	8	protein modification by small protein conjugation	84	0.0130	5	0.0157	0.1666346	E
<input type="radio"/>	GO:0009164	5,6	nucleoside catabolic process	4	0.0006	1	0.0031	0.1694032	E
<input type="radio"/>	GO:0042981	6,7,9,5	regulation of apoptosis	4	0.0006	1	0.0031	0.1694032	E
<input type="radio"/>	GO:0006596	7,8	polyamine biosynthetic process	4	0.0006	1	0.0031	0.1694032	E
<input type="radio"/>	GO:0031328	7,6	positive regulation of cellular biosynthetic process	4	0.0006	1	0.0031	0.1694032	E
<input type="radio"/>	GO:0016036	8,7,6	cellular response to phosphate starvation	4	0.0006	1	0.0031	0.1694032	E
<input type="radio"/>	GO:0006491	10,9,8	N-glycan processing	4	0.0006	1	0.0031	0.1694032	E
<input type="radio"/>	GO:0006085	7	acetyl-CoA biosynthetic process	4	0.0006	1	0.0031	0.1694032	E
<input type="radio"/>	GO:0030071	8,10,6,9,7,5	regulation of mitotic metaphase/anaphase transition	4	0.0006	1	0.0031	0.1694032	E
<input type="radio"/>	GO:0009452	7	RNA capping	4	0.0006	1	0.0031	0.1694032	E
<input type="radio"/>	GO:0030042	9,6,7	actin filament depolymerization	4	0.0006	1	0.0031	0.1694032	E
<input type="radio"/>	GO:0030162	6,7,5	regulation of proteolysis	4	0.0006	1	0.0031	0.1694032	E
<input type="radio"/>	GO:0006751	7,6	glutathione catabolic process	4	0.0006	1	0.0031	0.1694032	E
<input type="radio"/>	GO:0018205	8	peptidyl-lysine modification	4	0.0006	1	0.0031	0.1694032	E
<input type="radio"/>	GO:0006592	8,9,6,5	ornithine biosynthetic process	4	0.0006	1	0.0031	0.1694032	E
<input type="radio"/>	GO:0018348	11,10,9	protein amino acid geranylgeranylation	4	0.0006	1	0.0031	0.1694032	E
<input type="radio"/>	GO:0042180	4	ketone metabolic process	4	0.0006	1	0.0031	0.1694032	E
<input type="radio"/>	GO:0006900	5,6	membrane budding	4	0.0006	1	0.0031	0.1694032	E
<input type="radio"/>	GO:0006529	8,9	asparagine biosynthetic process	4	0.0006	1	0.0031	0.1694032	E
<input type="radio"/>	GO:0006898	7,6	receptor-mediated endocytosis	4	0.0006	1	0.0031	0.1694032	E
<input type="radio"/>	GO:0018344	10,9,8	protein geranylgeranylation	4	0.0006	1	0.0031	0.1694032	E
<input type="radio"/>	GO:0006097	6,8	glyoxylate cycle	4	0.0006	1	0.0031	0.1694032	E
<input type="radio"/>	GO:0045727	8,7,6	positive regulation of protein biosynthetic process	4	0.0006	1	0.0031	0.1694032	E
<input type="radio"/>	GO:0000059	8,10,11,7,9	protein import into nucleus, docking	4	0.0006	1	0.0031	0.1694032	E
<input type="radio"/>	GO:0000304	6	response to singlet oxygen	4	0.0006	1	0.0031	0.1694032	E
<input type="radio"/>	GO:0009891	6,5	positive regulation of biosynthetic process	4	0.0006	1	0.0031	0.1694032	E
<input type="radio"/>	GO:0043067	5,6,8,4	regulation of programmed cell death	4	0.0006	1	0.0031	0.1694032	E
<input type="radio"/>	GO:0007124	6,4,8,9	pseudohyphal growth	61	0.0094	4	0.0125	0.1733899	E
<input type="radio"/>	GO:0046148	5	pigment biosynthetic process	19	0.0029	2	0.0063	0.1760097	E
<input type="radio"/>	GO:0006275	8,7	regulation of DNA replication	19	0.0029	2	0.0063	0.1760097	E
<input type="radio"/>	GO:0000122	10,9	negative regulation of transcription from RNA polymerase II promoter	63	0.0097	4	0.0125	0.1789529	E
<input type="radio"/>	GO:0045893	9,8	positive regulation of transcription, DNA-dependent	95	0.0147	5	0.0157	0.1796191	E
<input type="radio"/>	GO:0006468	8,7	protein amino acid phosphorylation	101	0.0156	5	0.0157	0.1813852	E
<input type="radio"/>	GO:0045941	8,7	positive regulation of transcription	101	0.0156	5	0.0157	0.1813852	E
<input type="radio"/>	GO:0006084	6	acetyl-CoA metabolic process	20	0.0031	2	0.0063	0.1859652	E
<input type="radio"/>	GO:0006353	8,7	transcription termination	20	0.0031	2	0.0063	0.1859652	E
<input type="radio"/>	GO:0009109	6	coenzyme catabolic process	20	0.0031	2	0.0063	0.1859652	E
<input type="radio"/>	GO:0006100	6	tricarboxylic acid cycle intermediate metabolic process	20	0.0031	2	0.0063	0.1859652	E
<input type="radio"/>	GO:0042440	4	pigment metabolic process	20	0.0031	2	0.0063	0.1859652	E
<input type="radio"/>	GO:0030148	7,6,8	sphingolipid biosynthetic process	20	0.0031	2	0.0063	0.1859652	E
<input type="radio"/>	GO:0051028	5,7,6,8	mRNA transport	66	0.0102	4	0.0125	0.1861535	E
<input type="radio"/>	GO:0006406	11,9,6,8,10,7	mRNA export from nucleus	66	0.0102	4	0.0125	0.1861535	E

<input type="checkbox"/>	GO:0006769	8,7	nicotinamide metabolic process	42	0.0065	3	0.0094	0.1919623	E
<input type="checkbox"/>	GO:0006979	4	response to oxidative stress	71	0.0110	4	0.0125	0.1950524	E
<input type="checkbox"/>	GO:0051187	5	cofactor catabolic process	21	0.0032	2	0.0063	0.1954481	E
<input type="checkbox"/>	GO:0006891	8,6,5,7	intra-Golgi vesicle-mediated transport	21	0.0032	2	0.0063	0.1954481	E
<input type="checkbox"/>	GO:0051246	5,4	regulation of protein metabolic process	72	0.0111	4	0.0125	0.1963690	E
<input type="checkbox"/>	GO:0006887	8,6,5,7	exocytosis	44	0.0068	3	0.0094	0.2002380	E
<input type="checkbox"/>	GO:0006752	6	group transfer coenzyme metabolic process	44	0.0068	3	0.0094	0.2002380	E
<input type="checkbox"/>	GO:0009098	8,9	leucine biosynthetic process	5	0.0008	1	0.0031	0.2013495	E
<input type="checkbox"/>	GO:0007329	11,10,7	positive regulation of transcription from RNA polymerase II promoter by pheromones	5	0.0008	1	0.0031	0.2013495	E
<input type="checkbox"/>	GO:0000738	6,7	DNA catabolic process, exonucleolytic	5	0.0008	1	0.0031	0.2013495	E
<input type="checkbox"/>	GO:0018377	9,8,7	protein myristoylation	5	0.0008	1	0.0031	0.2013495	E
<input type="checkbox"/>	GO:0016233	9	telomere capping	5	0.0008	1	0.0031	0.2013495	E
<input type="checkbox"/>	GO:0006499	10,11,9,8	N-terminal protein myristoylation	5	0.0008	1	0.0031	0.2013495	E
<input type="checkbox"/>	GO:0043407	8,9	negative regulation of MAPK activity	5	0.0008	1	0.0031	0.2013495	E
<input type="checkbox"/>	GO:0006639	6,5,7	acylglycerol metabolic process	5	0.0008	1	0.0031	0.2013495	E
<input type="checkbox"/>	GO:0051254	8,7	positive regulation of RNA metabolic process	5	0.0008	1	0.0031	0.2013495	E
<input type="checkbox"/>	GO:0006498	9,10,8,7	N-terminal protein lipidation	5	0.0008	1	0.0031	0.2013495	E
<input type="checkbox"/>	GO:0046487	5,7	glyoxylate metabolic process	5	0.0008	1	0.0031	0.2013495	E
<input type="checkbox"/>	GO:0006662	4	glycerol ether metabolic process	5	0.0008	1	0.0031	0.2013495	E
<input type="checkbox"/>	GO:0006813	7,8	potassium ion transport	5	0.0008	1	0.0031	0.2013495	E
<input type="checkbox"/>	GO:0030007	10,8	cellular potassium ion homeostasis	5	0.0008	1	0.0031	0.2013495	E
<input type="checkbox"/>	GO:0000173	10,11,8,9,7	inactivation of MAPK activity during osmolarity sensing	5	0.0008	1	0.0031	0.2013495	E
<input type="checkbox"/>	GO:0018319	10,9,8	protein amino acid myristoylation	5	0.0008	1	0.0031	0.2013495	E
<input type="checkbox"/>	GO:0000101	6,7,8	sulfur amino acid transport	5	0.0008	1	0.0031	0.2013495	E
<input type="checkbox"/>	GO:0042176	6,7,5	regulation of protein catabolic process	5	0.0008	1	0.0031	0.2013495	E
<input type="checkbox"/>	GO:0051083	8	cotranslational protein folding	5	0.0008	1	0.0031	0.2013495	E
<input type="checkbox"/>	GO:0051247	6,5	positive regulation of protein metabolic process	5	0.0008	1	0.0031	0.2013495	E
<input type="checkbox"/>	GO:0009264	6,7	deoxyribonucleotide catabolic process	5	0.0008	1	0.0031	0.2013495	E
<input type="checkbox"/>	GO:0006336	7,8,11	DNA replication-independent nucleosome assembly	5	0.0008	1	0.0031	0.2013495	E
<input type="checkbox"/>	GO:0009051	10,7,11,12,8	pentose-phosphate shunt, oxidative branch	5	0.0008	1	0.0031	0.2013495	E
<input type="checkbox"/>	GO:0006089	7	lactate metabolic process	5	0.0008	1	0.0031	0.2013495	E
<input type="checkbox"/>	GO:0006797	6	polyphosphate metabolic process	5	0.0008	1	0.0031	0.2013495	E
<input type="checkbox"/>	GO:0018342	9,8,7	protein prenylation	5	0.0008	1	0.0031	0.2013495	E
<input type="checkbox"/>	GO:0009371	10,9,6	positive regulation of transcription by pheromones	5	0.0008	1	0.0031	0.2013495	E
<input type="checkbox"/>	GO:0055075	9	potassium ion homeostasis	5	0.0008	1	0.0031	0.2013495	E
<input type="checkbox"/>	GO:0006638	5,6	neutral lipid metabolic process	5	0.0008	1	0.0031	0.2013495	E
<input type="checkbox"/>	GO:0006641	7,6,8	triacylglycerol metabolic process	5	0.0008	1	0.0031	0.2013495	E
<input type="checkbox"/>	GO:0018346	10,9,8	protein amino acid prenylation	5	0.0008	1	0.0031	0.2013495	E
<input type="checkbox"/>	GO:0016255	11,10,8,9,12	attachment of GPI anchor to protein	5	0.0008	1	0.0031	0.2013495	E
<input type="checkbox"/>	GO:0000188	9,10,8	inactivation of MAPK activity	5	0.0008	1	0.0031	0.2013495	E
<input type="checkbox"/>	GO:0000729	7,8,10,9	DNA double-strand break processing	5	0.0008	1	0.0031	0.2013495	E
<input type="checkbox"/>	GO:0044273	5	sulfur compound catabolic process	5	0.0008	1	0.0031	0.2013495	E

<input type="radio"/>	GO:0046486	5,6	glycerolipid metabolic process	5	0.0008	1	0.0031	0.2013495	E
<input type="radio"/>	GO:0051439	7,5,4	regulation of ubiquitin ligase activity during mitotic cell cycle	5	0.0008	1	0.0031	0.2013495	E
<input type="radio"/>	GO:0016078	7	tRNA catabolic process	5	0.0008	1	0.0031	0.2013495	E
<input type="radio"/>	GO:0006405	10,8,5,7,9,6	RNA export from nucleus	79	0.0122	4	0.0125	0.2014419	E
<input type="radio"/>	GO:0050657	5,6	nucleic acid transport	80	0.0124	4	0.0125	0.2016027	E
<input type="radio"/>	GO:0050658	4,6,5,7	RNA transport	80	0.0124	4	0.0125	0.2016027	E
<input type="radio"/>	GO:0051236	3,4,5	establishment of RNA localization	80	0.0124	4	0.0125	0.2016027	E
<input type="radio"/>	GO:0019362	7,6	pyridine nucleotide metabolic process	45	0.0069	3	0.0094	0.2040005	E
<input type="radio"/>	GO:0006312	7	mitotic recombination	45	0.0069	3	0.0094	0.2040005	E
<input type="radio"/>	GO:0007231	6,5	osmosensory signaling pathway	22	0.0034	2	0.0063	0.2044348	E
<input type="radio"/>	GO:0007120	8,6,10,7,11,5	axial cellular bud site selection	22	0.0034	2	0.0063	0.2044348	E
<input type="radio"/>	GO:0006311	10,8,7,5,9,6,4	meiotic gene conversion	22	0.0034	2	0.0063	0.2044348	E
<input type="radio"/>	GO:0000041	7,8	transition metal ion transport	46	0.0071	3	0.0094	0.2075098	E
<input type="radio"/>	GO:0006608	10,11,8,9,7	snRNP protein import into nucleus	23	0.0036	2	0.0063	0.2129073	E
<input type="radio"/>	GO:0006610	10,11,8,9,7	ribosomal protein import into nucleus	23	0.0036	2	0.0063	0.2129073	E
<input type="radio"/>	GO:0006607	10,11,8,9,7	NLS-bearing substrate import into nucleus	23	0.0036	2	0.0063	0.2129073	E
<input type="radio"/>	GO:0051030	5,7,6,8	snRNA transport	23	0.0036	2	0.0063	0.2129073	E
<input type="radio"/>	GO:0019748	3	secondary metabolic process	23	0.0036	2	0.0063	0.2129073	E
<input type="radio"/>	GO:0009408	5,4	response to heat	23	0.0036	2	0.0063	0.2129073	E
<input type="radio"/>	GO:0006408	11,9,6,8,10,7	snRNA export from nucleus	23	0.0036	2	0.0063	0.2129073	E
<input type="radio"/>	GO:0006818	4,5	hydrogen transport	24	0.0037	2	0.0063	0.2208527	E
<input type="radio"/>	GO:0007006	5,6	mitochondrial membrane organization and biogenesis	24	0.0037	2	0.0063	0.2208527	E
<input type="radio"/>	GO:0006576	5,6	biogenic amine metabolic process	24	0.0037	2	0.0063	0.2208527	E
<input type="radio"/>	GO:0015992	5,7,6,8	proton transport	24	0.0037	2	0.0063	0.2208527	E
<input type="radio"/>	GO:0010035	4	response to inorganic substance	24	0.0037	2	0.0063	0.2208527	E
<input type="radio"/>	GO:0007088	7,9,8,6	regulation of mitosis	55	0.0085	3	0.0094	0.2277992	E
<input type="radio"/>	GO:0006609	10,11,8,9,7	mRNA-binding (hnRNP) protein import into nucleus	25	0.0039	2	0.0063	0.2282628	E
<input type="radio"/>	GO:0045005	8,6	maintenance of fidelity during DNA-dependent DNA replication	25	0.0039	2	0.0063	0.2282628	E
<input type="radio"/>	GO:0006298	7,9,6	mismatch repair	25	0.0039	2	0.0063	0.2282628	E
<input type="radio"/>	GO:0006611	9,10,7,8	protein export from nucleus	56	0.0086	3	0.0094	0.2288481	E
<input type="radio"/>	GO:0006997	5	nuclear organization and biogenesis	57	0.0088	3	0.0094	0.2296720	E
<input type="radio"/>	GO:0000749	5	response to pheromone during conjugation with cellular fusion	57	0.0088	3	0.0094	0.2296720	E
<input type="radio"/>	GO:0045996	10,9,6	negative regulation of transcription by pheromones	6	0.0009	1	0.0031	0.2297457	E
<input type="radio"/>	GO:0006013	7,8	mannose metabolic process	6	0.0009	1	0.0031	0.2297457	E
<input type="radio"/>	GO:0031935	11,7,4,8,12,10	regulation of chromatin silencing	6	0.0009	1	0.0031	0.2297457	E
<input type="radio"/>	GO:0043405	8	regulation of MAPK activity	6	0.0009	1	0.0031	0.2297457	E
<input type="radio"/>	GO:0046020	11,10,7	negative regulation of transcription from RNA polymerase II promoter by pheromones	6	0.0009	1	0.0031	0.2297457	E
<input type="radio"/>	GO:0005979	8,7,9,10,6	regulation of glycogen biosynthetic process	6	0.0009	1	0.0031	0.2297457	E
<input type="radio"/>	GO:0031930	6	mitochondrial signaling pathway	6	0.0009	1	0.0031	0.2297457	E
<input type="radio"/>	GO:0016054	5	organic acid catabolic process	6	0.0009	1	0.0031	0.2297457	E
<input type="radio"/>	GO:0031938	12,8,5,9,13,11	regulation of chromatin silencing at telomere	6	0.0009	1	0.0031	0.2297457	E
<input type="radio"/>	GO:0051340	5	regulation of ligase activity	6	0.0009	1	0.0031	0.2297457	E

<input type="radio"/>	GO:0051438	6	regulation of ubiquitin ligase activity	6	0.0009	1	0.0031	0.2297457	E
<input type="radio"/>	GO:0019795	7,8	nonprotein amino acid biosynthetic process	6	0.0009	1	0.0031	0.2297457	E
<input type="radio"/>	GO:0045040	10,9,7,8	protein import into mitochondrial outer membrane	6	0.0009	1	0.0031	0.2297457	E
<input type="radio"/>	GO:0000070	9,7,5,8,6,4	mitotic sister chromatid segregation	59	0.0091	3	0.0094	0.2306671	E
<input type="radio"/>	GO:0006354	8,6,7	RNA elongation	59	0.0091	3	0.0094	0.2306671	E
<input type="radio"/>	GO:0031509	7,11	telomeric heterochromatin formation	60	0.0093	3	0.0094	0.2308507	E
<input type="radio"/>	GO:0006402	7	mRNA catabolic process	60	0.0093	3	0.0094	0.2308507	E
<input type="radio"/>	GO:0006348	11,7,8,12,10	chromatin silencing at telomere	60	0.0093	3	0.0094	0.2308507	E
<input type="radio"/>	GO:0051029	5,7,6,8	rRNA transport	26	0.0040	2	0.0063	0.2351332	E
<input type="radio"/>	GO:0006407	11,9,6,8,10,7	rRNA export from nucleus	26	0.0040	2	0.0063	0.2351332	E
<input type="radio"/>	GO:0051318	6,7,5	G1 phase	27	0.0042	2	0.0063	0.2414632	E
<input type="radio"/>	GO:0000080	7,8,6	G1 phase of mitotic cell cycle	27	0.0042	2	0.0063	0.2414632	E
<input type="radio"/>	GO:0009084	7,8	glutamine family amino acid biosynthetic process	27	0.0042	2	0.0063	0.2414632	E
<input type="radio"/>	GO:0009266	4	response to temperature stimulus	28	0.0043	2	0.0063	0.2472552	E
<input type="radio"/>	GO:0032005	7,6	signal transduction during conjugation with cellular fusion	28	0.0043	2	0.0063	0.2472552	E
<input type="radio"/>	GO:0042144	6	vacuole fusion, non-autophagic	28	0.0043	2	0.0063	0.2472552	E
<input type="radio"/>	GO:0000750	8,7,6	pheromone-dependent signal transduction during conjugation with cellular fusion	28	0.0043	2	0.0063	0.2472552	E
<input type="radio"/>	GO:0018193	7	peptidyl-amino acid modification	28	0.0043	2	0.0063	0.2472552	E
<input type="radio"/>	GO:0006999	6	nuclear pore organization and biogenesis	29	0.0045	2	0.0063	0.2525143	E
<input type="radio"/>	GO:0006409	11,9,6,8,10,7	tRNA export from nucleus	29	0.0045	2	0.0063	0.2525143	E
<input type="radio"/>	GO:0006109	5,4	regulation of carbohydrate metabolic process	29	0.0045	2	0.0063	0.2525143	E
<input type="radio"/>	GO:0032507	6,5,4	maintenance of cellular protein localization	29	0.0045	2	0.0063	0.2525143	E
<input type="radio"/>	GO:0051651	5,4,3	maintenance of cellular localization	29	0.0045	2	0.0063	0.2525143	E
<input type="radio"/>	GO:0000376	9	RNA splicing, via transesterification reactions with guanosine as nucleophile	7	0.0011	1	0.0031	0.2548626	E
<input type="radio"/>	GO:0000727	9,8	double-strand break repair via break-induced replication	7	0.0011	1	0.0031	0.2548626	E
<input type="radio"/>	GO:0000372	10	Group I intron splicing	7	0.0011	1	0.0031	0.2548626	E
<input type="radio"/>	GO:0007008	6,7	outer mitochondrial membrane organization and biogenesis	7	0.0011	1	0.0031	0.2548626	E
<input type="radio"/>	GO:0019722	7	calcium-mediated signaling	7	0.0011	1	0.0031	0.2548626	E
<input type="radio"/>	GO:0009225	5	nucleotide-sugar metabolic process	7	0.0011	1	0.0031	0.2548626	E
<input type="radio"/>	GO:0046856	7,9,8,10	phosphoinositide dephosphorylation	7	0.0011	1	0.0031	0.2548626	E
<input type="radio"/>	GO:0000710	11,9,8,6,5,10,7,4	meiotic mismatch repair	7	0.0011	1	0.0031	0.2548626	E
<input type="radio"/>	GO:0046839	6,7	phospholipid dephosphorylation	7	0.0011	1	0.0031	0.2548626	E
<input type="radio"/>	GO:0000289	11,9,10	poly(A) tail shortening	7	0.0011	1	0.0031	0.2548626	E
<input type="radio"/>	GO:0006265	6	DNA topological change	7	0.0011	1	0.0031	0.2548626	E
<input type="radio"/>	GO:0051348	6	negative regulation of transferase activity	7	0.0011	1	0.0031	0.2548626	E
<input type="radio"/>	GO:0009092	7,8	homoserine metabolic process	7	0.0011	1	0.0031	0.2548626	E
<input type="radio"/>	GO:0009166	5,6	nucleotide catabolic process	7	0.0011	1	0.0031	0.2548626	E
<input type="radio"/>	GO:0006415	8,7,6	translational termination	7	0.0011	1	0.0031	0.2548626	E
<input type="radio"/>	GO:0006469	7,8	negative regulation of protein kinase activity	7	0.0011	1	0.0031	0.2548626	E
<input type="radio"/>	GO:0009435	8,7,10,9	NAD biosynthetic process	7	0.0011	1	0.0031	0.2548626	E
<input type="radio"/>	GO:0000755	6,5	cytogamy	7	0.0011	1	0.0031	0.2548626	E

<input type="checkbox"/>	GO:0006595	6,7	polyamine metabolic process	7	0.0011	1	0.0031	0.2548626	E
<input type="checkbox"/>	GO:0046999	5,4	regulation of conjugation	30	0.0046	2	0.0063	0.2572480	E
<input type="checkbox"/>	GO:0046364	6,7	monosaccharide biosynthetic process	30	0.0046	2	0.0063	0.2572480	E
<input type="checkbox"/>	GO:0051031	5,7,6,8	tRNA transport	30	0.0046	2	0.0063	0.2572480	E
<input type="checkbox"/>	GO:0019319	7,8	hexose biosynthetic process	30	0.0046	2	0.0063	0.2572480	E
<input type="checkbox"/>	GO:0051128	5,4	regulation of cellular component organization and biogenesis	30	0.0046	2	0.0063	0.2572480	E
<input type="checkbox"/>	GO:0031137	6,5	regulation of conjugation with cellular fusion	30	0.0046	2	0.0063	0.2572480	E
<input type="checkbox"/>	GO:0006665	6,7	sphingolipid metabolic process	30	0.0046	2	0.0063	0.2572480	E
<input type="checkbox"/>	GO:0006575	5	amino acid derivative metabolic process	31	0.0048	2	0.0063	0.2614658	E
<input type="checkbox"/>	GO:0007121	8,6,10,7,11,5	bipolar cellular bud site selection	32	0.0049	2	0.0063	0.2651792	E
<input type="checkbox"/>	GO:0045047	9,8,7,6,5	protein targeting to ER	33	0.0051	2	0.0063	0.2684010	E
<input type="checkbox"/>	GO:0007186	6	G-protein coupled receptor protein signaling pathway	34	0.0053	2	0.0063	0.2711452	E
<input type="checkbox"/>	GO:0007117	6,5,4	budding cell bud growth	35	0.0054	2	0.0063	0.2734270	E
<input type="checkbox"/>	GO:0046165	5	alcohol biosynthetic process	35	0.0054	2	0.0063	0.2734270	E
<input type="checkbox"/>	GO:0048590	3	non-developmental growth	35	0.0054	2	0.0063	0.2734270	E
<input type="checkbox"/>	GO:0051252	7,6	regulation of RNA metabolic process	36	0.0056	2	0.0063	0.2752624	E
<input type="checkbox"/>	GO:0007119	7,6,5	budding cell isotropic bud growth	8	0.0012	1	0.0031	0.2769534	E
<input type="checkbox"/>	GO:0015940	7,8	pantothenate biosynthetic process	8	0.0012	1	0.0031	0.2769534	E
<input type="checkbox"/>	GO:0006566	7,8	threonine metabolic process	8	0.0012	1	0.0031	0.2769534	E
<input type="checkbox"/>	GO:0015939	7	pantothenate metabolic process	8	0.0012	1	0.0031	0.2769534	E
<input type="checkbox"/>	GO:0000019	9,8	regulation of mitotic recombination	8	0.0012	1	0.0031	0.2769534	E
<input type="checkbox"/>	GO:0016973	12,10,7,9,11,8	poly(A)+ mRNA export from nucleus	8	0.0012	1	0.0031	0.2769534	E
<input type="checkbox"/>	GO:0015677	9,10	copper ion import	8	0.0012	1	0.0031	0.2769534	E
<input type="checkbox"/>	GO:0000335	10,9,6	negative regulation of DNA transposition	8	0.0012	1	0.0031	0.2769534	E
<input type="checkbox"/>	GO:0043144	7	snoRNA processing	8	0.0012	1	0.0031	0.2769534	E
<input type="checkbox"/>	GO:0007323	9	peptide pheromone maturation	8	0.0012	1	0.0031	0.2769534	E
<input type="checkbox"/>	GO:0006828	8,9	manganese ion transport	8	0.0012	1	0.0031	0.2769534	E
<input type="checkbox"/>	GO:0006383	8,7	transcription from RNA polymerase III promoter	38	0.0059	2	0.0063	0.2776610	E
<input type="checkbox"/>	GO:0008643	4,5	carbohydrate transport	38	0.0059	2	0.0063	0.2776610	E
<input type="checkbox"/>	GO:0007031	5	peroxisome organization and biogenesis	40	0.0062	2	0.0063	0.2784797	E
<input type="checkbox"/>	GO:0046685	5	response to arsenic	9	0.0014	1	0.0031	0.2962541	E
<input type="checkbox"/>	GO:0030491	7,9,10,6,8	heteroduplex formation	9	0.0014	1	0.0031	0.2962541	E
<input type="checkbox"/>	GO:0009262	6	deoxyribonucleotide metabolic process	9	0.0014	1	0.0031	0.2962541	E
<input type="checkbox"/>	GO:0019933	8	cAMP-mediated signaling	9	0.0014	1	0.0031	0.2962541	E
<input type="checkbox"/>	GO:0030968	7,5,6	unfolded protein response	9	0.0014	1	0.0031	0.2962541	E
<input type="checkbox"/>	GO:0006635	7,9,8	fatty acid beta-oxidation	9	0.0014	1	0.0031	0.2962541	E
<input type="checkbox"/>	GO:0019935	7	cyclic-nucleotide-mediated signaling	9	0.0014	1	0.0031	0.2962541	E
<input type="checkbox"/>	GO:0006528	7,8	asparagine metabolic process	9	0.0014	1	0.0031	0.2962541	E
<input type="checkbox"/>	GO:0042138	11,9,8,5,6,10,7,4	meiotic DNA double-strand break formation	9	0.0014	1	0.0031	0.2962541	E
<input type="checkbox"/>	GO:0006984	6	ER-nuclear signaling pathway	9	0.0014	1	0.0031	0.2962541	E
<input type="checkbox"/>	GO:0000501	4	flocculation via cell wall protein-carbohydrate interaction	9	0.0014	1	0.0031	0.2962541	E
<input type="checkbox"/>	GO:0006760	5,7	folic acid and derivative metabolic process	9	0.0014	1	0.0031	0.2962541	E
<input type="checkbox"/>	GO:0000128	3	flocculation	9	0.0014	1	0.0031	0.2962541	E

<input type="radio"/>	GO:0006280	6	mutagenesis	9	0.0014	1	0.0031	0.2962541	E
<input type="radio"/>	GO:0046519	7,8	sphingoid metabolic process	10	0.0015	1	0.0031	0.3129849	E
<input type="radio"/>	GO:0006882	10,8	cellular zinc ion homeostasis	10	0.0015	1	0.0031	0.3129849	E
<input type="radio"/>	GO:0019363	7,6,8	pyridine nucleotide biosynthetic process	10	0.0015	1	0.0031	0.3129849	E
<input type="radio"/>	GO:0006791	5	sulfur utilization	10	0.0015	1	0.0031	0.3129849	E
<input type="radio"/>	GO:0051261	6	protein depolymerization	10	0.0015	1	0.0031	0.3129849	E
<input type="radio"/>	GO:0030846	10,9	transcription termination from Pol II promoter, RNA polymerase(A) coupled	10	0.0015	1	0.0031	0.3129849	E
<input type="radio"/>	GO:0006313	7,4	transposition, DNA-mediated	10	0.0015	1	0.0031	0.3129849	E
<input type="radio"/>	GO:0000337	9,8,5	regulation of DNA transposition	10	0.0015	1	0.0031	0.3129849	E
<input type="radio"/>	GO:0000103	6	sulfate assimilation	10	0.0015	1	0.0031	0.3129849	E
<input type="radio"/>	GO:0009068	7,8	aspartate family amino acid catabolic process	10	0.0015	1	0.0031	0.3129849	E
<input type="radio"/>	GO:0055069	9	zinc ion homeostasis	10	0.0015	1	0.0031	0.3129849	E
<input type="radio"/>	GO:0000161	7,8,6	MAPKKK cascade during osmolarity sensing	11	0.0017	1	0.0031	0.3273515	E
<input type="radio"/>	GO:0043085	5	positive regulation of enzyme activity	11	0.0017	1	0.0031	0.3273515	E
<input type="radio"/>	GO:0001101	4	response to acid	11	0.0017	1	0.0031	0.3273515	E
<input type="radio"/>	GO:0019321	6,7	pentose metabolic process	11	0.0017	1	0.0031	0.3273515	E
<input type="radio"/>	GO:0000055	11,12,7,9,10	ribosomal large subunit export from nucleus	11	0.0017	1	0.0031	0.3273515	E
<input type="radio"/>	GO:0019395	6,8,7	fatty acid oxidation	11	0.0017	1	0.0031	0.3273515	E
<input type="radio"/>	GO:0043086	5	negative regulation of enzyme activity	11	0.0017	1	0.0031	0.3273515	E
<input type="radio"/>	GO:0006972	5	hyperosmotic response	11	0.0017	1	0.0031	0.3273515	E
<input type="radio"/>	GO:0006098	9,10,11	pentose-phosphate shunt	11	0.0017	1	0.0031	0.3273515	E
<input type="radio"/>	GO:0016237	4,6	microautophagy	11	0.0017	1	0.0031	0.3273515	E
<input type="radio"/>	GO:0007039	7,8	vacuolar protein catabolic process	11	0.0017	1	0.0031	0.3273515	E
<input type="radio"/>	GO:0006284	7,6	base-excision repair	12	0.0019	1	0.0031	0.3395452	E
<input type="radio"/>	GO:0015914	5,6	phospholipid transport	12	0.0019	1	0.0031	0.3395452	E
<input type="radio"/>	GO:0000302	5	response to reactive oxygen species	12	0.0019	1	0.0031	0.3395452	E
<input type="radio"/>	GO:0008054	7,6,11,10,12	cyclin catabolic process	12	0.0019	1	0.0031	0.3395452	E
<input type="radio"/>	GO:0006915	6,8	apoptosis	13	0.0020	1	0.0031	0.3497445	E
<input type="radio"/>	GO:0008219	4,6	cell death	13	0.0020	1	0.0031	0.3497445	E
<input type="radio"/>	GO:0030258	5,6	lipid modification	13	0.0020	1	0.0031	0.3497445	E
<input type="radio"/>	GO:0012501	5,7	programmed cell death	13	0.0020	1	0.0031	0.3497445	E
<input type="radio"/>	GO:0016265	3	death	13	0.0020	1	0.0031	0.3497445	E
<input type="radio"/>	GO:0006272	9,8	leading strand elongation	14	0.0022	1	0.0031	0.3581156	E
<input type="radio"/>	GO:0045002	8,7	double-strand break repair via single-strand annealing	14	0.0022	1	0.0031	0.3581156	E
<input type="radio"/>	GO:0006734	9,8	NADH metabolic process	14	0.0022	1	0.0031	0.3581156	E
<input type="radio"/>	GO:0000011	6	vacuole inheritance	14	0.0022	1	0.0031	0.3581156	E
<input type="radio"/>	GO:0006825	8,9	copper ion transport	14	0.0022	1	0.0031	0.3581156	E
<input type="radio"/>	GO:0007118	7,6,5	budding cell apical bud growth	14	0.0022	1	0.0031	0.3581156	E
<input type="radio"/>	GO:0000028	9,7,8,6	ribosomal small subunit assembly and maintenance	14	0.0022	1	0.0031	0.3581156	E
<input type="radio"/>	GO:0042787	10,9,11	protein ubiquitination during ubiquitin-dependent protein catabolic process	14	0.0022	1	0.0031	0.3581156	E
<input type="radio"/>	GO:0006740	10,9	NADPH regeneration	14	0.0022	1	0.0031	0.3581156	E
<input type="radio"/>	GO:0031365	8	N-terminal protein amino acid modification	15	0.0023	1	0.0031	0.3648134	E
<input type="radio"/>	GO:0000737	6,7	DNA catabolic process, endonucleolytic	15	0.0023	1	0.0031	0.3648134	E

<input type="radio"/>	GO:0009894	5,4	regulation of catabolic process	15	0.0023	1	0.0031	0.3648134	E
<input type="radio"/>	GO:0000079	8,7,6	regulation of cyclin-dependent protein kinase activity	15	0.0023	1	0.0031	0.3648134	E
<input type="radio"/>	GO:0007091	9,7,5,8,6,4	mitotic metaphase/anaphase transition	15	0.0023	1	0.0031	0.3648134	E
<input type="radio"/>	GO:0006267	8,7	pre-replicative complex assembly	15	0.0023	1	0.0031	0.3648134	E
<input type="radio"/>	GO:0031145	11,10,12	anaphase-promoting complex-dependent proteasomal ubiquitin-dependent protein catabolic process	15	0.0023	1	0.0031	0.3648134	E
<input type="radio"/>	GO:0005978	8,7,9	glycogen biosynthetic process	15	0.0023	1	0.0031	0.3648134	E
<input type="radio"/>	GO:0046356	7	acetyl-CoA catabolic process	15	0.0023	1	0.0031	0.3648134	E
<input type="radio"/>	GO:0006099	8,7,6	tricarboxylic acid cycle	15	0.0023	1	0.0031	0.3648134	E
<input type="radio"/>	GO:0018409	9	peptide or protein amino-terminal blocking	15	0.0023	1	0.0031	0.3648134	E
<input type="radio"/>	GO:0031023	5	microtubule organizing center organization and biogenesis	16	0.0025	1	0.0031	0.3699817	E
<input type="radio"/>	GO:0048017	8	inositol lipid-mediated signaling	16	0.0025	1	0.0031	0.3699817	E
<input type="radio"/>	GO:0048015	7	phosphoinositide-mediated signaling	16	0.0025	1	0.0031	0.3699817	E
<input type="radio"/>	GO:0051300	5,4,6	spindle pole body organization and biogenesis	16	0.0025	1	0.0031	0.3699817	E
<input type="radio"/>	GO:0000741	6	karyogamy	17	0.0026	1	0.0031	0.3737545	E
<input type="radio"/>	GO:0006739	9,8	NADP metabolic process	17	0.0026	1	0.0031	0.3737545	E
<input type="radio"/>	GO:0016074	6	snoRNA metabolic process	17	0.0026	1	0.0031	0.3737545	E
<input type="radio"/>	GO:0007004	9	telomere maintenance via telomerase	17	0.0026	1	0.0031	0.3737545	E
<input type="radio"/>	GO:0000742	7,5	karyogamy during conjugation with cellular fusion	17	0.0026	1	0.0031	0.3737545	E
<input type="radio"/>	GO:0009116	5	nucleoside metabolic process	18	0.0028	1	0.0031	0.3762564	E
<input type="radio"/>	GO:0010038	5	response to metal ion	18	0.0028	1	0.0031	0.3762564	E
<input type="radio"/>	GO:0006273	9,8	lagging strand elongation	18	0.0028	1	0.0031	0.3762564	E
<input type="radio"/>	GO:0042401	6,7	biogenic amine biosynthetic process	18	0.0028	1	0.0031	0.3762564	E
<input type="radio"/>	GO:0000753	7,8,6	cellular morphogenesis during conjugation with cellular fusion	18	0.0028	1	0.0031	0.3762564	E
<input type="radio"/>	GO:0006378	9	mRNA polyadenylation	18	0.0028	1	0.0031	0.3762564	E
<input type="radio"/>	GO:0055065	8	metal ion homeostasis	19	0.0029	1	0.0031	0.3776029	E
<input type="radio"/>	GO:0043255	7,6,5	regulation of carbohydrate biosynthetic process	19	0.0029	1	0.0031	0.3776029	E
<input type="radio"/>	GO:0009267	7,6,5	cellular response to starvation	19	0.0029	1	0.0031	0.3776029	E
<input type="radio"/>	GO:0042594	6,4	response to starvation	19	0.0029	1	0.0031	0.3776029	E
<input type="radio"/>	GO:0000722	9,8	telomere maintenance via recombination	19	0.0029	1	0.0031	0.3776029	E
<input type="radio"/>	GO:0006875	9,7	cellular metal ion homeostasis	19	0.0029	1	0.0031	0.3776029	E
<input type="radio"/>	GO:0031669	6,5	cellular response to nutrient levels	19	0.0029	1	0.0031	0.3776029	E
<input type="radio"/>	GO:0031668	5,4	cellular response to extracellular stimulus	19	0.0029	1	0.0031	0.3776029	E
<input type="radio"/>	GO:0000209	10	protein polyubiquitination	20	0.0031	1	0.0031	0.3779014	E
<input type="radio"/>	GO:0006614	11,10,9,8,7	SRP-dependent cotranslational protein targeting to membrane	20	0.0031	1	0.0031	0.3779014	E
<input type="radio"/>	GO:0000165	7	MAPKKK cascade	20	0.0031	1	0.0031	0.3779014	E
<input type="radio"/>	GO:0015985	6,8,7,9	energy coupled proton transport, down electrochemical gradient	20	0.0031	1	0.0031	0.3779014	E
<input type="radio"/>	GO:0051231	5,4,9,7	spindle elongation	20	0.0031	1	0.0031	0.3779014	E
<input type="radio"/>	GO:0000022	6,5,10,8	mitotic spindle elongation	20	0.0031	1	0.0031	0.3779014	E
<input type="radio"/>	GO:0016579	9	protein deubiquitination	20	0.0031	1	0.0031	0.3779014	E
<input type="radio"/>	GO:0006826	7,8,9	iron ion transport	20	0.0031	1	0.0031	0.3779014	E
<input type="radio"/>	GO:0015986	8,10,7,9,11,5	ATP synthesis coupled proton transport	20	0.0031	1	0.0031	0.3779014	E
<input type="radio"/>	GO:0006754	7,9,6,8,10	ATP biosynthetic process	20	0.0031	1	0.0031	0.3779014	E

<input type="radio"/>	GO:0006753	7	nucleoside phosphate metabolic process	20	0.0031	1	0.0031	0.3779014	E
<input type="radio"/>	GO:0042398	6,5	amino acid derivative biosynthetic process	20	0.0031	1	0.0031	0.3779014	E
<input type="radio"/>	GO:0006308	5,6	DNA catabolic process	20	0.0031	1	0.0031	0.3779014	E
<input type="radio"/>	GO:0000767	6,7	cellular morphogenesis during conjugation	20	0.0031	1	0.0031	0.3779014	E
<input type="radio"/>	GO:0008150	1	biological process	6476	1.0000	319	1.0000	1.0000000	D
<input type="radio"/>	GO:0045324	8,6,7	late endosome to vacuole transport	21	0.0032	1	0.0031	0.3772517	D
<input type="radio"/>	GO:0051716	3	cellular response to stimulus	21	0.0032	1	0.0031	0.3772517	D
<input type="radio"/>	GO:0033554	4	cellular response to stress	21	0.0032	1	0.0031	0.3772517	D
<input type="radio"/>	GO:0019674	9,8	NAD metabolic process	21	0.0032	1	0.0031	0.3772517	D
<input type="radio"/>	GO:0046034	5,9	ATP metabolic process	21	0.0032	1	0.0031	0.3772517	D
<input type="radio"/>	GO:0006081	4	aldehyde metabolic process	21	0.0032	1	0.0031	0.3772517	D
<input type="radio"/>	GO:0009206	8,9	purine ribonucleoside triphosphate biosynthetic process	22	0.0034	1	0.0031	0.3757461	D
<input type="radio"/>	GO:0006513	10	protein monoubiquitination	22	0.0034	1	0.0031	0.3757461	D
<input type="radio"/>	GO:0030472	6,5,10	mitotic spindle organization and biogenesis in nucleus	22	0.0034	1	0.0031	0.3757461	D
<input type="radio"/>	GO:0044272	5	sulfur compound biosynthetic process	22	0.0034	1	0.0031	0.3757461	D
<input type="radio"/>	GO:0048284	5	organelle fusion	22	0.0034	1	0.0031	0.3757461	D
<input type="radio"/>	GO:0009145	7,8	purine nucleoside triphosphate biosynthetic process	22	0.0034	1	0.0031	0.3757461	D
<input type="radio"/>	GO:0007064	10,8,5,6,9,7,4	mitotic sister chromatid cohesion	22	0.0034	1	0.0031	0.3757461	D
<input type="radio"/>	GO:0006613	10,9,8,7,6	cotranslational protein targeting to membrane	23	0.0036	1	0.0031	0.3734702	D
<input type="radio"/>	GO:0006303	8,7	double-strand break repair via nonhomologous end joining	23	0.0036	1	0.0031	0.3734702	D
<input type="radio"/>	GO:0007534	6,8,7	gene conversion at mating-type locus	23	0.0036	1	0.0031	0.3734702	D
<input type="radio"/>	GO:0009144	7	purine nucleoside triphosphate metabolic process	23	0.0036	1	0.0031	0.3734702	D
<input type="radio"/>	GO:0007243	6	protein kinase cascade	23	0.0036	1	0.0031	0.3734702	D
<input type="radio"/>	GO:0009205	8	purine ribonucleoside triphosphate metabolic process	23	0.0036	1	0.0031	0.3734702	D
<input type="radio"/>	GO:0009201	7,8	ribonucleoside triphosphate biosynthetic process	24	0.0037	1	0.0031	0.3705035	D
<input type="radio"/>	GO:0006555	7,8,6	methionine metabolic process	24	0.0037	1	0.0031	0.3705035	D
<input type="radio"/>	GO:0000288	10,8,9	mRNA catabolic process, deadenylation-dependent decay	24	0.0037	1	0.0031	0.3705035	D
<input type="radio"/>	GO:0043631	8	RNA polyadenylation	24	0.0037	1	0.0031	0.3705035	D
<input type="radio"/>	GO:0009199	7	ribonucleoside triphosphate metabolic process	25	0.0039	1	0.0031	0.3669192	D
<input type="radio"/>	GO:0045859	7	regulation of protein kinase activity	25	0.0039	1	0.0031	0.3669192	D
<input type="radio"/>	GO:0043549	6	regulation of kinase activity	25	0.0039	1	0.0031	0.3669192	D
<input type="radio"/>	GO:0009250	7,8	glucan biosynthetic process	25	0.0039	1	0.0031	0.3669192	D
<input type="radio"/>	GO:0006379	8	mRNA cleavage	26	0.0040	1	0.0031	0.3627854	D
<input type="radio"/>	GO:0051338	5	regulation of transferase activity	26	0.0040	1	0.0031	0.3627854	D
<input type="radio"/>	GO:0015749	5,6	monosaccharide transport	26	0.0040	1	0.0031	0.3627854	D
<input type="radio"/>	GO:0008645	6,7	hexose transport	26	0.0040	1	0.0031	0.3627854	D
<input type="radio"/>	GO:0042274	6,5	ribosomal small subunit biogenesis and assembly	26	0.0040	1	0.0031	0.3627854	D
<input type="radio"/>	GO:0009142	6,7	nucleoside triphosphate biosynthetic process	27	0.0042	1	0.0031	0.3581646	D
<input type="radio"/>	GO:0009636	4	response to toxin	28	0.0043	1	0.0031	0.3531147	D
<input type="radio"/>	GO:0000054	10,11,6,8,9	ribosome export from nucleus	28	0.0043	1	0.0031	0.3531147	D
<input type="radio"/>	GO:0006094	8,9	gluconeogenesis	28	0.0043	1	0.0031	0.3531147	D

<input type="checkbox"/>	GO:0006885	7	regulation of pH	29	0.0045	1	0.0031	0.3476892	D
<input type="checkbox"/>	GO:0007533	5,7,6	mating type switching	29	0.0045	1	0.0031	0.3476892	D
<input type="checkbox"/>	GO:0009141	6	nucleoside triphosphate metabolic process	30	0.0046	1	0.0031	0.3419373	D
<input type="checkbox"/>	GO:0006893	9,7,6,8	Golgi to plasma membrane transport	30	0.0046	1	0.0031	0.3419373	D
<input type="checkbox"/>	GO:0043487	8,7	regulation of RNA stability	30	0.0046	1	0.0031	0.3419373	D
<input type="checkbox"/>	GO:0043488	9,8,7	regulation of mRNA stability	30	0.0046	1	0.0031	0.3419373	D
<input type="checkbox"/>	GO:0007062	7,4	sister chromatid cohesion	31	0.0048	1	0.0031	0.3359041	D
<input type="checkbox"/>	GO:0022616	6	DNA strand elongation	32	0.0049	1	0.0031	0.3296314	D
<input type="checkbox"/>	GO:0043039	7,8	tRNA aminoacylation	32	0.0049	1	0.0031	0.3296314	D
<input type="checkbox"/>	GO:0006418	8,7,9,6	tRNA aminoacylation for protein translation	32	0.0049	1	0.0031	0.3296314	D
<input type="checkbox"/>	GO:0006271	8,7	DNA strand elongation during DNA replication	32	0.0049	1	0.0031	0.3296314	D
<input type="checkbox"/>	GO:0043038	6,7	amino acid activation	32	0.0049	1	0.0031	0.3296314	D
<input type="checkbox"/>	GO:0005977	7,6,8	glycogen metabolic process	32	0.0049	1	0.0031	0.3296314	D
<input type="checkbox"/>	GO:0000096	6,7,5	sulfur amino acid metabolic process	33	0.0051	1	0.0031	0.3231573	D
<input type="checkbox"/>	GO:0055067	8	monovalent inorganic cation homeostasis	34	0.0053	1	0.0031	0.3165169	D
<input type="checkbox"/>	GO:0006007	8,9	glucose catabolic process	34	0.0053	1	0.0031	0.3165169	D
<input type="checkbox"/>	GO:0030004	9,7	cellular monovalent inorganic cation homeostasis	34	0.0053	1	0.0031	0.3165169	D
<input type="checkbox"/>	GO:0006869	4,5	lipid transport	34	0.0053	1	0.0031	0.3165169	D
<input type="checkbox"/>	GO:0003006	3,4	reproductive developmental process	35	0.0054	1	0.0031	0.3097423	D
<input type="checkbox"/>	GO:0007530	4,5	sex determination	35	0.0054	1	0.0031	0.3097423	D
<input type="checkbox"/>	GO:0000726	7,6	non-recombinational repair	35	0.0054	1	0.0031	0.3097423	D
<input type="checkbox"/>	GO:0007531	4,6,5	mating type determination	35	0.0054	1	0.0031	0.3097423	D
<input type="checkbox"/>	GO:0031667	5	response to nutrient levels	37	0.0057	1	0.0031	0.2959052	D
<input type="checkbox"/>	GO:0009991	4	response to extracellular stimulus	37	0.0057	1	0.0031	0.2959052	D
<input type="checkbox"/>	GO:0009605	3	response to external stimulus	37	0.0057	1	0.0031	0.2959052	D
<input type="checkbox"/>	GO:0006879	10,8	cellular iron ion homeostasis	38	0.0059	1	0.0031	0.2888939	D
<input type="checkbox"/>	GO:0055072	9	iron ion homeostasis	38	0.0059	1	0.0031	0.2888939	D
<input type="checkbox"/>	GO:0009152	7,8	purine ribonucleotide biosynthetic process	38	0.0059	1	0.0031	0.2888939	D
<input type="checkbox"/>	GO:0006112	5	energy reserve metabolic process	39	0.0060	1	0.0031	0.2818512	D
<input type="checkbox"/>	GO:0019320	7,8	hexose catabolic process	39	0.0060	1	0.0031	0.2818512	D
<input type="checkbox"/>	GO:0001302	5	replicative cell aging	39	0.0060	1	0.0031	0.2818512	D
<input type="checkbox"/>	GO:0006612	9,7,8	protein targeting to membrane	39	0.0060	1	0.0031	0.2818512	D
<input type="checkbox"/>	GO:0030476	8,6,7	spore wall assembly (sensu Fungi)	42	0.0065	2	0.0063	0.2778609	D
<input type="checkbox"/>	GO:0042244	5,6	spore wall assembly	42	0.0065	2	0.0063	0.2778609	D
<input type="checkbox"/>	GO:0001403	6,4,8,9	invasive growth (sensu Saccharomyces)	42	0.0065	2	0.0063	0.2778609	D
<input type="checkbox"/>	GO:0009064	6,7	glutamine family amino acid metabolic process	43	0.0066	2	0.0063	0.2770572	D
<input type="checkbox"/>	GO:0006367	8,9,7	transcription initiation from RNA polymerase II promoter	44	0.0068	2	0.0063	0.2759477	D
<input type="checkbox"/>	GO:0007052	5,4,9	mitotic spindle organization and biogenesis	44	0.0068	2	0.0063	0.2759477	D
<input type="checkbox"/>	GO:0048308	5	organelle inheritance	40	0.0062	1	0.0031	0.2747972	D
<input type="checkbox"/>	GO:0009260	6,7	ribonucleotide biosynthetic process	40	0.0062	1	0.0031	0.2747972	D
<input type="checkbox"/>	GO:0050790	4	regulation of catalytic activity	45	0.0069	2	0.0063	0.2745499	D
<input type="checkbox"/>	GO:0065009	3	regulation of a molecular function	46	0.0071	2	0.0063	0.2728810	D
<input type="checkbox"/>	GO:0007051	8	spindle organization and biogenesis	47	0.0073	2	0.0063	0.2709581	D

<input type="radio"/>	GO:0000027	9,7,8,6	ribosomal large subunit assembly and maintenance	41	0.0063	1	0.0031	0.2677500	D
<input type="radio"/>	GO:0006164	6,7	purine nucleotide biosynthetic process	41	0.0063	1	0.0031	0.2677500	D
<input type="radio"/>	GO:0009150	7	purine ribonucleotide metabolic process	41	0.0063	1	0.0031	0.2677500	D
<input type="radio"/>	GO:0048468	3,5	cell development	52	0.0080	2	0.0063	0.2580979	D
<input type="radio"/>	GO:0006368	9,7,8	RNA elongation from RNA polymerase II promoter	53	0.0082	2	0.0063	0.2549838	D
<input type="radio"/>	GO:0009259	6	ribonucleotide metabolic process	43	0.0066	1	0.0031	0.2537409	D
<input type="radio"/>	GO:0042257	8,7	ribosomal subunit assembly	55	0.0085	2	0.0063	0.2483270	D
<input type="radio"/>	GO:0007131	10,8,7,5,9,6,4	meiotic recombination	55	0.0085	2	0.0063	0.2483270	D
<input type="radio"/>	GO:0046365	6,7	monosaccharide catabolic process	44	0.0068	1	0.0031	0.2468071	D
<input type="radio"/>	GO:0031167	8,9	rRNA methylation	44	0.0068	1	0.0031	0.2468071	D
<input type="radio"/>	GO:0006944	5	membrane fusion	59	0.0091	2	0.0063	0.2336544	D
<input type="radio"/>	GO:0009165	5,6	nucleotide biosynthetic process	59	0.0091	2	0.0063	0.2336544	D
<input type="radio"/>	GO:0006119	7,4	oxidative phosphorylation	46	0.0071	1	0.0031	0.2331407	D
<input type="radio"/>	GO:0006073	6,7	glucan metabolic process	46	0.0071	1	0.0031	0.2331407	D
<input type="radio"/>	GO:0007264	6	small GTPase mediated signal transduction	61	0.0094	3	0.0094	0.2308333	D
<input type="radio"/>	GO:0000819	7,4	sister chromatid segregation	62	0.0096	3	0.0094	0.2306217	D
<input type="radio"/>	GO:0006006	7,8	glucose metabolic process	65	0.0100	3	0.0094	0.2288896	D
<input type="radio"/>	GO:0030468	8,5,9	establishment of cell polarity (sensu Fungi)	66	0.0102	3	0.0094	0.2279698	D
<input type="radio"/>	GO:0030467	7,4,8	establishment and/or maintenance of cell polarity (sensu Fungi)	66	0.0102	3	0.0094	0.2279698	D
<input type="radio"/>	GO:0007105	6,4	cytokinesis, site selection	66	0.0102	3	0.0094	0.2279698	D
<input type="radio"/>	GO:0000282	7,9,5,6,10	cellular bud site selection	66	0.0102	3	0.0094	0.2279698	D
<input type="radio"/>	GO:0006417	7,6,5	regulation of translation	47	0.0073	1	0.0031	0.2264282	D
<input type="radio"/>	GO:0046164	5	alcohol catabolic process	47	0.0073	1	0.0031	0.2264282	D
<input type="radio"/>	GO:0006163	6	purine nucleotide metabolic process	47	0.0073	1	0.0031	0.2264282	D
<input type="radio"/>	GO:0043623	7,6	cellular protein complex assembly	69	0.0107	3	0.0094	0.2242826	D
<input type="radio"/>	GO:0006401	6	RNA catabolic process	74	0.0114	3	0.0094	0.2154687	D
<input type="radio"/>	GO:0030005	9,7	cellular di-, tri-valent inorganic cation homeostasis	64	0.0099	2	0.0063	0.2136821	D
<input type="radio"/>	GO:0055066	8	di-, tri-valent inorganic cation homeostasis	64	0.0099	2	0.0063	0.2136821	D
<input type="radio"/>	GO:0007569	4	cell aging	49	0.0076	1	0.0031	0.2132863	D
<input type="radio"/>	GO:0007568	3	aging	49	0.0076	1	0.0031	0.2132863	D
<input type="radio"/>	GO:0016197	7,5,6	endosome transport	49	0.0076	1	0.0031	0.2132863	D
<input type="radio"/>	GO:0046483	4	heterocycle metabolic process	76	0.0117	3	0.0094	0.2111702	D
<input type="radio"/>	GO:0042255	7,6	ribosome assembly	66	0.0102	2	0.0063	0.2054290	D
<input type="radio"/>	GO:0043414	6	biopolymer methylation	83	0.0128	4	0.0125	0.2013029	D
<input type="radio"/>	GO:0032259	5	methylation	83	0.0128	4	0.0125	0.2013029	D
<input type="radio"/>	GO:0007033	5	vacuole organization and biogenesis	67	0.0103	2	0.0063	0.2012781	D
<input type="radio"/>	GO:0031326	6,5	regulation of cellular biosynthetic process	67	0.0103	2	0.0063	0.2012781	D
<input type="radio"/>	GO:0008033	7	tRNA processing	84	0.0130	4	0.0125	0.2009533	D
<input type="radio"/>	GO:0019318	6,7	hexose metabolic process	85	0.0131	4	0.0125	0.2004849	D
<input type="radio"/>	GO:0006403	4	RNA localization	90	0.0139	4	0.0125	0.1964877	D
<input type="radio"/>	GO:0000082	8,5,6,7,4	G1/S transition of mitotic cell cycle	52	0.0080	1	0.0031	0.1943771	D
<input type="radio"/>	GO:0006400	7,8	tRNA modification	52	0.0080	1	0.0031	0.1943771	D
<input type="radio"/>	GO:0005996	5,6	monosaccharide metabolic process	92	0.0142	4	0.0125	0.1941877	D

<input type="radio"/>	GO:0009889	5,4	regulation of biosynthetic process	69	0.0107	2	0.0063	0.1929618	D
<input type="radio"/>	GO:0030447	3	filamentous growth	94	0.0145	4	0.0125	0.1915336	D
<input type="radio"/>	GO:0030010	7,4,8	establishment of cell polarity	103	0.0159	5	0.0157	0.1812033	D
<input type="radio"/>	GO:0030437	7,6	sporulation (sensu Fungi)	108	0.0167	5	0.0157	0.1792082	D
<input type="radio"/>	GO:0048622	6,5	reproductive sporulation	108	0.0167	5	0.0157	0.1792082	D
<input type="radio"/>	GO:0051168	9,7,8	nuclear export	102	0.0158	4	0.0125	0.1779919	D
<input type="radio"/>	GO:0016049	5,3,7,8	cell growth	102	0.0158	4	0.0125	0.1779919	D
<input type="radio"/>	GO:0009117	5	nucleotide metabolic process	111	0.0171	5	0.0157	0.1770431	D
<input type="radio"/>	GO:0006970	4	response to osmotic stress	89	0.0137	3	0.0094	0.1765073	D
<input type="radio"/>	GO:0007163	6,3,7	establishment and/or maintenance of cell polarity	115	0.0178	5	0.0157	0.1731591	D
<input type="radio"/>	GO:0009628	3	response to abiotic stimulus	117	0.0181	5	0.0157	0.1708338	D
<input type="radio"/>	GO:0007127	9,7,6,8,5	meiosis I	75	0.0116	2	0.0063	0.1683173	D
<input type="radio"/>	GO:0006310	6	DNA recombination	122	0.0188	6	0.0188	0.1662882	D
<input type="radio"/>	GO:0019725	5,3	cellular homeostasis	128	0.0198	6	0.0188	0.1647623	D
<input type="radio"/>	GO:0051169	7,5,6	nuclear transport	129	0.0199	6	0.0188	0.1642793	D
<input type="radio"/>	GO:0006913	8,6,7	nucleocytoplasmic transport	129	0.0199	6	0.0188	0.1642793	D
<input type="radio"/>	GO:0030435	5	sporulation	123	0.0190	5	0.0157	0.1625619	D
<input type="radio"/>	GO:0007067	8,6,7,5	mitosis	127	0.0196	5	0.0157	0.1561618	D
<input type="radio"/>	GO:0000087	7,5,6	M phase of mitotic cell cycle	129	0.0199	5	0.0157	0.1527524	D
<input type="radio"/>	GO:0008361	4,6,7	regulation of cell size	129	0.0199	5	0.0157	0.1527524	D
<input type="radio"/>	GO:0001510	7	RNA methylation	60	0.0093	1	0.0031	0.1493841	D
<input type="radio"/>	GO:0006725	4	aromatic compound metabolic process	60	0.0093	1	0.0031	0.1493841	D
<input type="radio"/>	GO:0008380	7	RNA splicing	132	0.0204	5	0.0157	0.1474267	D
<input type="radio"/>	GO:0000226	7	microtubule cytoskeleton organization and biogenesis	81	0.0125	2	0.0063	0.1448792	D
<input type="radio"/>	GO:0051726	5,4	regulation of cell cycle	167	0.0258	8	0.0251	0.1443915	D
<input type="radio"/>	GO:0000074	6,5	regulation of progression through cell cycle	167	0.0258	8	0.0251	0.1443915	D
<input type="radio"/>	GO:0050801	6	ion homeostasis	119	0.0184	4	0.0125	0.1403605	D
<input type="radio"/>	GO:0007059	3	chromosome segregation	119	0.0184	4	0.0125	0.1403605	D
<input type="radio"/>	GO:0043543	7	protein amino acid acylation	62	0.0096	1	0.0031	0.1394400	D
<input type="radio"/>	GO:0055080	7	cation homeostasis	102	0.0158	3	0.0094	0.1378920	D
<input type="radio"/>	GO:0030003	8,6	cellular cation homeostasis	102	0.0158	3	0.0094	0.1378920	D
<input type="radio"/>	GO:0022414	3,2	reproductive process	183	0.0283	9	0.0282	0.1370617	D
<input type="radio"/>	GO:0048878	5	chemical homeostasis	121	0.0187	4	0.0125	0.1356504	D
<input type="radio"/>	GO:0016310	6	phosphorylation	155	0.0239	6	0.0188	0.1350620	D
<input type="radio"/>	GO:0006338	9	chromatin remodeling	155	0.0239	6	0.0188	0.1350620	D
<input type="radio"/>	GO:0048869	3	cellular developmental process	173	0.0267	7	0.0219	0.1316443	D
<input type="radio"/>	GO:0030154	4	cell differentiation	173	0.0267	7	0.0219	0.1316443	D
<input type="radio"/>	GO:0042273	6,5	ribosomal large subunit biogenesis and assembly	64	0.0099	1	0.0031	0.1300182	D
<input type="radio"/>	GO:0006897	6,5	endocytosis	86	0.0133	2	0.0063	0.1267400	D
<input type="radio"/>	GO:0006623	9,8,7,6	protein targeting to vacuole	67	0.0103	1	0.0031	0.1168464	D
<input type="radio"/>	GO:0065008	3	regulation of biological quality	260	0.0401	12	0.0376	0.1160279	D
<input type="radio"/>	GO:0000375	8	RNA splicing, via transesterification reactions	110	0.0170	3	0.0094	0.1153715	D
<input type="radio"/>	GO:0016569	9	covalent chromatin modification	91	0.0141	2	0.0063	0.1100923	D
<input type="radio"/>	GO:0016570	10,8	histone modification	91	0.0141	2	0.0063	0.1100923	D

<input type="checkbox"/>	GO:0051329	7,5,6	interphase of mitotic cell cycle	112	0.0173	3	0.0094	0.1100432	D
<input type="checkbox"/>	GO:0051325	6,5	interphase	112	0.0173	3	0.0094	0.1100432	D
<input type="checkbox"/>	GO:0006892	8,6,5,7	post-Golgi vesicle-mediated transport	69	0.0107	1	0.0031	0.1086883	D
<input type="checkbox"/>	GO:0044265	5	cellular macromolecule catabolic process	314	0.0485	14	0.0439	0.1024580	D
<input type="checkbox"/>	GO:0055082	6,4	cellular chemical homeostasis	115	0.0178	3	0.0094	0.1023163	D
<input type="checkbox"/>	GO:0006873	7,5	cellular ion homeostasis	115	0.0178	3	0.0094	0.1023163	D
<input type="checkbox"/>	GO:0006397	7	mRNA processing	157	0.0242	5	0.0157	0.0996178	D
<input type="checkbox"/>	GO:0010324	5	membrane invagination	96	0.0148	2	0.0063	0.0950289	D
<input type="checkbox"/>	GO:0065003	5,4	macromolecular complex assembly	328	0.0506	14	0.0439	0.0938225	D
<input type="checkbox"/>	GO:0009057	4	macromolecule catabolic process	345	0.0533	15	0.0470	0.0937703	D
<input type="checkbox"/>	GO:0040007	2	growth	141	0.0218	4	0.0125	0.0909946	D
<input type="checkbox"/>	GO:0009653	4,3	anatomical structure morphogenesis	248	0.0383	9	0.0282	0.0821160	D
<input type="checkbox"/>	GO:0032989	4,5	cellular structure morphogenesis	248	0.0383	9	0.0282	0.0821160	D
<input type="checkbox"/>	GO:0048856	3	anatomical structure development	248	0.0383	9	0.0282	0.0821160	D
<input type="checkbox"/>	GO:0000902	5,6	cell morphogenesis	248	0.0383	9	0.0282	0.0821160	D
<input type="checkbox"/>	GO:0007017	6	microtubule-based process	101	0.0156	2	0.0063	0.0815607	D
<input type="checkbox"/>	GO:0016044	4	membrane organization and biogenesis	188	0.0290	6	0.0188	0.0815249	D
<input type="checkbox"/>	GO:0051276	5	chromosome organization and biogenesis	572	0.0883	27	0.0846	0.0796483	D
<input type="checkbox"/>	GO:0016071	6	mRNA metabolic process	210	0.0324	7	0.0219	0.0794229	D
<input type="checkbox"/>	GO:0007001	6	chromosome organization and biogenesis (sensu Eukaryota)	567	0.0876	26	0.0815	0.0770353	D
<input type="checkbox"/>	GO:0000377	9	RNA splicing, via transesterification reactions with bulged adenosine as nucleophile	103	0.0159	2	0.0063	0.0766111	D
<input type="checkbox"/>	GO:0022607	4	cellular component assembly	471	0.0727	20	0.0627	0.0722273	D
<input type="checkbox"/>	GO:0044275	6	cellular carbohydrate catabolic process	80	0.0124	1	0.0031	0.0719503	D
<input type="checkbox"/>	GO:0016052	5	carbohydrate catabolic process	80	0.0124	1	0.0031	0.0719503	D
<input type="checkbox"/>	GO:0006412	6,5	translation	688	0.1062	32	0.1003	0.0713169	D
<input type="checkbox"/>	GO:0006259	5	DNA metabolic process	523	0.0808	22	0.0690	0.0646104	D
<input type="checkbox"/>	GO:0016568	8	chromatin modification	223	0.0344	7	0.0219	0.0625870	D
<input type="checkbox"/>	GO:0000278	4	mitotic cell cycle	266	0.0411	9	0.0282	0.0620832	D
<input type="checkbox"/>	GO:0000154	7,8	rRNA modification	85	0.0131	1	0.0031	0.0592362	D
<input type="checkbox"/>	GO:0007034	7,5,6	vacuolar transport	114	0.0176	2	0.0063	0.0535676	D
<input type="checkbox"/>	GO:0006325	7	establishment and/or maintenance of chromatin architecture	253	0.0391	8	0.0251	0.0533263	D
<input type="checkbox"/>	GO:0006323	6	DNA packaging	253	0.0391	8	0.0251	0.0533263	D
<input type="checkbox"/>	GO:0032502	2	developmental process	436	0.0673	16	0.0502	0.0441150	D
<input type="checkbox"/>	GO:0043283	4	biopolymer metabolic process	2230	0.3443	103	0.3229	0.0346139	D
<input type="checkbox"/>	GO:0022402	4,3	cell cycle process	439	0.0678	15	0.0470	0.0300844	D
<input type="checkbox"/>	GO:0000398	8,10	nuclear mRNA splicing, via spliceosome	102	0.0158	1	0.0031	0.0298174	D
<input type="checkbox"/>	GO:0000279	6,5	M phase	258	0.0398	7	0.0219	0.0291843	D
<input type="checkbox"/>	GO:0006996	4	organelle organization and biogenesis	1388	0.2143	60	0.1881	0.0288049	D
<input type="checkbox"/>	GO:0032196	3	transposition	105	0.0162	1	0.0031	0.0263250	D
<input type="checkbox"/>	GO:0009451	6	RNA modification	139	0.0215	2	0.0063	0.0221719	D
<input type="checkbox"/>	GO:0007049	3	cell cycle	458	0.0707	15	0.0470	0.0214665	D
<input type="checkbox"/>	GO:0022618	6,5	protein-RNA complex assembly	144	0.0222	2	0.0063	0.0184134	D
<input type="checkbox"/>	GO:0022403	5,4	cell cycle phase	353	0.0545	10	0.0313	0.0169237	D
<input type="checkbox"/>	GO:0051321	4	meiotic cell cycle	148	0.0229	2	0.0063	0.0158406	D

<input type="radio"/>	GO:0051327	7,5,6	M phase of meiotic cell cycle	148	0.0229	2	0.0063	0.0158406	D
<input type="radio"/>	GO:0007126	8,6,7,5	meiosis	148	0.0229	2	0.0063	0.0158406	D
<input type="radio"/>	GO:0006396	6	RNA processing	491	0.0758	15	0.0470	0.0111405	D
<input type="radio"/>	GO:0016070	5	RNA metabolic process	1058	0.1634	40	0.1254	0.0103766	D
<input type="radio"/>	GO:0006139	4	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	1532	0.2366	61	0.1912	0.0078489	D
<input type="radio"/>	GO:0006364	6,7	rRNA processing	249	0.0384	4	0.0125	0.0034824	D
<input type="radio"/>	GO:0016072	6	rRNA metabolic process	256	0.0395	4	0.0125	0.0027067	D
<input type="radio"/>	GO:0043284	5	biopolymer biosynthetic process	354	0.0547	7	0.0219	0.0018761	D
<input type="radio"/>	GO:0042254	5	ribosome biogenesis and assembly	410	0.0633	7	0.0219	0.0002788	D
<input type="radio"/>	GO:0022613	4	ribonucleoprotein complex biogenesis and assembly	483	0.0746	7	0.0219	1.829757E-05	D
<input type="radio"/>	GO:0006414	7,6	translational elongation	313	0.0483	2	0.0063	1.316062E-05	D