

GO-Stats Results

Your dataset contains **186** 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:0006139	4	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	1532	0.2366	82	0.4409	2.510383E-10	E
<input type="radio"/> GO:0009987	2	cellular process	4654	0.7187	168	0.9032	2.889861E-10	E
<input type="radio"/> GO:0006259	5	DNA metabolic process	523	0.0808	38	0.2043	3.854371E-08	E
<input type="radio"/> GO:0008152	2	metabolic process	3516	0.5429	136	0.7312	3.961568E-08	E
<input type="radio"/> GO:0016070	5	RNA metabolic process	1058	0.1634	59	0.3172	6.393940E-08	E
<input type="radio"/> GO:0044238	3	primary metabolic process	3247	0.5014	128	0.6882	7.238003E-08	E
<input type="radio"/> GO:0044237	3	cellular metabolic process	3403	0.5255	132	0.7097	8.862501E-08	E
<input type="radio"/> GO:0016043	3	cellular component organization and biogenesis	2264	0.3496	98	0.5269	2.061521E-07	E
<input type="radio"/> GO:0006325	7	establishment and/or maintenance of chromatin architecture	253	0.0391	23	0.1237	5.604353E-07	E
<input type="radio"/> GO:0006323	6	DNA packaging	253	0.0391	23	0.1237	5.604353E-07	E
<input type="radio"/> GO:0007001	6	chromosome organization and biogenesis (sensu Eukaryota)	567	0.0876	37	0.1989	8.443296E-07	E
<input type="radio"/> GO:0016568	8	chromatin modification	223	0.0344	21	0.1129	1.006333E-06	E
<input type="radio"/> GO:0051276	5	chromosome organization and biogenesis	572	0.0883	37	0.1989	1.039381E-06	E
<input type="radio"/> GO:0043283	4	biopolymer metabolic process	2230	0.3443	94	0.5054	1.720219E-06	E
<input type="radio"/> GO:0043170	3	macromolecule metabolic process	2841	0.4387	112	0.6022	2.041164E-06	E
<input type="radio"/> GO:0006996	4	organelle organization and biogenesis	1388	0.2143	65	0.3495	6.078712E-06	E
<input type="radio"/> GO:0016071	6	mRNA metabolic process	210	0.0324	18	0.0968	2.115842E-05	E
<input type="radio"/> GO:0006338	9	chromatin remodeling	155	0.0239	14	0.0753	9.869394E-05	E
<input type="radio"/> GO:0065007	2	biological regulation	948	0.1464	45	0.2419	0.0001607	E
<input type="radio"/> GO:0006401	6	RNA catabolic process	74	0.0114	9	0.0484	0.0001982	E
<input type="radio"/> GO:0006402	7	mRNA catabolic process	60	0.0093	8	0.0430	0.0002380	E
<input type="radio"/> GO:0065008	3	regulation of biological quality	260	0.0401	18	0.0968	0.0002928	E

<input type="radio"/>	GO:0006261	7	DNA-dependent DNA replication	97	0.0150	10	0.0538	0.0003372	E
<input type="radio"/>	GO:0006260	6	DNA replication	117	0.0181	11	0.0591	0.0003781	E
<input type="radio"/>	GO:0006396	6	RNA processing	491	0.0758	27	0.1452	0.0004138	E
<input type="radio"/>	GO:0006183	9,10	GTP biosynthetic process	2	0.0003	2	0.0108	0.0008206	E
<input type="radio"/>	GO:0046039	9	GTP metabolic process	2	0.0003	2	0.0108	0.0008206	E
<input type="radio"/>	GO:0051169	7,5,6	nuclear transport	129	0.0199	11	0.0591	0.0008291	E
<input type="radio"/>	GO:0006913	8,6,7	nucleocytoplasmic transport	129	0.0199	11	0.0591	0.0008291	E
<input type="radio"/>	GO:0032774	6	RNA biosynthetic process	524	0.0809	27	0.1452	0.0010301	E
<input type="radio"/>	GO:0022607	4	cellular component assembly	471	0.0727	25	0.1344	0.0010479	E
<input type="radio"/>	GO:0042592	4	homeostatic process	134	0.0207	11	0.0591	0.0011139	E
<input type="radio"/>	GO:0006620	10,9,8,7,6	posttranslational protein targeting to membrane	8	0.0012	3	0.0161	0.0011316	E
<input type="radio"/>	GO:0043543	7	protein amino acid acylation	62	0.0096	7	0.0376	0.0015063	E
<input type="radio"/>	GO:0050801	6	ion homeostasis	119	0.0184	10	0.0538	0.0015401	E
<input type="radio"/>	GO:0000184	8	mRNA catabolic process, nonsense-mediated decay	9	0.0014	3	0.0161	0.0016493	E
<input type="radio"/>	GO:0048878	5	chemical homeostasis	121	0.0187	10	0.0538	0.0017314	E
<input type="radio"/>	GO:0000398	8,10	nuclear mRNA splicing, via spliceosome	102	0.0158	9	0.0484	0.0018698	E
<input type="radio"/>	GO:0055080	7	cation homeostasis	102	0.0158	9	0.0484	0.0018698	E
<input type="radio"/>	GO:0030003	8,6	cellular cation homeostasis	102	0.0158	9	0.0484	0.0018698	E
<input type="radio"/>	GO:0006351	7,6	transcription, DNA-dependent	522	0.0806	26	0.1398	0.0019286	E
<input type="radio"/>	GO:0006473	8	protein amino acid acetylation	48	0.0074	6	0.0323	0.0019384	E
<input type="radio"/>	GO:0000377	9	RNA splicing, via transesterification reactions with bulged adenosine as nucleophile	103	0.0159	9	0.0484	0.0019919	E
<input type="radio"/>	GO:0051327	7,5,6	M phase of meiotic cell cycle	148	0.0229	11	0.0591	0.0023389	E
<input type="radio"/>	GO:0007126	8,6,7,5	meiosis	148	0.0229	11	0.0591	0.0023389	E
<input type="radio"/>	GO:0051321	4	meiotic cell cycle	148	0.0229	11	0.0591	0.0023389	E
<input type="radio"/>	GO:0050896	2	response to stimulus	763	0.1178	34	0.1828	0.0025328	E
<input type="radio"/>	GO:0019725	5,3	cellular homeostasis	128	0.0198	10	0.0538	0.0025500	E
<input type="radio"/>	GO:0031323	5,4	regulation of cellular metabolic process	507	0.0783	25	0.1344	0.0025951	E
<input type="radio"/>	GO:0006350	5	transcription	567	0.0876	27	0.1452	0.0028381	E
<input type="radio"/>	GO:0000375	8	RNA splicing, via transesterification reactions	110	0.0170	9	0.0484	0.0030256	E
<input type="radio"/>	GO:0032200	7	telomere organization and biogenesis	274	0.0423	16	0.0860	0.0030938	E
<input type="radio"/>	GO:0000723	8	telomere maintenance	274	0.0423	16	0.0860	0.0030938	E
<input type="radio"/>	GO:0008380	7	RNA splicing	132	0.0204	10	0.0538	0.0031346	E
<input type="radio"/>	GO:0016569	9	covalent chromatin modification	91	0.0141	8	0.0430	0.0032974	E
<input type="radio"/>	GO:0016570	10,8	histone modification	91	0.0141	8	0.0430	0.0032974	E
<input type="radio"/>	GO:0006397	7	mRNA processing	157	0.0242	11	0.0591	0.0035566	E
<input type="radio"/>	GO:0006352	7,8,6	transcription initiation	55	0.0085	6	0.0323	0.0037533	E
<input type="radio"/>	GO:0016072	6	rRNA metabolic process	256	0.0395	15	0.0806	0.0039102	E
<input type="radio"/>	GO:0065004	6,5	protein-DNA complex assembly	74	0.0114	7	0.0376	0.0039234	E
<input type="radio"/>	GO:0055082	6,4	cellular chemical homeostasis	115	0.0178	9	0.0484	0.0039794	E
<input type="radio"/>	GO:0006873	7,5	cellular ion homeostasis	115	0.0178	9	0.0484	0.0039794	E
<input type="radio"/>	GO:0045814	5	negative regulation of gene expression, epigenetic	95	0.0147	8	0.0430	0.0042117	E
<input type="radio"/>	GO:0006342	10,6,7,11,9	chromatin silencing	95	0.0147	8	0.0430	0.0042117	E
<input type="radio"/>	GO:0016458	5	gene silencing	95	0.0147	8	0.0430	0.0042117	E

<input type="radio"/>	GO:0031507	6,10	heterochromatin formation	95	0.0147	8	0.0430	0.0042117	E
<input type="radio"/>	GO:0016573	11,9	histone acetylation	40	0.0062	5	0.0269	0.0045083	E
<input type="radio"/>	GO:0050794	4,3	regulation of cellular process	738	0.1140	32	0.1720	0.0046511	E
<input type="radio"/>	GO:0006333	8	chromatin assembly or disassembly	119	0.0184	9	0.0484	0.0048891	E
<input type="radio"/>	GO:0019222	4,3	regulation of metabolic process	538	0.0831	25	0.1344	0.0050667	E
<input type="radio"/>	GO:0040029	4	regulation of gene expression, epigenetic	100	0.0154	8	0.0430	0.0055970	E
<input type="radio"/>	GO:0046907	6,4,5	intracellular transport	545	0.0842	25	0.1344	0.0058168	E
<input type="radio"/>	GO:0006950	3	response to stress	488	0.0754	23	0.1237	0.0058564	E
<input type="radio"/>	GO:0022403	5,4	cell cycle phase	353	0.0545	18	0.0968	0.0064883	E
<input type="radio"/>	GO:0033036	3	macromolecule localization	382	0.0590	19	0.1022	0.0067251	E
<input type="radio"/>	GO:0050789	3	regulation of biological process	761	0.1175	32	0.1720	0.0067742	E
<input type="radio"/>	GO:0000054	10,11,6,8,9	ribosome export from nucleus	28	0.0043	4	0.0215	0.0068000	E
<input type="radio"/>	GO:0051641	4,3	cellular localization	642	0.0991	28	0.1505	0.0068709	E
<input type="radio"/>	GO:0031497	5,9	chromatin assembly	104	0.0161	8	0.0430	0.0069175	E
<input type="radio"/>	GO:0031324	6,5	negative regulation of cellular metabolic process	198	0.0306	12	0.0645	0.0069290	E
<input type="radio"/>	GO:0006364	6,7	rRNA processing	249	0.0384	14	0.0753	0.0069624	E
<input type="radio"/>	GO:0019219	6,5	regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	440	0.0679	21	0.1129	0.0070311	E
<input type="radio"/>	GO:0030005	9,7	cellular di-, tri-valent inorganic cation homeostasis	64	0.0099	6	0.0323	0.0075141	E
<input type="radio"/>	GO:0055066	8	di-, tri-valent inorganic cation homeostasis	64	0.0099	6	0.0323	0.0075141	E
<input type="radio"/>	GO:0000114	10,8,9,5,7,4	G1-specific transcription in mitotic cell cycle	15	0.0023	3	0.0161	0.0075198	E
<input type="radio"/>	GO:0031365	8	N-terminal protein amino acid modification	15	0.0023	3	0.0161	0.0075198	E
<input type="radio"/>	GO:0018409	9	peptide or protein amino-terminal blocking	15	0.0023	3	0.0161	0.0075198	E
<input type="radio"/>	GO:0046688	6	response to copper ion	5	0.0008	2	0.0108	0.0075260	E
<input type="radio"/>	GO:0006885	7	regulation of pH	29	0.0045	4	0.0215	0.0076653	E
<input type="radio"/>	GO:0045934	7,6	negative regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	179	0.0276	11	0.0591	0.0084773	E
<input type="radio"/>	GO:0006417	7,6,5	regulation of translation	47	0.0073	5	0.0269	0.0086065	E
<input type="radio"/>	GO:0045892	9,8	negative regulation of transcription, DNA-dependent	156	0.0241	10	0.0538	0.0089482	E
<input type="radio"/>	GO:0000279	6,5	M phase	258	0.0398	14	0.0753	0.0090122	E
<input type="radio"/>	GO:0009892	5,4	negative regulation of metabolic process	208	0.0321	12	0.0645	0.0096057	E
<input type="radio"/>	GO:0006974	4	response to DNA damage stimulus	234	0.0361	13	0.0699	0.0096279	E
<input type="radio"/>	GO:0007049	3	cell cycle	458	0.0707	21	0.1129	0.0100953	E
<input type="radio"/>	GO:0051649	5,3,4	establishment of cellular localization	606	0.0936	26	0.1398	0.0101837	E
<input type="radio"/>	GO:0006271	8,7	DNA strand elongation during DNA replication	32	0.0049	4	0.0215	0.0106501	E
<input type="radio"/>	GO:0022616	6	DNA strand elongation	32	0.0049	4	0.0215	0.0106501	E
<input type="radio"/>	GO:0017148	8,7,6	negative regulation of protein biosynthetic process	6	0.0009	2	0.0108	0.0109680	E
<input type="radio"/>	GO:0031327	7,6	negative regulation of cellular biosynthetic process	6	0.0009	2	0.0108	0.0109680	E
<input type="radio"/>	GO:0016481	8,7	negative regulation of transcription	162	0.0250	10	0.0538	0.0111391	E
<input type="radio"/>	GO:0042254	5	ribosome biogenesis and assembly	410	0.0633	19	0.1022	0.0122024	E
<input type="radio"/>	GO:0009719	3	response to endogenous stimulus	243	0.0375	13	0.0699	0.0123661	E
<input type="radio"/>	GO:0006273	9,8	lagging strand elongation	18	0.0028	3	0.0161	0.0123721	E

<input type="checkbox"/>	GO:0010038	5	response to metal ion	18	0.0028	3	0.0161	0.0123721	E
<input type="checkbox"/>	GO:0065003	5,4	macromolecular complex assembly	328	0.0506	16	0.0860	0.0131301	E
<input type="checkbox"/>	GO:0043331	4	response to dsRNA	7	0.0011	2	0.0108	0.0149186	E
<input type="checkbox"/>	GO:0043330	5,6	response to exogenous dsRNA	7	0.0011	2	0.0108	0.0149186	E
<input type="checkbox"/>	GO:0051707	3,4	response to other organism	7	0.0011	2	0.0108	0.0149186	E
<input type="checkbox"/>	GO:0019722	7	calcium-mediated signaling	7	0.0011	2	0.0108	0.0149186	E
<input type="checkbox"/>	GO:0009615	4,5	response to virus	7	0.0011	2	0.0108	0.0149186	E
<input type="checkbox"/>	GO:0051252	7,6	regulation of RNA metabolic process	36	0.0056	4	0.0215	0.0155562	E
<input type="checkbox"/>	GO:0022613	4	ribonucleoprotein complex biogenesis and assembly	483	0.0746	21	0.1129	0.0157397	E
<input type="checkbox"/>	GO:0006826	7,8,9	iron ion transport	20	0.0031	3	0.0161	0.0163188	E
<input type="checkbox"/>	GO:0051168	9,7,8	nuclear export	102	0.0158	7	0.0376	0.0181676	E
<input type="checkbox"/>	GO:0006383	8,7	transcription from RNA polymerase III promoter	38	0.0059	4	0.0215	0.0184074	E
<input type="checkbox"/>	GO:0055072	9	iron ion homeostasis	38	0.0059	4	0.0215	0.0184074	E
<input type="checkbox"/>	GO:0006879	10,8	cellular iron ion homeostasis	38	0.0059	4	0.0215	0.0184074	E
<input type="checkbox"/>	GO:0033212	11,9	iron assimilation	8	0.0012	2	0.0108	0.0193257	E
<input type="checkbox"/>	GO:0009890	6,5	negative regulation of biosynthetic process	8	0.0012	2	0.0108	0.0193257	E
<input type="checkbox"/>	GO:0022402	4,3	cell cycle process	439	0.0678	19	0.1022	0.0204306	E
<input type="checkbox"/>	GO:0006348	11,7,8,12,10	chromatin silencing at telomere	60	0.0093	5	0.0269	0.0211324	E
<input type="checkbox"/>	GO:0031509	7,11	telomeric heterochromatin formation	60	0.0093	5	0.0269	0.0211324	E
<input type="checkbox"/>	GO:0000003	2	reproduction	323	0.0499	15	0.0806	0.0213471	E
<input type="checkbox"/>	GO:0042221	3	response to chemical stimulus	382	0.0590	17	0.0914	0.0214158	E
<input type="checkbox"/>	GO:0048308	5	organelle inheritance	40	0.0062	4	0.0215	0.0215197	E
<input type="checkbox"/>	GO:0048523	5,4	negative regulation of cellular process	239	0.0369	12	0.0645	0.0221366	E
<input type="checkbox"/>	GO:0045184	3,4,5	establishment of protein localization	296	0.0457	14	0.0753	0.0221937	E
<input type="checkbox"/>	GO:0007534	6,8,7	gene conversion at mating-type locus	23	0.0036	3	0.0161	0.0232558	E
<input type="checkbox"/>	GO:0006629	4	lipid metabolic process	242	0.0374	12	0.0645	0.0237021	E
<input type="checkbox"/>	GO:0048519	4	negative regulation of biological process	242	0.0374	12	0.0645	0.0237021	E
<input type="checkbox"/>	GO:0006474	10,9	N-terminal protein amino acid acetylation	9	0.0014	2	0.0108	0.0241404	E
<input type="checkbox"/>	GO:0008104	4	protein localization	330	0.0510	15	0.0806	0.0243428	E
<input type="checkbox"/>	GO:0006886	7,5,6	intracellular protein transport	274	0.0423	13	0.0699	0.0254989	E
<input type="checkbox"/>	GO:0016575	11,9	histone deacetylation	24	0.0037	3	0.0161	0.0258243	E
<input type="checkbox"/>	GO:0051452	12,9,10	cellular pH reduction	24	0.0037	3	0.0161	0.0258243	E
<input type="checkbox"/>	GO:0010035	4	response to inorganic substance	24	0.0037	3	0.0161	0.0258243	E
<input type="checkbox"/>	GO:0006890	8,6,5,7	retrograde vesicle-mediated transport, Golgi to ER	24	0.0037	3	0.0161	0.0258243	E
<input type="checkbox"/>	GO:0045851	8	pH reduction	24	0.0037	3	0.0161	0.0258243	E
<input type="checkbox"/>	GO:0007035	13,10,6,11	vacuolar acidification	24	0.0037	3	0.0161	0.0258243	E
<input type="checkbox"/>	GO:0006281	6,5	DNA repair	193	0.0298	10	0.0538	0.0279156	E
<input type="checkbox"/>	GO:0051704	2	multi-organism process	139	0.0215	8	0.0430	0.0279711	E
<input type="checkbox"/>	GO:0006289	7,6	nucleotide-excision repair	44	0.0068	4	0.0215	0.0284994	E
<input type="checkbox"/>	GO:0006367	8,9,7	transcription initiation from RNA polymerase II promoter	44	0.0068	4	0.0215	0.0284994	E
<input type="checkbox"/>	GO:0030641	10,8	cellular hydrogen ion homeostasis	25	0.0039	3	0.0161	0.0285135	E
<input type="checkbox"/>	GO:0051453	11,8,9	regulation of cellular pH	25	0.0039	3	0.0161	0.0285135	E
<input type="checkbox"/>	GO:0015031	4,5,6	protein transport	280	0.0432	13	0.0699	0.0286947	E
<input type="checkbox"/>	GO:0051253	8,7	negative regulation of RNA metabolic process	1	0.0002	1	0.0054	0.0287214	E

<input type="radio"/>	GO:0048025	10,9,12	negative regulation of nuclear mRNA splicing, via spliceosome	1	0.0002	1	0.0054	0.0287214	E
<input type="radio"/>	GO:0030635	8	acetate derivative metabolic process	1	0.0002	1	0.0054	0.0287214	E
<input type="radio"/>	GO:0032218	5,6	riboflavin transport	1	0.0002	1	0.0054	0.0287214	E
<input type="radio"/>	GO:0042357	6,7	thiamin diphosphate metabolic process	1	0.0002	1	0.0054	0.0287214	E
<input type="radio"/>	GO:0006419	9,8,10,7	alanyl-tRNA aminoacylation	1	0.0002	1	0.0054	0.0287214	E
<input type="radio"/>	GO:0050686	9,8	negative regulation of mRNA processing	1	0.0002	1	0.0054	0.0287214	E
<input type="radio"/>	GO:0006266	6	DNA ligation	1	0.0002	1	0.0054	0.0287214	E
<input type="radio"/>	GO:0009237	5	siderophore metabolic process	1	0.0002	1	0.0054	0.0287214	E
<input type="radio"/>	GO:0009229	7,8	thiamin diphosphate biosynthetic process	1	0.0002	1	0.0054	0.0287214	E
<input type="radio"/>	GO:0006657	10,9,11	CDP-choline pathway	1	0.0002	1	0.0054	0.0287214	E
<input type="radio"/>	GO:0000040	8,9,10	low affinity iron ion transport	1	0.0002	1	0.0054	0.0287214	E
<input type="radio"/>	GO:0030636	8,9	acetate derivative biosynthetic process	1	0.0002	1	0.0054	0.0287214	E
<input type="radio"/>	GO:0042255	7,6	ribosome assembly	66	0.0102	5	0.0269	0.0291224	E
<input type="radio"/>	GO:0030846	10,9	transcription termination from Pol II promoter, RNA polymerase(A) coupled	10	0.0015	2	0.0108	0.0293170	E
<input type="radio"/>	GO:0051179	2	localization	1051	0.1623	37	0.1989	0.0303820	E
<input type="radio"/>	GO:0006312	7	mitotic recombination	45	0.0069	4	0.0215	0.0303948	E
<input type="radio"/>	GO:0006366	8,7	transcription from RNA polymerase II promoter	343	0.0530	15	0.0806	0.0304788	E
<input type="radio"/>	GO:0031326	6,5	regulation of cellular biosynthetic process	67	0.0103	5	0.0269	0.0305823	E
<input type="radio"/>	GO:0006476	8	protein amino acid deacetylation	26	0.0040	3	0.0161	0.0313182	E
<input type="radio"/>	GO:0006605	8,6,7	protein targeting	258	0.0398	12	0.0645	0.0330423	E
<input type="radio"/>	GO:0009889	5,4	regulation of biosynthetic process	69	0.0107	5	0.0269	0.0336065	E
<input type="radio"/>	GO:0000080	7,8,6	G1 phase of mitotic cell cycle	27	0.0042	3	0.0161	0.0342334	E
<input type="radio"/>	GO:0051318	6,7,5	G1 phase	27	0.0042	3	0.0161	0.0342334	E
<input type="radio"/>	GO:0030447	3	filamentous growth	94	0.0145	6	0.0323	0.0346631	E
<input type="radio"/>	GO:0000055	11,12,7,9,10	ribosomal large subunit export from nucleus	11	0.0017	2	0.0108	0.0348122	E
<input type="radio"/>	GO:0006384	8,9,7	transcription initiation from RNA polymerase III promoter	11	0.0017	2	0.0108	0.0348122	E
<input type="radio"/>	GO:0006979	4	response to oxidative stress	71	0.0110	5	0.0269	0.0367645	E
<input type="radio"/>	GO:0006310	6	DNA recombination	122	0.0188	7	0.0376	0.0372462	E
<input type="radio"/>	GO:0006906	6,5	vesicle fusion	28	0.0043	3	0.0161	0.0372534	E
<input type="radio"/>	GO:0018193	7	peptidyl-amino acid modification	28	0.0043	3	0.0161	0.0372534	E
<input type="radio"/>	GO:0051246	5,4	regulation of protein metabolic process	72	0.0111	5	0.0269	0.0383916	E
<input type="radio"/>	GO:0006464	6	protein modification process	520	0.0803	20	0.1075	0.0398013	E
<input type="radio"/>	GO:0007533	5,7,6	mating type switching	29	0.0045	3	0.0161	0.0403726	E
<input type="radio"/>	GO:0006284	7,6	base-excision repair	12	0.0019	2	0.0108	0.0405857	E
<input type="radio"/>	GO:0051170	9,7,8	nuclear import	50	0.0077	4	0.0215	0.0406969	E
<input type="radio"/>	GO:0006606	9,10,7,8,6	protein import into nucleus	50	0.0077	4	0.0215	0.0406969	E
<input type="radio"/>	GO:0007127	9,7,6,8,5	meiosis I	75	0.0116	5	0.0269	0.0434546	E
<input type="radio"/>	GO:0043488	9,8,7	regulation of mRNA stability	30	0.0046	3	0.0161	0.0435851	E
<input type="radio"/>	GO:0043487	8,7	regulation of RNA stability	30	0.0046	3	0.0161	0.0435851	E
<input type="radio"/>	GO:0051234	2,3	establishment of localization	1004	0.1550	34	0.1828	0.0447824	E
<input type="radio"/>	GO:0008361	4,6,7	regulation of cell size	129	0.0199	7	0.0376	0.0454967	E
<input type="radio"/>	GO:0008610	5,4,6	lipid biosynthetic process	129	0.0199	7	0.0376	0.0454967	E
<input type="radio"/>	GO:0016049	5,3,7,8	cell growth	102	0.0158	6	0.0323	0.0455926	E
<input type="radio"/>	GO:0006810	3,4	transport	981	0.1515	33	0.1774	0.0480418	E

<input type="checkbox"/>	GO:0019538	4	protein metabolic process	1547	0.2389	49	0.2634	0.0493412	E
<input type="checkbox"/>	GO:0016126	6,7,8	sterol biosynthetic process	32	0.0049	3	0.0161	0.0502662	E
<input type="checkbox"/>	GO:0006694	6,5,7	steroid biosynthetic process	32	0.0049	3	0.0161	0.0502662	E
<input type="checkbox"/>	GO:0042257	8,7	ribosomal subunit assembly	55	0.0085	4	0.0215	0.0522015	E
<input type="checkbox"/>	GO:0000463	8,9	maturation of LSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	14	0.0022	2	0.0108	0.0528184	E
<input type="checkbox"/>	GO:0000028	9,7,8,6	ribosomal small subunit assembly and maintenance	14	0.0022	2	0.0108	0.0528184	E
<input type="checkbox"/>	GO:0000470	7,8	maturation of LSU-rRNA	14	0.0022	2	0.0108	0.0528184	E
<input type="checkbox"/>	GO:0044267	5	cellular protein metabolic process	1498	0.2313	47	0.2527	0.0536181	E
<input type="checkbox"/>	GO:0045047	9,8,7,6,5	protein targeting to ER	33	0.0051	3	0.0161	0.0537226	E
<input type="checkbox"/>	GO:0006611	9,10,7,8	protein export from nucleus	56	0.0086	4	0.0215	0.0546236	E
<input type="checkbox"/>	GO:0045449	7,6	regulation of transcription	386	0.0596	15	0.0806	0.0547882	E
<input type="checkbox"/>	GO:0010043	6	response to zinc ion	2	0.0003	1	0.0054	0.0558016	E
<input type="checkbox"/>	GO:0051488	8	anaphase-promoting complex activation	2	0.0003	1	0.0054	0.0558016	E
<input type="checkbox"/>	GO:0016114	7,6,8,5	terpenoid biosynthetic process	2	0.0003	1	0.0054	0.0558016	E
<input type="checkbox"/>	GO:0046497	8,7	nicotinate nucleotide metabolic process	2	0.0003	1	0.0054	0.0558016	E
<input type="checkbox"/>	GO:0006434	9,8,10,7	seryl-tRNA aminoacylation	2	0.0003	1	0.0054	0.0558016	E
<input type="checkbox"/>	GO:0051598	9,11,8,10,7	meiotic recombination checkpoint	2	0.0003	1	0.0054	0.0558016	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	0.0054	0.0558016	E
<input type="checkbox"/>	GO:0033313	8,7	meiotic cell cycle checkpoint	2	0.0003	1	0.0054	0.0558016	E
<input type="checkbox"/>	GO:0006721	6,7,4	terpenoid metabolic process	2	0.0003	1	0.0054	0.0558016	E
<input type="checkbox"/>	GO:0048309	6	endoplasmic reticulum inheritance	2	0.0003	1	0.0054	0.0558016	E
<input type="checkbox"/>	GO:0032445	8,9	fructose import	2	0.0003	1	0.0054	0.0558016	E
<input type="checkbox"/>	GO:0007128	10,8,7,9,6	meiotic prophase I	2	0.0003	1	0.0054	0.0558016	E
<input type="checkbox"/>	GO:0006269	8,6,7	DNA replication, synthesis of RNA primer	2	0.0003	1	0.0054	0.0558016	E
<input type="checkbox"/>	GO:0033215	12,10	iron assimilation by reduction and transport	2	0.0003	1	0.0054	0.0558016	E
<input type="checkbox"/>	GO:0046037	9	GMP metabolic process	2	0.0003	1	0.0054	0.0558016	E
<input type="checkbox"/>	GO:0051324	7,6,5	prophase	2	0.0003	1	0.0054	0.0558016	E
<input type="checkbox"/>	GO:0015755	7,8	fructose transport	2	0.0003	1	0.0054	0.0558016	E
<input type="checkbox"/>	GO:0051437	8,6,5	positive regulation of ubiquitin ligase activity during mitotic cell cycle	2	0.0003	1	0.0054	0.0558016	E
<input type="checkbox"/>	GO:0019358	9,7,8	nicotinate nucleotide salvage	2	0.0003	1	0.0054	0.0558016	E
<input type="checkbox"/>	GO:0019365	8,6,7	pyridine nucleotide salvage	2	0.0003	1	0.0054	0.0558016	E
<input type="checkbox"/>	GO:0043687	7	post-translational protein modification	388	0.0599	15	0.0806	0.0560064	E
<input type="checkbox"/>	GO:0044260	4	cellular macromolecule metabolic process	1552	0.2397	48	0.2581	0.0568673	E
<input type="checkbox"/>	GO:0015674	6,7	di-, tri-valent inorganic cation transport	34	0.0053	3	0.0161	0.0572480	E
<input type="checkbox"/>	GO:0055067	8	monovalent inorganic cation homeostasis	34	0.0053	3	0.0161	0.0572480	E
<input type="checkbox"/>	GO:0030004	9,7	cellular monovalent inorganic cation homeostasis	34	0.0053	3	0.0161	0.0572480	E
<input type="checkbox"/>	GO:0006355	8,7	regulation of transcription, DNA-dependent	359	0.0554	14	0.0753	0.0585228	E
<input type="checkbox"/>	GO:0007018	8,7,6	microtubule-based movement	15	0.0023	2	0.0108	0.0592090	E
<input type="checkbox"/>	GO:0030473	8,9,6,7	nuclear migration, microtubule-mediated	15	0.0023	2	0.0108	0.0592090	E
<input type="checkbox"/>	GO:0009117	5	nucleotide metabolic process	111	0.0171	6	0.0323	0.0592320	E
<input type="checkbox"/>	GO:0007530	4,5	sex determination	35	0.0054	3	0.0161	0.0608363	E
<input type="checkbox"/>	GO:0003006	3,4	reproductive developmental process	35	0.0054	3	0.0161	0.0608363	E
<input type="checkbox"/>	GO:0007531	4,6,5	mating type determination	35	0.0054	3	0.0161	0.0608363	E

<input type="radio"/>	GO:0040007	2	growth	141	0.0218	7	0.0376	0.0610075	E
<input type="radio"/>	GO:0009058	3	biosynthetic process	1249	0.1929	39	0.2097	0.0614186	E
<input type="radio"/>	GO:0006944	5	membrane fusion	59	0.0091	4	0.0215	0.0620909	E
<input type="radio"/>	GO:0032502	2	developmental process	436	0.0673	16	0.0860	0.0645039	E
<input type="radio"/>	GO:0022618	6,5	protein-RNA complex assembly	144	0.0222	7	0.0376	0.0650769	E
<input type="radio"/>	GO:0006767	5	water-soluble vitamin metabolic process	89	0.0137	5	0.0269	0.0699125	E
<input type="radio"/>	GO:0006766	4	vitamin metabolic process	89	0.0137	5	0.0269	0.0699125	E
<input type="radio"/>	GO:0000747	4	conjugation with cellular fusion	118	0.0182	6	0.0323	0.0705107	E
<input type="radio"/>	GO:0000746	3	conjugation	118	0.0182	6	0.0323	0.0705107	E
<input type="radio"/>	GO:0019953	3	sexual reproduction	118	0.0182	6	0.0323	0.0705107	E
<input type="radio"/>	GO:0043285	5	biopolymer catabolic process	277	0.0428	11	0.0591	0.0714353	E
<input type="radio"/>	GO:0006403	4	RNA localization	90	0.0139	5	0.0269	0.0719272	E
<input type="radio"/>	GO:0030705	7,5,6	cytoskeleton-dependent intracellular transport	17	0.0026	2	0.0108	0.0723835	E
<input type="radio"/>	GO:0006113	5	fermentation	17	0.0026	2	0.0108	0.0723835	E
<input type="radio"/>	GO:0009653	4,3	anatomical structure morphogenesis	248	0.0383	10	0.0538	0.0752137	E
<input type="radio"/>	GO:0000902	5,6	cell morphogenesis	248	0.0383	10	0.0538	0.0752137	E
<input type="radio"/>	GO:0048856	3	anatomical structure development	248	0.0383	10	0.0538	0.0752137	E
<input type="radio"/>	GO:0032989	4,5	cellular structure morphogenesis	248	0.0383	10	0.0538	0.0752137	E
<input type="radio"/>	GO:0006612	9,7,8	protein targeting to membrane	39	0.0060	3	0.0161	0.0756953	E
<input type="radio"/>	GO:0042401	6,7	biogenic amine biosynthetic process	18	0.0028	2	0.0108	0.0791117	E
<input type="radio"/>	GO:0051248	6,5	negative regulation of protein metabolic process	18	0.0028	2	0.0108	0.0791117	E
<input type="radio"/>	GO:0000084	8,7,6	S phase of mitotic cell cycle	18	0.0028	2	0.0108	0.0791117	E
<input type="radio"/>	GO:0006369	9,8	transcription termination from RNA polymerase II promoter	18	0.0028	2	0.0108	0.0791117	E
<input type="radio"/>	GO:0006378	9	mRNA polyadenylation	18	0.0028	2	0.0108	0.0791117	E
<input type="radio"/>	GO:0000183	11,7,8,12,10	chromatin silencing at rDNA	18	0.0028	2	0.0108	0.0791117	E
<input type="radio"/>	GO:0048024	9,8,11	regulation of nuclear mRNA splicing, via spliceosome	3	0.0005	1	0.0054	0.0813106	E
<input type="radio"/>	GO:0006114	7,6	glycerol biosynthetic process	3	0.0005	1	0.0054	0.0813106	E
<input type="radio"/>	GO:0019413	7,8	acetate biosynthetic process	3	0.0005	1	0.0054	0.0813106	E
<input type="radio"/>	GO:0051443	7	positive regulation of ubiquitin ligase activity	3	0.0005	1	0.0054	0.0813106	E
<input type="radio"/>	GO:0031684	7	heterotrimeric G-protein complex cycle	3	0.0005	1	0.0054	0.0813106	E
<input type="radio"/>	GO:0051351	6	positive regulation of ligase activity	3	0.0005	1	0.0054	0.0813106	E
<input type="radio"/>	GO:0050684	8,7	regulation of mRNA processing	3	0.0005	1	0.0054	0.0813106	E
<input type="radio"/>	GO:0046173	6	polyol biosynthetic process	3	0.0005	1	0.0054	0.0813106	E
<input type="radio"/>	GO:0006404	10,8,5,7,9,6	RNA import into nucleus	3	0.0005	1	0.0054	0.0813106	E
<input type="radio"/>	GO:0045033	6	peroxisome inheritance	3	0.0005	1	0.0054	0.0813106	E
<input type="radio"/>	GO:0007033	5	vacuole organization and biogenesis	67	0.0103	4	0.0215	0.0830572	E
<input type="radio"/>	GO:0051052	7,6	regulation of DNA metabolic process	41	0.0063	3	0.0161	0.0833440	E
<input type="radio"/>	GO:0009150	7	purine ribonucleotide metabolic process	41	0.0063	3	0.0161	0.0833440	E
<input type="radio"/>	GO:0043412	5	biopolymer modification	664	0.1025	21	0.1129	0.0838892	E
<input type="radio"/>	GO:0009059	4	macromolecule biosynthetic process	886	0.1368	26	0.1398	0.0847322	E
<input type="radio"/>	GO:0006275	8,7	regulation of DNA replication	19	0.0029	2	0.0108	0.0858998	E
<input type="radio"/>	GO:0044249	4	cellular biosynthetic process	366	0.0565	13	0.0699	0.0859202	E
<input type="radio"/>	GO:0001403	6,4,8,9	invasive growth (sensu Saccharomyces)	42	0.0065	3	0.0161	0.0872026	E
<input type="radio"/>	GO:0016125	5,6,7	sterol metabolic process	42	0.0065	3	0.0161	0.0872026	E

<input type="checkbox"/>	GO:0006412	6,5	translation	688	0.1062	21	0.1129	0.0894607	E
<input type="checkbox"/>	GO:0044255	4,5	cellular lipid metabolic process	229	0.0354	9	0.0484	0.0896275	E
<input type="checkbox"/>	GO:0009259	6	ribonucleotide metabolic process	43	0.0066	3	0.0161	0.0910765	E
<input type="checkbox"/>	GO:0008202	5,6	steroid metabolic process	43	0.0066	3	0.0161	0.0910765	E
<input type="checkbox"/>	GO:0000278	4	mitotic cell cycle	266	0.0411	10	0.0538	0.0915502	E
<input type="checkbox"/>	GO:0007097	7,8,5,6	nuclear migration	20	0.0031	2	0.0108	0.0927244	E
<input type="checkbox"/>	GO:0051320	7,6,5	S phase	20	0.0031	2	0.0108	0.0927244	E
<input type="checkbox"/>	GO:0051647	6,5	nucleus localization	20	0.0031	2	0.0108	0.0927244	E
<input type="checkbox"/>	GO:0006353	8,7	transcription termination	20	0.0031	2	0.0108	0.0927244	E
<input type="checkbox"/>	GO:0042398	6,5	amino acid derivative biosynthetic process	20	0.0031	2	0.0108	0.0927244	E
<input type="checkbox"/>	GO:0040023	6,7,4,5	establishment of nucleus localization	20	0.0031	2	0.0108	0.0927244	E
<input type="checkbox"/>	GO:0007017	6	microtubule-based process	101	0.0156	5	0.0269	0.0944598	E
<input type="checkbox"/>	GO:0009057	4	macromolecule catabolic process	345	0.0533	12	0.0645	0.0959954	E
<input type="checkbox"/>	GO:0019362	7,6	pyridine nucleotide metabolic process	45	0.0069	3	0.0161	0.0988483	E
<input type="checkbox"/>	GO:0006891	8,6,5,7	intra-Golgi vesicle-mediated transport	21	0.0032	2	0.0108	0.0995640	E
<input type="checkbox"/>	GO:0044265	5	cellular macromolecule catabolic process	314	0.0485	11	0.0591	0.1004045	E
<input type="checkbox"/>	GO:0051186	4	cofactor metabolic process	170	0.0263	7	0.0376	0.1008189	E
<input type="checkbox"/>	GO:0000041	7,8	transition metal ion transport	46	0.0071	3	0.0161	0.1027356	E
<input type="checkbox"/>	GO:0000743	9,10,8,7,6	nuclear migration during conjugation with cellular fusion	4	0.0006	1	0.0054	0.1053156	E
<input type="checkbox"/>	GO:0030071	8,10,6,9,7,5	regulation of mitotic metaphase/anaphase transition	4	0.0006	1	0.0054	0.1053156	E
<input type="checkbox"/>	GO:0016180	7	snRNA processing	4	0.0006	1	0.0054	0.1053156	E
<input type="checkbox"/>	GO:0018344	10,9,8	protein geranylgeranylation	4	0.0006	1	0.0054	0.1053156	E
<input type="checkbox"/>	GO:0006278	7	RNA-dependent DNA replication	4	0.0006	1	0.0054	0.1053156	E
<input type="checkbox"/>	GO:0000059	8,10,11,7,9	protein import into nucleus, docking	4	0.0006	1	0.0054	0.1053156	E
<input type="checkbox"/>	GO:0046337	5,7,8	phosphatidylethanolamine metabolic process	4	0.0006	1	0.0054	0.1053156	E
<input type="checkbox"/>	GO:0046323	8,9	glucose import	4	0.0006	1	0.0054	0.1053156	E
<input type="checkbox"/>	GO:0000735	7,9,8	removal of nonhomologous ends	4	0.0006	1	0.0054	0.1053156	E
<input type="checkbox"/>	GO:0006646	7,8,9,6,10	phosphatidylethanolamine biosynthetic process	4	0.0006	1	0.0054	0.1053156	E
<input type="checkbox"/>	GO:0006827	8,9,10	high affinity iron ion transport	4	0.0006	1	0.0054	0.1053156	E
<input type="checkbox"/>	GO:0000771	6,4	agglutination	4	0.0006	1	0.0054	0.1053156	E
<input type="checkbox"/>	GO:0046335	6,7,8,9	ethanolamine biosynthetic process	4	0.0006	1	0.0054	0.1053156	E
<input type="checkbox"/>	GO:0000752	7,5,6	agglutination during conjugation with cellular fusion	4	0.0006	1	0.0054	0.1053156	E
<input type="checkbox"/>	GO:0043173	5	nucleotide salvage	4	0.0006	1	0.0054	0.1053156	E
<input type="checkbox"/>	GO:0019439	5	aromatic compound catabolic process	4	0.0006	1	0.0054	0.1053156	E
<input type="checkbox"/>	GO:0000731	7,6	DNA synthesis during DNA repair	4	0.0006	1	0.0054	0.1053156	E
<input type="checkbox"/>	GO:0007157	5	heterophilic cell adhesion	4	0.0006	1	0.0054	0.1053156	E
<input type="checkbox"/>	GO:0042439	6,7	ethanolamine and derivative metabolic process	4	0.0006	1	0.0054	0.1053156	E
<input type="checkbox"/>	GO:0006580	5,7,8	ethanolamine metabolic process	4	0.0006	1	0.0054	0.1053156	E
<input type="checkbox"/>	GO:0018348	11,10,9	protein amino acid geranylgeranylation	4	0.0006	1	0.0054	0.1053156	E
<input type="checkbox"/>	GO:0000350	8,7,10,12	generation of catalytic spliceosome for second transesterification step	4	0.0006	1	0.0054	0.1053156	E
<input type="checkbox"/>	GO:0031204	9,11,10,7,8	posttranslational protein targeting to membrane, translocation	4	0.0006	1	0.0054	0.1053156	E
<input type="checkbox"/>	GO:0042723	6	thiamin and derivative metabolic process	22	0.0034	2	0.0108	0.1063985	E
<input type="checkbox"/>	GO:0000145	7,8	purine nucleoside triphosphate	22	0.0034	2	0.0108	0.1063985	E

<input type="radio"/>	GO:0009143	7,8	biosynthetic process	22	0.0034	2	0.0108	0.1063985	E
<input type="radio"/>	GO:0009206	8,9	purine ribonucleoside triphosphate biosynthetic process	22	0.0034	2	0.0108	0.1063985	E
<input type="radio"/>	GO:0006311	10,8,7,5,9,6,4	meiotic gene conversion	22	0.0034	2	0.0108	0.1063985	E
<input type="radio"/>	GO:0040020	7,9,8,6	regulation of meiosis	22	0.0034	2	0.0108	0.1063985	E
<input type="radio"/>	GO:0006163	6	purine nucleotide metabolic process	47	0.0073	3	0.0161	0.1066171	E
<input type="radio"/>	GO:0032940	6,4,5	secretion by cell	250	0.0386	9	0.0484	0.1093178	E
<input type="radio"/>	GO:0046903	3,4	secretion	250	0.0386	9	0.0484	0.1093178	E
<input type="radio"/>	GO:0042157	6	lipoprotein metabolic process	48	0.0074	3	0.0161	0.1104877	E
<input type="radio"/>	GO:0006497	8,7,6	protein amino acid lipidation	48	0.0074	3	0.0161	0.1104877	E
<input type="radio"/>	GO:0042158	7,5	lipoprotein biosynthetic process	48	0.0074	3	0.0161	0.1104877	E
<input type="radio"/>	GO:0017038	5,6,7	protein import	109	0.0168	5	0.0269	0.1106354	E
<input type="radio"/>	GO:0044248	4	cellular catabolic process	425	0.0656	13	0.0699	0.1125855	E
<input type="radio"/>	GO:0009205	8	purine ribonucleoside triphosphate metabolic process	23	0.0036	2	0.0108	0.1132094	E
<input type="radio"/>	GO:0009144	7	purine nucleoside triphosphate metabolic process	23	0.0036	2	0.0108	0.1132094	E
<input type="radio"/>	GO:0009056	3	catabolic process	438	0.0676	13	0.0699	0.1148336	E
<input type="radio"/>	GO:0006405	10,8,5,7,9,6	RNA export from nucleus	79	0.0122	4	0.0215	0.1151923	E
<input type="radio"/>	GO:0051325	6,5	interphase	112	0.0173	5	0.0269	0.1165113	E
<input type="radio"/>	GO:0051329	7,5,6	interphase of mitotic cell cycle	112	0.0173	5	0.0269	0.1165113	E
<input type="radio"/>	GO:0050658	4,6,5,7	RNA transport	80	0.0124	4	0.0215	0.1178052	E
<input type="radio"/>	GO:0051236	3,4,5	establishment of RNA localization	80	0.0124	4	0.0215	0.1178052	E
<input type="radio"/>	GO:0050657	5,6	nucleic acid transport	80	0.0124	4	0.0215	0.1178052	E
<input type="radio"/>	GO:0043631	8	RNA polyadenylation	24	0.0037	2	0.0108	0.1199797	E
<input type="radio"/>	GO:0009201	7,8	ribonucleoside triphosphate biosynthetic process	24	0.0037	2	0.0108	0.1199797	E
<input type="radio"/>	GO:0006576	5,6	biogenic amine metabolic process	24	0.0037	2	0.0108	0.1199797	E
<input type="radio"/>	GO:0048468	3,5	cell development	52	0.0080	3	0.0161	0.1257694	E
<input type="radio"/>	GO:0000724	8,7	double-strand break repair via homologous recombination	25	0.0039	2	0.0108	0.1266936	E
<input type="radio"/>	GO:0006298	7,9,6	mismatch repair	25	0.0039	2	0.0108	0.1266936	E
<input type="radio"/>	GO:0009199	7	ribonucleoside triphosphate metabolic process	25	0.0039	2	0.0108	0.1266936	E
<input type="radio"/>	GO:0009607	3	response to biotic stimulus	25	0.0039	2	0.0108	0.1266936	E
<input type="radio"/>	GO:0045005	8,6	maintenance of fidelity during DNA-dependent DNA replication	25	0.0039	2	0.0108	0.1266936	E
<input type="radio"/>	GO:0051083	8	cotranslational protein folding	5	0.0008	1	0.0054	0.1278815	E
<input type="radio"/>	GO:0006498	9,10,8,7	N-terminal protein lipidation	5	0.0008	1	0.0054	0.1278815	E
<input type="radio"/>	GO:0043087	6	regulation of GTPase activity	5	0.0008	1	0.0054	0.1278815	E
<input type="radio"/>	GO:0018346	10,9,8	protein amino acid prenylation	5	0.0008	1	0.0054	0.1278815	E
<input type="radio"/>	GO:0018377	9,8,7	protein myristoylation	5	0.0008	1	0.0054	0.1278815	E
<input type="radio"/>	GO:0051439	7,5,4	regulation of ubiquitin ligase activity during mitotic cell cycle	5	0.0008	1	0.0054	0.1278815	E
<input type="radio"/>	GO:0032447	9	protein urmylation	5	0.0008	1	0.0054	0.1278815	E
<input type="radio"/>	GO:0016337	4	cell-cell adhesion	5	0.0008	1	0.0054	0.1278815	E
<input type="radio"/>	GO:0018319	10,9,8	protein amino acid myristoylation	5	0.0008	1	0.0054	0.1278815	E
<input type="radio"/>	GO:0043137	7,10,6,9	DNA replication, removal of RNA primer	5	0.0008	1	0.0054	0.1278815	E
<input type="radio"/>	GO:0000730	7,9,10,8,6	DNA recombinase assembly	5	0.0008	1	0.0054	0.1278815	E
<input type="radio"/>	GO:0000076	11,9,8,10	DNA replication checkpoint	5	0.0008	1	0.0054	0.1278815	E
<input type="radio"/>	GO:0000707	11,9,8,5,6,10,7,4	meiotic DNA recombinase assembly	5	0.0008	1	0.0054	0.1278815	E

<input type="checkbox"/>	GO:0015680	7,5,9,6,10	intracellular copper ion transport	5	0.0008	1	0.0054	0.1278815	E
<input type="checkbox"/>	GO:0006499	10,11,9,8	N-terminal protein myristoylation	5	0.0008	1	0.0054	0.1278815	E
<input type="checkbox"/>	GO:0018342	9,8,7	protein prenylation	5	0.0008	1	0.0054	0.1278815	E
<input type="checkbox"/>	GO:0008645	6,7	hexose transport	26	0.0040	2	0.0108	0.1333366	E
<input type="checkbox"/>	GO:0015749	5,6	monosaccharide transport	26	0.0040	2	0.0108	0.1333366	E
<input type="checkbox"/>	GO:0042274	6,5	ribosomal small subunit biogenesis and assembly	26	0.0040	2	0.0108	0.1333366	E
<input type="checkbox"/>	GO:0045045	7,5,4,6	secretory pathway	243	0.0375	8	0.0430	0.1344019	E
<input type="checkbox"/>	GO:0051301	3	cell division	246	0.0380	8	0.0430	0.1361144	E
<input type="checkbox"/>	GO:0007131	10,8,7,5,9,6,4	meiotic recombination	55	0.0085	3	0.0161	0.1369001	E
<input type="checkbox"/>	GO:0006066	4	alcohol metabolic process	163	0.0252	6	0.0323	0.1388363	E
<input type="checkbox"/>	GO:0009142	6,7	nucleoside triphosphate biosynthetic process	27	0.0042	2	0.0108	0.1398955	E
<input type="checkbox"/>	GO:0006733	6	oxidoreduction coenzyme metabolic process	56	0.0086	3	0.0161	0.1405267	E
<input type="checkbox"/>	GO:0051640	5,4	organelle localization	56	0.0086	3	0.0161	0.1405267	E
<input type="checkbox"/>	GO:0015931	4,5	nucleobase, nucleoside, nucleotide and nucleic acid transport	90	0.0139	4	0.0215	0.1425722	E
<input type="checkbox"/>	GO:0000749	5	response to pheromone during conjugation with cellular fusion	57	0.0088	3	0.0161	0.1441055	E
<input type="checkbox"/>	GO:0006302	7,6	double-strand break repair	57	0.0088	3	0.0161	0.1441055	E
<input type="checkbox"/>	GO:0000750	8,7,6	pheromone-dependent signal transduction during conjugation with cellular fusion	28	0.0043	2	0.0108	0.1463582	E
<input type="checkbox"/>	GO:0043624	7,6	cellular protein complex disassembly	28	0.0043	2	0.0108	0.1463582	E
<input type="checkbox"/>	GO:0043241	6,5	protein complex disassembly	28	0.0043	2	0.0108	0.1463582	E
<input type="checkbox"/>	GO:0032005	7,6	signal transduction during conjugation with cellular fusion	28	0.0043	2	0.0108	0.1463582	E
<input type="checkbox"/>	GO:0008654	7,6,8	phospholipid biosynthetic process	58	0.0090	3	0.0161	0.1476334	E
<input type="checkbox"/>	GO:0006720	5,6	isoprenoid metabolic process	6	0.0009	1	0.0054	0.1490706	E
<input type="checkbox"/>	GO:0008299	6,5,7	isoprenoid biosynthetic process	6	0.0009	1	0.0054	0.1490706	E
<input type="checkbox"/>	GO:0046021	10,8,5,6,9,7,4	regulation of transcription from RNA polymerase II promoter, mitotic	6	0.0009	1	0.0054	0.1490706	E
<input type="checkbox"/>	GO:0007029	5	endoplasmic reticulum organization and biogenesis	6	0.0009	1	0.0054	0.1490706	E
<input type="checkbox"/>	GO:0006083	7	acetate metabolic process	6	0.0009	1	0.0054	0.1490706	E
<input type="checkbox"/>	GO:0000717	8,7	nucleotide-excision repair, DNA duplex unwinding	6	0.0009	1	0.0054	0.1490706	E
<input type="checkbox"/>	GO:0045143	10,8,7,5,9,6,4	homologous chromosome segregation	6	0.0009	1	0.0054	0.1490706	E
<input type="checkbox"/>	GO:0033214	12,10	iron assimilation by chelation and transport	6	0.0009	1	0.0054	0.1490706	E
<input type="checkbox"/>	GO:0045041	10,9,8,7	protein import into mitochondrial intermembrane space	6	0.0009	1	0.0054	0.1490706	E
<input type="checkbox"/>	GO:0015892	13,11,8,9,5,10,6	siderophore-iron transport	6	0.0009	1	0.0054	0.1490706	E
<input type="checkbox"/>	GO:0006000	7,8	fructose metabolic process	6	0.0009	1	0.0054	0.1490706	E
<input type="checkbox"/>	GO:0051340	5	regulation of ligase activity	6	0.0009	1	0.0054	0.1490706	E
<input type="checkbox"/>	GO:0051438	6	regulation of ubiquitin ligase activity	6	0.0009	1	0.0054	0.1490706	E
<input type="checkbox"/>	GO:0006013	7,8	mannose metabolic process	6	0.0009	1	0.0054	0.1490706	E
<input type="checkbox"/>	GO:0007070	11,9,6,7,10,8,5	negative regulation of transcription from RNA polymerase II promoter, mitotic	6	0.0009	1	0.0054	0.1490706	E
<input type="checkbox"/>	GO:0015758	7,8	glucose transport	6	0.0009	1	0.0054	0.1490706	E
<input type="checkbox"/>	GO:0032297	10,8,9	negative regulation of DNA replication initiation	6	0.0009	1	0.0054	0.1490706	E
<input type="checkbox"/>	GO:0048869	3	cellular developmental process	173	0.0267	6	0.0323	0.1493815	E
<input type="checkbox"/>	GO:0030154	4	cell differentiation	173	0.0267	6	0.0323	0.1493815	E

<input type="checkbox"/>	GO:0000070	9,7,5,8,6,4	mitotic sister chromatid segregation	59	0.0091	3	0.0161	0.1511073	E
<input type="checkbox"/>	GO:0007010	5	cytoskeleton organization and biogenesis	227	0.0351	7	0.0376	0.1514544	E
<input type="checkbox"/>	GO:0019236	4	response to pheromone	94	0.0145	4	0.0215	0.1515654	E
<input type="checkbox"/>	GO:0000725	7,6	recombinational repair	29	0.0045	2	0.0108	0.1527137	E
<input type="checkbox"/>	GO:0051656	6,3,5,4	establishment of organelle localization	29	0.0045	2	0.0108	0.1527137	E
<input type="checkbox"/>	GO:0007154	3	cell communication	240	0.0371	7	0.0376	0.1540115	E
<input type="checkbox"/>	GO:0006725	4	aromatic compound metabolic process	60	0.0093	3	0.0161	0.1545242	E
<input type="checkbox"/>	GO:0006732	5	coenzyme metabolic process	136	0.0210	5	0.0269	0.1562040	E
<input type="checkbox"/>	GO:0022414	3,2	reproductive process	183	0.0283	6	0.0323	0.1573642	E
<input type="checkbox"/>	GO:0006812	5,6	cation transport	97	0.0150	4	0.0215	0.1578895	E
<input type="checkbox"/>	GO:0031137	6,5	regulation of conjugation with cellular fusion	30	0.0046	2	0.0108	0.1589520	E
<input type="checkbox"/>	GO:0009141	6	nucleoside triphosphate metabolic process	30	0.0046	2	0.0108	0.1589520	E
<input type="checkbox"/>	GO:0006893	9,7,6,8	Golgi to plasma membrane transport	30	0.0046	2	0.0108	0.1589520	E
<input type="checkbox"/>	GO:0030466	11,7,8,12,10	chromatin silencing at silent mating-type cassette	30	0.0046	2	0.0108	0.1589520	E
<input type="checkbox"/>	GO:0046999	5,4	regulation of conjugation	30	0.0046	2	0.0108	0.1589520	E
<input type="checkbox"/>	GO:0000819	7,4	sister chromatid segregation	62	0.0096	3	0.0161	0.1611764	E
<input type="checkbox"/>	GO:0030001	6,7	metal ion transport	62	0.0096	3	0.0161	0.1611764	E
<input type="checkbox"/>	GO:0032505	4,3	reproduction of a single-celled organism	194	0.0300	6	0.0323	0.1630496	E
<input type="checkbox"/>	GO:0006575	5	amino acid derivative metabolic process	31	0.0048	2	0.0108	0.1650640	E
<input type="checkbox"/>	GO:0042273	6,5	ribosomal large subunit biogenesis and assembly	64	0.0099	3	0.0161	0.1675701	E
<input type="checkbox"/>	GO:0006621	7,6,5,4	protein retention in ER	7	0.0011	1	0.0054	0.1689428	E
<input type="checkbox"/>	GO:0006656	9,8,10	phosphatidylcholine biosynthetic process	7	0.0011	1	0.0054	0.1689428	E
<input type="checkbox"/>	GO:0007068	10,8,6,9,7,5	negative regulation of transcription, mitotic	7	0.0011	1	0.0054	0.1689428	E
<input type="checkbox"/>	GO:0006265	6	DNA topological change	7	0.0011	1	0.0054	0.1689428	E
<input type="checkbox"/>	GO:0045896	9,7,5,8,6,4	regulation of transcription, mitotic	7	0.0011	1	0.0054	0.1689428	E
<input type="checkbox"/>	GO:0045835	8,10,9,7	negative regulation of meiosis	7	0.0011	1	0.0054	0.1689428	E
<input type="checkbox"/>	GO:0000710	11,9,8,6,5,10,7,4	meiotic mismatch repair	7	0.0011	1	0.0054	0.1689428	E
<input type="checkbox"/>	GO:0019932	6	second-messenger-mediated signaling	32	0.0049	2	0.0108	0.1710417	E
<input type="checkbox"/>	GO:0006418	8,7,9,6	tRNA aminoacylation for protein translation	32	0.0049	2	0.0108	0.1710417	E
<input type="checkbox"/>	GO:0043038	6,7	amino acid activation	32	0.0049	2	0.0108	0.1710417	E
<input type="checkbox"/>	GO:0032984	5	macromolecular complex disassembly	32	0.0049	2	0.0108	0.1710417	E
<input type="checkbox"/>	GO:0043039	7,8	tRNA aminoacylation	32	0.0049	2	0.0108	0.1710417	E
<input type="checkbox"/>	GO:0006270	8,6	DNA replication initiation	33	0.0051	2	0.0108	0.1768777	E
<input type="checkbox"/>	GO:0000910	4	cytokinesis	109	0.0168	4	0.0215	0.1790660	E
<input type="checkbox"/>	GO:0048193	7,5,6	Golgi vesicle transport	166	0.0256	5	0.0269	0.1795467	E
<input type="checkbox"/>	GO:0051726	5,4	regulation of cell cycle	167	0.0258	5	0.0269	0.1797791	E
<input type="checkbox"/>	GO:0000074	6,5	regulation of progression through cell cycle	167	0.0258	5	0.0269	0.1797791	E
<input type="checkbox"/>	GO:0000466	8,9	maturation of 5.8S rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	34	0.0053	2	0.0108	0.1825655	E
<input type="checkbox"/>	GO:0006360	8,7	transcription from RNA polymerase I promoter	34	0.0053	2	0.0108	0.1825655	E
<input type="checkbox"/>	GO:0007186	6	G-protein coupled receptor protein signaling pathway	34	0.0053	2	0.0108	0.1825655	E
<input type="checkbox"/>	GO:0006811	4,5	ion transport	115	0.0178	4	0.0215	0.1869698	E
<input type="checkbox"/>	GO:0015677	9,10	copper ion import	8	0.0012	1	0.0054	0.1875559	E

<input type="radio"/>	GO:0016973	12,10,7,9,11,8	poly(A)+ mRNA export from nucleus	8	0.0012	1	0.0054	0.1875559	E
<input type="radio"/>	GO:0046015	10,8,9,6	regulation of transcription by glucose	8	0.0012	1	0.0054	0.1875559	E
<input type="radio"/>	GO:0043144	7	snoRNA processing	8	0.0012	1	0.0054	0.1875559	E
<input type="radio"/>	GO:0009306	7,5,4,6	protein secretion	8	0.0012	1	0.0054	0.1875559	E
<input type="radio"/>	GO:0000019	9,8	regulation of mitotic recombination	8	0.0012	1	0.0054	0.1875559	E
<input type="radio"/>	GO:0008156	9,8	negative regulation of DNA replication	8	0.0012	1	0.0054	0.1875559	E
<input type="radio"/>	GO:0000726	7,6	non-recombinational repair	35	0.0054	2	0.0108	0.1880995	E
<input type="radio"/>	GO:0042493	4	response to drug	121	0.0187	4	0.0215	0.1930165	E
<input type="radio"/>	GO:0006399	6	tRNA metabolic process	121	0.0187	4	0.0215	0.1930165	E
<input type="radio"/>	GO:0022411	4	cellular component disassembly	36	0.0056	2	0.0108	0.1934747	E
<input type="radio"/>	GO:0000460	7,8	maturation of 5.8S rRNA	36	0.0056	2	0.0108	0.1934747	E
<input type="radio"/>	GO:0006643	5,6	membrane lipid metabolic process	125	0.0193	4	0.0215	0.1960227	E
<input type="radio"/>	GO:0007067	8,6,7,5	mitosis	127	0.0196	4	0.0215	0.1972236	E
<input type="radio"/>	GO:0000087	7,5,6	M phase of mitotic cell cycle	129	0.0199	4	0.0215	0.1982267	E
<input type="radio"/>	GO:0007242	5	intracellular signaling cascade	137	0.0212	4	0.0215	0.2003301	E
<input type="radio"/>	GO:0008643	4,5	carbohydrate transport	38	0.0059	2	0.0108	0.2037317	E
<input type="radio"/>	GO:0009152	7,8	purine ribonucleotide biosynthetic process	38	0.0059	2	0.0108	0.2037317	E
<input type="radio"/>	GO:0046467	6,5,7	membrane lipid biosynthetic process	78	0.0120	3	0.0161	0.2039151	E
<input type="radio"/>	GO:0007155	3	cell adhesion	9	0.0014	1	0.0054	0.2049653	E
<input type="radio"/>	GO:0006071	6	glycerol metabolic process	9	0.0014	1	0.0054	0.2049653	E
<input type="radio"/>	GO:0051180	4,5	vitamin transport	9	0.0014	1	0.0054	0.2049653	E
<input type="radio"/>	GO:0015891	4,5	siderophore transport	9	0.0014	1	0.0054	0.2049653	E
<input type="radio"/>	GO:0000393	7,6,9,11	spliceosomal conformational changes to generate catalytic conformation	9	0.0014	1	0.0054	0.2049653	E
<input type="radio"/>	GO:0019751	5	polyol metabolic process	9	0.0014	1	0.0054	0.2049653	E
<input type="radio"/>	GO:0006874	10,8	cellular calcium ion homeostasis	9	0.0014	1	0.0054	0.2049653	E
<input type="radio"/>	GO:0030847	10,9	transcription termination from Pol II promoter, RNA polymerase(A)-independent	9	0.0014	1	0.0054	0.2049653	E
<input type="radio"/>	GO:0030952	6	establishment and/or maintenance of cytoskeleton polarity	9	0.0014	1	0.0054	0.2049653	E
<input type="radio"/>	GO:0046470	8,9	phosphatidylcholine metabolic process	9	0.0014	1	0.0054	0.2049653	E
<input type="radio"/>	GO:0006280	6	mutagenesis	9	0.0014	1	0.0054	0.2049653	E
<input type="radio"/>	GO:0030950	8,7	establishment and/or maintenance of actin cytoskeleton polarity	9	0.0014	1	0.0054	0.2049653	E
<input type="radio"/>	GO:0006283	8,7	transcription-coupled nucleotide-excision repair	9	0.0014	1	0.0054	0.2049653	E
<input type="radio"/>	GO:0022610	2	biological adhesion	9	0.0014	1	0.0054	0.2049653	E
<input type="radio"/>	GO:0006760	5,7	folic acid and derivative metabolic process	9	0.0014	1	0.0054	0.2049653	E
<input type="radio"/>	GO:0055074	9	calcium ion homeostasis	9	0.0014	1	0.0054	0.2049653	E
<input type="radio"/>	GO:0046474	8,7,9	glycerophospholipid biosynthetic process	39	0.0060	2	0.0108	0.2086068	E
<input type="radio"/>	GO:0001302	5	replicative cell aging	39	0.0060	2	0.0108	0.2086068	E
<input type="radio"/>	GO:0006888	8,6,5,7	ER to Golgi vesicle-mediated transport	81	0.0125	3	0.0161	0.2096222	E
<input type="radio"/>	GO:0009260	6,7	ribonucleotide biosynthetic process	40	0.0062	2	0.0108	0.2133093	E
<input type="radio"/>	GO:0006457	6	protein folding	84	0.0130	3	0.0161	0.2145720	E
<input type="radio"/>	GO:0032446	8	protein modification by small protein conjugation	84	0.0130	3	0.0161	0.2145720	E
<input type="radio"/>	GO:0019954	3	asexual reproduction	85	0.0131	3	0.0161	0.2160544	E
<input type="radio"/>	GO:0007114	5,4	cell budding	85	0.0131	3	0.0161	0.2160544	E
<input type="radio"/>	GO:0006164	6,7	purine nucleotide biosynthetic process	41	0.0063	2	0.0108	0.2178372	E

<input type="radio"/>	GO:0000027	9,7,8,6	ribosomal large subunit assembly and maintenance	41	0.0063	2	0.0108	0.2178372	E
<input type="radio"/>	GO:0032506	5,3	cytokinetic process	88	0.0136	3	0.0161	0.2200036	E
<input type="radio"/>	GO:0000103	6	sulfate assimilation	10	0.0015	1	0.0054	0.2212243	E
<input type="radio"/>	GO:0008298	5	intracellular mRNA localization	10	0.0015	1	0.0054	0.2212243	E
<input type="radio"/>	GO:0009096	8,7,9	aromatic amino acid family biosynthetic process, anthranilate pathway	10	0.0015	1	0.0054	0.2212243	E
<input type="radio"/>	GO:0006616	9,12,11,7,10,8	SRP-dependent cotranslational protein targeting to membrane, translocation	10	0.0015	1	0.0054	0.2212243	E
<input type="radio"/>	GO:0000162	9,8,7,10	tryptophan biosynthetic process	10	0.0015	1	0.0054	0.2212243	E
<input type="radio"/>	GO:0006791	5	sulfur utilization	10	0.0015	1	0.0054	0.2212243	E
<input type="radio"/>	GO:0006882	10,8	cellular zinc ion homeostasis	10	0.0015	1	0.0054	0.2212243	E
<input type="radio"/>	GO:0006568	7,8,6	tryptophan metabolic process	10	0.0015	1	0.0054	0.2212243	E
<input type="radio"/>	GO:0006446	8,7,6	regulation of translational initiation	10	0.0015	1	0.0054	0.2212243	E
<input type="radio"/>	GO:0055069	9	zinc ion homeostasis	10	0.0015	1	0.0054	0.2212243	E
<input type="radio"/>	GO:0051336	5	regulation of hydrolase activity	10	0.0015	1	0.0054	0.2212243	E
<input type="radio"/>	GO:0042434	6	indole derivative metabolic process	10	0.0015	1	0.0054	0.2212243	E
<input type="radio"/>	GO:0006586	6,7	indolalkylamine metabolic process	10	0.0015	1	0.0054	0.2212243	E
<input type="radio"/>	GO:0042430	5	indole and derivative metabolic process	10	0.0015	1	0.0054	0.2212243	E
<input type="radio"/>	GO:0046219	7,8,6	indolalkylamine biosynthetic process	10	0.0015	1	0.0054	0.2212243	E
<input type="radio"/>	GO:0030174	9,7,8	regulation of DNA replication initiation	10	0.0015	1	0.0054	0.2212243	E
<input type="radio"/>	GO:0042435	7,5	indole derivative biosynthetic process	10	0.0015	1	0.0054	0.2212243	E
<input type="radio"/>	GO:0006769	8,7	nicotinamide metabolic process	42	0.0065	2	0.0108	0.2221888	E
<input type="radio"/>	GO:0006644	6,7	phospholipid metabolic process	97	0.0150	3	0.0161	0.2275179	E
<input type="radio"/>	GO:0006468	8,7	protein amino acid phosphorylation	101	0.0156	3	0.0161	0.2288911	E
<input type="radio"/>	GO:0030010	7,4,8	establishment of cell polarity	103	0.0159	3	0.0161	0.2291556	E
<input type="radio"/>	GO:0007052	5,4,9	mitotic spindle organization and biogenesis	44	0.0068	2	0.0108	0.2303595	E
<input type="radio"/>	GO:0031505	6	chitin- and beta-glucan-containing cell wall organization and biogenesis	44	0.0068	2	0.0108	0.2303595	E
<input type="radio"/>	GO:0050790	4	regulation of catalytic activity	45	0.0069	2	0.0108	0.2341775	E
<input type="radio"/>	GO:0065002	8,6,7	intracellular protein transport across a membrane	11	0.0017	1	0.0054	0.2363843	E
<input type="radio"/>	GO:0030503	5,7,4	regulation of cell redox homeostasis	11	0.0017	1	0.0054	0.2363843	E
<input type="radio"/>	GO:0031163	5	metallo-sulfur cluster assembly	11	0.0017	1	0.0054	0.2363843	E
<input type="radio"/>	GO:0043085	5	positive regulation of enzyme activity	11	0.0017	1	0.0054	0.2363843	E
<input type="radio"/>	GO:0007021	7	tubulin folding	11	0.0017	1	0.0054	0.2363843	E
<input type="radio"/>	GO:0045454	6,4	cell redox homeostasis	11	0.0017	1	0.0054	0.2363843	E
<input type="radio"/>	GO:0001558	5,6,4,8,9	regulation of cell growth	11	0.0017	1	0.0054	0.2363843	E
<input type="radio"/>	GO:0016226	6	iron-sulfur cluster assembly	11	0.0017	1	0.0054	0.2363843	E
<input type="radio"/>	GO:0007109	7,6,5,4	cytokinesis, completion of separation	11	0.0017	1	0.0054	0.2363843	E
<input type="radio"/>	GO:0065009	3	regulation of a molecular function	46	0.0071	2	0.0108	0.2378172	E
<input type="radio"/>	GO:0007051	8	spindle organization and biogenesis	47	0.0073	2	0.0108	0.2412791	E
<input type="radio"/>	GO:0007569	4	cell aging	49	0.0076	2	0.0108	0.2476723	E
<input type="radio"/>	GO:0007568	3	aging	49	0.0076	2	0.0108	0.2476723	E
<input type="radio"/>	GO:0006904	9,5,7,6,8	vesicle docking during exocytosis	12	0.0019	1	0.0054	0.2504946	E
<input type="radio"/>	GO:0007166	5	cell surface receptor linked signal transduction	52	0.0080	2	0.0108	0.2559545	E
<input type="radio"/>	GO:0000075	7,6	cell cycle checkpoint	53	0.0082	2	0.0108	0.2583732	E
<input type="radio"/>	GO:0006368	9,7,8	RNA elongation from RNA polymerase II promoter	53	0.0082	2	0.0108	0.2583732	E

<input type="checkbox"/>	GO:0007088	7,9,8,6	regulation of mitosis	55	0.0085	2	0.0108	0.2627101	E
<input type="checkbox"/>	GO:0000920	6,4	cell separation during cytokinesis	13	0.0020	1	0.0054	0.2636025	E
<input type="checkbox"/>	GO:0006450	8,7,6	regulation of translational fidelity	13	0.0020	1	0.0054	0.2636025	E
<input type="checkbox"/>	GO:0040008	4,3	regulation of growth	13	0.0020	1	0.0054	0.2636025	E
<input type="checkbox"/>	GO:0006301	7,6	postreplication repair	13	0.0020	1	0.0054	0.2636025	E
<input type="checkbox"/>	GO:0031929	6	TOR signaling pathway	13	0.0020	1	0.0054	0.2636025	E
<input type="checkbox"/>	GO:0006537	8,9	glutamate biosynthetic process	13	0.0020	1	0.0054	0.2636025	E
<input type="checkbox"/>	GO:0006038	9,10,7,8,11	cell wall chitin biosynthetic process	13	0.0020	1	0.0054	0.2636025	E
<input type="checkbox"/>	GO:0006997	5	nuclear organization and biogenesis	57	0.0088	2	0.0108	0.2663958	E
<input type="checkbox"/>	GO:0009165	5,6	nucleotide biosynthetic process	59	0.0091	2	0.0108	0.2694516	E
<input type="checkbox"/>	GO:0006354	8,6,7	RNA elongation	59	0.0091	2	0.0108	0.2694516	E
<input type="checkbox"/>	GO:0006650	7,8	glycerophospholipid metabolic process	60	0.0093	2	0.0108	0.2707504	E
<input type="checkbox"/>	GO:0007124	6,4,8,9	pseudohyphal growth	61	0.0094	2	0.0108	0.2719005	E
<input type="checkbox"/>	GO:0000122	10,9	negative regulation of transcription from RNA polymerase II promoter	63	0.0097	2	0.0108	0.2737671	E
<input type="checkbox"/>	GO:0051028	5,7,6,8	mRNA transport	66	0.0102	2	0.0108	0.2755317	E
<input type="checkbox"/>	GO:0030467	7,4,8	establishment and/or maintenance of cell polarity (sensu Fungi)	66	0.0102	2	0.0108	0.2755317	E
<input type="checkbox"/>	GO:0016567	9	protein ubiquitination	66	0.0102	2	0.0108	0.2755317	E
<input type="checkbox"/>	GO:0006406	11,9,6,8,10,7	mRNA export from nucleus	66	0.0102	2	0.0108	0.2755317	E
<input type="checkbox"/>	GO:0030468	8,5,9	establishment of cell polarity (sensu Fungi)	66	0.0102	2	0.0108	0.2755317	E
<input type="checkbox"/>	GO:0000282	7,9,5,6,10	cellular bud site selection	66	0.0102	2	0.0108	0.2755317	E
<input type="checkbox"/>	GO:0007105	6,4	cytokinesis, site selection	66	0.0102	2	0.0108	0.2755317	E
<input type="checkbox"/>	GO:0006825	8,9	copper ion transport	14	0.0022	1	0.0054	0.2757537	E
<input type="checkbox"/>	GO:0006037	8,9,6,7,10	cell wall chitin metabolic process	14	0.0022	1	0.0054	0.2757537	E
<input type="checkbox"/>	GO:0000394	8	RNA splicing, via endonucleolytic cleavage and ligation	14	0.0022	1	0.0054	0.2757537	E
<input type="checkbox"/>	GO:0006272	9,8	leading strand elongation	14	0.0022	1	0.0054	0.2757537	E
<input type="checkbox"/>	GO:0048278	4,5,6	vesicle docking	14	0.0022	1	0.0054	0.2757537	E
<input type="checkbox"/>	GO:0006388	9,8	tRNA splicing	14	0.0022	1	0.0054	0.2757537	E
<input type="checkbox"/>	GO:0000011	6	vacuole inheritance	14	0.0022	1	0.0054	0.2757537	E
<input type="checkbox"/>	GO:0045002	8,7	double-strand break repair via single-strand annealing	14	0.0022	1	0.0054	0.2757537	E
<input type="checkbox"/>	GO:0045990	9,7,8,5	regulation of transcription by carbon catabolites	14	0.0022	1	0.0054	0.2757537	E
<input type="checkbox"/>	GO:0022406	3	membrane docking	14	0.0022	1	0.0054	0.2757537	E
<input type="checkbox"/>	GO:0006892	8,6,5,7	post-Golgi vesicle-mediated transport	69	0.0107	2	0.0108	0.2761338	E
<input type="checkbox"/>	GO:0006031	9,7,8,10	chitin biosynthetic process	15	0.0023	1	0.0054	0.2869920	E
<input type="checkbox"/>	GO:0007091	9,7,5,8,6,4	mitotic metaphase/anaphase transition	15	0.0023	1	0.0054	0.2869920	E
<input type="checkbox"/>	GO:0000737	6,7	DNA catabolic process, endonucleolytic	15	0.0023	1	0.0054	0.2869920	E
<input type="checkbox"/>	GO:0016073	6	snRNA metabolic process	15	0.0023	1	0.0054	0.2869920	E
<input type="checkbox"/>	GO:0031145	11,10,12	anaphase-promoting complex-dependent proteasomal ubiquitin-dependent protein catabolic process	15	0.0023	1	0.0054	0.2869920	E
<input type="checkbox"/>	GO:0032392	6	DNA geometric change	16	0.0025	1	0.0054	0.2973594	E
<input type="checkbox"/>	GO:0032508	7	DNA duplex unwinding	16	0.0025	1	0.0054	0.2973594	E
<input type="checkbox"/>	GO:0010383	7,5,6	cell wall polysaccharide metabolic process	16	0.0025	1	0.0054	0.2973594	E
<input type="checkbox"/>	GO:0006536	7,8	glutamate metabolic process	16	0.0025	1	0.0054	0.2973594	E
<input type="checkbox"/>	GO:0009073	7,6,8	aromatic amino acid family biosynthetic process	16	0.0025	1	0.0054	0.2973594	E

<input type="radio"/>	GO:0016074	6	snoRNA metabolic process	17	0.0026	1	0.0054	0.3068965	E
<input type="radio"/>	GO:0045003	9,8	double-strand break repair via synthesis-dependent strand annealing	17	0.0026	1	0.0054	0.3068965	E
<input type="radio"/>	GO:0009167	8	purine ribonucleoside monophosphate metabolic process	17	0.0026	1	0.0054	0.3068965	E
<input type="radio"/>	GO:0046349	6,7	amino sugar biosynthetic process	17	0.0026	1	0.0054	0.3068965	E
<input type="radio"/>	GO:0006030	8,6,7,9	chitin metabolic process	17	0.0026	1	0.0054	0.3068965	E
<input type="radio"/>	GO:0016053	5	organic acid biosynthetic process	17	0.0026	1	0.0054	0.3068965	E
<input type="radio"/>	GO:0006045	8,9	N-acetylglucosamine biosynthetic process	17	0.0026	1	0.0054	0.3068965	E
<input type="radio"/>	GO:0000742	7,5	karyogamy during conjugation with cellular fusion	17	0.0026	1	0.0054	0.3068965	E
<input type="radio"/>	GO:0000741	6	karyogamy	17	0.0026	1	0.0054	0.3068965	E
<input type="radio"/>	GO:0006042	7,8	glucosamine biosynthetic process	17	0.0026	1	0.0054	0.3068965	E
<input type="radio"/>	GO:0046394	6	carboxylic acid biosynthetic process	17	0.0026	1	0.0054	0.3068965	E
<input type="radio"/>	GO:0009161	7	ribonucleoside monophosphate metabolic process	17	0.0026	1	0.0054	0.3068965	E
<input type="radio"/>	GO:0045132	9,7,8,6,4	meiotic chromosome segregation	17	0.0026	1	0.0054	0.3068965	E
<input type="radio"/>	GO:0009126	7	purine nucleoside monophosphate metabolic process	18	0.0028	1	0.0054	0.3156419	E
<input type="radio"/>	GO:0031570	8,7	DNA integrity checkpoint	18	0.0028	1	0.0054	0.3156419	E
<input type="radio"/>	GO:0007584	6,4	response to nutrient	18	0.0028	1	0.0054	0.3156419	E
<input type="radio"/>	GO:0019438	5	aromatic compound biosynthetic process	18	0.0028	1	0.0054	0.3156419	E
<input type="radio"/>	GO:0000018	8,7	regulation of DNA recombination	18	0.0028	1	0.0054	0.3156419	E
<input type="radio"/>	GO:0055065	8	metal ion homeostasis	19	0.0029	1	0.0054	0.3236332	E
<input type="radio"/>	GO:0006875	9,7	cellular metal ion homeostasis	19	0.0029	1	0.0054	0.3236332	E
<input type="radio"/>	GO:0006044	7,8	N-acetylglucosamine metabolic process	19	0.0029	1	0.0054	0.3236332	E
<input type="radio"/>	GO:0009123	6	nucleoside monophosphate metabolic process	19	0.0029	1	0.0054	0.3236332	E
<input type="radio"/>	GO:0006041	6,7	glucosamine metabolic process	19	0.0029	1	0.0054	0.3236332	E
<input type="radio"/>	GO:0043094	4	metabolic compound salvage	19	0.0029	1	0.0054	0.3236332	E
<input type="radio"/>	GO:0006040	5,6	amino sugar metabolic process	19	0.0029	1	0.0054	0.3236332	E
<input type="radio"/>	GO:0042724	7	thiamin and derivative biosynthetic process	20	0.0031	1	0.0054	0.3309060	E
<input type="radio"/>	GO:0051231	5,4,9,7	spindle elongation	20	0.0031	1	0.0054	0.3309060	E
<input type="radio"/>	GO:0006772	7	thiamin metabolic process	20	0.0031	1	0.0054	0.3309060	E
<input type="radio"/>	GO:0006614	11,10,9,8,7	SRP-dependent cotranslational protein targeting to membrane	20	0.0031	1	0.0054	0.3309060	E
<input type="radio"/>	GO:0000022	6,5,10,8	mitotic spindle elongation	20	0.0031	1	0.0054	0.3309060	E
<input type="radio"/>	GO:0006308	5,6	DNA catabolic process	20	0.0031	1	0.0054	0.3309060	E
<input type="radio"/>	GO:0051053	8,7	negative regulation of DNA metabolic process	20	0.0031	1	0.0054	0.3309060	E
<input type="radio"/>	GO:0019674	9,8	NAD metabolic process	21	0.0032	1	0.0054	0.3374949	E
<input type="radio"/>	GO:0009072	6,5,7	aromatic amino acid family metabolic process	21	0.0032	1	0.0054	0.3374949	E
<input type="radio"/>	GO:0006513	10	protein monoubiquitination	22	0.0034	1	0.0054	0.3434329	E
<input type="radio"/>	GO:0048284	5	organelle fusion	22	0.0034	1	0.0054	0.3434329	E
<input type="radio"/>	GO:0030472	6,5,10	mitotic spindle organization and biogenesis in nucleus	22	0.0034	1	0.0054	0.3434329	E
<input type="radio"/>	GO:0007064	10,8,5,6,9,7,4	mitotic sister chromatid cohesion	22	0.0034	1	0.0054	0.3434329	E
<input type="radio"/>	GO:0043044	10	ATP-dependent chromatin remodeling	23	0.0036	1	0.0054	0.3487518	E
<input type="radio"/>	GO:0006303	8,7	double-strand break repair via nonhomologous end joining	23	0.0036	1	0.0054	0.3487518	E
<input type="radio"/>	GO:0006613	10,9,8,7,6	cotranslational protein targeting to membrane	23	0.0036	1	0.0054	0.3487518	E

<input type="radio"/>	GO:0019748	3	secondary metabolic process	23	0.0036	1	0.0054	0.3487518	E
<input type="radio"/>	GO:0051278	8,7	chitin- and beta-glucan-containing cell wall polysaccharide biosynthetic process	24	0.0037	1	0.0054	0.3534819	E
<input type="radio"/>	GO:0006818	4,5	hydrogen transport	24	0.0037	1	0.0054	0.3534819	E
<input type="radio"/>	GO:0006096	9,10	glycolysis	24	0.0037	1	0.0054	0.3534819	E
<input type="radio"/>	GO:0015992	5,7,6,8	proton transport	24	0.0037	1	0.0054	0.3534819	E
<input type="radio"/>	GO:0048311	7,6	mitochondrion distribution	26	0.0040	1	0.0054	0.3612917	E
<input type="radio"/>	GO:0006506	10,9,8,7,11	GPI anchor biosynthetic process	26	0.0040	1	0.0054	0.3612917	E
<input type="radio"/>	GO:0010382	6,4	cell wall metabolic process	26	0.0040	1	0.0054	0.3612917	E
<input type="radio"/>	GO:0000001	8,7,6	mitochondrion inheritance	26	0.0040	1	0.0054	0.3612917	E
<input type="radio"/>	GO:0051029	5,7,6,8	rRNA transport	26	0.0040	1	0.0054	0.3612917	E
<input type="radio"/>	GO:0006407	11,9,6,8,10,7	rRNA export from nucleus	26	0.0040	1	0.0054	0.3612917	E
<input type="radio"/>	GO:0006505	9,10	GPI anchor metabolic process	27	0.0042	1	0.0054	0.3644263	E
<input type="radio"/>	GO:0009084	7,8	glutamine family amino acid biosynthetic process	27	0.0042	1	0.0054	0.3644263	E
<input type="radio"/>	GO:0051646	6,5	mitochondrion localization	27	0.0042	1	0.0054	0.3644263	E
<input type="radio"/>	GO:0046489	9,8,10	phosphoinositide biosynthetic process	28	0.0043	1	0.0054	0.3670822	E
<input type="radio"/>	GO:0009636	4	response to toxin	28	0.0043	1	0.0054	0.3670822	E
<input type="radio"/>	GO:0042144	6	vacuole fusion, non-autophagic	28	0.0043	1	0.0054	0.3670822	E
<input type="radio"/>	GO:0032507	6,5,4	maintenance of cellular protein localization	29	0.0045	1	0.0054	0.3692842	E
<input type="radio"/>	GO:0006409	11,9,6,8,10,7	tRNA export from nucleus	29	0.0045	1	0.0054	0.3692842	E
<input type="radio"/>	GO:0006470	8,7	protein amino acid dephosphorylation	29	0.0045	1	0.0054	0.3692842	E
<input type="radio"/>	GO:0051651	5,4,3	maintenance of cellular localization	29	0.0045	1	0.0054	0.3692842	E
<input type="radio"/>	GO:0045185	5,4,3	maintenance of protein localization	30	0.0046	1	0.0054	0.3710559	E
<input type="radio"/>	GO:0051031	5,7,6,8	tRNA transport	30	0.0046	1	0.0054	0.3710559	E
<input type="radio"/>	GO:0006665	6,7	sphingolipid metabolic process	30	0.0046	1	0.0054	0.3710559	E
<input type="radio"/>	GO:0007062	7,4	sister chromatid cohesion	31	0.0048	1	0.0054	0.3724202	E
<input type="radio"/>	GO:0015672	6,7	monovalent inorganic cation transport	32	0.0049	1	0.0054	0.3733988	E
<input type="radio"/>	GO:0007121	8,6,10,7,11,5	bipolar cellular bud site selection	32	0.0049	1	0.0054	0.3733988	E
<input type="radio"/>	GO:0042546	6	cell wall biogenesis	33	0.0051	1	0.0054	0.3740126	E
<input type="radio"/>	GO:0009272	7	chitin- and beta-glucan-containing cell wall biogenesis	33	0.0051	1	0.0054	0.3740126	E
<input type="radio"/>	GO:0051235	3,2	maintenance of localization	33	0.0051	1	0.0054	0.3740126	E
<input type="radio"/>	GO:0006869	4,5	lipid transport	34	0.0053	1	0.0054	0.3742818	E
<input type="radio"/>	GO:0006007	8,9	glucose catabolic process	34	0.0053	1	0.0054	0.3742818	E
<input type="radio"/>	GO:0008150	1	biological process	6476	1.0000	186	1.0000	1.0000000	D
<input type="radio"/>	GO:0046165	5	alcohol biosynthetic process	35	0.0054	1	0.0054	0.3742254	D
<input type="radio"/>	GO:0009605	3	response to external stimulus	37	0.0057	1	0.0054	0.3732087	D
<input type="radio"/>	GO:0009991	4	response to extracellular stimulus	37	0.0057	1	0.0054	0.3732087	D
<input type="radio"/>	GO:0031667	5	response to nutrient levels	37	0.0057	1	0.0054	0.3732087	D
<input type="radio"/>	GO:0019320	7,8	hexose catabolic process	39	0.0060	1	0.0054	0.3711005	D
<input type="radio"/>	GO:0043681	6,7,8	protein import into mitochondrion	40	0.0062	1	0.0054	0.3696770	D
<input type="radio"/>	GO:0007031	5	peroxisome organization and biogenesis	40	0.0062	1	0.0054	0.3696770	D
<input type="radio"/>	GO:0000271	6,7	polysaccharide biosynthetic process	41	0.0063	1	0.0054	0.3680271	D
<input type="radio"/>	GO:0016311	6	dephosphorylation	41	0.0063	1	0.0054	0.3680271	D
<input type="radio"/>	GO:0042244	5,6	spore wall assembly	42	0.0065	1	0.0054	0.3661649	D
<input type="radio"/>	GO:0030476	8,6,7	spore wall assembly (sensu Fungi)	42	0.0065	1	0.0054	0.3661649	D

<input type="radio"/>	GO:0030384	8,9	phosphoinositide metabolic process	43	0.0066	1	0.0054	0.3641039	D
<input type="radio"/>	GO:0009064	6,7	glutamine family amino acid metabolic process	43	0.0066	1	0.0054	0.3641039	D
<input type="radio"/>	GO:0046365	6,7	monosaccharide catabolic process	44	0.0068	1	0.0054	0.3618570	D
<input type="radio"/>	GO:0006752	6	group transfer coenzyme metabolic process	44	0.0068	1	0.0054	0.3618570	D
<input type="radio"/>	GO:0006887	8,6,5,7	exocytosis	44	0.0068	1	0.0054	0.3618570	D
<input type="radio"/>	GO:0000462	8,9	maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	45	0.0069	1	0.0054	0.3594366	D
<input type="radio"/>	GO:0030490	7,8	maturation of SSU-rRNA	45	0.0069	1	0.0054	0.3594366	D
<input type="radio"/>	GO:0046164	5	alcohol catabolic process	47	0.0073	1	0.0054	0.3541217	D
<input type="radio"/>	GO:0006631	5,7,6	fatty acid metabolic process	47	0.0073	1	0.0054	0.3541217	D
<input type="radio"/>	GO:0006413	7,6	translational initiation	49	0.0076	1	0.0054	0.3482473	D
<input type="radio"/>	GO:0006400	7,8	tRNA modification	52	0.0080	1	0.0054	0.3385598	D
<input type="radio"/>	GO:0006626	9,8,7,6	protein targeting to mitochondrion	52	0.0080	1	0.0054	0.3385598	D
<input type="radio"/>	GO:0007015	8	actin filament organization	61	0.0094	1	0.0054	0.3052634	D
<input type="radio"/>	GO:0007264	6	small GTPase mediated signal transduction	61	0.0094	1	0.0054	0.3052634	D
<input type="radio"/>	GO:0043161	10,9,11	proteasomal ubiquitin-dependent protein catabolic process	63	0.0097	1	0.0054	0.2973488	D
<input type="radio"/>	GO:0006839	7,5,6	mitochondrial transport	65	0.0100	1	0.0054	0.2893422	D
<input type="radio"/>	GO:0005976	5	polysaccharide metabolic process	65	0.0100	1	0.0054	0.2893422	D
<input type="radio"/>	GO:0006006	7,8	glucose metabolic process	65	0.0100	1	0.0054	0.2893422	D
<input type="radio"/>	GO:0044264	5,6	cellular polysaccharide metabolic process	65	0.0100	1	0.0054	0.2893422	D
<input type="radio"/>	GO:0009108	6	coenzyme biosynthetic process	66	0.0102	1	0.0054	0.2853157	D
<input type="radio"/>	GO:0006790	4	sulfur metabolic process	67	0.0103	1	0.0054	0.2812793	D
<input type="radio"/>	GO:0006623	9,8,7,6	protein targeting to vacuole	67	0.0103	1	0.0054	0.2812793	D
<input type="radio"/>	GO:0046483	4	heterocycle metabolic process	76	0.0117	2	0.0108	0.2735331	D
<input type="radio"/>	GO:0043623	7,6	cellular protein complex assembly	69	0.0107	1	0.0054	0.2731925	D
<input type="radio"/>	GO:0000226	7	microtubule cytoskeleton organization and biogenesis	81	0.0125	2	0.0108	0.2687479	D
<input type="radio"/>	GO:0008033	7	tRNA processing	84	0.0130	2	0.0108	0.2649015	D
<input type="radio"/>	GO:0006512	8	ubiquitin cycle	88	0.0136	2	0.0108	0.2588073	D
<input type="radio"/>	GO:0006486	8,7,6	protein amino acid glycosylation	73	0.0113	1	0.0054	0.2570582	D
<input type="radio"/>	GO:0043413	6	biopolymer glycosylation	73	0.0113	1	0.0054	0.2570582	D
<input type="radio"/>	GO:0016051	5	carbohydrate biosynthetic process	77	0.0119	1	0.0054	0.2411327	D
<input type="radio"/>	GO:0009101	7,5	glycoprotein biosynthetic process	78	0.0120	1	0.0054	0.2372025	D
<input type="radio"/>	GO:0009100	6	glycoprotein metabolic process	79	0.0122	1	0.0054	0.2332968	D
<input type="radio"/>	GO:0051188	5	cofactor biosynthetic process	79	0.0122	1	0.0054	0.2332968	D
<input type="radio"/>	GO:0016052	5	carbohydrate catabolic process	80	0.0124	1	0.0054	0.2294176	D
<input type="radio"/>	GO:0044275	6	cellular carbohydrate catabolic process	80	0.0124	1	0.0054	0.2294176	D
<input type="radio"/>	GO:0048622	6,5	reproductive sporulation	108	0.0167	3	0.0161	0.2286644	D
<input type="radio"/>	GO:0030437	7,6	sporulation (sensu Fungi)	108	0.0167	3	0.0161	0.2286644	D
<input type="radio"/>	GO:0009309	5,6	amine biosynthetic process	114	0.0176	3	0.0161	0.2260873	D
<input type="radio"/>	GO:0007163	6,3,7	establishment and/or maintenance of cell polarity	115	0.0178	3	0.0161	0.2254657	D
<input type="radio"/>	GO:0044271	5,4	nitrogen compound biosynthetic process	115	0.0178	3	0.0161	0.2254657	D
<input type="radio"/>	GO:0006461	6,5	protein complex assembly	116	0.0179	3	0.0161	0.2247929	D
<input type="radio"/>	GO:0007059	3	chromosome segregation	119	0.0184	3	0.0161	0.2224806	D
<input type="radio"/>	GO:0008652	6,7	amino acid biosynthetic process	106	0.0164	2	0.0108	0.2221696	D

<input type="radio"/>	GO:0030036	7	actin cytoskeleton organization and biogenesis	107	0.0165	2	0.0108	0.2198617	D
<input type="radio"/>	GO:0030435	5	sporulation	123	0.0190	3	0.0161	0.2187626	D
<input type="radio"/>	GO:0009060	6	aerobic respiration	84	0.0130	1	0.0054	0.2141984	D
<input type="radio"/>	GO:0007005	5	mitochondrion organization and biogenesis	110	0.0170	2	0.0108	0.2128523	D
<input type="radio"/>	GO:0019318	6,7	hexose metabolic process	85	0.0131	1	0.0054	0.2104752	D
<input type="radio"/>	GO:0030029	6	actin filament-based process	112	0.0173	2	0.0108	0.2081244	D
<input type="radio"/>	GO:0006897	6,5	endocytosis	86	0.0133	1	0.0054	0.2067870	D
<input type="radio"/>	GO:0007034	7,5,6	vacuolar transport	114	0.0176	2	0.0108	0.2033667	D
<input type="radio"/>	GO:0045333	5	cellular respiration	89	0.0137	1	0.0054	0.1959438	D
<input type="radio"/>	GO:0006970	4	response to osmotic stress	89	0.0137	1	0.0054	0.1959438	D
<input type="radio"/>	GO:0015980	4	energy derivation by oxidation of organic compounds	145	0.0224	3	0.0161	0.1889116	D
<input type="radio"/>	GO:0005996	5,6	monosaccharide metabolic process	92	0.0142	1	0.0054	0.1854504	D
<input type="radio"/>	GO:0048610	3,4	reproductive cellular process	149	0.0230	3	0.0161	0.1823859	D
<input type="radio"/>	GO:0022413	5,4	reproductive process in single-celled organism	149	0.0230	3	0.0161	0.1823859	D
<input type="radio"/>	GO:0016044	4	membrane organization and biogenesis	188	0.0290	5	0.0269	0.1774173	D
<input type="radio"/>	GO:0032787	6	monocarboxylic acid metabolic process	126	0.0195	2	0.0108	0.1747807	D
<input type="radio"/>	GO:0016310	6	phosphorylation	155	0.0239	3	0.0161	0.1722898	D
<input type="radio"/>	GO:0010324	5	membrane invagination	96	0.0148	1	0.0054	0.1720339	D
<input type="radio"/>	GO:0007047	5	cell wall organization and biogenesis	200	0.0309	5	0.0269	0.1707710	D
<input type="radio"/>	GO:0045229	4	external encapsulating structure organization and biogenesis	200	0.0309	5	0.0269	0.1707710	D
<input type="radio"/>	GO:0006519	4	amino acid and derivative metabolic process	202	0.0312	5	0.0269	0.1693631	D
<input type="radio"/>	GO:0007165	4	signal transduction	209	0.0323	6	0.0323	0.1656692	D
<input type="radio"/>	GO:0006520	5,6	amino acid metabolic process	187	0.0289	4	0.0215	0.1630491	D
<input type="radio"/>	GO:0009308	4	amine metabolic process	228	0.0352	6	0.0323	0.1613587	D
<input type="radio"/>	GO:0045941	8,7	positive regulation of transcription	101	0.0156	1	0.0054	0.1562238	D
<input type="radio"/>	GO:0006807	3	nitrogen compound metabolic process	251	0.0388	7	0.0376	0.1535461	D
<input type="radio"/>	GO:0006357	9,8	regulation of transcription from RNA polymerase II promoter	221	0.0341	5	0.0269	0.1527540	D
<input type="radio"/>	GO:0045935	7,6	positive regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	108	0.0167	1	0.0054	0.1359189	D
<input type="radio"/>	GO:0006793	4	phosphorus metabolic process	212	0.0327	4	0.0215	0.1295679	D
<input type="radio"/>	GO:0006796	5	phosphate metabolic process	212	0.0327	4	0.0215	0.1295679	D
<input type="radio"/>	GO:0006091	3	generation of precursor metabolites and energy	183	0.0283	3	0.0161	0.1247070	D
<input type="radio"/>	GO:0031325	6,5	positive regulation of cellular metabolic process	116	0.0179	1	0.0054	0.1152992	D
<input type="radio"/>	GO:0009893	5,4	positive regulation of metabolic process	116	0.0179	1	0.0054	0.1152992	D
<input type="radio"/>	GO:0009628	3	response to abiotic stimulus	117	0.0181	1	0.0054	0.1129105	D
<input type="radio"/>	GO:0048518	4	positive regulation of biological process	124	0.0191	1	0.0054	0.0973132	D
<input type="radio"/>	GO:0048522	5,4	positive regulation of cellular process	124	0.0191	1	0.0054	0.0973132	D
<input type="radio"/>	GO:0006082	4	organic acid metabolic process	314	0.0485	6	0.0323	0.0891829	D
<input type="radio"/>	GO:0019752	5	carboxylic acid metabolic process	314	0.0485	6	0.0323	0.0891829	D
<input type="radio"/>	GO:0016192	4,5	vesicle-mediated transport	328	0.0506	6	0.0323	0.0766294	D
<input type="radio"/>	GO:0006508	6	proteolysis	178	0.0275	2	0.0108	0.0753068	D
<input type="radio"/>	GO:0009451	6	RNA modification	139	0.0215	1	0.0054	0.0699843	D
<input type="radio"/>	GO:0019941	8,7,9	modification-dependent protein catabolic	148	0.0228	1	0.0054	0.0570616	D

<input type="checkbox"/>	GO:0019941	9,7,8	process	148	0.0229	1	0.0054	0.0570046	<input type="checkbox"/>
<input type="checkbox"/>	GO:0006511	9,8,10	ubiquitin-dependent protein catabolic process	148	0.0229	1	0.0054	0.0570646	<input type="checkbox"/>
<input type="checkbox"/>	GO:0051603	7,8	proteolysis involved in cellular protein catabolic process	151	0.0233	1	0.0054	0.0532621	<input type="checkbox"/>
<input type="checkbox"/>	GO:0043632	6	modification-dependent macromolecule catabolic process	155	0.0239	1	0.0054	0.0485503	<input type="checkbox"/>
<input type="checkbox"/>	GO:0044257	6,7	cellular protein catabolic process	160	0.0247	1	0.0054	0.0431974	<input type="checkbox"/>
<input type="checkbox"/>	GO:0044262	5	cellular carbohydrate metabolic process	213	0.0329	2	0.0108	0.0381254	<input type="checkbox"/>
<input type="checkbox"/>	GO:0030163	6,5	protein catabolic process	173	0.0267	1	0.0054	0.0317235	<input type="checkbox"/>
<input type="checkbox"/>	GO:0005975	4	carbohydrate metabolic process	233	0.0360	2	0.0108	0.0251153	<input type="checkbox"/>
<input type="checkbox"/>	GO:0043284	5	biopolymer biosynthetic process	354	0.0547	3	0.0161	0.0054548	<input type="checkbox"/>
<input type="checkbox"/>	GO:0006414	7,6	translational elongation	313	0.0483	2	0.0108	0.0040801	<input type="checkbox"/>