

GO-Stats Results

Your dataset contains **799** 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:0022613	4	ribonucleoprotein complex biogenesis and assembly	483	0.0746	215	0.2691	3.243243E-74	E
<input type="radio"/> GO:0042254	5	ribosome biogenesis and assembly	410	0.0633	191	0.2390	5.595199E-69	E
<input type="radio"/> GO:0009987	2	cellular process	4654	0.7187	732	0.9161	1.743542E-45	E
<input type="radio"/> GO:0006139	4	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	1532	0.2366	357	0.4468	4.841747E-42	E
<input type="radio"/> GO:0006396	6	RNA processing	491	0.0758	171	0.2140	3.803117E-39	E
<input type="radio"/> GO:0006996	4	organelle organization and biogenesis	1388	0.2143	328	0.4105	1.074381E-38	E
<input type="radio"/> GO:0016043	3	cellular component organization and biogenesis	2264	0.3496	453	0.5670	2.806947E-38	E
<input type="radio"/> GO:0016070	5	RNA metabolic process	1058	0.1634	272	0.3404	3.034026E-37	E
<input type="radio"/> GO:0016072	6	rRNA metabolic process	256	0.0395	108	0.1352	9.628789E-32	E
<input type="radio"/> GO:0006364	6,7	rRNA processing	249	0.0384	104	0.1302	5.482138E-30	E
<input type="radio"/> GO:0008152	2	metabolic process	3516	0.5429	577	0.7222	9.641343E-26	E
<input type="radio"/> GO:0044238	3	primary metabolic process	3247	0.5014	542	0.6783	2.120387E-24	E
<input type="radio"/> GO:0044237	3	cellular metabolic process	3403	0.5255	556	0.6959	8.082449E-23	E
<input type="radio"/> GO:0042273	6,5	ribosomal large subunit biogenesis and assembly	64	0.0099	42	0.0526	1.672340E-20	E
<input type="radio"/> GO:0000460	7,8	maturation of 5.8S rRNA	36	0.0056	29	0.0363	1.222792E-17	E
<input type="radio"/> GO:0000466	8,9	maturation of 5.8S rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	34	0.0053	27	0.0338	5.493389E-16	E
<input type="radio"/> GO:0022618	6,5	protein-RNA complex assembly	144	0.0222	58	0.0726	9.101849E-15	E
<input type="radio"/> GO:0043283	4	biopolymer metabolic process	2230	0.3443	381	0.4768	6.151671E-14	E
<input type="radio"/> GO:0030490	7,8	maturation of SSU-rRNA	45	0.0069	28	0.0350	3.768537E-12	E
<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	28	0.0350	3.768537E-12	E

<input type="radio"/>	GO:0043170	3	macromolecule metabolic process	2841	0.4387	452	0.5657	2.581480E-12	E
<input type="radio"/>	GO:0006399	6	tRNA metabolic process	121	0.0187	48	0.0601	1.361111E-11	E
<input type="radio"/>	GO:0006520	5,6	amino acid metabolic process	187	0.0289	60	0.0751	4.423457E-10	E
<input type="radio"/>	GO:0006519	4	amino acid and derivative metabolic process	202	0.0312	63	0.0788	4.705826E-10	E
<input type="radio"/>	GO:0008033	7	tRNA processing	84	0.0130	36	0.0451	1.990519E-09	E
<input type="radio"/>	GO:0065003	5,4	macromolecular complex assembly	328	0.0506	84	0.1051	8.968112E-09	E
<input type="radio"/>	GO:0006400	7,8	tRNA modification	52	0.0080	26	0.0325	3.708831E-08	E
<input type="radio"/>	GO:0006725	4	aromatic compound metabolic process	60	0.0093	28	0.0350	5.206356E-08	E
<input type="radio"/>	GO:0044249	4	cellular biosynthetic process	366	0.0565	88	0.1101	1.016410E-07	E
<input type="radio"/>	GO:0042255	7,6	ribosome assembly	66	0.0102	29	0.0363	1.423325E-07	E
<input type="radio"/>	GO:0000027	9,7,8,6	ribosomal large subunit assembly and maintenance	41	0.0063	22	0.0275	2.125010E-07	E
<input type="radio"/>	GO:0000479	8,9	endonucleolytic cleavage of tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	20	0.0031	15	0.0188	2.140170E-07	E
<input type="radio"/>	GO:0000478	7,8	endonucleolytic cleavages during rRNA processing	20	0.0031	15	0.0188	2.140170E-07	E
<input type="radio"/>	GO:0000447	9,10	endonucleolytic cleavage between SSU-rRNA and 5.8S rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	20	0.0031	15	0.0188	2.140170E-07	E
<input type="radio"/>	GO:0008652	6,7	amino acid biosynthetic process	106	0.0164	38	0.0476	2.750876E-07	E
<input type="radio"/>	GO:0022607	4	cellular component assembly	471	0.0727	104	0.1302	3.550861E-07	E
<input type="radio"/>	GO:0009308	4	amine metabolic process	228	0.0352	62	0.0776	4.218749E-07	E
<input type="radio"/>	GO:0009309	5,6	amine biosynthetic process	114	0.0176	39	0.0488	7.676336E-07	E
<input type="radio"/>	GO:0044271	5,4	nitrogen compound biosynthetic process	115	0.0178	39	0.0488	1.022793E-06	E
<input type="radio"/>	GO:0000470	7,8	maturation of LSU-rRNA	14	0.0022	12	0.0150	1.028737E-06	E
<input type="radio"/>	GO:0000463	8,9	maturation of LSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	14	0.0022	12	0.0150	1.028737E-06	E
<input type="radio"/>	GO:0006807	3	nitrogen compound metabolic process	251	0.0388	64	0.0801	3.612316E-06	E
<input type="radio"/>	GO:0006360	8,7	transcription from RNA polymerase I promoter	34	0.0053	18	0.0225	1.312243E-05	E
<input type="radio"/>	GO:0006413	7,6	translational initiation	49	0.0076	22	0.0275	1.541006E-05	E
<input type="radio"/>	GO:0042257	8,7	ribosomal subunit assembly	55	0.0085	23	0.0288	3.675545E-05	E
<input type="radio"/>	GO:0006913	8,6,7	nucleocytoplasmic transport	129	0.0199	39	0.0488	3.710269E-05	E
<input type="radio"/>	GO:0051169	7,5,6	nuclear transport	129	0.0199	39	0.0488	3.710269E-05	E
<input type="radio"/>	GO:0006206	6	pyrimidine base metabolic process	17	0.0026	12	0.0150	4.737857E-05	E
<input type="radio"/>	GO:0051168	9,7,8	nuclear export	102	0.0158	33	0.0413	7.157357E-05	E
<input type="radio"/>	GO:0019856	7,6	pyrimidine base biosynthetic process	15	0.0023	11	0.0138	9.757927E-05	E
<input type="radio"/>	GO:0046483	4	heterocycle metabolic process	76	0.0117	27	0.0338	0.0001340	E
<input type="radio"/>	GO:0009112	5	nucleobase metabolic process	31	0.0048	16	0.0200	0.0001381	E
<input type="radio"/>	GO:0000054	10,11,6,8,9	ribosome export from nucleus	28	0.0043	15	0.0188	0.0001834	E

<input type="checkbox"/>	GO:0019752	5	carboxylic acid metabolic process	314	0.0485	70	0.0876	0.0002093	E
<input type="checkbox"/>	GO:0006082	4	organic acid metabolic process	314	0.0485	70	0.0876	0.0002093	E
<input type="checkbox"/>	GO:0006611	9,10,7,8	protein export from nucleus	56	0.0086	22	0.0275	0.0002694	E
<input type="checkbox"/>	GO:0046112	6,5	nucleobase biosynthetic process	21	0.0032	12	0.0150	0.0013381	E
<input type="checkbox"/>	GO:0016071	6	mRNA metabolic process	210	0.0324	50	0.0626	0.0016151	E
<input type="checkbox"/>	GO:0009101	7,5	glycoprotein biosynthetic process	78	0.0120	24	0.0300	0.0110469	E
<input type="checkbox"/>	GO:0008380	7	RNA splicing	132	0.0204	34	0.0426	0.0129812	E
<input type="checkbox"/>	GO:0009100	6	glycoprotein metabolic process	79	0.0122	24	0.0300	0.0139453	E
<input type="checkbox"/>	GO:0019438	5	aromatic compound biosynthetic process	18	0.0028	10	0.0125	0.0152160	E
<input type="checkbox"/>	GO:0009451	6	RNA modification	139	0.0215	35	0.0438	0.0162926	E
<input type="checkbox"/>	GO:0030488	8,9	tRNA methylation	15	0.0023	9	0.0113	0.0184703	E
<input type="checkbox"/>	GO:0006696	7,8,9	ergosterol biosynthetic process	26	0.0040	12	0.0150	0.0229460	E
<input type="checkbox"/>	GO:0008204	6,7,8	ergosterol metabolic process	26	0.0040	12	0.0150	0.0229460	E
<input type="checkbox"/>	GO:0006220	6	pyrimidine nucleotide metabolic process	7	0.0011	6	0.0075	0.0270000	E
<input type="checkbox"/>	GO:0009123	6	nucleoside monophosphate metabolic process	19	0.0029	10	0.0125	0.0281980	E
<input type="checkbox"/>	GO:0009073	7,6,8	aromatic amino acid family biosynthetic process	16	0.0025	9	0.0113	0.0370558	E
<input type="checkbox"/>	GO:0009081	6,7	branched chain family amino acid metabolic process	16	0.0025	9	0.0113	0.0370558	E
<input type="checkbox"/>	GO:0009082	7,8	branched chain family amino acid biosynthetic process	13	0.0020	8	0.0100	0.0442117	E
<input type="checkbox"/>	GO:0006260	6	DNA replication	117	0.0181	30	0.0375	0.0443304	E
<input type="checkbox"/>	GO:0006401	6	RNA catabolic process	74	0.0114	22	0.0275	0.0448531	E
<input type="checkbox"/>	GO:0006351	7,6	transcription, DNA-dependent	522	0.0806	93	0.1164	0.0490947	E
<input type="checkbox"/>	GO:0032774	6	RNA biosynthetic process	524	0.0809	93	0.1164	0.0564004	E
<input type="checkbox"/>	GO:0006350	5	transcription	567	0.0876	99	0.1239	0.0619651	E
<input type="checkbox"/>	GO:0009066	6,7	aspartate family amino acid metabolic process	46	0.0071	16	0.0200	0.0651407	E
<input type="checkbox"/>	GO:0009124	6,7	nucleoside monophosphate biosynthetic process	17	0.0026	9	0.0113	0.0691139	E
<input type="checkbox"/>	GO:0031323	5,4	regulation of cellular metabolic process	507	0.0783	90	0.1126	0.0727678	E
<input type="checkbox"/>	GO:0016125	5,6,7	sterol metabolic process	42	0.0065	15	0.0188	0.0785320	E
<input type="checkbox"/>	GO:0009072	6,5,7	aromatic amino acid family metabolic process	21	0.0032	10	0.0125	0.0829592	E
<input type="checkbox"/>	GO:0006383	8,7	transcription from RNA polymerase III promoter	38	0.0059	14	0.0175	0.0931924	E
<input type="checkbox"/>	GO:0008202	5,6	steroid metabolic process	43	0.0066	15	0.0188	0.1059070	E
<input type="checkbox"/>	GO:0006486	8,7,6	protein amino acid glycosylation	73	0.0113	21	0.0263	0.1097457	E
<input type="checkbox"/>	GO:0043413	6	biopolymer glycosylation	73	0.0113	21	0.0263	0.1097457	E
<input type="checkbox"/>	GO:0009116	5	nucleoside metabolic process	18	0.0028	9	0.0113	0.1213211	E
<input type="checkbox"/>	GO:0009126	7	purine nucleoside monophosphate metabolic process	18	0.0028	9	0.0113	0.1213211	E
<input type="checkbox"/>	GO:0015931	4,5	nucleobase, nucleoside, nucleotide and nucleic acid transport	90	0.0139	24	0.0300	0.1303394	E
<input type="checkbox"/>	GO:0006261	7	DNA-dependent DNA replication	97	0.0150	25	0.0313	0.1676598	E
<input type="checkbox"/>	GO:0016073	6	snRNA metabolic process	15	0.0023	8	0.0100	0.1702557	E
<input type="checkbox"/>	GO:0043094	4	metabolic compound salvage	19	0.0029	9	0.0113	0.2023121	E
<input type="checkbox"/>	GO:0006397	7	mRNA processing	157	0.0242	35	0.0438	0.2045515	E
<input type="checkbox"/>	GO:0016126	6,7,8	sterol biosynthetic process	32	0.0049	12	0.0150	0.2456545	E
<input type="checkbox"/>	GO:0006694	6,5,7	steroid biosynthetic process	32	0.0049	12	0.0150	0.2456545	E
<input type="checkbox"/>	GO:0009262	6	deoxyribonucleotide metabolic process	9	0.0014	6	0.0075	0.2494282	E

<input type="radio"/>	GO:0018193	7	peptidyl-amino acid modification	28	0.0043	11	0.0138	0.2825412	E
<input type="radio"/>	GO:0045943	10,9	positive regulation of transcription from RNA polymerase I promoter	4	0.0006	4	0.0050	0.2916572	E
<input type="radio"/>	GO:0009127	7,8	purine nucleoside monophosphate biosynthetic process	16	0.0025	8	0.0100	0.2988236	E
<input type="radio"/>	GO:0006403	4	RNA localization	90	0.0139	23	0.0288	0.3375910	E
<input type="radio"/>	GO:0000398	8,10	nuclear mRNA splicing, via spliceosome	102	0.0158	25	0.0313	0.3700944	E
<input type="radio"/>	GO:0000377	9	RNA splicing, via transesterification reactions with bulged adenosine as nucleophile	103	0.0159	25	0.0313	0.4293694	E
<input type="radio"/>	GO:0016074	6	snoRNA metabolic process	17	0.0026	8	0.0100	0.4953307	E
<input type="radio"/>	GO:0009161	7	ribonucleoside monophosphate metabolic process	17	0.0026	8	0.0100	0.4953307	E
<input type="radio"/>	GO:0009167	8	purine ribonucleoside monophosphate metabolic process	17	0.0026	8	0.0100	0.4953307	E
<input type="radio"/>	GO:0019222	4,3	regulation of metabolic process	538	0.0831	90	0.1126	0.4992326	E
<input type="radio"/>	GO:0000375	8	RNA splicing, via transesterification reactions	110	0.0170	26	0.0325	0.5057125	E
<input type="radio"/>	GO:0019219	6,5	regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	440	0.0679	76	0.0951	0.5258771	E
<input type="radio"/>	GO:0006446	8,7,6	regulation of translational initiation	10	0.0015	6	0.0075	0.5471066	E
<input type="radio"/>	GO:0006402	7	mRNA catabolic process	60	0.0093	17	0.0213	0.5729398	E
<input type="radio"/>	GO:0040029	4	regulation of gene expression, epigenetic	100	0.0154	24	0.0300	0.6475644	E
<input type="radio"/>	GO:0007049	3	cell cycle	458	0.0707	78	0.0976	0.6671927	E
<input type="radio"/>	GO:0009075	6,7	histidine family amino acid metabolic process	14	0.0022	7	0.0088	0.7408701	E
<input type="radio"/>	GO:0006547	7,8	histidine metabolic process	14	0.0022	7	0.0088	0.7408701	E
<input type="radio"/>	GO:0000105	8,9	histidine biosynthetic process	14	0.0022	7	0.0088	0.7408701	E
<input type="radio"/>	GO:0009076	7,8	histidine family amino acid biosynthetic process	14	0.0022	7	0.0088	0.7408701	E
<input type="radio"/>	GO:0006405	10,8,5,7,9,6	RNA export from nucleus	79	0.0122	20	0.0250	0.8891301	E
<input type="radio"/>	GO:0045449	7,6	regulation of transcription	386	0.0596	67	0.0839	0.9153812	E
<input type="radio"/>	GO:0006355	8,7	regulation of transcription, DNA-dependent	359	0.0554	63	0.0788	0.9667154	E
<input type="radio"/>	GO:0000173	10,11,8,9,7	inactivation of MAPK activity during osmolarity sensing	5	0.0008	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0019878	9,10	lysine biosynthetic process via amino adipic acid	8	0.0012	2	0.0025	1.0000000	E
<input type="radio"/>	GO:0046019	10,9,6	regulation of transcription from RNA polymerase II promoter by pheromones	10	0.0015	3	0.0038	1.0000000	E
<input type="radio"/>	GO:0000097	7,8,6	sulfur amino acid biosynthetic process	13	0.0020	5	0.0063	1.0000000	E
<input type="radio"/>	GO:0046656	7,8,9	folic acid biosynthetic process	2	0.0003	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0019284	9,7,8,6,10	methionine biosynthetic process from S-adenosylmethionine	1	0.0002	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0046125	7	pyrimidine deoxyribonucleoside metabolic process	3	0.0005	2	0.0025	1.0000000	E
<input type="radio"/>	GO:0016571	11,9,10,8	histone methylation	18	0.0028	4	0.0050	1.0000000	E
<input type="radio"/>	GO:0030030	7,6,8	cell projection organization and biogenesis	8	0.0012	2	0.0025	1.0000000	E
<input type="radio"/>	GO:0006568	7,8,6	tryptophan metabolic process	10	0.0015	4	0.0050	1.0000000	E
<input type="radio"/>	GO:0009226	5,6	nucleotide-sugar biosynthetic process	2	0.0003	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0006488	10,9,8	dolichol-linked oligosaccharide biosynthetic process	11	0.0017	2	0.0025	1.0000000	E
<input type="radio"/>	GO:0045740	9,8	positive regulation of DNA replication	2	0.0003	2	0.0025	1.0000000	E
<input type="radio"/>	GO:0006452	8,7,6	translational frameshifting	3	0.0005	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0016077	7	snoRNA catabolic process	4	0.0006	2	0.0025	1.0000000	E
<input type="radio"/>	GO:0016180	7	snRNA processing	4	0.0006	2	0.0025	1.0000000	E

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<input type="radio"/>	GO:0009225	5	nucleotide-sugar metabolic process	7	0.0011	2	0.0025	1.0000000	E
<input type="radio"/>	GO:0031497	5,9	chromatin assembly	104	0.0161	24	0.0300	1.0000000	E
<input type="radio"/>	GO:0008610	5,4,6	lipid biosynthetic process	129	0.0199	24	0.0300	1.0000000	E
<input type="radio"/>	GO:0015940	7,8	pantothenate biosynthetic process	8	0.0012	3	0.0038	1.0000000	E
<input type="radio"/>	GO:0000390	7,9,11	spliceosome disassembly	4	0.0006	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0000032	8,6,9,7	cell wall mannoprotein biosynthetic process	12	0.0019	6	0.0075	1.0000000	E
<input type="radio"/>	GO:0007001	6	chromosome organization and biogenesis (sensu Eukaryota)	567	0.0876	87	0.1089	1.0000000	E
<input type="radio"/>	GO:0015867	8,9	ATP transport	3	0.0005	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0000320	7,6	re-entry into mitotic cell cycle	3	0.0005	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0015959	9	diadenosine polyphosphate metabolic process	1	0.0002	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0051439	7,5,4	regulation of ubiquitin ligase activity during mitotic cell cycle	5	0.0008	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0009220	7,8	pyrimidine ribonucleotide biosynthetic process	2	0.0003	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0033353	7,6	S-adenosylmethionine cycle	1	0.0002	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0015865	6,7	purine nucleotide transport	4	0.0006	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0009133	6,7	nucleoside diphosphate biosynthetic process	2	0.0003	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0006221	6,7	pyrimidine nucleotide biosynthetic process	5	0.0008	4	0.0050	1.0000000	E
<input type="radio"/>	GO:0000481	7,8	maturation of 5S rRNA	1	0.0002	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0043433	9,8	negative regulation of transcription factor activity	1	0.0002	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0009213	8,9	pyrimidine deoxyribonucleoside triphosphate catabolic process	1	0.0002	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0006259	5	DNA metabolic process	523	0.0808	82	0.1026	1.0000000	E
<input type="radio"/>	GO:0008156	9,8	negative regulation of DNA replication	8	0.0012	2	0.0025	1.0000000	E
<input type="radio"/>	GO:0009141	6	nucleoside triphosphate metabolic process	30	0.0046	4	0.0050	1.0000000	E
<input type="radio"/>	GO:0009264	6,7	deoxyribonucleotide catabolic process	5	0.0008	3	0.0038	1.0000000	E
<input type="radio"/>	GO:0046020	11,10,7	negative regulation of transcription from RNA polymerase II promoter by pheromones	6	0.0009	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0033313	8,7	meiotic cell cycle checkpoint	2	0.0003	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0016568	8	chromatin modification	223	0.0344	33	0.0413	1.0000000	E
<input type="radio"/>	GO:0043174	5	nucleoside salvage	6	0.0009	3	0.0038	1.0000000	E
<input type="radio"/>	GO:0019860	7	uracil metabolic process	1	0.0002	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0030468	8,5,9	establishment of cell polarity (sensu Fungi)	66	0.0102	15	0.0188	1.0000000	E
<input type="radio"/>	GO:0007000	6	nucleolus organization and biogenesis	2	0.0003	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0008298	5	intracellular mRNA localization	10	0.0015	3	0.0038	1.0000000	E
<input type="radio"/>	GO:0009166	5,6	nucleotide catabolic process	7	0.0011	3	0.0038	1.0000000	E
<input type="radio"/>	GO:0006544	7,8	glycine metabolic process	6	0.0009	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0031935	11,7,4,8,12,10	regulation of chromatin silencing	6	0.0009	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0030497	8,7,9,6	fatty acid elongation	4	0.0006	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0006408	11,9,6,8,10,7	snRNA export from nucleus	23	0.0036	7	0.0088	1.0000000	E
<input type="radio"/>	GO:0001301	9,5	progressive alteration of chromatin during cell aging	10	0.0015	2	0.0025	1.0000000	E
<input type="radio"/>	GO:0000056	11,12,7,9,10	ribosomal small subunit export from nucleus	7	0.0011	3	0.0038	1.0000000	E
<input type="radio"/>	GO:0006612	9,7,8	protein targeting to membrane	39	0.0060	7	0.0088	1.0000000	E
<input type="radio"/>	GO:0065004	6,5	protein-DNA complex assembly	74	0.0114	10	0.0125	1.0000000	E

<input type="radio"/>	GO:0009615	4,5	response to virus	7	0.0011	2	0.0025	1.0000000	E
<input type="radio"/>	GO:0045005	8,6	maintenance of fidelity during DNA-dependent DNA replication	25	0.0039	7	0.0088	1.0000000	E
<input type="radio"/>	GO:0018319	10,9,8	protein amino acid myristoylation	5	0.0008	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0015858	5,6	nucleoside transport	3	0.0005	2	0.0025	1.0000000	E
<input type="radio"/>	GO:0045934	7,6	negative regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	179	0.0276	30	0.0375	1.0000000	E
<input type="radio"/>	GO:0000351	8,7,10,11,12,13	assembly of spliceosomal tri-snRNP U4/U6.U5	1	0.0002	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0019954	3	asexual reproduction	85	0.0131	14	0.0175	1.0000000	E
<input type="radio"/>	GO:0006605	8,6,7	protein targeting	258	0.0398	47	0.0588	1.0000000	E
<input type="radio"/>	GO:0043407	8,9	negative regulation of MAPK activity	5	0.0008	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0006869	4,5	lipid transport	34	0.0053	5	0.0063	1.0000000	E
<input type="radio"/>	GO:0042440	4	pigment metabolic process	20	0.0031	4	0.0050	1.0000000	E
<input type="radio"/>	GO:0032502	2	developmental process	436	0.0673	60	0.0751	1.0000000	E
<input type="radio"/>	GO:0033013	5	tetrapyrrole metabolic process	14	0.0022	3	0.0038	1.0000000	E
<input type="radio"/>	GO:0008361	4,6,7	regulation of cell size	129	0.0199	20	0.0250	1.0000000	E
<input type="radio"/>	GO:0017148	8,7,6	negative regulation of protein biosynthetic process	6	0.0009	2	0.0025	1.0000000	E
<input type="radio"/>	GO:0031509	7,11	telomeric heterochromatin formation	60	0.0093	14	0.0175	1.0000000	E
<input type="radio"/>	GO:0031327	7,6	negative regulation of cellular biosynthetic process	6	0.0009	2	0.0025	1.0000000	E
<input type="radio"/>	GO:0006098	9,10,11	pentose-phosphate shunt	11	0.0017	3	0.0038	1.0000000	E
<input type="radio"/>	GO:0031565	8,7	cytokinesis checkpoint	4	0.0006	3	0.0038	1.0000000	E
<input type="radio"/>	GO:0033238	6,5	regulation of amine metabolic process	1	0.0002	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0007131	10,8,7,5,9,6,4	meiotic recombination	55	0.0085	11	0.0138	1.0000000	E
<input type="radio"/>	GO:0045815	5	positive regulation of gene expression, epigenetic	9	0.0014	2	0.0025	1.0000000	E
<input type="radio"/>	GO:0046073	9	dTMP metabolic process	1	0.0002	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0015772	5,6	oligosaccharide transport	1	0.0002	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0065009	3	regulation of a molecular function	46	0.0071	9	0.0113	1.0000000	E
<input type="radio"/>	GO:0000742	7,5	karyogamy during conjugation with cellular fusion	17	0.0026	3	0.0038	1.0000000	E
<input type="radio"/>	GO:0045893	9,8	positive regulation of transcription, DNA-dependent	95	0.0147	16	0.0200	1.0000000	E
<input type="radio"/>	GO:0006334	6,7,10	nucleosome assembly	13	0.0020	3	0.0038	1.0000000	E
<input type="radio"/>	GO:0051246	5,4	regulation of protein metabolic process	72	0.0111	15	0.0188	1.0000000	E
<input type="radio"/>	GO:0032259	5	methylation	83	0.0128	16	0.0200	1.0000000	E
<input type="radio"/>	GO:0009092	7,8	homoserine metabolic process	7	0.0011	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0000090	7,8,9,6	mitotic anaphase	6	0.0009	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0001323	4,5,6	age-dependent general metabolic decline during chronological cell aging	6	0.0009	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0051301	3	cell division	246	0.0380	34	0.0426	1.0000000	E
<input type="radio"/>	GO:0043038	6,7	amino acid activation	32	0.0049	10	0.0125	1.0000000	E
<input type="radio"/>	GO:0045132	9,7,8,6,4	meiotic chromosome segregation	17	0.0026	4	0.0050	1.0000000	E
<input type="radio"/>	GO:0015939	7	pantothenate metabolic process	8	0.0012	3	0.0038	1.0000000	E
<input type="radio"/>	GO:0016236	4	macroautophagy	6	0.0009	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0051052	7,6	regulation of DNA metabolic process	41	0.0063	9	0.0113	1.0000000	E
<input type="radio"/>	GO:0046394	6	carboxylic acid biosynthetic process	17	0.0026	5	0.0063	1.0000000	E
<input type="radio"/>	GO:0009149	7,8	pyrimidine nucleoside triphosphate catabolic process	1	0.0002	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0032506	5,3	cytokinetic process	88	0.0136	19	0.0238	1.0000000	E

<input type="radio"/>	GO:0046489	9,8,10	phosphoinositide biosynthetic process	28	0.0043	5	0.0063	1.0000000	E
<input type="radio"/>	GO:0009204	7,8	deoxyribonucleoside triphosphate catabolic process	2	0.0003	2	0.0025	1.0000000	E
<input type="radio"/>	GO:0044270	5,4	nitrogen compound catabolic process	32	0.0049	4	0.0050	1.0000000	E
<input type="radio"/>	GO:0048518	4	positive regulation of biological process	124	0.0191	22	0.0275	1.0000000	E
<input type="radio"/>	GO:0007569	4	cell aging	49	0.0076	7	0.0088	1.0000000	E
<input type="radio"/>	GO:0031929	6	TOR signaling pathway	13	0.0020	2	0.0025	1.0000000	E
<input type="radio"/>	GO:0009371	10,9,6	positive regulation of transcription by pheromones	5	0.0008	3	0.0038	1.0000000	E
<input type="radio"/>	GO:0006285	7,8	base-excision repair, AP site formation	3	0.0005	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0040031	7	snRNA modification	7	0.0011	4	0.0050	1.0000000	E
<input type="radio"/>	GO:0051030	5,7,6,8	snRNA transport	23	0.0036	7	0.0088	1.0000000	E
<input type="radio"/>	GO:0006418	8,7,9,6	tRNA aminoacylation for protein translation	32	0.0049	10	0.0125	1.0000000	E
<input type="radio"/>	GO:0009132	6	nucleoside diphosphate metabolic process	3	0.0005	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0009143	6,7	nucleoside triphosphate catabolic process	3	0.0005	2	0.0025	1.0000000	E
<input type="radio"/>	GO:0048024	9,8,11	regulation of nuclear mRNA splicing, via spliceosome	3	0.0005	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0006430	9,8,10,7	lysyl-tRNA aminoacylation	2	0.0003	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0000388	8,7,6,10,12	spliceosome conformational change to release U4 (or U4atac) and U1 (or U11)	2	0.0003	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0050685	9,8	positive regulation of mRNA processing	2	0.0003	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0048878	5	chemical homeostasis	121	0.0187	15	0.0188	1.0000000	E
<input type="radio"/>	GO:0006301	7,6	postreplication repair	13	0.0020	2	0.0025	1.0000000	E
<input type="radio"/>	GO:0009113	7,6	purine base biosynthetic process	6	0.0009	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0010032	7	meiotic chromosome condensation	2	0.0003	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0006388	9,8	tRNA splicing	14	0.0022	5	0.0063	1.0000000	E
<input type="radio"/>	GO:0030847	10,9	transcription termination from Pol II promoter, RNA polymerase(A)-independent	9	0.0014	2	0.0025	1.0000000	E
<input type="radio"/>	GO:0018205	8	peptidyl-lysine modification	4	0.0006	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0009119	6	ribonucleoside metabolic process	13	0.0020	5	0.0063	1.0000000	E
<input type="radio"/>	GO:0006620	10,9,8,7,6	posttranslational protein targeting to membrane	8	0.0012	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0009177	8,9	pyrimidine deoxyribonucleoside monophosphate biosynthetic process	1	0.0002	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0006862	5,6	nucleotide transport	5	0.0008	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0006421	9,8,10,7	asparaginyl-tRNA aminoacylation	1	0.0002	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0006560	7,8	proline metabolic process	7	0.0011	2	0.0025	1.0000000	E
<input type="radio"/>	GO:0007264	6	small GTPase mediated signal transduction	61	0.0094	8	0.0100	1.0000000	E
<input type="radio"/>	GO:0009208	8	pyrimidine ribonucleoside triphosphate metabolic process	2	0.0003	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0006276	3	plasmid maintenance	11	0.0017	2	0.0025	1.0000000	E
<input type="radio"/>	GO:0018409	9	peptide or protein amino-terminal blocking	15	0.0023	4	0.0050	1.0000000	E
<input type="radio"/>	GO:0048523	5,4	negative regulation of cellular process	239	0.0369	35	0.0438	1.0000000	E
<input type="radio"/>	GO:0051348	6	negative regulation of transferase activity	7	0.0011	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0009165	5,6	nucleotide biosynthetic process	59	0.0091	14	0.0175	1.0000000	E
<input type="radio"/>	GO:0006555	7,8,6	methionine metabolic process	24	0.0037	8	0.0100	1.0000000	E
<input type="radio"/>	GO:0007105	6,4	cytokinesis, site selection	66	0.0102	15	0.0188	1.0000000	E
<input type="radio"/>	GO:0043331	4	response to dsRNA	7	0.0011	2	0.0025	1.0000000	E
<input type="radio"/>	GO:0006499	10,11,9,8	N-terminal protein myristoylation	5	0.0008	1	0.0013	1.0000000	E

<input type="radio"/>	GO:0007064	10,8,5,6,9,7,4	mitotic sister chromatid cohesion	22	0.0034	6	0.0075	1.0000000	E
<input type="radio"/>	GO:0000266	6	mitochondrial fission	5	0.0008	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0006493	9,8,7	protein amino acid O-linked glycosylation	16	0.0025	5	0.0063	1.0000000	E
<input type="radio"/>	GO:0015806	7,8,9	S-methylmethionine transport	1	0.0002	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0019858	7	cytosine metabolic process	1	0.0002	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0010383	7,5,6	cell wall polysaccharide metabolic process	16	0.0025	2	0.0025	1.0000000	E
<input type="radio"/>	GO:0000750	8,7,6	pheromone-dependent signal transduction during conjugation with cellular fusion	28	0.0043	4	0.0050	1.0000000	E
<input type="radio"/>	GO:0006817	7,8	phosphate transport	10	0.0015	3	0.0038	1.0000000	E
<input type="radio"/>	GO:0001402	5,4	signal transduction during filamentous growth	7	0.0011	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0006521	7,6	regulation of amino acid metabolic process	1	0.0002	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0051444	7	negative regulation of ubiquitin ligase activity	3	0.0005	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0006566	7,8	threonine metabolic process	8	0.0012	3	0.0038	1.0000000	E
<input type="radio"/>	GO:0032261	6,7	purine nucleotide salvage	2	0.0003	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0051438	6	regulation of ubiquitin ligase activity	6	0.0009	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0006323	6	DNA packaging	253	0.0391	37	0.0463	1.0000000	E
<input type="radio"/>	GO:0006450	8,7,6	regulation of translational fidelity	13	0.0020	3	0.0038	1.0000000	E
<input type="radio"/>	GO:0009129	7	pyrimidine nucleoside monophosphate metabolic process	1	0.0002	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0051029	5,7,6,8	rRNA transport	26	0.0040	9	0.0113	1.0000000	E
<input type="radio"/>	GO:0006474	10,9	N-terminal protein amino acid acetylation	9	0.0014	2	0.0025	1.0000000	E
<input type="radio"/>	GO:0006066	4	alcohol metabolic process	163	0.0252	22	0.0275	1.0000000	E
<input type="radio"/>	GO:0007535	6,8,4,7	donor selection	5	0.0008	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0016576	11,9,8	histone dephosphorylation	2	0.0003	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0030474	5,6,4,7	spindle pole body duplication	14	0.0022	3	0.0038	1.0000000	E
<input type="radio"/>	GO:0030261	6	chromosome condensation	11	0.0017	2	0.0025	1.0000000	E
<input type="radio"/>	GO:0009063	6,7	amino acid catabolic process	29	0.0045	4	0.0050	1.0000000	E
<input type="radio"/>	GO:0009310	5,6	amine catabolic process	32	0.0049	4	0.0050	1.0000000	E
<input type="radio"/>	GO:0032940	6,4,5	secretion by cell	250	0.0386	35	0.0438	1.0000000	E
<input type="radio"/>	GO:0042044	4,5	fluid transport	3	0.0005	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0030641	10,8	cellular hydrogen ion homeostasis	25	0.0039	4	0.0050	1.0000000	E
<input type="radio"/>	GO:0008615	8	pyridoxine biosynthetic process	1	0.0002	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0033559	6,8,7	unsaturated fatty acid metabolic process	1	0.0002	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0015918	5,6	sterol transport	15	0.0023	2	0.0025	1.0000000	E
<input type="radio"/>	GO:0046087	8	cytidine metabolic process	2	0.0003	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0006425	9,8,10,7	glutaminyl-tRNA aminoacylation	1	0.0002	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0009168	8,9	purine ribonucleoside monophosphate biosynthetic process	15	0.0023	7	0.0088	1.0000000	E
<input type="radio"/>	GO:0001302	5	replicative cell aging	39	0.0060	7	0.0088	1.0000000	E
<input type="radio"/>	GO:0051453	11,8,9	regulation of cellular pH	25	0.0039	4	0.0050	1.0000000	E
<input type="radio"/>	GO:0043623	7,6	cellular protein complex assembly	69	0.0107	11	0.0138	1.0000000	E
<input type="radio"/>	GO:0016237	4,6	microautophagy	11	0.0017	3	0.0038	1.0000000	E
<input type="radio"/>	GO:0006374	9,11	nuclear mRNA splicing via U2-type spliceosome	15	0.0023	6	0.0075	1.0000000	E
<input type="radio"/>	GO:0030004	9,7	cellular monovalent inorganic cation homeostasis	34	0.0053	5	0.0063	1.0000000	E
<input type="radio"/>	GO:0007533	5,7,6	mating type switching	29	0.0045	4	0.0050	1.0000000	E
<input type="radio"/>	GO:0006241	9,10	CTP biosynthetic process	2	0.0003	1	0.0013	1.0000000	E

<input type="radio"/>	GO:0008104	4	protein localization	330	0.0510	53	0.0663	1.0000000	E
<input type="radio"/>	GO:0016481	8,7	negative regulation of transcription	162	0.0250	28	0.0350	1.0000000	E
<input type="radio"/>	GO:0045039	10,9,7,8	protein import into mitochondrial inner membrane	8	0.0012	3	0.0038	1.0000000	E
<input type="radio"/>	GO:0000162	9,8,7,10	tryptophan biosynthetic process	10	0.0015	4	0.0050	1.0000000	E
<input type="radio"/>	GO:0006997	5	nuclear organization and biogenesis	57	0.0088	12	0.0150	1.0000000	E
<input type="radio"/>	GO:0007021	7	tubulin folding	11	0.0017	4	0.0050	1.0000000	E
<input type="radio"/>	GO:0051704	2	multi-organism process	139	0.0215	21	0.0263	1.0000000	E
<input type="radio"/>	GO:0044272	5	sulfur compound biosynthetic process	22	0.0034	6	0.0075	1.0000000	E
<input type="radio"/>	GO:0009260	6,7	ribonucleotide biosynthetic process	40	0.0062	8	0.0100	1.0000000	E
<input type="radio"/>	GO:0043096	7,6	purine base salvage	1	0.0002	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0000070	9,7,5,8,6,4	mitotic sister chromatid segregation	59	0.0091	8	0.0100	1.0000000	E
<input type="radio"/>	GO:0000413	8	protein peptidyl-prolyl isomerization	1	0.0002	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0031384	6,8,11,10,9,7,12	regulation of initiation of mating projection growth	4	0.0006	2	0.0025	1.0000000	E
<input type="radio"/>	GO:0009196	8	pyrimidine deoxyribonucleoside diphosphate metabolic process	1	0.0002	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0006376	8,7,10,12,3	mRNA splice site selection	6	0.0009	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0009435	8,7,10,9	NAD biosynthetic process	7	0.0011	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0040020	7,9,8,6	regulation of meiosis	22	0.0034	4	0.0050	1.0000000	E
<input type="radio"/>	GO:0019413	7,8	acetate biosynthetic process	3	0.0005	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0044419	3	interspecies interaction between organisms	2	0.0003	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0009889	5,4	regulation of biosynthetic process	69	0.0107	15	0.0188	1.0000000	E
<input type="radio"/>	GO:0009452	7	RNA capping	4	0.0006	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0000754	8,7,5	adaptation to pheromone during conjugation with cellular fusion	15	0.0023	2	0.0025	1.0000000	E
<input type="radio"/>	GO:0051090	8,7	regulation of transcription factor activity	1	0.0002	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0008272	7,8	sulfate transport	3	0.0005	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0046131	7	pyrimidine ribonucleoside metabolic process	2	0.0003	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0006283	8,7	transcription-coupled nucleotide-excision repair	9	0.0014	2	0.0025	1.0000000	E
<input type="radio"/>	GO:0031532	8	actin cytoskeleton reorganization	4	0.0006	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0007531	4,6,5	mating type determination	35	0.0054	5	0.0063	1.0000000	E
<input type="radio"/>	GO:0046219	7,8,6	indolalkylamine biosynthetic process	10	0.0015	4	0.0050	1.0000000	E
<input type="radio"/>	GO:0000412	11,9	histone peptidyl-prolyl isomerization	1	0.0002	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0015721	7,8	bile acid and bile salt transport	1	0.0002	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0006056	7	mannoprotein metabolic process	12	0.0019	6	0.0075	1.0000000	E
<input type="radio"/>	GO:0055069	9	zinc ion homeostasis	10	0.0015	2	0.0025	1.0000000	E
<input type="radio"/>	GO:0006431	9,8,10,7	methionyl-tRNA aminoacylation	3	0.0005	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0006885	7	regulation of pH	29	0.0045	4	0.0050	1.0000000	E
<input type="radio"/>	GO:0051247	6,5	positive regulation of protein metabolic process	5	0.0008	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0009200	7	deoxyribonucleoside triphosphate metabolic process	4	0.0006	3	0.0038	1.0000000	E
<input type="radio"/>	GO:0006629	4	lipid metabolic process	242	0.0374	33	0.0413	1.0000000	E
<input type="radio"/>	GO:0006529	8,9	asparagine biosynthetic process	4	0.0006	2	0.0025	1.0000000	E
<input type="radio"/>	GO:0000710	11,9,8,6,5,10,7,4	meiotic mismatch repair	7	0.0011	2	0.0025	1.0000000	E
<input type="radio"/>	GO:0007020	8	microtubule nucleation	23	0.0036	5	0.0063	1.0000000	E
<input type="radio"/>	GO:0043248	8,7	proteasome assembly	7	0.0011	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0042434	6	indole derivative metabolic process	10	0.0015	4	0.0050	1.0000000	E

<input type="radio"/>	GO:0043039	7,8	tRNA aminoacylation	32	0.0049	10	0.0125	1.0000000	E
<input type="radio"/>	GO:0006636	8,7,9,6	unsaturated fatty acid biosynthetic process	1	0.0002	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0007120	8,6,10,7,11,5	axial cellular bud site selection	22	0.0034	5	0.0063	1.0000000	E
<input type="radio"/>	GO:0051726	5,4	regulation of cell cycle	167	0.0258	26	0.0325	1.0000000	E
<input type="radio"/>	GO:0006407	11,9,6,8,10,7	rRNA export from nucleus	26	0.0040	9	0.0113	1.0000000	E
<input type="radio"/>	GO:0006530	8,9	asparagine catabolic process	5	0.0008	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0000921	8,7	septin ring assembly	9	0.0014	3	0.0038	1.0000000	E
<input type="radio"/>	GO:0000370	8,9,7,10,11,12,13	U2-type nuclear mRNA branch site recognition	3	0.0005	2	0.0025	1.0000000	E
<input type="radio"/>	GO:0042398	6,5	amino acid derivative biosynthetic process	20	0.0031	7	0.0088	1.0000000	E
<input type="radio"/>	GO:0031382	9,8,10,7	mating projection biogenesis	7	0.0011	2	0.0025	1.0000000	E
<input type="radio"/>	GO:0046036	9	CTP metabolic process	2	0.0003	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0006163	6	purine nucleotide metabolic process	47	0.0073	11	0.0138	1.0000000	E
<input type="radio"/>	GO:0000092	8,9,10,7	mitotic anaphase B	5	0.0008	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0000747	4	conjugation with cellular fusion	118	0.0182	17	0.0213	1.0000000	E
<input type="radio"/>	GO:0006235	9,10	dTTP biosynthetic process	1	0.0002	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0006998	5,6	nuclear membrane organization and biogenesis	7	0.0011	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0009892	5,4	negative regulation of metabolic process	208	0.0321	33	0.0413	1.0000000	E
<input type="radio"/>	GO:0000245	7,6,9,11	spliceosome assembly	19	0.0029	7	0.0088	1.0000000	E
<input type="radio"/>	GO:0006576	5,6	biogenic amine metabolic process	24	0.0037	5	0.0063	1.0000000	E
<input type="radio"/>	GO:0051649	5,3,4	establishment of cellular localization	606	0.0936	95	0.1189	1.0000000	E
<input type="radio"/>	GO:0031325	6,5	positive regulation of cellular metabolic process	116	0.0179	20	0.0250	1.0000000	E
<input type="radio"/>	GO:0042558	5	pteridine and derivative metabolic process	2	0.0003	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0006047	8,6,9	UDP-N-acetylglucosamine metabolic process	2	0.0003	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0000282	7,9,5,6,10	cellular bud site selection	66	0.0102	15	0.0188	1.0000000	E
<input type="radio"/>	GO:0009130	7,8	pyrimidine nucleoside monophosphate biosynthetic process	1	0.0002	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0045941	8,7	positive regulation of transcription	101	0.0156	16	0.0200	1.0000000	E
<input type="radio"/>	GO:0000741	6	karyogamy	17	0.0026	3	0.0038	1.0000000	E
<input type="radio"/>	GO:0015862	7,8	uridine transport	1	0.0002	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0016458	5	gene silencing	95	0.0147	22	0.0275	1.0000000	E
<input type="radio"/>	GO:0006275	8,7	regulation of DNA replication	19	0.0029	5	0.0063	1.0000000	E
<input type="radio"/>	GO:0000321	9,8,7,6	re-entry into mitotic cell cycle after pheromone arrest	3	0.0005	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0006596	7,8	polyamine biosynthetic process	4	0.0006	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0046040	9	IMP metabolic process	14	0.0022	6	0.0075	1.0000000	E
<input type="radio"/>	GO:0006891	8,6,5,7	intra-Golgi vesicle-mediated transport	21	0.0032	5	0.0063	1.0000000	E
<input type="radio"/>	GO:0006633	7,6,8,5	fatty acid biosynthetic process	13	0.0020	4	0.0050	1.0000000	E
<input type="radio"/>	GO:0007090	8,9,7,6	regulation of S phase of mitotic cell cycle	3	0.0005	3	0.0038	1.0000000	E
<input type="radio"/>	GO:0051300	5,4,6	spindle pole body organization and biogenesis	16	0.0025	4	0.0050	1.0000000	E
<input type="radio"/>	GO:0015864	6,7	pyrimidine nucleoside transport	2	0.0003	2	0.0025	1.0000000	E
<input type="radio"/>	GO:0001510	7	RNA methylation	60	0.0093	11	0.0138	1.0000000	E
<input type="radio"/>	GO:0009105	7,6	lipoic acid biosynthetic process	1	0.0002	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0030026	10,8	cellular manganese ion homeostasis	5	0.0008	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0007232	7,6	osmosensory signaling pathway via Sho1 osmosensor	5	0.0008	1	0.0013	1.0000000	E

<input type="radio"/>	GO:0015861	7,8	cytidine transport	1	0.0002	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0033205	5,4	cytokinesis during cell cycle	7	0.0011	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0051324	7,6,5	prophase	2	0.0003	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0006665	6,7	sphingolipid metabolic process	30	0.0046	5	0.0063	1.0000000	E
<input type="radio"/>	GO:0006378	9	mRNA polyadenylation	18	0.0028	4	0.0050	1.0000000	E
<input type="radio"/>	GO:0000226	7	microtubule cytoskeleton organization and biogenesis	81	0.0125	11	0.0138	1.0000000	E
<input type="radio"/>	GO:0050658	4,6,5,7	RNA transport	80	0.0124	20	0.0250	1.0000000	E
<input type="radio"/>	GO:0007130	11,9,8,6,5,10,7,4	synaptonemal complex assembly	6	0.0009	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0006213	6	pyrimidine nucleoside metabolic process	5	0.0008	4	0.0050	1.0000000	E
<input type="radio"/>	GO:0006570	7,6,8	tyrosine metabolic process	1	0.0002	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0006816	7,8	calcium ion transport	5	0.0008	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0008655	5	pyrimidine salvage	5	0.0008	3	0.0038	1.0000000	E
<input type="radio"/>	GO:0042168	6,7,5	heme metabolic process	14	0.0022	3	0.0038	1.0000000	E
<input type="radio"/>	GO:0006739	9,8	NADP metabolic process	17	0.0026	3	0.0038	1.0000000	E
<input type="radio"/>	GO:0007118	7,6,5	budding cell apical bud growth	14	0.0022	2	0.0025	1.0000000	E
<input type="radio"/>	GO:0006778	5,6	porphyrin metabolic process	14	0.0022	3	0.0038	1.0000000	E
<input type="radio"/>	GO:0050000	6,5	chromosome localization	4	0.0006	3	0.0038	1.0000000	E
<input type="radio"/>	GO:0031578	9,11,10,8	mitotic cell cycle spindle orientation checkpoint	4	0.0006	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0051568	12,10,11,9	histone H3-K4 methylation	1	0.0002	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0000725	7,6	recombinational repair	29	0.0045	5	0.0063	1.0000000	E
<input type="radio"/>	GO:0002097	8,9	tRNA wobble base modification	1	0.0002	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0018202	8	peptidyl-histidine modification	5	0.0008	4	0.0050	1.0000000	E
<input type="radio"/>	GO:0000731	7,6	DNA synthesis during DNA repair	4	0.0006	3	0.0038	1.0000000	E
<input type="radio"/>	GO:0045045	7,5,4,6	secretory pathway	243	0.0375	35	0.0438	1.0000000	E
<input type="radio"/>	GO:0006286	8,7	base-excision repair, base-free sugar-phosphate removal	1	0.0002	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0009211	8	pyrimidine deoxyribonucleoside triphosphate metabolic process	2	0.0003	2	0.0025	1.0000000	E
<input type="radio"/>	GO:0009396	6,7,8	folic acid and derivative biosynthetic process	6	0.0009	2	0.0025	1.0000000	E
<input type="radio"/>	GO:0051234	2,3	establishment of localization	1004	0.1550	132	0.1652	1.0000000	E
<input type="radio"/>	GO:0006284	7,6	base-excision repair	12	0.0019	3	0.0038	1.0000000	E
<input type="radio"/>	GO:0006451	8,7,6	translational readthrough	2	0.0003	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0030466	11,7,8,12,10	chromatin silencing at silent mating-type cassette	30	0.0046	8	0.0100	1.0000000	E
<input type="radio"/>	GO:0000348	7,8,6,10,12	nuclear mRNA branch site recognition	4	0.0006	2	0.0025	1.0000000	E
<input type="radio"/>	GO:0000734	7,9,8	gene conversion at mating-type locus, DNA repair synthesis	1	0.0002	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0006828	8,9	manganese ion transport	8	0.0012	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0031106	7	septin ring organization	9	0.0014	3	0.0038	1.0000000	E
<input type="radio"/>	GO:0006608	10,11,8,9,7	snRNP protein import into nucleus	23	0.0036	7	0.0088	1.0000000	E
<input type="radio"/>	GO:0006083	7	acetate metabolic process	6	0.0009	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0051340	5	regulation of ligase activity	6	0.0009	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0051031	5,7,6,8	tRNA transport	30	0.0046	8	0.0100	1.0000000	E
<input type="radio"/>	GO:0043629	9	ncRNA polyadenylation	5	0.0008	3	0.0038	1.0000000	E
<input type="radio"/>	GO:0010043	6	response to zinc ion	2	0.0003	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0006461	6,5	protein complex assembly	116	0.0179	16	0.0200	1.0000000	E
<input type="radio"/>	GO:0015887	5,6	pantothenate transport	1	0.0002	1	0.0013	1.0000000	E

<input type="radio"/>	GO:0007068	10,8,6,9,7,5	negative regulation of transcription, mitotic	7	0.0011	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0000079	8,7,6	regulation of cyclin-dependent protein kinase activity	15	0.0023	6	0.0075	1.0000000	E
<input type="radio"/>	GO:0000337	9,8,5	regulation of DNA transposition	10	0.0015	2	0.0025	1.0000000	E
<input type="radio"/>	GO:0006505	9,10	GPI anchor metabolic process	27	0.0042	4	0.0050	1.0000000	E
<input type="radio"/>	GO:0030010	7,4,8	establishment of cell polarity	103	0.0159	22	0.0275	1.0000000	E
<input type="radio"/>	GO:0007231	6,5	osmosensory signaling pathway	22	0.0034	3	0.0038	1.0000000	E
<input type="radio"/>	GO:0015817	7,8,9	histidine transport	1	0.0002	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0009084	7,8	glutamine family amino acid biosynthetic process	27	0.0042	4	0.0050	1.0000000	E
<input type="radio"/>	GO:0007532	9,5,7,8,6	regulation of transcription, mating-type specific	8	0.0012	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0031119	8,9	tRNA pseudouridine synthesis	4	0.0006	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0010382	6,4	cell wall metabolic process	26	0.0040	6	0.0075	1.0000000	E
<input type="radio"/>	GO:0006839	7,5,6	mitochondrial transport	65	0.0100	12	0.0150	1.0000000	E
<input type="radio"/>	GO:0043101	5	purine salvage	9	0.0014	5	0.0063	1.0000000	E
<input type="radio"/>	GO:0048284	5	organelle fusion	22	0.0034	4	0.0050	1.0000000	E
<input type="radio"/>	GO:0045143	10,8,7,5,9,6,4	homologous chromosome segregation	6	0.0009	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0000074	6,5	regulation of progression through cell cycle	167	0.0258	26	0.0325	1.0000000	E
<input type="radio"/>	GO:0006561	8,9	proline biosynthetic process	3	0.0005	2	0.0025	1.0000000	E
<input type="radio"/>	GO:0006740	10,9	NADPH regeneration	14	0.0022	3	0.0038	1.0000000	E
<input type="radio"/>	GO:0042157	6	lipoprotein metabolic process	48	0.0074	6	0.0075	1.0000000	E
<input type="radio"/>	GO:0033036	3	macromolecule localization	382	0.0590	65	0.0814	1.0000000	E
<input type="radio"/>	GO:0006298	7,9,6	mismatch repair	25	0.0039	7	0.0088	1.0000000	E
<input type="radio"/>	GO:0007568	3	aging	49	0.0076	7	0.0088	1.0000000	E
<input type="radio"/>	GO:0042256	8,7	mature ribosome assembly	1	0.0002	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0006379	8	mRNA cleavage	26	0.0040	9	0.0113	1.0000000	E
<input type="radio"/>	GO:0006308	5,6	DNA catabolic process	20	0.0031	4	0.0050	1.0000000	E
<input type="radio"/>	GO:0051318	6,7,5	G1 phase	27	0.0042	7	0.0088	1.0000000	E
<input type="radio"/>	GO:0000723	8	telomere maintenance	274	0.0423	42	0.0526	1.0000000	E
<input type="radio"/>	GO:0000302	5	response to reactive oxygen species	12	0.0019	2	0.0025	1.0000000	E
<input type="radio"/>	GO:0050684	8,7	regulation of mRNA processing	3	0.0005	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0043634	8	polyadenylation-dependent ncRNA catabolic process	7	0.0011	3	0.0038	1.0000000	E
<input type="radio"/>	GO:0022411	4	cellular component disassembly	36	0.0056	8	0.0100	1.0000000	E
<input type="radio"/>	GO:0043173	5	nucleotide salvage	4	0.0006	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0006720	5,6	isoprenoid metabolic process	6	0.0009	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0006479	9,7	protein amino acid methylation	23	0.0036	5	0.0063	1.0000000	E
<input type="radio"/>	GO:0019478	7,8	D-amino acid catabolic process	1	0.0002	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0046942	5,6	carboxylic acid transport	54	0.0083	9	0.0113	1.0000000	E
<input type="radio"/>	GO:0018216	9,10,8	peptidyl-arginine methylation	1	0.0002	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0006353	8,7	transcription termination	20	0.0031	4	0.0050	1.0000000	E
<input type="radio"/>	GO:0000917	6,4	barrier septum formation	3	0.0005	2	0.0025	1.0000000	E
<input type="radio"/>	GO:0015849	4,5	organic acid transport	55	0.0085	9	0.0113	1.0000000	E
<input type="radio"/>	GO:0009069	6,7	serine family amino acid metabolic process	24	0.0037	7	0.0088	1.0000000	E
<input type="radio"/>	GO:0017038	5,6,7	protein import	109	0.0168	21	0.0263	1.0000000	E
<input type="radio"/>	GO:0006270	8,6	DNA replication initiation	33	0.0051	9	0.0113	1.0000000	E
<input type="radio"/>	GO:0046083	7	adenine metabolic process	3	0.0005	2	0.0025	1.0000000	E

<input type="radio"/>	GO:0010410	8,6,7	hemicellulose metabolic process	2	0.0003	2	0.0025	1.0000000	E
<input type="radio"/>	GO:0018201	8	peptidyl-glycine modification	1	0.0002	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0009086	8,9,7	methionine biosynthetic process	7	0.0011	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0006528	7,8	asparagine metabolic process	9	0.0014	3	0.0038	1.0000000	E
<input type="radio"/>	GO:0043405	8	regulation of MAPK activity	6	0.0009	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0009891	6,5	positive regulation of biosynthetic process	4	0.0006	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0051170	9,7,8	nuclear import	50	0.0077	12	0.0150	1.0000000	E
<input type="radio"/>	GO:0006152	6,7	purine nucleoside catabolic process	1	0.0002	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0009070	7,8	serine family amino acid biosynthetic process	12	0.0019	5	0.0063	1.0000000	E
<input type="radio"/>	GO:0006146	8,7	adenine catabolic process	1	0.0002	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0007059	3	chromosome segregation	119	0.0184	19	0.0238	1.0000000	E
<input type="radio"/>	GO:0032297	10,8,9	negative regulation of DNA replication initiation	6	0.0009	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0006487	9,8,7	protein amino acid N-linked glycosylation	48	0.0074	14	0.0175	1.0000000	E
<input type="radio"/>	GO:0051028	5,7,6,8	mRNA transport	66	0.0102	17	0.0213	1.0000000	E
<input type="radio"/>	GO:0050794	4,3	regulation of cellular process	738	0.1140	114	0.1427	1.0000000	E
<input type="radio"/>	GO:0006865	5,6,7	amino acid transport	39	0.0060	5	0.0063	1.0000000	E
<input type="radio"/>	GO:0007007	6,7	inner mitochondrial membrane organization and biogenesis	12	0.0019	3	0.0038	1.0000000	E
<input type="radio"/>	GO:0006367	8,9,7	transcription initiation from RNA polymerase II promoter	44	0.0068	6	0.0075	1.0000000	E
<input type="radio"/>	GO:0022616	6	DNA strand elongation	32	0.0049	8	0.0100	1.0000000	E
<input type="radio"/>	GO:0009373	9,8,5	regulation of transcription by pheromones	10	0.0015	3	0.0038	1.0000000	E
<input type="radio"/>	GO:0000335	10,9,6	negative regulation of DNA transposition	8	0.0012	2	0.0025	1.0000000	E
<input type="radio"/>	GO:0007089	8,9,7,6	traversing start control point of mitotic cell cycle	6	0.0009	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0050790	4	regulation of catalytic activity	45	0.0069	9	0.0113	1.0000000	E
<input type="radio"/>	GO:0006610	10,11,8,9,7	ribosomal protein import into nucleus	23	0.0036	7	0.0088	1.0000000	E
<input type="radio"/>	GO:0050789	3	regulation of biological process	761	0.1175	114	0.1427	1.0000000	E
<input type="radio"/>	GO:0009209	8,9	pyrimidine ribonucleoside triphosphate biosynthetic process	2	0.0003	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0043630	9,10	ncRNA polyadenylation during polyadenylation-dependent ncRNA catabolic process	5	0.0008	3	0.0038	1.0000000	E
<input type="radio"/>	GO:0043007	7	maintenance of rDNA	1	0.0002	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0043549	6	regulation of kinase activity	25	0.0039	7	0.0088	1.0000000	E
<input type="radio"/>	GO:0007128	10,8,7,9,6	meiotic prophase I	2	0.0003	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0016076	7	snRNA catabolic process	4	0.0006	2	0.0025	1.0000000	E
<input type="radio"/>	GO:0009189	7,8	deoxyribonucleoside diphosphate biosynthetic process	1	0.0002	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0031023	5	microtubule organizing center organization and biogenesis	16	0.0025	4	0.0050	1.0000000	E
<input type="radio"/>	GO:0000087	7,5,6	M phase of mitotic cell cycle	129	0.0199	18	0.0225	1.0000000	E
<input type="radio"/>	GO:0009202	7,8	deoxyribonucleoside triphosphate biosynthetic process	2	0.0003	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0006267	8,7	pre-replicative complex assembly	15	0.0023	3	0.0038	1.0000000	E
<input type="radio"/>	GO:0016075	7	rRNA catabolic process	5	0.0008	3	0.0038	1.0000000	E
<input type="radio"/>	GO:0046160	7,8,6	heme a metabolic process	3	0.0005	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0032185	6	septin cytoskeleton organization and biogenesis	9	0.0014	3	0.0038	1.0000000	E
<input type="radio"/>	GO:0045896	9,7,5,8,6,4	regulation of transcription, mitotic	7	0.0011	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0006360	8,9	transcription termination from RNA	18	0.0028	3	0.0038	1.0000000	E

<input type="radio"/>	GO:0006309	7,9	polymerase II promoter	18	0.0028	5	0.0038	1.0000000	E
<input type="radio"/>	GO:0032984	5	macromolecular complex disassembly	32	0.0049	8	0.0100	1.0000000	E
<input type="radio"/>	GO:0009263	6,7	deoxyribonucleotide biosynthetic process	3	0.0005	2	0.0025	1.0000000	E
<input type="radio"/>	GO:0001308	11,7,10	loss of chromatin silencing during replicative cell aging	8	0.0012	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0000115	10,9,8,5,7,4	S-phase-specific transcription in mitotic cell cycle	1	0.0002	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0007051	8	spindle organization and biogenesis	47	0.0073	6	0.0075	1.0000000	E
<input type="radio"/>	GO:0000753	7,8,6	cellular morphogenesis during conjugation with cellular fusion	18	0.0028	3	0.0038	1.0000000	E
<input type="radio"/>	GO:0018004	10,9	N-terminal protein formylation	1	0.0002	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0009446	8,9	putrescine biosynthetic process	1	0.0002	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0046999	5,4	regulation of conjugation	30	0.0046	4	0.0050	1.0000000	E
<input type="radio"/>	GO:0031383	5,7,10,9,8,6,11	regulation of mating projection biogenesis	6	0.0009	2	0.0025	1.0000000	E
<input type="radio"/>	GO:0043102	6,5,7	amino acid salvage	3	0.0005	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0015781	6,7	pyrimidine nucleotide-sugar transport	2	0.0003	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0006586	6,7	indolalkylamine metabolic process	10	0.0015	4	0.0050	1.0000000	E
<input type="radio"/>	GO:0065007	2	biological regulation	948	0.1464	139	0.1740	1.0000000	E
<input type="radio"/>	GO:0043681	6,7,8	protein import into mitochondrion	40	0.0062	8	0.0100	1.0000000	E
<input type="radio"/>	GO:0016562	6,11,10,8,9,7	protein import into peroxisome matrix, receptor recycling	5	0.0008	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0002098	9,10	tRNA wobble uridine modification	1	0.0002	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0046907	6,4,5	intracellular transport	545	0.0842	89	0.1114	1.0000000	E
<input type="radio"/>	GO:0006873	7,5	cellular ion homeostasis	115	0.0178	15	0.0188	1.0000000	E
<input type="radio"/>	GO:0045996	10,9,6	negative regulation of transcription by pheromones	6	0.0009	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0051225	5,9	spindle assembly	3	0.0005	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0009893	5,4	positive regulation of metabolic process	116	0.0179	20	0.0250	1.0000000	E
<input type="radio"/>	GO:0016259	7,8,6	selenocysteine metabolic process	1	0.0002	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0008213	8	protein amino acid alkylation	23	0.0036	5	0.0063	1.0000000	E
<input type="radio"/>	GO:0006342	10,6,7,11,9	chromatin silencing	95	0.0147	22	0.0275	1.0000000	E
<input type="radio"/>	GO:0007062	7,4	sister chromatid cohesion	31	0.0048	9	0.0113	1.0000000	E
<input type="radio"/>	GO:0000819	7,4	sister chromatid segregation	62	0.0096	9	0.0113	1.0000000	E
<input type="radio"/>	GO:0009138	7	pyrimidine nucleoside diphosphate metabolic process	1	0.0002	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0009102	6,7,8	biotin biosynthetic process	7	0.0011	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0000372	10	Group I intron splicing	7	0.0011	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0046513	9,8,10	ceramide biosynthetic process	4	0.0006	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0046903	3,4	secretion	250	0.0386	35	0.0438	1.0000000	E
<input type="radio"/>	GO:0043543	7	protein amino acid acylation	62	0.0096	8	0.0100	1.0000000	E
<input type="radio"/>	GO:0006797	6	polyphosphate metabolic process	5	0.0008	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0006784	8,7,9	heme a biosynthetic process	3	0.0005	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0048519	4	negative regulation of biological process	242	0.0374	35	0.0438	1.0000000	E
<input type="radio"/>	GO:0043241	6,5	protein complex disassembly	28	0.0043	7	0.0088	1.0000000	E
<input type="radio"/>	GO:0007093	8,10,9,7	mitotic cell cycle checkpoint	27	0.0042	4	0.0050	1.0000000	E
<input type="radio"/>	GO:0031137	6,5	regulation of conjugation with cellular fusion	30	0.0046	4	0.0050	1.0000000	E
<input type="radio"/>	GO:0006333	8	chromatin assembly or disassembly	119	0.0184	24	0.0300	1.0000000	E
<input type="radio"/>	GO:0051252	7,6	regulation of RNA metabolic process	36	0.0056	5	0.0063	1.0000000	E
<input type="radio"/>	GO:0042274	6,5	ribosomal small subunit biogenesis and assembly	26	0.0040	6	0.0075	1.0000000	E

<input type="checkbox"/>	GO:0006626	9,8,7,6	protein targeting to mitochondrion	52	0.0080	8	0.0100	1.0000000	E
<input type="checkbox"/>	GO:0016311	6	dephosphorylation	41	0.0063	8	0.0100	1.0000000	E
<input type="checkbox"/>	GO:0000415	9,11,14,8,12,13,10	negative regulation of histone H3-K36 methylation	1	0.0002	1	0.0013	1.0000000	E
<input type="checkbox"/>	GO:0051179	2	localization	1051	0.1623	137	0.1715	1.0000000	E
<input type="checkbox"/>	GO:0007127	9,7,6,8,5	meiosis I	75	0.0116	14	0.0175	1.0000000	E
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<input type="checkbox"/>	GO:0032200	7	telomere organization and biogenesis	274	0.0423	42	0.0526	1.0000000	E
<input type="checkbox"/>	GO:0006790	4	sulfur metabolic process	67	0.0103	12	0.0150	1.0000000	E
<input type="checkbox"/>	GO:0009067	7,8	aspartate family amino acid biosynthetic process	20	0.0031	6	0.0075	1.0000000	E
<input type="checkbox"/>	GO:0006537	8,9	glutamate biosynthetic process	13	0.0020	2	0.0025	1.0000000	E
<input type="checkbox"/>	GO:0050801	6	ion homeostasis	119	0.0184	15	0.0188	1.0000000	E
<input type="checkbox"/>	GO:0006310	6	DNA recombination	122	0.0188	19	0.0238	1.0000000	E
<input type="checkbox"/>	GO:0032005	7,6	signal transduction during conjugation with cellular fusion	28	0.0043	4	0.0050	1.0000000	E
<input type="checkbox"/>	GO:0015857	7,8	uracil transport	1	0.0002	1	0.0013	1.0000000	E
<input type="checkbox"/>	GO:0032392	6	DNA geometric change	16	0.0025	2	0.0025	1.0000000	E
<input type="checkbox"/>	GO:0016233	9	telomere capping	5	0.0008	1	0.0013	1.0000000	E
<input type="checkbox"/>	GO:0032990	5,6	cell part morphogenesis	8	0.0012	2	0.0025	1.0000000	E
<input type="checkbox"/>	GO:0042787	10,9,11	protein ubiquitination during ubiquitin-dependent protein catabolic process	14	0.0022	2	0.0025	1.0000000	E
<input type="checkbox"/>	GO:0045892	9,8	negative regulation of transcription, DNA-dependent	156	0.0241	26	0.0325	1.0000000	E
<input type="checkbox"/>	GO:0015851	5,6	nucleobase transport	3	0.0005	2	0.0025	1.0000000	E
<input type="checkbox"/>	GO:0030011	7,4,8	maintenance of cell polarity	8	0.0012	1	0.0013	1.0000000	E
<input type="checkbox"/>	GO:0032988	6	protein-RNA complex disassembly	4	0.0006	1	0.0013	1.0000000	E
<input type="checkbox"/>	GO:0000767	6,7	cellular morphogenesis during conjugation	20	0.0031	3	0.0038	1.0000000	E
<input type="checkbox"/>	GO:0046516	6	hypusine metabolic process	2	0.0003	2	0.0025	1.0000000	E
<input type="checkbox"/>	GO:0065008	3	regulation of biological quality	260	0.0401	35	0.0438	1.0000000	E
<input type="checkbox"/>	GO:0000304	6	response to singlet oxygen	4	0.0006	1	0.0013	1.0000000	E
<input type="checkbox"/>	GO:0018377	9,8,7	protein myristoylation	5	0.0008	1	0.0013	1.0000000	E
<input type="checkbox"/>	GO:0007023	8	post-chaperonin tubulin folding pathway	5	0.0008	1	0.0013	1.0000000	E
<input type="checkbox"/>	GO:0046148	5	pigment biosynthetic process	19	0.0029	4	0.0050	1.0000000	E
<input type="checkbox"/>	GO:0006621	7,6,5,4	protein retention in ER	7	0.0011	1	0.0013	1.0000000	E
<input type="checkbox"/>	GO:0009298	9,6,7,10	GDP-mannose biosynthetic process	2	0.0003	1	0.0013	1.0000000	E
<input type="checkbox"/>	GO:0006168	8,7	adenine salvage	1	0.0002	1	0.0013	1.0000000	E
<input type="checkbox"/>	GO:0000086	8,5,6,7,4	G2/M transition of mitotic cell cycle	35	0.0054	8	0.0100	1.0000000	E
<input type="checkbox"/>	GO:0000083	10,9,6,5,7,8,4	G1/S-specific transcription in mitotic cell cycle	12	0.0019	3	0.0038	1.0000000	E
<input type="checkbox"/>	GO:0055067	8	monovalent inorganic cation homeostasis	34	0.0053	5	0.0063	1.0000000	E
<input type="checkbox"/>	GO:0042278	6	purine nucleoside metabolic process	12	0.0019	5	0.0063	1.0000000	E
<input type="checkbox"/>	GO:0030384	8,9	phosphoinositide metabolic process	43	0.0066	6	0.0075	1.0000000	E
<input type="checkbox"/>	GO:0006892	8,6,5,7	post-Golgi vesicle-mediated transport	69	0.0107	11	0.0138	1.0000000	E
<input type="checkbox"/>	GO:0006829	8,9	zinc ion transport	7	0.0011	2	0.0025	1.0000000	E
<input type="checkbox"/>	GO:0000046	5,6	autophagic vacuole fusion	1	0.0002	1	0.0013	1.0000000	E
<input type="checkbox"/>	GO:0006457	6	protein folding	84	0.0130	11	0.0138	1.0000000	E
<input type="checkbox"/>	GO:0000301	9,7,6,8	retrograde transport, vesicle recycling within Golgi	4	0.0006	2	0.0025	1.0000000	E
<input type="checkbox"/>	GO:0043137	7,10,6,9	DNA replication, removal of RNA primer	5	0.0008	1	0.0013	1.0000000	E

<input type="checkbox"/>	GO:0007346	7,5,6	regulation of progression through mitotic cell cycle	13	0.0020	5	0.0063	1.0000000	E
<input type="checkbox"/>	GO:0000354	7,8,6,10,12	cis assembly of pre-catalytic spliceosome	2	0.0003	1	0.0013	1.0000000	E
<input type="checkbox"/>	GO:0006595	6,7	polyamine metabolic process	7	0.0011	1	0.0013	1.0000000	E
<input type="checkbox"/>	GO:0043412	5	biopolymer modification	664	0.1025	102	0.1277	1.0000000	E
<input type="checkbox"/>	GO:0051436	8,6,5	negative regulation of ubiquitin ligase activity during mitotic cell cycle	3	0.0005	1	0.0013	1.0000000	E
<input type="checkbox"/>	GO:0045814	5	negative regulation of gene expression, epigenetic	95	0.0147	22	0.0275	1.0000000	E
<input type="checkbox"/>	GO:0006167	9,10	AMP biosynthetic process	1	0.0002	1	0.0013	1.0000000	E
<input type="checkbox"/>	GO:0006188	9,10	IMP biosynthetic process	14	0.0022	6	0.0075	1.0000000	E
<input type="checkbox"/>	GO:0046077	9	dUDP metabolic process	1	0.0002	1	0.0013	1.0000000	E
<input type="checkbox"/>	GO:0043633	7	modification-dependent RNA catabolic process	7	0.0011	3	0.0038	1.0000000	E
<input type="checkbox"/>	GO:0033261	7,8,6	regulation of progression through S phase	5	0.0008	3	0.0038	1.0000000	E
<input type="checkbox"/>	GO:0006835	6,7	dicarboxylic acid transport	3	0.0005	1	0.0013	1.0000000	E
<input type="checkbox"/>	GO:0046515	7,6	hypusine biosynthetic process	2	0.0003	2	0.0025	1.0000000	E
<input type="checkbox"/>	GO:0006048	9,7,10	UDP-N-acetylglucosamine biosynthetic process	2	0.0003	1	0.0013	1.0000000	E
<input type="checkbox"/>	GO:0031060	7,9,12,6,10,11,8	regulation of histone methylation	1	0.0002	1	0.0013	1.0000000	E
<input type="checkbox"/>	GO:0042816	6	vitamin B6 metabolic process	8	0.0012	1	0.0013	1.0000000	E
<input type="checkbox"/>	GO:0015856	7,8	cytosine transport	1	0.0002	1	0.0013	1.0000000	E
<input type="checkbox"/>	GO:0009148	7,8	pyrimidine nucleoside triphosphate biosynthetic process	1	0.0002	1	0.0013	1.0000000	E
<input type="checkbox"/>	GO:0001324	5,6,7	age-dependent response to oxidative stress during chronological cell aging	6	0.0009	1	0.0013	1.0000000	E
<input type="checkbox"/>	GO:0031120	8	snRNA pseudouridine synthesis	7	0.0011	4	0.0050	1.0000000	E
<input type="checkbox"/>	GO:0007234	7,6	osmosensory signaling pathway via two-component system	3	0.0005	1	0.0013	1.0000000	E
<input type="checkbox"/>	GO:0051188	5	cofactor biosynthetic process	79	0.0122	10	0.0125	1.0000000	E
<input type="checkbox"/>	GO:0010412	9,7,8	mannan metabolic process	2	0.0003	2	0.0025	1.0000000	E
<input type="checkbox"/>	GO:0000280	3	nuclear division	2	0.0003	1	0.0013	1.0000000	E
<input type="checkbox"/>	GO:0000349	8,7,10,12	generation of catalytic spliceosome for first transesterification step	4	0.0006	1	0.0013	1.0000000	E
<input type="checkbox"/>	GO:0000135	9,8	septin checkpoint	4	0.0006	3	0.0038	1.0000000	E
<input type="checkbox"/>	GO:0006888	8,6,5,7	ER to Golgi vesicle-mediated transport	81	0.0125	11	0.0138	1.0000000	E
<input type="checkbox"/>	GO:0006614	11,10,9,8,7	SRP-dependent cotranslational protein targeting to membrane	20	0.0031	4	0.0050	1.0000000	E
<input type="checkbox"/>	GO:0009653	4,3	anatomical structure morphogenesis	248	0.0383	42	0.0526	1.0000000	E
<input type="checkbox"/>	GO:0000244	7,6,10,12	assembly of spliceosomal tri-snRNP	3	0.0005	2	0.0025	1.0000000	E
<input type="checkbox"/>	GO:0006970	4	response to osmotic stress	89	0.0137	11	0.0138	1.0000000	E
<input type="checkbox"/>	GO:0009061	6	anaerobic respiration	2	0.0003	1	0.0013	1.0000000	E
<input type="checkbox"/>	GO:0006357	9,8	regulation of transcription from RNA polymerase II promoter	221	0.0341	32	0.0401	1.0000000	E
<input type="checkbox"/>	GO:0000101	6,7,8	sulfur amino acid transport	5	0.0008	1	0.0013	1.0000000	E
<input type="checkbox"/>	GO:0030150	10,9,8,7	protein import into mitochondrial matrix	22	0.0034	4	0.0050	1.0000000	E
<input type="checkbox"/>	GO:0031344	4,6,8,7,5,9	regulation of cell projection organization and biogenesis	6	0.0009	2	0.0025	1.0000000	E
<input type="checkbox"/>	GO:0006231	9,10	dTMP biosynthetic process	1	0.0002	1	0.0013	1.0000000	E
<input type="checkbox"/>	GO:0000080	7,8,6	G1 phase of mitotic cell cycle	27	0.0042	7	0.0088	1.0000000	E
<input type="checkbox"/>	GO:0009120	6	deoxyribonucleoside metabolic process	3	0.0005	2	0.0025	1.0000000	E
<input type="checkbox"/>	GO:0015031	4,5,6	protein transport	280	0.0432	49	0.0613	1.0000000	E
<input type="checkbox"/>	GO:0006426	9,8,10,7	glycyl-tRNA aminoacylation	2	0.0003	1	0.0013	1.0000000	E
<input type="checkbox"/>	GO:0000217	8,9	pyrimidine deoxyribonucleoside	1	0.0002	1	0.0013	1.0000000	E

<input type="radio"/>	GO:0009212	9,9	triphosphate biosynthetic process	1	0.0002	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0045292	10,12	nuclear mRNA cis splicing, via U2-type spliceosome	1	0.0002	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0046488	9,10	phosphatidylinositol metabolic process	3	0.0005	2	0.0025	1.0000000	E
<input type="radio"/>	GO:0017183	10,4	peptidyl-diphthamide biosynthetic process from peptidyl-histidine	5	0.0008	4	0.0050	1.0000000	E
<input type="radio"/>	GO:0031326	6,5	regulation of cellular biosynthetic process	67	0.0103	15	0.0188	1.0000000	E
<input type="radio"/>	GO:0007534	6,8,7	gene conversion at mating-type locus	23	0.0036	3	0.0038	1.0000000	E
<input type="radio"/>	GO:0045859	7	regulation of protein kinase activity	25	0.0039	7	0.0088	1.0000000	E
<input type="radio"/>	GO:0006617	8,12,11,7,10,9	SRP-dependent cotranslational protein targeting to membrane, signal sequence recognition	7	0.0011	4	0.0050	1.0000000	E
<input type="radio"/>	GO:0043330	5,6	response to exogenous dsRNA	7	0.0011	2	0.0025	1.0000000	E
<input type="radio"/>	GO:0003006	3,4	reproductive developmental process	35	0.0054	5	0.0063	1.0000000	E
<input type="radio"/>	GO:0015729	7,8	oxaloacetate transport	1	0.0002	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0032989	4,5	cellular structure morphogenesis	248	0.0383	42	0.0526	1.0000000	E
<input type="radio"/>	GO:0015746	7,8	citrate transport	1	0.0002	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0000117	10,9,6,5,7,8,4	G2/M-specific transcription in mitotic cell cycle	3	0.0005	2	0.0025	1.0000000	E
<input type="radio"/>	GO:0006356	9,8	regulation of transcription from RNA polymerase I promoter	8	0.0012	5	0.0063	1.0000000	E
<input type="radio"/>	GO:0006280	6	mutagenesis	9	0.0014	3	0.0038	1.0000000	E
<input type="radio"/>	GO:0000727	9,8	double-strand break repair via break-induced replication	7	0.0011	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0055075	9	potassium ion homeostasis	5	0.0008	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0000078	9,11,10,8,6,7	cell morphogenesis checkpoint	2	0.0003	2	0.0025	1.0000000	E
<input type="radio"/>	GO:0030037	5,4,9	actin filament reorganization during cell cycle	4	0.0006	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0043570	6	maintenance of DNA repeat elements	1	0.0002	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0022401	7,6	adaptation of signaling pathway	15	0.0023	2	0.0025	1.0000000	E
<input type="radio"/>	GO:0007571	3,4	age-dependent general metabolic decline	7	0.0011	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0051236	3,4,5	establishment of RNA localization	80	0.0124	20	0.0250	1.0000000	E
<input type="radio"/>	GO:0048858	6,7	cell projection morphogenesis	8	0.0012	2	0.0025	1.0000000	E
<input type="radio"/>	GO:0009186	7	deoxyribonucleoside diphosphate metabolic process	1	0.0002	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0006820	5,6	anion transport	17	0.0026	4	0.0050	1.0000000	E
<input type="radio"/>	GO:0006427	9,8,10,7	histidyl-tRNA aminoacylation	1	0.0002	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0043631	8	RNA polyadenylation	24	0.0037	7	0.0088	1.0000000	E
<input type="radio"/>	GO:0031938	12,8,5,9,13,11	regulation of chromatin silencing at telomere	6	0.0009	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0051666	5,4	actin cortical patch localization	2	0.0003	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0019988	7,8,9,6	charged-tRNA modification	2	0.0003	2	0.0025	1.0000000	E
<input type="radio"/>	GO:0046416	6,7	D-amino acid metabolic process	1	0.0002	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0046021	10,8,5,6,9,7,4	regulation of transcription from RNA polymerase II promoter, mitotic	6	0.0009	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0007126	8,6,7,5	meiosis	148	0.0229	23	0.0288	1.0000000	E
<input type="radio"/>	GO:0030007	10,8	cellular potassium ion homeostasis	5	0.0008	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0006824	7,8,9	cobalt ion transport	2	0.0003	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0046498	6	S-adenosylhomocysteine metabolic process	1	0.0002	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0006549	7,8	isoleucine metabolic process	3	0.0005	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0046113	6,5	nucleobase catabolic process	1	0.0002	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0042819	7	vitamin B6 biosynthetic process	1	0.0002	1	0.0013	1.0000000	E

<input type="radio"/>	GO:0000082	8,5,6,7,4	G1/S transition of mitotic cell cycle	52	0.0080	11	0.0138	1.0000000	E
<input type="radio"/>	GO:0043001	10,8,7,9	Golgi to plasma membrane protein transport	5	0.0008	3	0.0038	1.0000000	E
<input type="radio"/>	GO:0000391	8,10,12	U2-dependent spliceosome disassembly	4	0.0006	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0045935	7,6	positive regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	108	0.0167	19	0.0238	1.0000000	E
<input type="radio"/>	GO:0007025	8	beta-tubulin folding	3	0.0005	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0006506	10,9,8,7,11	GPI anchor biosynthetic process	26	0.0040	4	0.0050	1.0000000	E
<input type="radio"/>	GO:0009223	7,8	pyrimidine deoxyribonucleotide catabolic process	1	0.0002	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0006831	9,10	low-affinity zinc ion transport	1	0.0002	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0009176	8	pyrimidine deoxyribonucleoside monophosphate metabolic process	1	0.0002	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0016584	6,10	nucleosome positioning	3	0.0005	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0006843	8,6,7,9	mitochondrial citrate transport	1	0.0002	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0009096	8,7,9	aromatic amino acid family biosynthetic process, anthranilate pathway	10	0.0015	4	0.0050	1.0000000	E
<input type="radio"/>	GO:0051327	7,5,6	M phase of meiotic cell cycle	148	0.0229	23	0.0288	1.0000000	E
<input type="radio"/>	GO:0030491	7,9,10,6,8	heteroduplex formation	9	0.0014	2	0.0025	1.0000000	E
<input type="radio"/>	GO:0008612	8,7,9	hypusine biosynthetic process from peptidyl-lysine	1	0.0002	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0009259	6	ribonucleotide metabolic process	43	0.0066	9	0.0113	1.0000000	E
<input type="radio"/>	GO:0007119	7,6,5	budding cell isotropic bud growth	8	0.0012	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0007067	8,6,7,5	mitosis	127	0.0196	17	0.0213	1.0000000	E
<input type="radio"/>	GO:0048026	10,9,12	positive regulation of nuclear mRNA splicing, via spliceosome	2	0.0003	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0006271	8,7	DNA strand elongation during DNA replication	32	0.0049	8	0.0100	1.0000000	E
<input type="radio"/>	GO:0006545	8,9	glycine biosynthetic process	2	0.0003	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0000912	6,5,9,4	cytokinesis, formation of actomyosin apparatus	3	0.0005	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0006164	6,7	purine nucleotide biosynthetic process	41	0.0063	9	0.0113	1.0000000	E
<input type="radio"/>	GO:0009068	7,8	aspartate family amino acid catabolic process	10	0.0015	2	0.0025	1.0000000	E
<input type="radio"/>	GO:0007006	5,6	mitochondrial membrane organization and biogenesis	24	0.0037	3	0.0038	1.0000000	E
<input type="radio"/>	GO:0006406	11,9,6,8,10,7	mRNA export from nucleus	66	0.0102	17	0.0213	1.0000000	E
<input type="radio"/>	GO:0045047	9,8,7,6,5	protein targeting to ER	33	0.0051	7	0.0088	1.0000000	E
<input type="radio"/>	GO:0046686	6	response to cadmium ion	4	0.0006	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0031056	6,8,11,5,9,7	regulation of histone modification	2	0.0003	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0045041	10,9,8,7	protein import into mitochondrial intermembrane space	6	0.0009	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0051083	8	cotranslational protein folding	5	0.0008	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0048856	3	anatomical structure development	248	0.0383	42	0.0526	1.0000000	E
<input type="radio"/>	GO:0006345	10,6,9	loss of chromatin silencing	9	0.0014	2	0.0025	1.0000000	E
<input type="radio"/>	GO:0006886	7,5,6	intracellular protein transport	274	0.0423	49	0.0613	1.0000000	E
<input type="radio"/>	GO:0051053	8,7	negative regulation of DNA metabolic process	20	0.0031	4	0.0050	1.0000000	E
<input type="radio"/>	GO:0022403	5,4	cell cycle phase	353	0.0545	58	0.0726	1.0000000	E
<input type="radio"/>	GO:0000414	8,10,13,7,11,12,9	regulation of histone H3-K36 methylation	1	0.0002	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0000279	6,5	M phase	258	0.0398	38	0.0476	1.0000000	E
<input type="radio"/>	GO:0051338	5	regulation of transferase activity	26	0.0040	7	0.0088	1.0000000	E
<input type="radio"/>	GO:0046037	9	GMP metabolic process	2	0.0003	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0046520	8,7,9	sphingoid biosynthetic process	4	0.0006	1	0.0013	1.0000000	E

<input type="radio"/>	GO:0030467	7,4,8	establishment and/or maintenance of cell polarity (sensu Fungi)	66	0.0102	15	0.0188	1.0000000	E
<input type="radio"/>	GO:0000188	9,10,8	inactivation of MAPK activity	5	0.0008	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0006387	8	snRNA capping	1	0.0002	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0006607	10,11,8,9,7	NLS-bearing substrate import into nucleus	23	0.0036	7	0.0088	1.0000000	E
<input type="radio"/>	GO:0009147	7	pyrimidine nucleoside triphosphate metabolic process	4	0.0006	3	0.0038	1.0000000	E
<input type="radio"/>	GO:0007266	8	Rho protein signal transduction	17	0.0026	5	0.0063	1.0000000	E
<input type="radio"/>	GO:0019673	8,6,9	GDP-mannose metabolic process	2	0.0003	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0006438	9,8,10,7	valyl-tRNA aminoacylation	1	0.0002	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0007117	6,5,4	budding cell bud growth	35	0.0054	7	0.0088	1.0000000	E
<input type="radio"/>	GO:0051320	7,6,5	S phase	20	0.0031	5	0.0063	1.0000000	E
<input type="radio"/>	GO:0006278	7	RNA-dependent DNA replication	4	0.0006	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0007103	6,7,5,8	spindle pole body duplication in nuclear envelope	13	0.0020	3	0.0038	1.0000000	E
<input type="radio"/>	GO:0051325	6,5	interphase	112	0.0173	25	0.0313	1.0000000	E
<input type="radio"/>	GO:0046075	9	dTTP metabolic process	1	0.0002	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0000160	5	two-component signal transduction system (phosphorelay)	3	0.0005	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0032264	7,8	IMP salvage	1	0.0002	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0006338	9	chromatin remodeling	155	0.0239	28	0.0350	1.0000000	E
<input type="radio"/>	GO:0001881	5,7	receptor recycling	5	0.0008	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0045787	6,7,5	positive regulation of progression through cell cycle	3	0.0005	2	0.0025	1.0000000	E
<input type="radio"/>	GO:0040007	2	growth	141	0.0218	18	0.0225	1.0000000	E
<input type="radio"/>	GO:0015785	7,8	UDP-galactose transport	1	0.0002	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0009058	3	biosynthetic process	1249	0.1929	177	0.2215	1.0000000	E
<input type="radio"/>	GO:0042542	6	response to hydrogen peroxide	4	0.0006	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0000096	6,7,5	sulfur amino acid metabolic process	33	0.0051	10	0.0125	1.0000000	E
<input type="radio"/>	GO:0009117	5	nucleotide metabolic process	111	0.0171	25	0.0313	1.0000000	E
<input type="radio"/>	GO:0017182	9	peptidyl-diphthamide metabolic process	5	0.0008	4	0.0050	1.0000000	E
<input type="radio"/>	GO:0000084	8,7,6	S phase of mitotic cell cycle	18	0.0028	5	0.0063	1.0000000	E
<input type="radio"/>	GO:0006144	6	purine base metabolic process	14	0.0022	4	0.0050	1.0000000	E
<input type="radio"/>	GO:0016579	9	protein deubiquitination	20	0.0031	3	0.0038	1.0000000	E
<input type="radio"/>	GO:0030031	8,7,9	cell projection biogenesis	8	0.0012	2	0.0025	1.0000000	E
<input type="radio"/>	GO:0031569	10,12,11,9	G2/M transition size control checkpoint	1	0.0002	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0006833	5,6	water transport	3	0.0005	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0007530	4,5	sex determination	35	0.0054	5	0.0063	1.0000000	E
<input type="radio"/>	GO:0006227	9,10	dUDP biosynthetic process	1	0.0002	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0000055	11,12,7,9,10	ribosomal large subunit export from nucleus	11	0.0017	4	0.0050	1.0000000	E
<input type="radio"/>	GO:0006491	10,9,8	N-glycan processing	4	0.0006	2	0.0025	1.0000000	E
<input type="radio"/>	GO:0042435	7,5	indole derivative biosynthetic process	10	0.0015	4	0.0050	1.0000000	E
<input type="radio"/>	GO:0007135	9,7,6,8,5	meiosis II	4	0.0006	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0006348	11,7,8,12,10	chromatin silencing at telomere	60	0.0093	14	0.0175	1.0000000	E
<input type="radio"/>	GO:0006311	10,8,7,5,9,6,4	meiotic gene conversion	22	0.0034	5	0.0063	1.0000000	E
<input type="radio"/>	GO:0006359	9,8	regulation of transcription from RNA polymerase III promoter	7	0.0011	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0009150	7	purine ribonucleotide metabolic process	41	0.0063	8	0.0100	1.0000000	E
<input type="radio"/>	GO:0000387	5,9,11	spliceosomal snRNP biogenesis	3	0.0005	2	0.0025	1.0000000	E

<input type="checkbox"/>	GO:0032447	9	protein urmylation	5	0.0008	3	0.0038	1.0000000	E
<input type="checkbox"/>	GO:0006855	5,6	multidrug transport	8	0.0012	1	0.0013	1.0000000	E
<input type="checkbox"/>	GO:0006810	3,4	transport	981	0.1515	131	0.1640	1.0000000	E
<input type="checkbox"/>	GO:0042430	5	indole and derivative metabolic process	10	0.0015	4	0.0050	1.0000000	E
<input type="checkbox"/>	GO:0006289	7,6	nucleotide-excision repair	44	0.0068	6	0.0075	1.0000000	E
<input type="checkbox"/>	GO:0015780	5,6	nucleotide-sugar transport	4	0.0006	2	0.0025	1.0000000	E
<input type="checkbox"/>	GO:0007163	6,3,7	establishment and/or maintenance of cell polarity	115	0.0178	24	0.0300	1.0000000	E
<input type="checkbox"/>	GO:0045727	8,7,6	positive regulation of protein biosynthetic process	4	0.0006	1	0.0013	1.0000000	E
<input type="checkbox"/>	GO:0016053	5	organic acid biosynthetic process	17	0.0026	5	0.0063	1.0000000	E
<input type="checkbox"/>	GO:0017196	11,9,10	N-terminal peptidyl-methionine acetylation	3	0.0005	1	0.0013	1.0000000	E
<input type="checkbox"/>	GO:0000076	11,9,8,10	DNA replication checkpoint	5	0.0008	1	0.0013	1.0000000	E
<input type="checkbox"/>	GO:0009164	5,6	nucleoside catabolic process	4	0.0006	2	0.0025	1.0000000	E
<input type="checkbox"/>	GO:0015855	6,7	pyrimidine transport	2	0.0003	2	0.0025	1.0000000	E
<input type="checkbox"/>	GO:0031506	7,5,8,6	cell wall glycoprotein biosynthetic process	12	0.0019	6	0.0075	1.0000000	E
<input type="checkbox"/>	GO:0051321	4	meiotic cell cycle	148	0.0229	23	0.0288	1.0000000	E
<input type="checkbox"/>	GO:0000075	7,6	cell cycle checkpoint	53	0.0082	10	0.0125	1.0000000	E
<input type="checkbox"/>	GO:0006449	8,7,9,6	regulation of translational termination	3	0.0005	1	0.0013	1.0000000	E
<input type="checkbox"/>	GO:0045851	8	pH reduction	24	0.0037	4	0.0050	1.0000000	E
<input type="checkbox"/>	GO:0006893	9,7,6,8	Golgi to plasma membrane transport	30	0.0046	6	0.0075	1.0000000	E
<input type="checkbox"/>	GO:0045944	10,9	positive regulation of transcription from RNA polymerase II promoter	76	0.0117	10	0.0125	1.0000000	E
<input type="checkbox"/>	GO:0006556	8,7,6,9,5	S-adenosylmethionine biosynthetic process	2	0.0003	2	0.0025	1.0000000	E
<input type="checkbox"/>	GO:0019344	8,9,7	cysteine biosynthetic process	2	0.0003	2	0.0025	1.0000000	E
<input type="checkbox"/>	GO:0006145	7,6	purine base catabolic process	1	0.0002	1	0.0013	1.0000000	E
<input type="checkbox"/>	GO:0006166	6,8	purine ribonucleoside salvage	6	0.0009	3	0.0038	1.0000000	E
<input type="checkbox"/>	GO:0007070	11,9,6,7,10,8,5	negative regulation of transcription from RNA polymerase II promoter, mitotic	6	0.0009	1	0.0013	1.0000000	E
<input type="checkbox"/>	GO:0031385	6,8,11,10,9,7,12	regulation of termination of mating projection growth	5	0.0008	1	0.0013	1.0000000	E
<input type="checkbox"/>	GO:0000746	3	conjugation	118	0.0182	17	0.0213	1.0000000	E
<input type="checkbox"/>	GO:0046128	7	purine ribonucleoside metabolic process	11	0.0017	4	0.0050	1.0000000	E
<input type="checkbox"/>	GO:0006779	6,7	porphyrin biosynthetic process	13	0.0020	3	0.0038	1.0000000	E
<input type="checkbox"/>	GO:0043488	9,8,7	regulation of mRNA stability	30	0.0046	4	0.0050	1.0000000	E
<input type="checkbox"/>	GO:0009890	6,5	negative regulation of biosynthetic process	8	0.0012	2	0.0025	1.0000000	E
<input type="checkbox"/>	GO:0016078	7	tRNA catabolic process	5	0.0008	2	0.0025	1.0000000	E
<input type="checkbox"/>	GO:0018195	8	peptidyl-arginine modification	2	0.0003	2	0.0025	1.0000000	E
<input type="checkbox"/>	GO:0031328	7,6	positive regulation of cellular biosynthetic process	4	0.0006	1	0.0013	1.0000000	E
<input type="checkbox"/>	GO:0043414	6	biopolymer methylation	83	0.0128	16	0.0200	1.0000000	E
<input type="checkbox"/>	GO:0048285	5	organelle fission	6	0.0009	1	0.0013	1.0000000	E
<input type="checkbox"/>	GO:0006498	9,10,8,7	N-terminal protein lipidation	5	0.0008	1	0.0013	1.0000000	E
<input type="checkbox"/>	GO:0006273	9,8	lagging strand elongation	18	0.0028	6	0.0075	1.0000000	E
<input type="checkbox"/>	GO:0045835	8,10,9,7	negative regulation of meiosis	7	0.0011	1	0.0013	1.0000000	E
<input type="checkbox"/>	GO:0000394	8	RNA splicing, via endonucleolytic cleavage and ligation	14	0.0022	5	0.0063	1.0000000	E
<input type="checkbox"/>	GO:0006313	7,4	transposition, DNA-mediated	10	0.0015	2	0.0025	1.0000000	E
<input type="checkbox"/>	GO:0006541	7,8	glutamine metabolic process	2	0.0003	1	0.0013	1.0000000	E

<input type="checkbox"/>	GO:0045184	3,4,5	establishment of protein localization	296	0.0457	50	0.0626	1.0000000	E
<input type="checkbox"/>	GO:0022402	4,3	cell cycle process	439	0.0678	74	0.0926	1.0000000	E
<input type="checkbox"/>	GO:0009157	7,8	deoxyribonucleoside monophosphate biosynthetic process	1	0.0002	1	0.0013	1.0000000	E
<input type="checkbox"/>	GO:0046500	6,5	S-adenosylmethionine metabolic process	3	0.0005	3	0.0038	1.0000000	E
<input type="checkbox"/>	GO:0000114	10,8,9,5,7,4	G1-specific transcription in mitotic cell cycle	15	0.0023	4	0.0050	1.0000000	E
<input type="checkbox"/>	GO:0007580	10,6	extrachromosomal circular DNA accumulation during cell aging	2	0.0003	1	0.0013	1.0000000	E
<input type="checkbox"/>	GO:0007076	10,8,5,6,9,7,4	mitotic chromosome condensation	9	0.0014	2	0.0025	1.0000000	E
<input type="checkbox"/>	GO:0042158	7,5	lipoprotein biosynthetic process	48	0.0074	6	0.0075	1.0000000	E
<input type="checkbox"/>	GO:0007010	5	cytoskeleton organization and biogenesis	227	0.0351	33	0.0413	1.0000000	E
<input type="checkbox"/>	GO:0006244	6,7	pyrimidine nucleotide catabolic process	1	0.0002	1	0.0013	1.0000000	E
<input type="checkbox"/>	GO:0032508	7	DNA duplex unwinding	16	0.0025	2	0.0025	1.0000000	E
<input type="checkbox"/>	GO:0048280	7,6	vesicle fusion with Golgi apparatus	1	0.0002	1	0.0013	1.0000000	E
<input type="checkbox"/>	GO:0006272	9,8	leading strand elongation	14	0.0022	5	0.0063	1.0000000	E
<input type="checkbox"/>	GO:0051322	6,7,5	anaphase	6	0.0009	1	0.0013	1.0000000	E
<input type="checkbox"/>	GO:0009847	5	spore germination	2	0.0003	1	0.0013	1.0000000	E
<input type="checkbox"/>	GO:0042559	6	pteridine and derivative biosynthetic process	2	0.0003	1	0.0013	1.0000000	E
<input type="checkbox"/>	GO:0030259	6,7	lipid glycosylation	1	0.0002	1	0.0013	1.0000000	E
<input type="checkbox"/>	GO:0006613	10,9,8,7,6	cotranslational protein targeting to membrane	23	0.0036	5	0.0063	1.0000000	E
<input type="checkbox"/>	GO:0030148	7,6,8	sphingolipid biosynthetic process	20	0.0031	3	0.0038	1.0000000	E
<input type="checkbox"/>	GO:0018256	8	protein amino acid formylation	1	0.0002	1	0.0013	1.0000000	E
<input type="checkbox"/>	GO:0000737	6,7	DNA catabolic process, endonucleolytic	15	0.0023	3	0.0038	1.0000000	E
<input type="checkbox"/>	GO:0035055	10,9,12	regulation of nuclear mRNA splicing via U2-type spliceosome	2	0.0003	1	0.0013	1.0000000	E
<input type="checkbox"/>	GO:0006730	4	one-carbon compound metabolic process	97	0.0150	20	0.0250	1.0000000	E
<input type="checkbox"/>	GO:0031567	9,11,10,8	cell size control checkpoint	1	0.0002	1	0.0013	1.0000000	E
<input type="checkbox"/>	GO:0031146	11,10,12	SCF-dependent proteasomal ubiquitin-dependent protein catabolic process	8	0.0012	1	0.0013	1.0000000	E
<input type="checkbox"/>	GO:0006432	9,8,10,7	phenylalanyl-tRNA aminoacylation	3	0.0005	2	0.0025	1.0000000	E
<input type="checkbox"/>	GO:0006013	7,8	mannose metabolic process	6	0.0009	1	0.0013	1.0000000	E
<input type="checkbox"/>	GO:0051452	12,9,10	cellular pH reduction	24	0.0037	4	0.0050	1.0000000	E
<input type="checkbox"/>	GO:0006534	7,8,6	cysteine metabolic process	4	0.0006	2	0.0025	1.0000000	E
<input type="checkbox"/>	GO:0007035	13,10,6,11	vacuolar acidification	24	0.0037	4	0.0050	1.0000000	E
<input type="checkbox"/>	GO:0007323	9	peptide pheromone maturation	8	0.0012	2	0.0025	1.0000000	E
<input type="checkbox"/>	GO:0006325	7	establishment and/or maintenance of chromatin architecture	253	0.0391	37	0.0463	1.0000000	E
<input type="checkbox"/>	GO:0008614	7	pyridoxine metabolic process	8	0.0012	1	0.0013	1.0000000	E
<input type="checkbox"/>	GO:0031507	6,10	heterochromatin formation	95	0.0147	22	0.0275	1.0000000	E
<input type="checkbox"/>	GO:0006429	9,8,10,7	leucyl-tRNA aminoacylation	2	0.0003	1	0.0013	1.0000000	E
<input type="checkbox"/>	GO:0051276	5	chromosome organization and biogenesis	572	0.0883	87	0.1089	1.0000000	E
<input type="checkbox"/>	GO:0006999	6	nuclear pore organization and biogenesis	29	0.0045	8	0.0100	1.0000000	E
<input type="checkbox"/>	GO:0008283	3	cell proliferation	5	0.0008	2	0.0025	1.0000000	E
<input type="checkbox"/>	GO:0015914	5,6	phospholipid transport	12	0.0019	3	0.0038	1.0000000	E
<input type="checkbox"/>	GO:0009152	7,8	purine ribonucleotide biosynthetic process	38	0.0059	7	0.0088	1.0000000	E
<input type="checkbox"/>	GO:0007030	5	Golgi organization and biogenesis	3	0.0005	1	0.0013	1.0000000	E
<input type="checkbox"/>	GO:0006979	4	response to oxidative stress	71	0.0110	11	0.0138	1.0000000	E
<input type="checkbox"/>	GO:0045910	9,8	negative regulation of DNA recombination	12	0.0019	2	0.0025	1.0000000	E

<input type="radio"/>	GO:0001718	8,7,11,10,9	conversion of met-tRNAf to fmet-tRNA	1	0.0002	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0043624	7,6	cellular protein complex disassembly	28	0.0043	7	0.0088	1.0000000	E
<input type="radio"/>	GO:0051352	6	negative regulation of ligase activity	3	0.0005	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0006464	6	protein modification process	520	0.0803	72	0.0901	1.0000000	E
<input type="radio"/>	GO:0031032	8	actomyosin structure organization and biogenesis	3	0.0005	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0006553	7,8	lysine metabolic process	9	0.0014	3	0.0038	1.0000000	E
<input type="radio"/>	GO:0000902	5,6	cell morphogenesis	248	0.0383	42	0.0526	1.0000000	E
<input type="radio"/>	GO:0051254	8,7	positive regulation of RNA metabolic process	5	0.0008	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0031365	8	N-terminal protein amino acid modification	15	0.0023	4	0.0050	1.0000000	E
<input type="radio"/>	GO:0006281	6,5	DNA repair	193	0.0298	26	0.0325	1.0000000	E
<input type="radio"/>	GO:0006057	8,6	mannoprotein biosynthetic process	12	0.0019	6	0.0075	1.0000000	E
<input type="radio"/>	GO:0030472	6,5,10	mitotic spindle organization and biogenesis in nucleus	22	0.0034	5	0.0063	1.0000000	E
<input type="radio"/>	GO:0051598	9,11,8,10,7	meiotic recombination checkpoint	2	0.0003	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0006567	8,9	threonine catabolic process	3	0.0005	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0030174	9,7,8	regulation of DNA replication initiation	10	0.0015	2	0.0025	1.0000000	E
<input type="radio"/>	GO:0006661	10,9,11	phosphatidylinositol biosynthetic process	2	0.0003	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0007121	8,6,10,7,11,5	bipolar cellular bud site selection	32	0.0049	4	0.0050	1.0000000	E
<input type="radio"/>	GO:0016036	8,7,6	cellular response to phosphate starvation	4	0.0006	2	0.0025	1.0000000	E
<input type="radio"/>	GO:0009219	7	pyrimidine deoxyribonucleotide metabolic process	3	0.0005	3	0.0038	1.0000000	E
<input type="radio"/>	GO:0006536	7,8	glutamate metabolic process	16	0.0025	2	0.0025	1.0000000	E
<input type="radio"/>	GO:0009197	8,9	pyrimidine deoxyribonucleoside diphosphate biosynthetic process	1	0.0002	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0031576	9,11,10,8	G2/M transition checkpoint	1	0.0002	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0051707	3,4	response to other organism	7	0.0011	2	0.0025	1.0000000	E
<input type="radio"/>	GO:0051503	7,8	adenine nucleotide transport	3	0.0005	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0055082	6,4	cellular chemical homeostasis	115	0.0178	15	0.0188	1.0000000	E
<input type="radio"/>	GO:0043487	8,7	regulation of RNA stability	30	0.0046	4	0.0050	1.0000000	E
<input type="radio"/>	GO:0009162	7	deoxyribonucleoside monophosphate metabolic process	1	0.0002	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0015698	6,7	inorganic anion transport	16	0.0025	4	0.0050	1.0000000	E
<input type="radio"/>	GO:0006882	10,8	cellular zinc ion homeostasis	10	0.0015	2	0.0025	1.0000000	E
<input type="radio"/>	GO:0033014	6	tetrapyrrole biosynthetic process	13	0.0020	3	0.0038	1.0000000	E
<input type="radio"/>	GO:0009098	8,9	leucine biosynthetic process	5	0.0008	3	0.0038	1.0000000	E
<input type="radio"/>	GO:0019953	3	sexual reproduction	118	0.0182	17	0.0213	1.0000000	E
<input type="radio"/>	GO:0046107	8,7	uracil biosynthetic process	1	0.0002	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0006575	5	amino acid derivative metabolic process	31	0.0048	10	0.0125	1.0000000	E
<input type="radio"/>	GO:0006282	8,7,6	regulation of DNA repair	2	0.0003	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0015837	4,5	amine transport	50	0.0077	7	0.0088	1.0000000	E
<input type="radio"/>	GO:0006470	8,7	protein amino acid dephosphorylation	29	0.0045	5	0.0063	1.0000000	E
<input type="radio"/>	GO:0006417	7,6,5	regulation of translation	47	0.0073	14	0.0175	1.0000000	E
<input type="radio"/>	GO:0043112	6	receptor metabolic process	5	0.0008	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0048522	5,4	positive regulation of cellular process	124	0.0191	22	0.0275	1.0000000	E
<input type="radio"/>	GO:0050657	5,6	nucleic acid transport	80	0.0124	20	0.0250	1.0000000	E
<input type="radio"/>	GO:0048590	3	non-developmental growth	35	0.0054	7	0.0088	1.0000000	E
<input type="radio"/>	GO:0006606	9,10,7,8,6	protein import into nucleus	50	0.0077	12	0.0150	1.0000000	E

<input type="radio"/>	GO:0000910	4	cytokinesis	109	0.0168	22	0.0275	1.0000000	E
<input type="radio"/>	GO:0051054	8,7	positive regulation of DNA metabolic process	3	0.0005	2	0.0025	1.0000000	E
<input type="radio"/>	GO:0042401	6,7	biogenic amine biosynthetic process	18	0.0028	5	0.0063	1.0000000	E
<input type="radio"/>	GO:0006352	7,8,6	transcription initiation	55	0.0085	7	0.0088	1.0000000	E
<input type="radio"/>	GO:0009218	7	pyrimidine ribonucleotide metabolic process	2	0.0003	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0051641	4,3	cellular localization	642	0.0991	97	0.1214	1.0000000	E
<input type="radio"/>	GO:0006279	7	premeiotic DNA synthesis	5	0.0008	3	0.0038	1.0000000	E
<input type="radio"/>	GO:0007004	9	telomere maintenance via telomerase	17	0.0026	4	0.0050	1.0000000	E
<input type="radio"/>	GO:0006842	6,7	tricarboxylic acid transport	2	0.0003	2	0.0025	1.0000000	E
<input type="radio"/>	GO:0009156	7,8	ribonucleoside monophosphate biosynthetic process	15	0.0023	7	0.0088	1.0000000	E
<input type="radio"/>	GO:0007017	6	microtubule-based process	101	0.0156	13	0.0163	1.0000000	E
<input type="radio"/>	GO:0006609	10,11,8,9,7	mRNA-binding (hnRNP) protein import into nucleus	25	0.0039	7	0.0088	1.0000000	E
<input type="radio"/>	GO:0009083	7,8	branched chain family amino acid catabolic process	4	0.0006	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0007088	7,9,8,6	regulation of mitosis	55	0.0085	7	0.0088	1.0000000	E
<input type="radio"/>	GO:0006760	5,7	folic acid and derivative metabolic process	9	0.0014	2	0.0025	1.0000000	E
<input type="radio"/>	GO:0046033	9	AMP metabolic process	1	0.0002	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0009064	6,7	glutamine family amino acid metabolic process	43	0.0066	7	0.0088	1.0000000	E
<input type="radio"/>	GO:0043144	7	snoRNA processing	8	0.0012	3	0.0038	1.0000000	E
<input type="radio"/>	GO:0006768	5,7,6	biotin metabolic process	7	0.0011	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0043086	5	negative regulation of enzyme activity	11	0.0017	2	0.0025	1.0000000	E
<input type="radio"/>	GO:0006551	7,8	leucine metabolic process	7	0.0011	3	0.0038	1.0000000	E
<input type="radio"/>	GO:0009445	7,8	putrescine metabolic process	1	0.0002	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0006366	8,7	transcription from RNA polymerase II promoter	343	0.0530	46	0.0576	1.0000000	E
<input type="radio"/>	GO:0016050	5	vesicle organization and biogenesis	16	0.0025	2	0.0025	1.0000000	E
<input type="radio"/>	GO:0019748	3	secondary metabolic process	23	0.0036	4	0.0050	1.0000000	E
<input type="radio"/>	GO:0018008	11,12,9,10	N-terminal peptidyl-glycine N-myristoylation	1	0.0002	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0000459	7,8	exonucleolytic trimming during rRNA processing	1	0.0002	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0006268	8	DNA unwinding during replication	10	0.0015	2	0.0025	1.0000000	E
<input type="radio"/>	GO:0045141	9,7,5,8,6,4	telomere clustering	2	0.0003	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0046474	8,7,9	glycerophospholipid biosynthetic process	39	0.0060	5	0.0063	1.0000000	E
<input type="radio"/>	GO:0009221	7,8	pyrimidine deoxyribonucleotide biosynthetic process	2	0.0003	2	0.0025	1.0000000	E
<input type="radio"/>	GO:0030100	6,7,5	regulation of endocytosis	3	0.0005	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0006497	8,7,6	protein amino acid lipidation	48	0.0074	6	0.0075	1.0000000	E
<input type="radio"/>	GO:0046135	6,7	pyrimidine nucleoside catabolic process	2	0.0003	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0048250	8,6,9,7,10	mitochondrial iron ion transport	2	0.0003	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0031324	6,5	negative regulation of cellular metabolic process	198	0.0306	33	0.0413	1.0000000	E
<input type="radio"/>	GO:0018345	9,8,7	protein palmitoylation	8	0.0012	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0042138	11,9,8,5,6,10,7,4	meiotic DNA double-strand break formation	9	0.0014	3	0.0038	1.0000000	E
<input type="radio"/>	GO:0007029	5	endoplasmic reticulum organization and biogenesis	6	0.0009	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0006783	7,6,8	heme biosynthetic process	13	0.0020	3	0.0038	1.0000000	E
<input type="radio"/>	GO:0006469	7,8	negative regulation of protein kinase activity	7	0.0011	1	0.0013	1.0000000	E

<input type="radio"/>	GO:0006085	7	acetyl-CoA biosynthetic process	4	0.0006	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0048193	7,5,6	Golgi vesicle transport	166	0.0256	22	0.0275	1.0000000	E
<input type="radio"/>	GO:0035057	11,10,13	positive regulation of nuclear mRNA splicing via U2-type spliceosome	2	0.0003	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0018318	10,9,8	protein amino acid palmitoylation	8	0.0012	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0044255	4,5	cellular lipid metabolic process	229	0.0354	32	0.0401	1.0000000	E
<input type="radio"/>	GO:0000278	4	mitotic cell cycle	266	0.0411	46	0.0576	1.0000000	E
<input type="radio"/>	GO:0015677	9,10	copper ion import	8	0.0012	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0018206	8	peptidyl-methionine modification	3	0.0005	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0009085	8,9	lysine biosynthetic process	9	0.0014	3	0.0038	1.0000000	E
<input type="radio"/>	GO:0008299	6,5,7	isoprenoid biosynthetic process	6	0.0009	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0006672	8,9	ceramide metabolic process	8	0.0012	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0007329	11,10,7	positive regulation of transcription from RNA polymerase II promoter by pheromones	5	0.0008	3	0.0038	1.0000000	E
<input type="radio"/>	GO:0051329	7,5,6	interphase of mitotic cell cycle	112	0.0173	25	0.0313	1.0000000	E
<input type="radio"/>	GO:0015802	6,7,8	basic amino acid transport	9	0.0014	2	0.0025	1.0000000	E
<input type="radio"/>	GO:0030969	8,6,7	UFP-specific transcription factor mRNA processing during unfolded protein response	2	0.0003	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0046072	9	dTDP metabolic process	1	0.0002	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0019307	8,9	mannose biosynthetic process	2	0.0003	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0000915	7,6,10,5	cytokinesis, contractile ring formation	3	0.0005	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0045144	10,8,7,5,9,6,4	meiotic sister chromatid segregation	4	0.0006	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0000273	6,5	lipoic acid metabolic process	1	0.0002	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0006233	9,10	dTDP biosynthetic process	1	0.0002	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0055071	9	manganese ion homeostasis	5	0.0008	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0007265	7	Ras protein signal transduction	39	0.0060	6	0.0075	1.0000000	E
<input type="radio"/>	GO:0019509	7,8,6,9	methionine salvage	3	0.0005	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0000288	10,8,9	mRNA catabolic process, deadenylation-dependent decay	24	0.0037	4	0.0050	1.0000000	E
<input type="radio"/>	GO:0000360	8,9,7,11,13	cis assembly of U2-type pre-catalytic spliceosome	1	0.0002	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0008315	10,8,7,5,9,6,4	meiotic G2/MI transition	1	0.0002	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0009139	7,8	pyrimidine nucleoside diphosphate biosynthetic process	1	0.0002	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0000376	9	RNA splicing, via transesterification reactions with quanosine as nucleophile	7	0.0011	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0032263	7,8	GMP salvage	1	0.0002	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0000903	6,4,8,7,9	cellular morphogenesis during vegetative growth	8	0.0012	2	0.0025	1.0000000	E
<input type="radio"/>	GO:0006415	8,7,6	translational termination	7	0.0011	3	0.0038	1.0000000	E
<input type="radio"/>	GO:0006409	11,9,6,8,10,7	tRNA export from nucleus	29	0.0045	8	0.0100	1.0000000	E
<input type="radio"/>	GO:0001306	4,5	age-dependent response to oxidative stress	6	0.0009	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0046655	6,8	folic acid metabolic process	2	0.0003	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0045332	5,7,6,8	phospholipid translocation	7	0.0011	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0016255	11,10,8,9,12	attachment of GPI anchor to protein	5	0.0008	1	0.0013	1.0000000	E
<input type="radio"/>	GO:0006080	10,8,9	substituted mannan metabolic process	2	0.0003	2	0.0025	1.0000000	E
<input type="radio"/>	GO:0007114	5,4	cell budding	85	0.0131	14	0.0175	1.0000000	E
<input type="radio"/>	GO:0006096	9,10	glycolysis	24	0.0037	1	0.0013	1.0000000	D
<input type="radio"/>	GO:0009201	7,8	ribonucleoside triphosphate biosynthetic process	24	0.0037	1	0.0013	1.0000000	D

<input type="checkbox"/>	GO:0007109	7,6,5,4	cytokinesis, completion of separation	11	0.0017	1	0.0013	1.0000000	D
<input type="checkbox"/>	GO:0030001	6,7	metal ion transport	62	0.0096	6	0.0075	1.0000000	D
<input type="checkbox"/>	GO:0044248	4	cellular catabolic process	425	0.0656	44	0.0551	1.0000000	D
<input type="checkbox"/>	GO:0006118	4	electron transport	33	0.0051	3	0.0038	1.0000000	D
<input type="checkbox"/>	GO:0001300	5	chronological cell aging	13	0.0020	1	0.0013	1.0000000	D
<input type="checkbox"/>	GO:0016265	3	death	13	0.0020	1	0.0013	1.0000000	D
<input type="checkbox"/>	GO:0006006	7,8	glucose metabolic process	65	0.0100	6	0.0075	1.0000000	D
<input type="checkbox"/>	GO:0000128	3	flocculation	9	0.0014	1	0.0013	1.0000000	D
<input type="checkbox"/>	GO:0019674	9,8	NAD metabolic process	21	0.0032	2	0.0025	1.0000000	D
<input type="checkbox"/>	GO:0044262	5	cellular carbohydrate metabolic process	213	0.0329	13	0.0163	1.0000000	D
<input type="checkbox"/>	GO:0006887	8,6,5,7	exocytosis	44	0.0068	4	0.0050	1.0000000	D
<input type="checkbox"/>	GO:0007165	4	signal transduction	209	0.0323	23	0.0288	1.0000000	D
<input type="checkbox"/>	GO:0006081	4	aldehyde metabolic process	21	0.0032	1	0.0013	1.0000000	D
<input type="checkbox"/>	GO:0016226	6	iron-sulfur cluster assembly	11	0.0017	1	0.0013	1.0000000	D
<input type="checkbox"/>	GO:0006769	8,7	nicotinamide metabolic process	42	0.0065	5	0.0063	1.0000000	D
<input type="checkbox"/>	GO:0015893	4,5	drug transport	13	0.0020	1	0.0013	1.0000000	D
<input type="checkbox"/>	GO:0043161	10,9,11	proteasomal ubiquitin-dependent protein catabolic process	63	0.0097	4	0.0050	1.0000000	D
<input type="checkbox"/>	GO:0051180	4,5	vitamin transport	9	0.0014	1	0.0013	1.0000000	D
<input type="checkbox"/>	GO:0000154	7,8	rRNA modification	85	0.0131	8	0.0100	1.0000000	D
<input type="checkbox"/>	GO:0000724	8,7	double-strand break repair via homologous recombination	25	0.0039	3	0.0038	1.0000000	D
<input type="checkbox"/>	GO:0006045	8,9	N-acetylglucosamine biosynthetic process	17	0.0026	1	0.0013	1.0000000	D
<input type="checkbox"/>	GO:0030036	7	actin cytoskeleton organization and biogenesis	107	0.0165	13	0.0163	1.0000000	D
<input type="checkbox"/>	GO:0006007	8,9	glucose catabolic process	34	0.0053	4	0.0050	1.0000000	D
<input type="checkbox"/>	GO:0006974	4	response to DNA damage stimulus	234	0.0361	28	0.0350	1.0000000	D
<input type="checkbox"/>	GO:0006986	4,5	response to unfolded protein	18	0.0028	1	0.0013	1.0000000	D
<input type="checkbox"/>	GO:0009966	5,4	regulation of signal transduction	26	0.0040	2	0.0025	1.0000000	D
<input type="checkbox"/>	GO:0055072	9	iron ion homeostasis	38	0.0059	4	0.0050	1.0000000	D
<input type="checkbox"/>	GO:0046470	8,9	phosphatidylcholine metabolic process	9	0.0014	1	0.0013	1.0000000	D
<input type="checkbox"/>	GO:0006650	7,8	glycerophospholipid metabolic process	60	0.0093	7	0.0088	1.0000000	D
<input type="checkbox"/>	GO:0009056	3	catabolic process	438	0.0676	45	0.0563	1.0000000	D
<input type="checkbox"/>	GO:0016051	5	carbohydrate biosynthetic process	77	0.0119	3	0.0038	1.0000000	D
<input type="checkbox"/>	GO:0000051	4,3	urea cycle intermediate metabolic process	15	0.0023	1	0.0013	1.0000000	D
<input type="checkbox"/>	GO:0016567	9	protein ubiquitination	66	0.0102	4	0.0050	1.0000000	D
<input type="checkbox"/>	GO:0032446	8	protein modification by small protein conjugation	84	0.0130	7	0.0088	1.0000000	D
<input type="checkbox"/>	GO:0006767	5	water-soluble vitamin metabolic process	89	0.0137	7	0.0088	1.0000000	D
<input type="checkbox"/>	GO:0043085	5	positive regulation of enzyme activity	11	0.0017	1	0.0013	1.0000000	D
<input type="checkbox"/>	GO:0007129	10,8,7,5,9,6,4	synapsis	10	0.0015	1	0.0013	1.0000000	D
<input type="checkbox"/>	GO:0042493	4	response to drug	121	0.0187	14	0.0175	1.0000000	D
<input type="checkbox"/>	GO:0031118	8,9	rRNA pseudouridine synthesis	31	0.0048	1	0.0013	1.0000000	D
<input type="checkbox"/>	GO:0042221	3	response to chemical stimulus	382	0.0590	42	0.0526	1.0000000	D
<input type="checkbox"/>	GO:0019319	7,8	hexose biosynthetic process	30	0.0046	2	0.0025	1.0000000	D
<input type="checkbox"/>	GO:0000393	7,6,9,11	spliceosomal conformational changes to generate catalytic conformation	9	0.0014	1	0.0013	1.0000000	D
<input type="checkbox"/>	GO:0030258	5,6	lipid modification	13	0.0020	1	0.0013	1.0000000	D
<input type="checkbox"/>	GO:0005977	7,6,8	glycogen metabolic process	32	0.0049	2	0.0025	1.0000000	D

<input type="radio"/>	GO:0006473	8	protein amino acid acetylation	48	0.0074	5	0.0063	1.0000000	D
<input type="radio"/>	GO:0008150	1	biological process	6476	1.0000	799	1.0000	1.0000000	D
<input type="radio"/>	GO:0045333	5	cellular respiration	89	0.0137	6	0.0075	1.0000000	D
<input type="radio"/>	GO:0031667	5	response to nutrient levels	37	0.0057	2	0.0025	1.0000000	D
<input type="radio"/>	GO:0000028	9,7,8,6	ribosomal small subunit assembly and maintenance	14	0.0022	1	0.0013	1.0000000	D
<input type="radio"/>	GO:0032505	4,3	reproduction of a single-celled organism	194	0.0300	21	0.0263	1.0000000	D
<input type="radio"/>	GO:0006094	8,9	gluconeogenesis	28	0.0043	1	0.0013	1.0000000	D
<input type="radio"/>	GO:0019320	7,8	hexose catabolic process	39	0.0060	4	0.0050	1.0000000	D
<input type="radio"/>	GO:0019538	4	protein metabolic process	1547	0.2389	161	0.2015	1.0000000	D
<input type="radio"/>	GO:0009060	6	aerobic respiration	84	0.0130	5	0.0063	1.0000000	D
<input type="radio"/>	GO:0044265	5	cellular macromolecule catabolic process	314	0.0485	33	0.0413	1.0000000	D
<input type="radio"/>	GO:0007243	6	protein kinase cascade	23	0.0036	2	0.0025	1.0000000	D
<input type="radio"/>	GO:0007047	5	cell wall organization and biogenesis	200	0.0309	20	0.0250	1.0000000	D
<input type="radio"/>	GO:0000726	7,6	non-recombinational repair	35	0.0054	1	0.0013	1.0000000	D
<input type="radio"/>	GO:0006906	6,5	vesicle fusion	28	0.0043	2	0.0025	1.0000000	D
<input type="radio"/>	GO:0009065	7,8	glutamine family amino acid catabolic process	13	0.0020	1	0.0013	1.0000000	D
<input type="radio"/>	GO:0000165	7	MAPKKK cascade	20	0.0031	1	0.0013	1.0000000	D
<input type="radio"/>	GO:0000122	10,9	negative regulation of transcription from RNA polymerase II promoter	63	0.0097	4	0.0050	1.0000000	D
<input type="radio"/>	GO:0046164	5	alcohol catabolic process	47	0.0073	4	0.0050	1.0000000	D
<input type="radio"/>	GO:0051049	5,4	regulation of transport	11	0.0017	1	0.0013	1.0000000	D
<input type="radio"/>	GO:0008643	4,5	carbohydrate transport	38	0.0059	3	0.0038	1.0000000	D
<input type="radio"/>	GO:0009199	7	ribonucleoside triphosphate metabolic process	25	0.0039	1	0.0013	1.0000000	D
<input type="radio"/>	GO:0043255	7,6,5	regulation of carbohydrate biosynthetic process	19	0.0029	1	0.0013	1.0000000	D
<input type="radio"/>	GO:0022413	5,4	reproductive process in single-celled organism	149	0.0230	14	0.0175	1.0000000	D
<input type="radio"/>	GO:0009607	3	response to biotic stimulus	25	0.0039	3	0.0038	1.0000000	D
<input type="radio"/>	GO:0001304	10,6	progressive alteration of chromatin during replicative cell aging	9	0.0014	1	0.0013	1.0000000	D
<input type="radio"/>	GO:0030003	8,6	cellular cation homeostasis	102	0.0158	12	0.0150	1.0000000	D
<input type="radio"/>	GO:0045003	9,8	double-strand break repair via synthesis-dependent strand annealing	17	0.0026	2	0.0025	1.0000000	D
<input type="radio"/>	GO:0051186	4	cofactor metabolic process	170	0.0263	18	0.0225	1.0000000	D
<input type="radio"/>	GO:0030968	7,5,6	unfolded protein response	9	0.0014	1	0.0013	1.0000000	D
<input type="radio"/>	GO:0000722	9,8	telomere maintenance via recombination	19	0.0029	1	0.0013	1.0000000	D
<input type="radio"/>	GO:0046467	6,5,7	membrane lipid biosynthetic process	78	0.0120	9	0.0113	1.0000000	D
<input type="radio"/>	GO:0009059	4	macromolecule biosynthetic process	886	0.1368	87	0.1089	1.0000000	D
<input type="radio"/>	GO:0051128	5,4	regulation of cellular component organization and biogenesis	30	0.0046	3	0.0038	1.0000000	D
<input type="radio"/>	GO:0016570	10,8	histone modification	91	0.0141	8	0.0100	1.0000000	D
<input type="radio"/>	GO:0016569	9	covalent chromatin modification	91	0.0141	8	0.0100	1.0000000	D
<input type="radio"/>	GO:0000161	7,8,6	MAPKKK cascade during osmolarity sensing	11	0.0017	1	0.0013	1.0000000	D
<input type="radio"/>	GO:0050896	2	response to stimulus	763	0.1178	84	0.1051	1.0000000	D
<input type="radio"/>	GO:0006984	6	ER-nuclear signaling pathway	9	0.0014	1	0.0013	1.0000000	D
<input type="radio"/>	GO:0006042	7,8	glucosamine biosynthetic process	17	0.0026	1	0.0013	1.0000000	D
<input type="radio"/>	GO:0006513	10	protein monoubiquitination	22	0.0034	2	0.0025	1.0000000	D
<input type="radio"/>	GO:0030437	7,6	sporulation (sensu Fungi)	108	0.0167	7	0.0088	1.0000000	D

<input type="radio"/>	GO:0045229	4	external encapsulating structure organization and biogenesis	200	0.0309	20	0.0250	1.0000000	D
<input type="radio"/>	GO:0043632	6	modification-dependent macromolecule catabolic process	155	0.0239	10	0.0125	1.0000000	D
<input type="radio"/>	GO:0006625	9,8,6,7	protein targeting to peroxisome	20	0.0031	1	0.0013	1.0000000	D
<input type="radio"/>	GO:0000001	8,7,6	mitochondrion inheritance	26	0.0040	1	0.0013	1.0000000	D
<input type="radio"/>	GO:0006384	8,9,7	transcription initiation from RNA polymerase III promoter	11	0.0017	1	0.0013	1.0000000	D
<input type="radio"/>	GO:0030435	5	sporulation	123	0.0190	7	0.0088	1.0000000	D
<input type="radio"/>	GO:0006113	5	fermentation	17	0.0026	2	0.0025	1.0000000	D
<input type="radio"/>	GO:0006875	9,7	cellular metal ion homeostasis	19	0.0029	1	0.0013	1.0000000	D
<input type="radio"/>	GO:0006950	3	response to stress	488	0.0754	54	0.0676	1.0000000	D
<input type="radio"/>	GO:0000003	2	reproduction	323	0.0499	39	0.0488	1.0000000	D
<input type="radio"/>	GO:0051651	5,4,3	maintenance of cellular localization	29	0.0045	1	0.0013	1.0000000	D
<input type="radio"/>	GO:0000018	8,7	regulation of DNA recombination	18	0.0028	2	0.0025	1.0000000	D
<input type="radio"/>	GO:0044264	5,6	cellular polysaccharide metabolic process	65	0.0100	5	0.0063	1.0000000	D
<input type="radio"/>	GO:0006826	7,8,9	iron ion transport	20	0.0031	2	0.0025	1.0000000	D
<input type="radio"/>	GO:0051646	6,5	mitochondrion localization	27	0.0042	1	0.0013	1.0000000	D
<input type="radio"/>	GO:0006302	7,6	double-strand break repair	57	0.0088	5	0.0063	1.0000000	D
<input type="radio"/>	GO:0010035	4	response to inorganic substance	24	0.0037	2	0.0025	1.0000000	D
<input type="radio"/>	GO:0048468	3,5	cell development	52	0.0080	6	0.0075	1.0000000	D
<input type="radio"/>	GO:0051716	3	cellular response to stimulus	21	0.0032	2	0.0025	1.0000000	D
<input type="radio"/>	GO:0009651	5	response to salt stress	15	0.0023	1	0.0013	1.0000000	D
<input type="radio"/>	GO:0009968	6,5	negative regulation of signal transduction	17	0.0026	2	0.0025	1.0000000	D
<input type="radio"/>	GO:0043285	5	biopolymer catabolic process	277	0.0428	32	0.0401	1.0000000	D
<input type="radio"/>	GO:0042592	4	homeostatic process	134	0.0207	15	0.0188	1.0000000	D
<input type="radio"/>	GO:0030705	7,5,6	cytoskeleton-dependent intracellular transport	17	0.0026	1	0.0013	1.0000000	D
<input type="radio"/>	GO:0007052	5,4,9	mitotic spindle organization and biogenesis	44	0.0068	5	0.0063	1.0000000	D
<input type="radio"/>	GO:0046519	7,8	sphingoid metabolic process	10	0.0015	1	0.0013	1.0000000	D
<input type="radio"/>	GO:0046365	6,7	monosaccharide catabolic process	44	0.0068	4	0.0050	1.0000000	D
<input type="radio"/>	GO:0043486	11	histone exchange	9	0.0014	1	0.0013	1.0000000	D
<input type="radio"/>	GO:0007094	9,11,10,8	mitotic cell cycle spindle assembly checkpoint	20	0.0031	1	0.0013	1.0000000	D
<input type="radio"/>	GO:0006915	6,8	apoptosis	13	0.0020	1	0.0013	1.0000000	D
<input type="radio"/>	GO:0006825	8,9	copper ion transport	14	0.0022	1	0.0013	1.0000000	D
<input type="radio"/>	GO:0016573	11,9	histone acetylation	40	0.0062	3	0.0038	1.0000000	D
<input type="radio"/>	GO:0031570	8,7	DNA integrity checkpoint	18	0.0028	2	0.0025	1.0000000	D
<input type="radio"/>	GO:0016558	10,9,7,8,6	protein import into peroxisome matrix	17	0.0026	1	0.0013	1.0000000	D
<input type="radio"/>	GO:0007031	5	peroxisome organization and biogenesis	40	0.0062	2	0.0025	1.0000000	D
<input type="radio"/>	GO:0022406	3	membrane docking	14	0.0022	1	0.0013	1.0000000	D
<input type="radio"/>	GO:0045721	7,9,8,10,6,11	negative regulation of gluconeogenesis	9	0.0014	1	0.0013	1.0000000	D
<input type="radio"/>	GO:0009636	4	response to toxin	28	0.0043	2	0.0025	1.0000000	D
<input type="radio"/>	GO:0006890	8,6,5,7	retrograde vesicle-mediated transport, Golgi to ER	24	0.0037	2	0.0025	1.0000000	D
<input type="radio"/>	GO:0000920	6,4	cell separation during cytokinesis	13	0.0020	1	0.0013	1.0000000	D
<input type="radio"/>	GO:0000011	6	vacuole inheritance	14	0.0022	1	0.0013	1.0000000	D
<input type="radio"/>	GO:0031577	8,7	spindle checkpoint	24	0.0037	2	0.0025	1.0000000	D
<input type="radio"/>	GO:0000290	11,8,9,10	deadenylation-dependent decapping	9	0.0014	1	0.0013	1.0000000	D

<input type="radio"/>	GO:0048622	6,5	reproductive sporulation	108	0.0167	7	0.0088	1.0000000	D
<input type="radio"/>	GO:0055080	7	cation homeostasis	102	0.0158	12	0.0150	1.0000000	D
<input type="radio"/>	GO:0042144	6	vacuole fusion, non-autophagic	28	0.0043	3	0.0038	1.0000000	D
<input type="radio"/>	GO:0006303	8,7	double-strand break repair via nonhomologous end joining	23	0.0036	1	0.0013	1.0000000	D
<input type="radio"/>	GO:0006631	5,7,6	fatty acid metabolic process	47	0.0073	4	0.0050	1.0000000	D
<input type="radio"/>	GO:0045185	5,4,3	maintenance of protein localization	30	0.0046	1	0.0013	1.0000000	D
<input type="radio"/>	GO:0046165	5	alcohol biosynthetic process	35	0.0054	2	0.0025	1.0000000	D
<input type="radio"/>	GO:0031167	8,9	rRNA methylation	44	0.0068	1	0.0013	1.0000000	D
<input type="radio"/>	GO:0006044	7,8	N-acetylglucosamine metabolic process	19	0.0029	1	0.0013	1.0000000	D
<input type="radio"/>	GO:0006749	6,5	glutathione metabolic process	14	0.0022	1	0.0013	1.0000000	D
<input type="radio"/>	GO:0007097	7,8,5,6	nuclear migration	20	0.0031	1	0.0013	1.0000000	D
<input type="radio"/>	GO:0016485	8	protein processing	38	0.0059	2	0.0025	1.0000000	D
<input type="radio"/>	GO:0009142	6,7	nucleoside triphosphate biosynthetic process	27	0.0042	2	0.0025	1.0000000	D
<input type="radio"/>	GO:0019362	7,6	pyridine nucleotide metabolic process	45	0.0069	5	0.0063	1.0000000	D
<input type="radio"/>	GO:0006511	9,8,10	ubiquitin-dependent protein catabolic process	148	0.0229	7	0.0088	1.0000000	D
<input type="radio"/>	GO:0016052	5	carbohydrate catabolic process	80	0.0124	4	0.0050	1.0000000	D
<input type="radio"/>	GO:0009267	7,6,5	cellular response to starvation	19	0.0029	2	0.0025	1.0000000	D
<input type="radio"/>	GO:0006972	5	hyperosmotic response	11	0.0017	1	0.0013	1.0000000	D
<input type="radio"/>	GO:0042147	8,6,7	retrograde transport, endosome to Golgi	17	0.0026	1	0.0013	1.0000000	D
<input type="radio"/>	GO:0030154	4	cell differentiation	173	0.0267	14	0.0175	1.0000000	D
<input type="radio"/>	GO:0006732	5	coenzyme metabolic process	136	0.0210	13	0.0163	1.0000000	D
<input type="radio"/>	GO:0007124	6,4,8,9	pseudohyphal growth	61	0.0094	7	0.0088	1.0000000	D
<input type="radio"/>	GO:0006040	5,6	amino sugar metabolic process	19	0.0029	1	0.0013	1.0000000	D
<input type="radio"/>	GO:0051640	5,4	organelle localization	56	0.0086	5	0.0063	1.0000000	D
<input type="radio"/>	GO:0006041	6,7	glucosamine metabolic process	19	0.0029	1	0.0013	1.0000000	D
<input type="radio"/>	GO:0040023	6,7,4,5	establishment of nucleus localization	20	0.0031	1	0.0013	1.0000000	D
<input type="radio"/>	GO:0019363	7,6,8	pyridine nucleotide biosynthetic process	10	0.0015	1	0.0013	1.0000000	D
<input type="radio"/>	GO:0007186	6	G-protein coupled receptor protein signaling pathway	34	0.0053	4	0.0050	1.0000000	D
<input type="radio"/>	GO:0006109	5,4	regulation of carbohydrate metabolic process	29	0.0045	1	0.0013	1.0000000	D
<input type="radio"/>	GO:0019725	5,3	cellular homeostasis	128	0.0198	15	0.0188	1.0000000	D
<input type="radio"/>	GO:0030029	6	actin filament-based process	112	0.0173	13	0.0163	1.0000000	D
<input type="radio"/>	GO:0006091	3	generation of precursor metabolites and energy	183	0.0283	13	0.0163	1.0000000	D
<input type="radio"/>	GO:0006914	3	autophagy	45	0.0069	4	0.0050	1.0000000	D
<input type="radio"/>	GO:0006512	8	ubiquitin cycle	88	0.0136	7	0.0088	1.0000000	D
<input type="radio"/>	GO:0007166	5	cell surface receptor linked signal transduction	52	0.0080	6	0.0075	1.0000000	D
<input type="radio"/>	GO:0007242	5	intracellular signaling cascade	137	0.0212	14	0.0175	1.0000000	D
<input type="radio"/>	GO:0032787	6	monocarboxylic acid metabolic process	126	0.0195	10	0.0125	1.0000000	D
<input type="radio"/>	GO:0000103	6	sulfate assimilation	10	0.0015	1	0.0013	1.0000000	D
<input type="radio"/>	GO:0051248	6,5	negative regulation of protein metabolic process	18	0.0028	2	0.0025	1.0000000	D
<input type="radio"/>	GO:0006766	4	vitamin metabolic process	89	0.0137	7	0.0088	1.0000000	D
<input type="radio"/>	GO:0051235	3,2	maintenance of localization	33	0.0051	1	0.0013	1.0000000	D
<input type="radio"/>	GO:0015674	6,7	di-, tri-valent inorganic cation transport	34	0.0053	4	0.0050	1.0000000	D
<input type="radio"/>	GO:0006112	5	energy reserve metabolic process	39	0.0060	2	0.0025	1.0000000	D

<input type="radio"/>	GO:0015718	6,7	monocarboxylic acid transport	10	0.0015	1	0.0013	1.0000000	D
<input type="radio"/>	GO:0009057	4	macromolecule catabolic process	345	0.0533	36	0.0451	1.0000000	D
<input type="radio"/>	GO:0016310	6	phosphorylation	155	0.0239	9	0.0113	1.0000000	D
<input type="radio"/>	GO:0006525	7,8,5,4	arginine metabolic process	15	0.0023	1	0.0013	1.0000000	D
<input type="radio"/>	GO:0009408	5,4	response to heat	23	0.0036	1	0.0013	1.0000000	D
<input type="radio"/>	GO:0010038	5	response to metal ion	18	0.0028	2	0.0025	1.0000000	D
<input type="radio"/>	GO:0051647	6,5	nucleus localization	20	0.0031	1	0.0013	1.0000000	D
<input type="radio"/>	GO:0030005	9,7	cellular di-, tri-valent inorganic cation homeostasis	64	0.0099	7	0.0088	1.0000000	D
<input type="radio"/>	GO:0006468	8,7	protein amino acid phosphorylation	101	0.0156	9	0.0113	1.0000000	D
<input type="radio"/>	GO:0007033	5	vacuole organization and biogenesis	67	0.0103	8	0.0100	1.0000000	D
<input type="radio"/>	GO:0022414	3,2	reproductive process	183	0.0283	19	0.0238	1.0000000	D
<input type="radio"/>	GO:0030447	3	filamentous growth	94	0.0145	10	0.0125	1.0000000	D
<input type="radio"/>	GO:0016192	4,5	vesicle-mediated transport	328	0.0506	35	0.0438	1.0000000	D
<input type="radio"/>	GO:0007005	5	mitochondrion organization and biogenesis	110	0.0170	10	0.0125	1.0000000	D
<input type="radio"/>	GO:0006623	9,8,7,6	protein targeting to vacuole	67	0.0103	4	0.0050	1.0000000	D
<input type="radio"/>	GO:0005976	5	polysaccharide metabolic process	65	0.0100	5	0.0063	1.0000000	D
<input type="radio"/>	GO:0009991	4	response to extracellular stimulus	37	0.0057	2	0.0025	1.0000000	D
<input type="radio"/>	GO:0006812	5,6	cation transport	97	0.0150	6	0.0075	1.0000000	D
<input type="radio"/>	GO:0006312	7	mitotic recombination	45	0.0069	3	0.0038	1.0000000	D
<input type="radio"/>	GO:0007034	7,5,6	vacuolar transport	114	0.0176	10	0.0125	1.0000000	D
<input type="radio"/>	GO:0043687	7	post-translational protein modification	388	0.0599	35	0.0438	1.0000000	D
<input type="radio"/>	GO:0006752	6	group transfer coenzyme metabolic process	44	0.0068	5	0.0063	1.0000000	D
<input type="radio"/>	GO:0042594	6,4	response to starvation	19	0.0029	2	0.0025	1.0000000	D
<input type="radio"/>	GO:0006791	5	sulfur utilization	10	0.0015	1	0.0013	1.0000000	D
<input type="radio"/>	GO:0008219	4,6	cell death	13	0.0020	1	0.0013	1.0000000	D
<input type="radio"/>	GO:0006643	5,6	membrane lipid metabolic process	125	0.0193	14	0.0175	1.0000000	D
<input type="radio"/>	GO:0009266	4	response to temperature stimulus	28	0.0043	2	0.0025	1.0000000	D
<input type="radio"/>	GO:0016197	7,5,6	endosome transport	49	0.0076	3	0.0038	1.0000000	D
<input type="radio"/>	GO:0016044	4	membrane organization and biogenesis	188	0.0290	18	0.0225	1.0000000	D
<input type="radio"/>	GO:0019941	8,7,9	modification-dependent protein catabolic process	148	0.0229	7	0.0088	1.0000000	D
<input type="radio"/>	GO:0030846	10,9	transcription termination from Pol II promoter, RNA polymerase(A) coupled	10	0.0015	1	0.0013	1.0000000	D
<input type="radio"/>	GO:0000749	5	response to pheromone during conjugation with cellular fusion	57	0.0088	6	0.0075	1.0000000	D
<input type="radio"/>	GO:0045786	6,7,5	negative regulation of progression through cell cycle	13	0.0020	1	0.0013	1.0000000	D
<input type="radio"/>	GO:0051231	5,4,9,7	spindle elongation	20	0.0031	1	0.0013	1.0000000	D
<input type="radio"/>	GO:0032507	6,5,4	maintenance of cellular protein localization	29	0.0045	1	0.0013	1.0000000	D
<input type="radio"/>	GO:0010324	5	membrane invagination	96	0.0148	11	0.0138	1.0000000	D
<input type="radio"/>	GO:0015980	4	energy derivation by oxidation of organic compounds	145	0.0224	10	0.0125	1.0000000	D
<input type="radio"/>	GO:0006111	8,7,9,10,6	regulation of gluconeogenesis	13	0.0020	1	0.0013	1.0000000	D
<input type="radio"/>	GO:0051656	6,3,5,4	establishment of organelle localization	29	0.0045	1	0.0013	1.0000000	D
<input type="radio"/>	GO:0007096	8,10,9,7	regulation of exit from mitosis	24	0.0037	2	0.0025	1.0000000	D
<input type="radio"/>	GO:0031163	5	metallo-sulfur cluster assembly	11	0.0017	1	0.0013	1.0000000	D
<input type="radio"/>	GO:0007015	8	actin filament organization	61	0.0094	6	0.0075	1.0000000	D
<input type="radio"/>	GO:0006090	7	pyruvate metabolic process	38	0.0059	2	0.0025	1.0000000	D

<input type="radio"/>	GO:0016049	5,3,7,8	cell growth	102	0.0158	11	0.0138	1.0000000	D
<input type="radio"/>	GO:0006368	9,7,8	RNA elongation from RNA polymerase II promoter	53	0.0082	4	0.0050	1.0000000	D
<input type="radio"/>	GO:0009110	5	vitamin biosynthetic process	46	0.0071	4	0.0050	1.0000000	D
<input type="radio"/>	GO:0009719	3	response to endogenous stimulus	243	0.0375	28	0.0350	1.0000000	D
<input type="radio"/>	GO:0030473	8,9,6,7	nuclear migration, microtubule-mediated	15	0.0023	1	0.0013	1.0000000	D
<input type="radio"/>	GO:0046349	6,7	amino sugar biosynthetic process	17	0.0026	1	0.0013	1.0000000	D
<input type="radio"/>	GO:0009108	6	coenzyme biosynthetic process	66	0.0102	7	0.0088	1.0000000	D
<input type="radio"/>	GO:0009628	3	response to abiotic stimulus	117	0.0181	13	0.0163	1.0000000	D
<input type="radio"/>	GO:0042244	5,6	spore wall assembly	42	0.0065	2	0.0025	1.0000000	D
<input type="radio"/>	GO:0006073	6,7	glucan metabolic process	46	0.0071	3	0.0038	1.0000000	D
<input type="radio"/>	GO:0000022	6,5,10,8	mitotic spindle elongation	20	0.0031	1	0.0013	1.0000000	D
<input type="radio"/>	GO:0000184	8	mRNA catabolic process, nonsense-mediated decay	9	0.0014	1	0.0013	1.0000000	D
<input type="radio"/>	GO:0048610	3,4	reproductive cellular process	149	0.0230	14	0.0175	1.0000000	D
<input type="radio"/>	GO:0042364	6	water-soluble vitamin biosynthetic process	46	0.0071	4	0.0050	1.0000000	D
<input type="radio"/>	GO:0045324	8,6,7	late endosome to vacuole transport	21	0.0032	1	0.0013	1.0000000	D
<input type="radio"/>	GO:0000041	7,8	transition metal ion transport	46	0.0071	5	0.0063	1.0000000	D
<input type="radio"/>	GO:0006644	6,7	phospholipid metabolic process	97	0.0150	9	0.0113	1.0000000	D
<input type="radio"/>	GO:0030433	9,11,10,12	ER-associated protein catabolic process	35	0.0054	3	0.0038	1.0000000	D
<input type="radio"/>	GO:0000209	10	protein polyubiquitination	20	0.0031	2	0.0025	1.0000000	D
<input type="radio"/>	GO:0008654	7,6,8	phospholipid biosynthetic process	58	0.0090	6	0.0075	1.0000000	D
<input type="radio"/>	GO:0045912	6,5	negative regulation of carbohydrate metabolic process	9	0.0014	1	0.0013	1.0000000	D
<input type="radio"/>	GO:0031669	6,5	cellular response to nutrient levels	19	0.0029	2	0.0025	1.0000000	D
<input type="radio"/>	GO:0006734	9,8	NADH metabolic process	14	0.0022	1	0.0013	1.0000000	D
<input type="radio"/>	GO:0006733	6	oxidoreduction coenzyme metabolic process	56	0.0086	5	0.0063	1.0000000	D
<input type="radio"/>	GO:0019236	4	response to pheromone	94	0.0145	11	0.0138	1.0000000	D
<input type="radio"/>	GO:0006896	9,8,7,6	Golgi to vacuole transport	24	0.0037	2	0.0025	1.0000000	D
<input type="radio"/>	GO:0048311	7,6	mitochondrion distribution	26	0.0040	1	0.0013	1.0000000	D
<input type="radio"/>	GO:0006515	8,9	misfolded or incompletely synthesized protein catabolic process	38	0.0059	3	0.0038	1.0000000	D
<input type="radio"/>	GO:0042770	5	DNA damage response, signal transduction	14	0.0022	1	0.0013	1.0000000	D
<input type="radio"/>	GO:0006879	10,8	cellular iron ion homeostasis	38	0.0059	4	0.0050	1.0000000	D
<input type="radio"/>	GO:0046685	5	response to arsenic	9	0.0014	1	0.0013	1.0000000	D
<input type="radio"/>	GO:0001403	6,4,8,9	invasive growth (sensu Saccharomyces)	42	0.0065	4	0.0050	1.0000000	D
<input type="radio"/>	GO:0048869	3	cellular developmental process	173	0.0267	14	0.0175	1.0000000	D
<input type="radio"/>	GO:0015846	5,6	polyamine transport	12	0.0019	1	0.0013	1.0000000	D
<input type="radio"/>	GO:0006084	6	acetyl-CoA metabolic process	20	0.0031	1	0.0013	1.0000000	D
<input type="radio"/>	GO:0000002	6	mitochondrial genome maintenance	31	0.0048	2	0.0025	1.0000000	D
<input type="radio"/>	GO:0000501	4	flocculation via cell wall protein-carbohydrate interaction	9	0.0014	1	0.0013	1.0000000	D
<input type="radio"/>	GO:0043044	10	ATP-dependent chromatin remodeling	23	0.0036	1	0.0013	1.0000000	D
<input type="radio"/>	GO:0044275	6	cellular carbohydrate catabolic process	80	0.0124	4	0.0050	1.0000000	D
<input type="radio"/>	GO:0055065	8	metal ion homeostasis	19	0.0029	1	0.0013	1.0000000	D
<input type="radio"/>	GO:0048308	5	organelle inheritance	40	0.0062	2	0.0025	1.0000000	D
<input type="radio"/>	GO:0009605	3	response to external stimulus	37	0.0057	2	0.0025	1.0000000	D
<input type="radio"/>	GO:0031668	5,4	cellular response to extracellular stimulus	19	0.0029	2	0.0025	1.0000000	D

<input type="radio"/>	GO:0012501	5,7	programmed cell death	13	0.0020	1	0.0013	1.0000000	D
<input type="radio"/>	GO:0006944	5	membrane fusion	59	0.0091	5	0.0063	1.0000000	D
<input type="radio"/>	GO:0006811	4,5	ion transport	115	0.0178	10	0.0125	1.0000000	D
<input type="radio"/>	GO:0051789	4	response to protein stimulus	18	0.0028	1	0.0013	1.0000000	D
<input type="radio"/>	GO:0001522	7	pseudouridine synthesis	39	0.0060	4	0.0050	1.0000000	D
<input type="radio"/>	GO:0006354	8,6,7	RNA elongation	59	0.0091	4	0.0050	1.0000000	D
<input type="radio"/>	GO:0000183	11,7,8,12,10	chromatin silencing at rDNA	18	0.0028	2	0.0025	1.0000000	D
<input type="radio"/>	GO:0044267	5	cellular protein metabolic process	1498	0.2313	155	0.1940	1.0000000	D
<input type="radio"/>	GO:0006116	10,9	NADH oxidation	11	0.0017	1	0.0013	1.0000000	D
<input type="radio"/>	GO:0048278	4,5,6	vesicle docking	14	0.0022	1	0.0013	1.0000000	D
<input type="radio"/>	GO:0019318	6,7	hexose metabolic process	85	0.0131	7	0.0088	1.0000000	D
<input type="radio"/>	GO:0006793	4	phosphorus metabolic process	212	0.0327	21	0.0263	1.0000000	D
<input type="radio"/>	GO:0005996	5,6	monosaccharide metabolic process	92	0.0142	7	0.0088	1.0000000	D
<input type="radio"/>	GO:0006897	6,5	endocytosis	86	0.0133	8	0.0100	1.0000000	D
<input type="radio"/>	GO:0055066	8	di-, tri-valent inorganic cation homeostasis	64	0.0099	7	0.0088	1.0000000	D
<input type="radio"/>	GO:0006895	8,9,6,7	Golgi to endosome transport	13	0.0020	1	0.0013	1.0000000	D
<input type="radio"/>	GO:0007018	8,7,6	microtubule-based movement	15	0.0023	1	0.0013	1.0000000	D
<input type="radio"/>	GO:0000077	9,8,6	DNA damage checkpoint	14	0.0022	1	0.0013	1.0000000	D
<input type="radio"/>	GO:0033554	4	cellular response to stress	21	0.0032	2	0.0025	1.0000000	D
<input type="radio"/>	GO:0006796	5	phosphate metabolic process	212	0.0327	21	0.0263	1.0000000	D
<input type="radio"/>	GO:0046364	6,7	monosaccharide biosynthetic process	30	0.0046	2	0.0025	1.0000000	D
<input type="radio"/>	GO:0007154	3	cell communication	240	0.0371	25	0.0313	1.0000000	D
<input type="radio"/>	GO:0043574	7,5,6	peroxisomal transport	20	0.0031	1	0.0013	1.0000000	D
<input type="radio"/>	GO:0030476	8,6,7	spore wall assembly (sensu Fungi)	42	0.0065	2	0.0025	1.0000000	D
<input type="radio"/>	GO:0051603	7,8	proteolysis involved in cellular protein catabolic process	151	0.0233	7	0.0088	0.9018385	D
<input type="radio"/>	GO:0006508	6	proteolysis	178	0.0275	9	0.0113	0.6510150	D
<input type="radio"/>	GO:0044260	4	cellular macromolecule metabolic process	1552	0.2397	158	0.1977	0.4972517	D
<input type="radio"/>	GO:0044257	6,7	cellular protein catabolic process	160	0.0247	7	0.0088	0.4086696	D
<input type="radio"/>	GO:0030163	6,5	protein catabolic process	173	0.0267	8	0.0100	0.3719355	D
<input type="radio"/>	GO:0005975	4	carbohydrate metabolic process	233	0.0360	13	0.0163	0.2922390	D
<input type="radio"/>	GO:0032196	3	transposition	105	0.0162	2	0.0025	0.1245641	D
<input type="radio"/>	GO:0006412	6,5	translation	688	0.1062	55	0.0688	0.0428671	D
<input type="radio"/>	GO:0006414	7,6	translational elongation	313	0.0483	3	0.0038	8.849858E-12	D
<input type="radio"/>	GO:0043284	5	biopolymer biosynthetic process	354	0.0547	3	0.0038	4.332150E-14	D