

GO-Stats Results

Your dataset contains **414** annotated gene products.

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

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

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

GO ID	Level	GO Term	RO	RF	DO	DF	P-value	E/D
<input type="radio"/> GO:0009987	2	cellular process	4654	0.7187	372	0.8986	2.287279E-20	E
<input type="radio"/> GO:0016043	3	cellular component organization and biogenesis	2264	0.3496	208	0.5024	1.511116E-11	E
<input type="radio"/> GO:0009112	5	nucleobase metabolic process	31	0.0048	13	0.0314	1.620246E-08	E
<input type="radio"/> GO:0022613	4	ribonucleoprotein complex biogenesis and assembly	483	0.0746	62	0.1498	2.726378E-08	E
<input type="radio"/> GO:0006139	4	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	1532	0.2366	143	0.3454	6.684433E-08	E
<input type="radio"/> GO:0044249	4	cellular biosynthetic process	366	0.0565	50	0.1208	9.612251E-08	E
<input type="radio"/> GO:0009101	7,5	glycoprotein biosynthetic process	78	0.0120	19	0.0459	2.184789E-07	E
<input type="radio"/> GO:0042254	5	ribosome biogenesis and assembly	410	0.0633	53	0.1280	2.340433E-07	E
<input type="radio"/> GO:0009100	6	glycoprotein metabolic process	79	0.0122	19	0.0459	2.699041E-07	E
<input type="radio"/> GO:0043413	6	biopolymer glycosylation	73	0.0113	18	0.0435	3.733889E-07	E
<input type="radio"/> GO:0006486	8,7,6	protein amino acid glycosylation	73	0.0113	18	0.0435	3.733889E-07	E
<input type="radio"/> GO:0008152	2	metabolic process	3516	0.5429	270	0.6522	8.259352E-07	E
<input type="radio"/> GO:0044238	3	primary metabolic process	3247	0.5014	252	0.6087	1.447318E-06	E
<input type="radio"/> GO:0044237	3	cellular metabolic process	3403	0.5255	261	0.6304	2.092212E-06	E
<input type="radio"/> GO:0046112	6,5	nucleobase biosynthetic process	21	0.0032	9	0.0217	2.220932E-06	E
<input type="radio"/> GO:0006725	4	aromatic compound metabolic process	60	0.0093	15	0.0362	2.862097E-06	E
<input type="radio"/> GO:0046483	4	heterocycle metabolic process	76	0.0117	17	0.0411	3.240834E-06	E
<input type="radio"/> GO:0009309	5,6	amine biosynthetic process	114	0.0176	21	0.0507	6.131593E-06	E
<input type="radio"/> GO:0008652	6,7	amino acid biosynthetic process	106	0.0164	20	0.0483	6.997618E-06	E
<input type="radio"/> GO:0044271	5,4	nitrogen compound biosynthetic process	115	0.0178	21	0.0507	7.038031E-06	E
<input type="radio"/> GO:0008202	5,6	steroid metabolic process	43	0.0066	12	0.0290	8.358470E-06	E

<input type="radio"/>	GO:0006996	4	organelle organization and biogenesis	1388	0.2143	123	0.2971	1.057766E-05	E
<input type="radio"/>	GO:0006446	8,7,6	regulation of translational initiation	10	0.0015	6	0.0145	1.067580E-05	E
<input type="radio"/>	GO:0006520	5,6	amino acid metabolic process	187	0.0289	28	0.0676	1.160870E-05	E
<input type="radio"/>	GO:0006694	6,5,7	steroid biosynthetic process	32	0.0049	10	0.0242	1.601600E-05	E
<input type="radio"/>	GO:0016126	6,7,8	sterol biosynthetic process	32	0.0049	10	0.0242	1.601600E-05	E
<input type="radio"/>	GO:0006696	7,8,9	ergosterol biosynthetic process	26	0.0040	9	0.0217	1.707377E-05	E
<input type="radio"/>	GO:0008204	6,7,8	ergosterol metabolic process	26	0.0040	9	0.0217	1.707377E-05	E
<input type="radio"/>	GO:0016070	5	RNA metabolic process	1058	0.1634	98	0.2367	1.771238E-05	E
<input type="radio"/>	GO:0006519	4	amino acid and derivative metabolic process	202	0.0312	29	0.0700	1.806041E-05	E
<input type="radio"/>	GO:0016125	5,6,7	sterol metabolic process	42	0.0065	11	0.0266	3.724051E-05	E
<input type="radio"/>	GO:0009070	7,8	serine family amino acid biosynthetic process	12	0.0019	6	0.0145	4.123214E-05	E
<input type="radio"/>	GO:0006206	6	pyrimidine base metabolic process	17	0.0026	7	0.0169	4.222575E-05	E
<input type="radio"/>	GO:0000460	7,8	maturation of 5.8S rRNA	36	0.0056	10	0.0242	4.870387E-05	E
<input type="radio"/>	GO:0009116	5	nucleoside metabolic process	18	0.0028	7	0.0169	6.474270E-05	E
<input type="radio"/>	GO:0009308	4	amine metabolic process	228	0.0352	30	0.0725	6.508060E-05	E
<input type="radio"/>	GO:0006396	6	RNA processing	491	0.0758	52	0.1256	7.594817E-05	E
<input type="radio"/>	GO:0006213	6	pyrimidine nucleoside metabolic process	5	0.0008	4	0.0097	7.716350E-05	E
<input type="radio"/>	GO:0045859	7	regulation of protein kinase activity	25	0.0039	8	0.0193	9.390734E-05	E
<input type="radio"/>	GO:0043549	6	regulation of kinase activity	25	0.0039	8	0.0193	9.390734E-05	E
<input type="radio"/>	GO:0043094	4	metabolic compound salvage	19	0.0029	7	0.0169	9.604888E-05	E
<input type="radio"/>	GO:0006144	6	purine base metabolic process	14	0.0022	6	0.0145	0.0001176	E
<input type="radio"/>	GO:0051338	5	regulation of transferase activity	26	0.0040	8	0.0193	0.0001271	E
<input type="radio"/>	GO:0006487	9,8,7	protein amino acid N-linked glycosylation	48	0.0074	11	0.0266	0.0001333	E
<input type="radio"/>	GO:0006807	3	nitrogen compound metabolic process	251	0.0388	31	0.0749	0.0001529	E
<input type="radio"/>	GO:0008033	7	tRNA processing	84	0.0130	15	0.0362	0.0001702	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	9	0.0217	0.0001706	E
<input type="radio"/>	GO:0000079	8,7,6	regulation of cyclin-dependent protein kinase activity	15	0.0023	6	0.0145	0.0001837	E
<input type="radio"/>	GO:0009113	7,6	purine base biosynthetic process	6	0.0009	4	0.0097	0.0002168	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	10	0.0242	0.0003411	E
<input type="radio"/>	GO:0030490	7,8	maturation of SSU-rRNA	45	0.0069	10	0.0242	0.0003411	E
<input type="radio"/>	GO:0009066	6,7	aspartate family amino acid metabolic process	46	0.0071	10	0.0242	0.0004084	E
<input type="radio"/>	GO:0042273	6,5	ribosomal large subunit biogenesis and assembly	64	0.0099	12	0.0290	0.0004606	E
<input type="radio"/>	GO:0009069	6,7	serine family amino acid metabolic process	24	0.0037	7	0.0169	0.0004764	E
<input type="radio"/>	GO:0006417	7,6,5	regulation of translation	47	0.0073	10	0.0242	0.0004862	E
<input type="radio"/>	GO:0009058	3	biosynthetic process	1249	0.1929	104	0.2512	0.0005035	E
<input type="radio"/>	GO:0000096	6,7,5	sulfur amino acid metabolic process	33	0.0051	8	0.0193	0.0007165	E

<input type="radio"/>	GO:0007346	7,5,6	regulation of progression through mitotic cell cycle	13	0.0020	5	0.0121	0.0007966	E
<input type="radio"/>	GO:0008610	5,4,6	lipid biosynthetic process	129	0.0199	18	0.0435	0.0008250	E
<input type="radio"/>	GO:0016072	6	rRNA metabolic process	256	0.0395	29	0.0700	0.0008914	E
<input type="radio"/>	GO:0009200	7	deoxyribonucleoside triphosphate metabolic process	4	0.0006	3	0.0072	0.0009721	E
<input type="radio"/>	GO:0006534	7,8,6	cysteine metabolic process	4	0.0006	3	0.0072	0.0009721	E
<input type="radio"/>	GO:0051301	3	cell division	246	0.0380	28	0.0676	0.0009984	E
<input type="radio"/>	GO:0000478	7,8	endonucleolytic cleavages during rRNA processing	20	0.0031	6	0.0145	0.0010264	E
<input type="radio"/>	GO:0000479	8,9	endonucleolytic cleavage of tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	20	0.0031	6	0.0145	0.0010264	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	6	0.0145	0.0010264	E
<input type="radio"/>	GO:0009075	6,7	histidine family amino acid metabolic process	14	0.0022	5	0.0121	0.0011607	E
<input type="radio"/>	GO:0006188	9,10	IMP biosynthetic process	14	0.0022	5	0.0121	0.0011607	E
<input type="radio"/>	GO:0009076	7,8	histidine family amino acid biosynthetic process	14	0.0022	5	0.0121	0.0011607	E
<input type="radio"/>	GO:0000105	8,9	histidine biosynthetic process	14	0.0022	5	0.0121	0.0011607	E
<input type="radio"/>	GO:0046040	9	IMP metabolic process	14	0.0022	5	0.0121	0.0011607	E
<input type="radio"/>	GO:0006547	7,8	histidine metabolic process	14	0.0022	5	0.0121	0.0011607	E
<input type="radio"/>	GO:0006364	6,7	rRNA processing	249	0.0384	28	0.0676	0.0011804	E
<input type="radio"/>	GO:0019752	5	carboxylic acid metabolic process	314	0.0485	33	0.0797	0.0014028	E
<input type="radio"/>	GO:0006082	4	organic acid metabolic process	314	0.0485	33	0.0797	0.0014028	E
<input type="radio"/>	GO:0050790	4	regulation of catalytic activity	45	0.0069	9	0.0217	0.0014099	E
<input type="radio"/>	GO:0007049	3	cell cycle	458	0.0707	44	0.1063	0.0015512	E
<input type="radio"/>	GO:0009168	8,9	purine ribonucleoside monophosphate biosynthetic process	15	0.0023	5	0.0121	0.0016308	E
<input type="radio"/>	GO:0009156	7,8	ribonucleoside monophosphate biosynthetic process	15	0.0023	5	0.0121	0.0016308	E
<input type="radio"/>	GO:0019856	7,6	pyrimidine base biosynthetic process	15	0.0023	5	0.0121	0.0016308	E
<input type="radio"/>	GO:0065009	3	regulation of a molecular function	46	0.0071	9	0.0217	0.0016424	E
<input type="radio"/>	GO:0031326	6,5	regulation of cellular biosynthetic process	67	0.0103	11	0.0266	0.0022120	E
<input type="radio"/>	GO:0009127	7,8	purine nucleoside monophosphate biosynthetic process	16	0.0025	5	0.0121	0.0022219	E
<input type="radio"/>	GO:0008655	5	pyrimidine salvage	5	0.0008	3	0.0072	0.0022759	E
<input type="radio"/>	GO:0007232	7,6	osmosensory signaling pathway via Sho1 osmosensor	5	0.0008	3	0.0072	0.0022759	E
<input type="radio"/>	GO:0006399	6	tRNA metabolic process	121	0.0187	16	0.0386	0.0025184	E
<input type="radio"/>	GO:0006413	7,6	translational initiation	49	0.0076	9	0.0217	0.0025196	E
<input type="radio"/>	GO:0009889	5,4	regulation of biosynthetic process	69	0.0107	11	0.0266	0.0027570	E
<input type="radio"/>	GO:0009167	8	purine ribonucleoside monophosphate metabolic process	17	0.0026	5	0.0121	0.0029485	E
<input type="radio"/>	GO:0009124	6,7	nucleoside monophosphate biosynthetic process	17	0.0026	5	0.0121	0.0029485	E
<input type="radio"/>	GO:0009161	7	ribonucleoside monophosphate metabolic process	17	0.0026	5	0.0121	0.0029485	E
<input type="radio"/>	GO:0031323	5,4	regulation of cellular metabolic process	507	0.0783	46	0.1111	0.0033293	E
<input type="radio"/>	GO:0009126	7	purine nucleoside monophosphate metabolic process	18	0.0028	5	0.0121	0.0038240	E
<input type="radio"/>	GO:0010410	8,6,7	hemicellulose metabolic process	2	0.0003	2	0.0048	0.0040776	E
<input type="radio"/>	GO:0009211	8	pyrimidine deoxyribonucleoside triphosphate metabolic process	2	0.0003	2	0.0048	0.0040776	E

<input type="checkbox"/>	GO:0009204	7,8	deoxyribonucleoside triphosphate catabolic process	2	0.0003	2	0.0048	0.0040776	E
<input type="checkbox"/>	GO:0006842	6,7	tricarboxylic acid transport	2	0.0003	2	0.0048	0.0040776	E
<input type="checkbox"/>	GO:0015855	6,7	pyrimidine transport	2	0.0003	2	0.0048	0.0040776	E
<input type="checkbox"/>	GO:0015864	6,7	pyrimidine nucleoside transport	2	0.0003	2	0.0048	0.0040776	E
<input type="checkbox"/>	GO:0010412	9,7,8	mannan metabolic process	2	0.0003	2	0.0048	0.0040776	E
<input type="checkbox"/>	GO:0006080	10,8,9	substituted mannan metabolic process	2	0.0003	2	0.0048	0.0040776	E
<input type="checkbox"/>	GO:0019344	8,9,7	cysteine biosynthetic process	2	0.0003	2	0.0048	0.0040776	E
<input type="checkbox"/>	GO:0050794	4,3	regulation of cellular process	738	0.1140	62	0.1498	0.0042500	E
<input type="checkbox"/>	GO:0006166	6,8	purine ribonucleoside salvage	6	0.0009	3	0.0072	0.0042626	E
<input type="checkbox"/>	GO:0043174	5	nucleoside salvage	6	0.0009	3	0.0072	0.0042626	E
<input type="checkbox"/>	GO:0006057	8,6	mannoprotein biosynthetic process	12	0.0019	4	0.0097	0.0048302	E
<input type="checkbox"/>	GO:0000032	8,6,9,7	cell wall mannoprotein biosynthetic process	12	0.0019	4	0.0097	0.0048302	E
<input type="checkbox"/>	GO:0006056	7	mannoprotein metabolic process	12	0.0019	4	0.0097	0.0048302	E
<input type="checkbox"/>	GO:0031506	7,5,8,6	cell wall glycoprotein biosynthetic process	12	0.0019	4	0.0097	0.0048302	E
<input type="checkbox"/>	GO:0009123	6	nucleoside monophosphate metabolic process	19	0.0029	5	0.0121	0.0048610	E
<input type="checkbox"/>	GO:0046148	5	pigment biosynthetic process	19	0.0029	5	0.0121	0.0048610	E
<input type="checkbox"/>	GO:0000074	6,5	regulation of progression through cell cycle	167	0.0258	19	0.0459	0.0052015	E
<input type="checkbox"/>	GO:0051726	5,4	regulation of cell cycle	167	0.0258	19	0.0459	0.0052015	E
<input type="checkbox"/>	GO:0065007	2	biological regulation	948	0.1464	76	0.1836	0.0052496	E
<input type="checkbox"/>	GO:0042440	4	pigment metabolic process	20	0.0031	5	0.0121	0.0060708	E
<input type="checkbox"/>	GO:0043283	4	biopolymer metabolic process	2230	0.3443	161	0.3889	0.0061669	E
<input type="checkbox"/>	GO:0009119	6	ribonucleoside metabolic process	13	0.0020	4	0.0097	0.0065344	E
<input type="checkbox"/>	GO:0006220	6	pyrimidine nucleotide metabolic process	7	0.0011	3	0.0072	0.0069857	E
<input type="checkbox"/>	GO:0032502	2	developmental process	436	0.0673	39	0.0942	0.0070354	E
<input type="checkbox"/>	GO:0050789	3	regulation of biological process	761	0.1175	62	0.1498	0.0071898	E
<input type="checkbox"/>	GO:0022402	4,3	cell cycle process	439	0.0678	39	0.0942	0.0076784	E
<input type="checkbox"/>	GO:0007047	5	cell wall organization and biogenesis	200	0.0309	21	0.0507	0.0078790	E
<input type="checkbox"/>	GO:0045229	4	external encapsulating structure organization and biogenesis	200	0.0309	21	0.0507	0.0078790	E
<input type="checkbox"/>	GO:0019222	4,3	regulation of metabolic process	538	0.0831	46	0.1111	0.0080037	E
<input type="checkbox"/>	GO:0022607	4	cellular component assembly	471	0.0727	41	0.0990	0.0086484	E
<input type="checkbox"/>	GO:0051246	5,4	regulation of protein metabolic process	72	0.0111	10	0.0242	0.0099077	E
<input type="checkbox"/>	GO:0043170	3	macromolecule metabolic process	2841	0.4387	198	0.4783	0.0100192	E
<input type="checkbox"/>	GO:0006351	7,6	transcription, DNA-dependent	522	0.0806	44	0.1063	0.0108093	E
<input type="checkbox"/>	GO:0019748	3	secondary metabolic process	23	0.0036	5	0.0121	0.0108265	E
<input type="checkbox"/>	GO:0022618	6,5	protein-RNA complex assembly	144	0.0222	16	0.0386	0.0109121	E
<input type="checkbox"/>	GO:0006400	7,8	tRNA modification	52	0.0080	8	0.0193	0.0112551	E
<input type="checkbox"/>	GO:0007166	5	cell surface receptor linked signal transduction	52	0.0080	8	0.0193	0.0112551	E
<input type="checkbox"/>	GO:0032774	6	RNA biosynthetic process	524	0.0809	44	0.1063	0.0113324	E
<input type="checkbox"/>	GO:0009219	7	pyrimidine deoxyribonucleotide metabolic process	3	0.0005	2	0.0048	0.0114543	E
<input type="checkbox"/>	GO:0046125	7	pyrimidine deoxyribonucleoside metabolic process	3	0.0005	2	0.0048	0.0114543	E
<input type="checkbox"/>	GO:0009143	6,7	nucleoside triphosphate catabolic process	3	0.0005	2	0.0048	0.0114543	E
<input type="checkbox"/>	GO:0046488	9,10	phosphatidylinositol metabolic process	3	0.0005	2	0.0048	0.0114543	E
<input type="checkbox"/>	GO:0007025	8	beta-tubulin folding	3	0.0005	2	0.0048	0.0114543	E
<input type="checkbox"/>	GO:0015851	5,6	nucleobase transport	3	0.0005	2	0.0048	0.0114543	E

<input type="radio"/>	GO:0009120	6	deoxyribonucleoside metabolic process	3	0.0005	2	0.0048	0.0114543	E
<input type="radio"/>	GO:0015858	5,6	nucleoside transport	3	0.0005	2	0.0048	0.0114543	E
<input type="radio"/>	GO:0042493	4	response to drug	121	0.0187	14	0.0338	0.0118467	E
<input type="radio"/>	GO:0000910	4	cytokinesis	109	0.0168	13	0.0314	0.0118696	E
<input type="radio"/>	GO:0045047	9,8,7,6,5	protein targeting to ER	33	0.0051	6	0.0145	0.0125417	E
<input type="radio"/>	GO:0007127	9,7,6,8,5	meiosis I	75	0.0116	10	0.0242	0.0125963	E
<input type="radio"/>	GO:0006555	7,8,6	methionine metabolic process	24	0.0037	5	0.0121	0.0128088	E
<input type="radio"/>	GO:0015698	6,7	inorganic anion transport	16	0.0025	4	0.0097	0.0136636	E
<input type="radio"/>	GO:0006493	9,8,7	protein amino acid O-linked glycosylation	16	0.0025	4	0.0097	0.0136636	E
<input type="radio"/>	GO:0032506	5,3	cytokinetic process	88	0.0136	11	0.0266	0.0140552	E
<input type="radio"/>	GO:0051649	5,3,4	establishment of cellular localization	606	0.0936	49	0.1184	0.0141349	E
<input type="radio"/>	GO:0051325	6,5	interphase	112	0.0173	13	0.0314	0.0141895	E
<input type="radio"/>	GO:0051329	7,5,6	interphase of mitotic cell cycle	112	0.0173	13	0.0314	0.0141895	E
<input type="radio"/>	GO:0006464	6	protein modification process	520	0.0803	43	0.1039	0.0143090	E
<input type="radio"/>	GO:0043101	5	purine salvage	9	0.0014	3	0.0072	0.0147028	E
<input type="radio"/>	GO:0006553	7,8	lysine metabolic process	9	0.0014	3	0.0072	0.0147028	E
<input type="radio"/>	GO:0009262	6	deoxyribonucleotide metabolic process	9	0.0014	3	0.0072	0.0147028	E
<input type="radio"/>	GO:0009085	8,9	lysine biosynthetic process	9	0.0014	3	0.0072	0.0147028	E
<input type="radio"/>	GO:0044255	4,5	cellular lipid metabolic process	229	0.0354	22	0.0531	0.0151113	E
<input type="radio"/>	GO:0006350	5	transcription	567	0.0876	46	0.1111	0.0154749	E
<input type="radio"/>	GO:0006790	4	sulfur metabolic process	67	0.0103	9	0.0217	0.0162234	E
<input type="radio"/>	GO:0007004	9	telomere maintenance via telomerase	17	0.0026	4	0.0097	0.0167338	E
<input type="radio"/>	GO:0006820	5,6	anion transport	17	0.0026	4	0.0097	0.0167338	E
<input type="radio"/>	GO:0007163	6,3,7	establishment and/or maintenance of cell polarity	115	0.0178	13	0.0314	0.0167849	E
<input type="radio"/>	GO:0006817	7,8	phosphate transport	10	0.0015	3	0.0072	0.0196692	E
<input type="radio"/>	GO:0046219	7,8,6	indolalkylamine biosynthetic process	10	0.0015	3	0.0072	0.0196692	E
<input type="radio"/>	GO:0042430	5	indole and derivative metabolic process	10	0.0015	3	0.0072	0.0196692	E
<input type="radio"/>	GO:0006568	7,8,6	tryptophan metabolic process	10	0.0015	3	0.0072	0.0196692	E
<input type="radio"/>	GO:0009096	8,7,9	aromatic amino acid family biosynthetic process, anthranilate pathway	10	0.0015	3	0.0072	0.0196692	E
<input type="radio"/>	GO:0042434	6	indole derivative metabolic process	10	0.0015	3	0.0072	0.0196692	E
<input type="radio"/>	GO:0000162	9,8,7,10	tryptophan biosynthetic process	10	0.0015	3	0.0072	0.0196692	E
<input type="radio"/>	GO:0006586	6,7	indolalkylamine metabolic process	10	0.0015	3	0.0072	0.0196692	E
<input type="radio"/>	GO:0042435	7,5	indole derivative biosynthetic process	10	0.0015	3	0.0072	0.0196692	E
<input type="radio"/>	GO:0042401	6,7	biogenic amine biosynthetic process	18	0.0028	4	0.0097	0.0201491	E
<input type="radio"/>	GO:0006259	5	DNA metabolic process	523	0.0808	42	0.1014	0.0204821	E
<input type="radio"/>	GO:0051641	4,3	cellular localization	642	0.0991	50	0.1208	0.0208829	E
<input type="radio"/>	GO:0009165	5,6	nucleotide biosynthetic process	59	0.0091	8	0.0193	0.0209947	E
<input type="radio"/>	GO:0032147	8,9	activation of protein kinase activity	4	0.0006	2	0.0048	0.0214505	E
<input type="radio"/>	GO:0006491	10,9,8	N-glycan processing	4	0.0006	2	0.0048	0.0214505	E
<input type="radio"/>	GO:0009147	7	pyrimidine nucleoside triphosphate metabolic process	4	0.0006	2	0.0048	0.0214505	E
<input type="radio"/>	GO:0007135	9,7,6,8,5	meiosis II	4	0.0006	2	0.0048	0.0214505	E
<input type="radio"/>	GO:0045144	10,8,7,5,9,6,4	meiotic sister chromatid segregation	4	0.0006	2	0.0048	0.0214505	E
<input type="radio"/>	GO:0016180	7	snRNA processing	4	0.0006	2	0.0048	0.0214505	E
<input type="radio"/>	GO:0006383	8,7	transcription from RNA polymerase III promoter	38	0.0059	6	0.0145	0.0225373	E

<input type="radio"/>	GO:0043241	6,5	protein complex disassembly	28	0.0043	5	0.0121	0.0227903	E
<input type="radio"/>	GO:0043624	7,6	cellular protein complex disassembly	28	0.0043	5	0.0121	0.0227903	E
<input type="radio"/>	GO:0006629	4	lipid metabolic process	242	0.0374	22	0.0531	0.0232107	E
<input type="radio"/>	GO:0043412	5	biopolymer modification	664	0.1025	51	0.1232	0.0233920	E
<input type="radio"/>	GO:0046907	6,4,5	intracellular transport	545	0.0842	43	0.1039	0.0234058	E
<input type="radio"/>	GO:0048610	3,4	reproductive cellular process	149	0.0230	15	0.0362	0.0248987	E
<input type="radio"/>	GO:0022413	5,4	reproductive process in single-celled organism	149	0.0230	15	0.0362	0.0248987	E
<input type="radio"/>	GO:0030435	5	sporulation	123	0.0190	13	0.0314	0.0250535	E
<input type="radio"/>	GO:0046128	7	purine ribonucleoside metabolic process	11	0.0017	3	0.0072	0.0253260	E
<input type="radio"/>	GO:0043085	5	positive regulation of enzyme activity	11	0.0017	3	0.0072	0.0253260	E
<input type="radio"/>	GO:0007021	7	tubulin folding	11	0.0017	3	0.0072	0.0253260	E
<input type="radio"/>	GO:0006066	4	alcohol metabolic process	163	0.0252	16	0.0386	0.0255812	E
<input type="radio"/>	GO:0048856	3	anatomical structure development	248	0.0383	22	0.0531	0.0276086	E
<input type="radio"/>	GO:0000902	5,6	cell morphogenesis	248	0.0383	22	0.0531	0.0276086	E
<input type="radio"/>	GO:0032989	4,5	cellular structure morphogenesis	248	0.0383	22	0.0531	0.0276086	E
<input type="radio"/>	GO:0009653	4,3	anatomical structure morphogenesis	248	0.0383	22	0.0531	0.0276086	E
<input type="radio"/>	GO:0009067	7,8	aspartate family amino acid biosynthetic process	20	0.0031	4	0.0097	0.0279802	E
<input type="radio"/>	GO:0042398	6,5	amino acid derivative biosynthetic process	20	0.0031	4	0.0097	0.0279802	E
<input type="radio"/>	GO:0000082	8,5,6,7,4	G1/S transition of mitotic cell cycle	52	0.0080	7	0.0169	0.0295859	E
<input type="radio"/>	GO:0019219	6,5	regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	440	0.0679	35	0.0845	0.0297279	E
<input type="radio"/>	GO:0006164	6,7	purine nucleotide biosynthetic process	41	0.0063	6	0.0145	0.0301603	E
<input type="radio"/>	GO:0000278	4	mitotic cell cycle	266	0.0411	23	0.0556	0.0305274	E
<input type="radio"/>	GO:0000083	10,9,6,5,7,8,4	G1/S-specific transcription in mitotic cell cycle	12	0.0019	3	0.0072	0.0316213	E
<input type="radio"/>	GO:0042278	6	purine nucleoside metabolic process	12	0.0019	3	0.0072	0.0316213	E
<input type="radio"/>	GO:0048523	5,4	negative regulation of cellular process	239	0.0369	21	0.0507	0.0317625	E
<input type="radio"/>	GO:0006575	5	amino acid derivative metabolic process	31	0.0048	5	0.0121	0.0323678	E
<input type="radio"/>	GO:0051169	7,5,6	nuclear transport	129	0.0199	13	0.0314	0.0324735	E
<input type="radio"/>	GO:0006913	8,6,7	nucleocytoplasmic transport	129	0.0199	13	0.0314	0.0324735	E
<input type="radio"/>	GO:0030010	7,4,8	establishment of cell polarity	103	0.0159	11	0.0266	0.0329195	E
<input type="radio"/>	GO:0042244	5,6	spore wall assembly	42	0.0065	6	0.0145	0.0329560	E
<input type="radio"/>	GO:0030476	8,6,7	spore wall assembly (sensu Fungi)	42	0.0065	6	0.0145	0.0329560	E
<input type="radio"/>	GO:0065003	5,4	macromolecular complex assembly	328	0.0506	27	0.0652	0.0334513	E
<input type="radio"/>	GO:0006279	7	premeiotic DNA synthesis	5	0.0008	2	0.0048	0.0334749	E
<input type="radio"/>	GO:0009264	6,7	deoxyribonucleotide catabolic process	5	0.0008	2	0.0048	0.0334749	E
<input type="radio"/>	GO:0008283	3	cell proliferation	5	0.0008	2	0.0048	0.0334749	E
<input type="radio"/>	GO:0032447	9	protein urmylation	5	0.0008	2	0.0048	0.0334749	E
<input type="radio"/>	GO:0033261	7,8,6	regulation of progression through S phase	5	0.0008	2	0.0048	0.0334749	E
<input type="radio"/>	GO:0006366	8,7	transcription from RNA polymerase II promoter	343	0.0530	28	0.0676	0.0336499	E
<input type="radio"/>	GO:0048519	4	negative regulation of biological process	242	0.0374	21	0.0507	0.0343470	E
<input type="radio"/>	GO:0046942	5,6	carboxylic acid transport	54	0.0083	7	0.0169	0.0343592	E
<input type="radio"/>	GO:0007105	6,4	cytokinesis, site selection	66	0.0102	8	0.0193	0.0344065	E
<input type="radio"/>	GO:0000282	7,9,5,6,10	cellular bud site selection	66	0.0102	8	0.0193	0.0344065	E
<input type="radio"/>	GO:0030468	8,5,9	establishment of cell polarity (sensu Fungi)	66	0.0102	8	0.0193	0.0344065	E
<input type="radio"/>	GO:0030467	7,4,9	establishment and/or maintenance of cell	66	0.0102	8	0.0193	0.0344065	E

<input type="radio"/>	GO:0050407	1,4,0	polarity (sensu Fungi)	60	0.0102	0	0.0195	0.0344005	E
<input type="radio"/>	GO:0051234	2,3	establishment of localization	1004	0.1550	71	0.1715	0.0344824	E
<input type="radio"/>	GO:0045045	7,5,4,6	secretory pathway	243	0.0375	21	0.0507	0.0352259	E
<input type="radio"/>	GO:0032984	5	macromolecular complex disassembly	32	0.0049	5	0.0121	0.0359274	E
<input type="radio"/>	GO:0048869	3	cellular developmental process	173	0.0267	16	0.0386	0.0361695	E
<input type="radio"/>	GO:0030154	4	cell differentiation	173	0.0267	16	0.0386	0.0361695	E
<input type="radio"/>	GO:0015849	4,5	organic acid transport	55	0.0085	7	0.0169	0.0368749	E
<input type="radio"/>	GO:0007131	10,8,7,5,9,6,4	meiotic recombination	55	0.0085	7	0.0169	0.0368749	E
<input type="radio"/>	GO:0006810	3,4	transport	981	0.1515	69	0.1667	0.0369846	E
<input type="radio"/>	GO:0044272	5	sulfur compound biosynthetic process	22	0.0034	4	0.0097	0.0370490	E
<input type="radio"/>	GO:0007231	6,5	osmosensory signaling pathway	22	0.0034	4	0.0097	0.0370490	E
<input type="radio"/>	GO:0040020	7,9,8,6	regulation of meiosis	22	0.0034	4	0.0097	0.0370490	E
<input type="radio"/>	GO:0000097	7,8,6	sulfur amino acid biosynthetic process	13	0.0020	3	0.0072	0.0384940	E
<input type="radio"/>	GO:0045786	6,7,5	negative regulation of progression through cell cycle	13	0.0020	3	0.0072	0.0384940	E
<input type="radio"/>	GO:0030447	3	filamentous growth	94	0.0145	10	0.0242	0.0397381	E
<input type="radio"/>	GO:0007001	6	chromosome organization and biogenesis (sensu Eukaryota)	567	0.0876	42	0.1014	0.0403269	E
<input type="radio"/>	GO:0022403	5,4	cell cycle phase	353	0.0545	28	0.0676	0.0405719	E
<input type="radio"/>	GO:0000003	2	reproduction	323	0.0499	26	0.0628	0.0405916	E
<input type="radio"/>	GO:0030437	7,6	sporulation (sensu Fungi)	108	0.0167	11	0.0266	0.0410694	E
<input type="radio"/>	GO:0048622	6,5	reproductive sporulation	108	0.0167	11	0.0266	0.0410694	E
<input type="radio"/>	GO:0046903	3,4	secretion	250	0.0386	21	0.0507	0.0415827	E
<input type="radio"/>	GO:0032940	6,4,5	secretion by cell	250	0.0386	21	0.0507	0.0415827	E
<input type="radio"/>	GO:0051276	5	chromosome organization and biogenesis	572	0.0883	42	0.1014	0.0427124	E
<input type="radio"/>	GO:0006281	6,5	DNA repair	193	0.0298	17	0.0411	0.0428334	E
<input type="radio"/>	GO:0051179	2	localization	1051	0.1623	72	0.1739	0.0431175	E
<input type="radio"/>	GO:0006360	8,7	transcription from RNA polymerase I promoter	34	0.0053	5	0.0121	0.0435413	E
<input type="radio"/>	GO:0007186	6	G-protein coupled receptor protein signaling pathway	34	0.0053	5	0.0121	0.0435413	E
<input type="radio"/>	GO:0000470	7,8	maturation of LSU-rRNA	14	0.0022	3	0.0072	0.0458768	E
<input type="radio"/>	GO:0006388	9,8	tRNA splicing	14	0.0022	3	0.0072	0.0458768	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	3	0.0072	0.0458768	E
<input type="radio"/>	GO:0000394	8	RNA splicing, via endonucleolytic cleavage and ligation	14	0.0022	3	0.0072	0.0458768	E
<input type="radio"/>	GO:0006272	9,8	leading strand elongation	14	0.0022	3	0.0072	0.0458768	E
<input type="radio"/>	GO:0006457	6	protein folding	84	0.0130	9	0.0217	0.0459801	E
<input type="radio"/>	GO:0009117	5	nucleotide metabolic process	111	0.0171	11	0.0266	0.0463028	E
<input type="radio"/>	GO:0051347	6	positive regulation of transferase activity	6	0.0009	2	0.0048	0.0470155	E
<input type="radio"/>	GO:0007130	11,9,8,6,5,10,7,4	synaptonemal complex assembly	6	0.0009	2	0.0048	0.0470155	E
<input type="radio"/>	GO:0008299	6,5,7	isoprenoid biosynthetic process	6	0.0009	2	0.0048	0.0470155	E
<input type="radio"/>	GO:0045860	7,8	positive regulation of protein kinase activity	6	0.0009	2	0.0048	0.0470155	E
<input type="radio"/>	GO:0006720	5,6	isoprenoid metabolic process	6	0.0009	2	0.0048	0.0470155	E
<input type="radio"/>	GO:0006576	5,6	biogenic amine metabolic process	24	0.0037	4	0.0097	0.0471975	E
<input type="radio"/>	GO:0007096	8,10,9,7	regulation of exit from mitosis	24	0.0037	4	0.0097	0.0471975	E
<input type="radio"/>	GO:0022414	3,2	reproductive process	183	0.0283	16	0.0386	0.0481752	E
<input type="radio"/>	GO:0006163	6	purine nucleotide metabolic process	47	0.0073	6	0.0145	0.0486099	E

<input type="checkbox"/>	GO:0050896	2	response to stimulus	763	0.1178	53	0.1280	0.0488989	E
<input type="checkbox"/>	GO:0040007	2	growth	141	0.0218	13	0.0314	0.0497872	E
<input type="checkbox"/>	GO:0000723	8	telomere maintenance	274	0.0423	22	0.0531	0.0499650	E
<input type="checkbox"/>	GO:0032200	7	telomere organization and biogenesis	274	0.0423	22	0.0531	0.0499650	E
<input type="checkbox"/>	GO:0022411	4	cellular component disassembly	36	0.0056	5	0.0121	0.0517380	E
<input type="checkbox"/>	GO:0008361	4,6,7	regulation of cell size	129	0.0199	12	0.0290	0.0533686	E
<input type="checkbox"/>	GO:0030488	8,9	tRNA methylation	15	0.0023	3	0.0072	0.0536986	E
<input type="checkbox"/>	GO:0006374	9,11	nuclear mRNA splicing via U2-type spliceosome	15	0.0023	3	0.0072	0.0536986	E
<input type="checkbox"/>	GO:0010382	6,4	cell wall metabolic process	26	0.0040	4	0.0097	0.0582315	E
<input type="checkbox"/>	GO:0006379	8	mRNA cleavage	26	0.0040	4	0.0097	0.0582315	E
<input type="checkbox"/>	GO:0006606	9,10,7,8,6	protein import into nucleus	50	0.0077	6	0.0145	0.0590913	E
<input type="checkbox"/>	GO:0051170	9,7,8	nuclear import	50	0.0077	6	0.0145	0.0590913	E
<input type="checkbox"/>	GO:0015931	4,5	nucleobase, nucleoside, nucleotide and nucleic acid transport	90	0.0139	9	0.0217	0.0595507	E
<input type="checkbox"/>	GO:0016481	8,7	negative regulation of transcription	162	0.0250	14	0.0338	0.0595538	E
<input type="checkbox"/>	GO:0009152	7,8	purine ribonucleotide biosynthetic process	38	0.0059	5	0.0121	0.0604135	E
<input type="checkbox"/>	GO:0007126	8,6,7,5	meiosis	148	0.0229	13	0.0314	0.0607919	E
<input type="checkbox"/>	GO:0051327	7,5,6	M phase of meiotic cell cycle	148	0.0229	13	0.0314	0.0607919	E
<input type="checkbox"/>	GO:0051321	4	meiotic cell cycle	148	0.0229	13	0.0314	0.0607919	E
<input type="checkbox"/>	GO:0001402	5,4	signal transduction during filamentous growth	7	0.0011	2	0.0048	0.0616302	E
<input type="checkbox"/>	GO:0009092	7,8	homoserine metabolic process	7	0.0011	2	0.0048	0.0616302	E
<input type="checkbox"/>	GO:0006415	8,7,6	translational termination	7	0.0011	2	0.0048	0.0616302	E
<input type="checkbox"/>	GO:0015833	4,5	peptide transport	7	0.0011	2	0.0048	0.0616302	E
<input type="checkbox"/>	GO:0009166	5,6	nucleotide catabolic process	7	0.0011	2	0.0048	0.0616302	E
<input type="checkbox"/>	GO:0009073	7,6,8	aromatic amino acid family biosynthetic process	16	0.0025	3	0.0072	0.0618864	E
<input type="checkbox"/>	GO:0032505	4,3	reproduction of a single-celled organism	194	0.0300	16	0.0386	0.0621093	E
<input type="checkbox"/>	GO:0045934	7,6	negative regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	179	0.0276	15	0.0362	0.0623783	E
<input type="checkbox"/>	GO:0006244	6,7	pyrimidine nucleotide catabolic process	1	0.0002	1	0.0024	0.0639284	E
<input type="checkbox"/>	GO:0009148	7,8	pyrimidine nucleoside triphosphate biosynthetic process	1	0.0002	1	0.0024	0.0639284	E
<input type="checkbox"/>	GO:0015878	5,6	biotin transport	1	0.0002	1	0.0024	0.0639284	E
<input type="checkbox"/>	GO:0046077	9	dUDP metabolic process	1	0.0002	1	0.0024	0.0639284	E
<input type="checkbox"/>	GO:0015721	7,8	bile acid and bile salt transport	1	0.0002	1	0.0024	0.0639284	E
<input type="checkbox"/>	GO:0015862	7,8	uridine transport	1	0.0002	1	0.0024	0.0639284	E
<input type="checkbox"/>	GO:0032979	8,7,6	protein insertion into mitochondrial membrane from inner side	1	0.0002	1	0.0024	0.0639284	E
<input type="checkbox"/>	GO:0006227	9,10	dUDP biosynthetic process	1	0.0002	1	0.0024	0.0639284	E
<input type="checkbox"/>	GO:0031576	9,11,10,8	G2/M transition checkpoint	1	0.0002	1	0.0024	0.0639284	E
<input type="checkbox"/>	GO:0009445	7,8	putrescine metabolic process	1	0.0002	1	0.0024	0.0639284	E
<input type="checkbox"/>	GO:0019858	7	cytosine metabolic process	1	0.0002	1	0.0024	0.0639284	E
<input type="checkbox"/>	GO:0032365	7,5,6	intracellular lipid transport	1	0.0002	1	0.0024	0.0639284	E
<input type="checkbox"/>	GO:0009197	8,9	pyrimidine deoxyribonucleoside diphosphate biosynthetic process	1	0.0002	1	0.0024	0.0639284	E
<input type="checkbox"/>	GO:0006235	9,10	dTTP biosynthetic process	1	0.0002	1	0.0024	0.0639284	E
<input type="checkbox"/>	GO:0015861	7,8	cytidine transport	1	0.0002	1	0.0024	0.0639284	E
<input type="checkbox"/>	GO:0030970	8,6,7	retrograde protein transport, ER to cytosol	1	0.0002	1	0.0024	0.0639284	E

<input type="radio"/>	GO:0009186	7	deoxyribonucleoside diphosphate metabolic process	1	0.0002	1	0.0024	0.0639284	E
<input type="radio"/>	GO:0032368	6,5	regulation of lipid transport	1	0.0002	1	0.0024	0.0639284	E
<input type="radio"/>	GO:0000360	8,9,7,11,13	cis assembly of U2-type pre-catalytic spliceosome	1	0.0002	1	0.0024	0.0639284	E
<input type="radio"/>	GO:0032978	7,6,5	protein insertion into membrane from inner side	1	0.0002	1	0.0024	0.0639284	E
<input type="radio"/>	GO:0009139	7,8	pyrimidine nucleoside diphosphate biosynthetic process	1	0.0002	1	0.0024	0.0639284	E
<input type="radio"/>	GO:0045736	8,9,7,6	negative regulation of cyclin-dependent protein kinase activity	1	0.0002	1	0.0024	0.0639284	E
<input type="radio"/>	GO:0015729	7,8	oxaloacetate transport	1	0.0002	1	0.0024	0.0639284	E
<input type="radio"/>	GO:0042256	8,7	mature ribosome assembly	1	0.0002	1	0.0024	0.0639284	E
<input type="radio"/>	GO:0019408	9,8,10	dolichol biosynthetic process	1	0.0002	1	0.0024	0.0639284	E
<input type="radio"/>	GO:0015806	7,8,9	S-methylmethionine transport	1	0.0002	1	0.0024	0.0639284	E
<input type="radio"/>	GO:0015817	7,8,9	histidine transport	1	0.0002	1	0.0024	0.0639284	E
<input type="radio"/>	GO:0032377	7,8,6	regulation of intracellular lipid transport	1	0.0002	1	0.0024	0.0639284	E
<input type="radio"/>	GO:0019346	8,9,7	transsulfuration	1	0.0002	1	0.0024	0.0639284	E
<input type="radio"/>	GO:0009212	8,9	pyrimidine deoxyribonucleoside triphosphate biosynthetic process	1	0.0002	1	0.0024	0.0639284	E
<input type="radio"/>	GO:0031567	9,11,10,8	cell size control checkpoint	1	0.0002	1	0.0024	0.0639284	E
<input type="radio"/>	GO:0002098	9,10	tRNA wobble uridine modification	1	0.0002	1	0.0024	0.0639284	E
<input type="radio"/>	GO:0015772	5,6	oligosaccharide transport	1	0.0002	1	0.0024	0.0639284	E
<input type="radio"/>	GO:0006521	7,6	regulation of amino acid metabolic process	1	0.0002	1	0.0024	0.0639284	E
<input type="radio"/>	GO:0006863	6,7	purine transport	1	0.0002	1	0.0024	0.0639284	E
<input type="radio"/>	GO:0033238	6,5	regulation of amine metabolic process	1	0.0002	1	0.0024	0.0639284	E
<input type="radio"/>	GO:0031569	10,12,11,9	G2/M transition size control checkpoint	1	0.0002	1	0.0024	0.0639284	E
<input type="radio"/>	GO:0002097	8,9	tRNA wobble base modification	1	0.0002	1	0.0024	0.0639284	E
<input type="radio"/>	GO:0019478	7,8	D-amino acid catabolic process	1	0.0002	1	0.0024	0.0639284	E
<input type="radio"/>	GO:0009196	8	pyrimidine deoxyribonucleoside diphosphate metabolic process	1	0.0002	1	0.0024	0.0639284	E
<input type="radio"/>	GO:0046072	9	dTDP metabolic process	1	0.0002	1	0.0024	0.0639284	E
<input type="radio"/>	GO:0046107	8,7	uracil biosynthetic process	1	0.0002	1	0.0024	0.0639284	E
<input type="radio"/>	GO:0019860	7	uracil metabolic process	1	0.0002	1	0.0024	0.0639284	E
<input type="radio"/>	GO:0046416	6,7	D-amino acid metabolic process	1	0.0002	1	0.0024	0.0639284	E
<input type="radio"/>	GO:0009213	8,9	pyrimidine deoxyribonucleoside triphosphate catabolic process	1	0.0002	1	0.0024	0.0639284	E
<input type="radio"/>	GO:0015857	7,8	uracil transport	1	0.0002	1	0.0024	0.0639284	E
<input type="radio"/>	GO:0009189	7,8	deoxyribonucleoside diphosphate biosynthetic process	1	0.0002	1	0.0024	0.0639284	E
<input type="radio"/>	GO:0009138	7	pyrimidine nucleoside diphosphate metabolic process	1	0.0002	1	0.0024	0.0639284	E
<input type="radio"/>	GO:0019348	8,9	dolichol metabolic process	1	0.0002	1	0.0024	0.0639284	E
<input type="radio"/>	GO:0045836	8,10,9,7	positive regulation of meiosis	1	0.0002	1	0.0024	0.0639284	E
<input type="radio"/>	GO:0000185	9,10,8	activation of MAPKKK activity	1	0.0002	1	0.0024	0.0639284	E
<input type="radio"/>	GO:0009446	8,9	putrescine biosynthetic process	1	0.0002	1	0.0024	0.0639284	E
<input type="radio"/>	GO:0015856	7,8	cytosine transport	1	0.0002	1	0.0024	0.0639284	E
<input type="radio"/>	GO:0000351	8,7,10,11,12,13	assembly of spliceosomal tri-snRNP U4/U6.U5	1	0.0002	1	0.0024	0.0639284	E
<input type="radio"/>	GO:0006233	9,10	dTDP biosynthetic process	1	0.0002	1	0.0024	0.0639284	E
<input type="radio"/>	GO:0008315	10,8,7,5,9,6,4	meiotic G2/MI transition	1	0.0002	1	0.0024	0.0639284	E
<input type="radio"/>	GO:0009149	7,8	pyrimidine nucleoside triphosphate catabolic process	1	0.0002	1	0.0024	0.0639284	E
<input type="radio"/>	GO:0009222	7,8	pyrimidine deoxyribonucleotide catabolic	1	0.0002	1	0.0024	0.0639284	E

<input type="radio"/>	GO:0009223	1,0	process	1	0.0002	1	0.0024	0.0639284	E
<input type="radio"/>	GO:0045292	10,12	nuclear mRNA cis splicing, via U2-type spliceosome	1	0.0002	1	0.0024	0.0639284	E
<input type="radio"/>	GO:0015746	7,8	citrate transport	1	0.0002	1	0.0024	0.0639284	E
<input type="radio"/>	GO:0006843	8,6,7,9	mitochondrial citrate transport	1	0.0002	1	0.0024	0.0639284	E
<input type="radio"/>	GO:0046075	9	dTTP metabolic process	1	0.0002	1	0.0024	0.0639284	E
<input type="radio"/>	GO:0006605	8,6,7	protein targeting	258	0.0398	20	0.0483	0.0641090	E
<input type="radio"/>	GO:0006886	7,5,6	intracellular protein transport	274	0.0423	21	0.0507	0.0642320	E
<input type="radio"/>	GO:0006612	9,7,8	protein targeting to membrane	39	0.0060	5	0.0121	0.0648954	E
<input type="radio"/>	GO:0006355	8,7	regulation of transcription, DNA-dependent	359	0.0554	26	0.0628	0.0670517	E
<input type="radio"/>	GO:0031324	6,5	negative regulation of cellular metabolic process	198	0.0306	16	0.0386	0.0671388	E
<input type="radio"/>	GO:0045184	3,4,5	establishment of protein localization	296	0.0457	22	0.0531	0.0692340	E
<input type="radio"/>	GO:0009260	6,7	ribonucleotide biosynthetic process	40	0.0062	5	0.0121	0.0694537	E
<input type="radio"/>	GO:0015031	4,5,6	protein transport	280	0.0432	21	0.0507	0.0695280	E
<input type="radio"/>	GO:0032005	7,6	signal transduction during conjugation with cellular fusion	28	0.0043	4	0.0097	0.0699344	E
<input type="radio"/>	GO:0042144	6	vacuole fusion, non-autophagic	28	0.0043	4	0.0097	0.0699344	E
<input type="radio"/>	GO:0000750	8,7,6	pheromone-dependent signal transduction during conjugation with cellular fusion	28	0.0043	4	0.0097	0.0699344	E
<input type="radio"/>	GO:0016074	6	snoRNA metabolic process	17	0.0026	3	0.0072	0.0703667	E
<input type="radio"/>	GO:0009968	6,5	negative regulation of signal transduction	17	0.0026	3	0.0072	0.0703667	E
<input type="radio"/>	GO:0051704	2	multi-organism process	139	0.0215	12	0.0290	0.0706279	E
<input type="radio"/>	GO:0033036	3	macromolecule localization	382	0.0590	27	0.0652	0.0706543	E
<input type="radio"/>	GO:0006974	4	response to DNA damage stimulus	234	0.0361	18	0.0435	0.0720479	E
<input type="radio"/>	GO:0045449	7,6	regulation of transcription	386	0.0596	27	0.0652	0.0727133	E
<input type="radio"/>	GO:0045892	9,8	negative regulation of transcription, DNA-dependent	156	0.0241	13	0.0314	0.0734352	E
<input type="radio"/>	GO:0009150	7	purine ribonucleotide metabolic process	41	0.0063	5	0.0121	0.0740734	E
<input type="radio"/>	GO:0016311	6	dephosphorylation	41	0.0063	5	0.0121	0.0740734	E
<input type="radio"/>	GO:0006470	8,7	protein amino acid dephosphorylation	29	0.0045	4	0.0097	0.0759656	E
<input type="radio"/>	GO:0015940	7,8	pantothenate biosynthetic process	8	0.0012	2	0.0048	0.0769401	E
<input type="radio"/>	GO:0006566	7,8	threonine metabolic process	8	0.0012	2	0.0048	0.0769401	E
<input type="radio"/>	GO:0006828	8,9	manganese ion transport	8	0.0012	2	0.0048	0.0769401	E
<input type="radio"/>	GO:0015939	7	pantothenate metabolic process	8	0.0012	2	0.0048	0.0769401	E
<input type="radio"/>	GO:0019878	9,10	lysine biosynthetic process via aminoadipic acid	8	0.0012	2	0.0048	0.0769401	E
<input type="radio"/>	GO:0018318	10,9,8	protein amino acid palmitoylation	8	0.0012	2	0.0048	0.0769401	E
<input type="radio"/>	GO:0030011	7,4,8	maintenance of cell polarity	8	0.0012	2	0.0048	0.0769401	E
<input type="radio"/>	GO:0043144	7	snoRNA processing	8	0.0012	2	0.0048	0.0769401	E
<input type="radio"/>	GO:0006620	10,9,8,7,6	posttranslational protein targeting to membrane	8	0.0012	2	0.0048	0.0769401	E
<input type="radio"/>	GO:0018345	9,8,7	protein palmitoylation	8	0.0012	2	0.0048	0.0769401	E
<input type="radio"/>	GO:0006352	7,8,6	transcription initiation	55	0.0085	6	0.0145	0.0776489	E
<input type="radio"/>	GO:0001403	6,4,8,9	invasive growth (sensu Saccharomyces)	42	0.0065	5	0.0121	0.0787390	E
<input type="radio"/>	GO:0042221	3	response to chemical stimulus	382	0.0590	26	0.0628	0.0788186	E
<input type="radio"/>	GO:0006369	9,8	transcription termination from RNA polymerase II promoter	18	0.0028	3	0.0072	0.0790669	E
<input type="radio"/>	GO:0019438	5	aromatic compound biosynthetic process	18	0.0028	3	0.0072	0.0790669	E
<input type="radio"/>	GO:0009892	5,4	negative regulation of metabolic process	208	0.0321	16	0.0386	0.0790736	E
<input type="radio"/>	GO:0008104	4	protein localization	330	0.0510	23	0.0556	0.0804572	E

<input type="radio"/>	GO:0009719	3	response to endogenous stimulus	243	0.0375	18	0.0435	0.0807898	E
<input type="radio"/>	GO:0006665	6,7	sphingolipid metabolic process	30	0.0046	4	0.0097	0.0820783	E
<input type="radio"/>	GO:0046999	5,4	regulation of conjugation	30	0.0046	4	0.0097	0.0820783	E
<input type="radio"/>	GO:0031137	6,5	regulation of conjugation with cellular fusion	30	0.0046	4	0.0097	0.0820783	E
<input type="radio"/>	GO:0009259	6	ribonucleotide metabolic process	43	0.0066	5	0.0121	0.0834355	E
<input type="radio"/>	GO:0008380	7	RNA splicing	132	0.0204	11	0.0266	0.0855507	E
<input type="radio"/>	GO:0006260	6	DNA replication	117	0.0181	10	0.0242	0.0868835	E
<input type="radio"/>	GO:0006367	8,9,7	transcription initiation from RNA polymerase II promoter	44	0.0068	5	0.0121	0.0881476	E
<input type="radio"/>	GO:0006752	6	group transfer coenzyme metabolic process	44	0.0068	5	0.0121	0.0881476	E
<input type="radio"/>	GO:0000746	3	conjugation	118	0.0182	10	0.0242	0.0888973	E
<input type="radio"/>	GO:0019953	3	sexual reproduction	118	0.0182	10	0.0242	0.0888973	E
<input type="radio"/>	GO:0000747	4	conjugation with cellular fusion	118	0.0182	10	0.0242	0.0888973	E
<input type="radio"/>	GO:0007059	3	chromosome segregation	119	0.0184	10	0.0242	0.0908860	E
<input type="radio"/>	GO:0000279	6,5	M phase	258	0.0398	18	0.0435	0.0920809	E
<input type="radio"/>	GO:0006280	6	mutagenesis	9	0.0014	2	0.0048	0.0926218	E
<input type="radio"/>	GO:0030847	10,9	transcription termination from Pol II promoter, RNA polymerase(A)-independent	9	0.0014	2	0.0048	0.0926218	E
<input type="radio"/>	GO:0006760	5,7	folic acid and derivative metabolic process	9	0.0014	2	0.0048	0.0926218	E
<input type="radio"/>	GO:0065008	3	regulation of biological quality	260	0.0401	18	0.0435	0.0932070	E
<input type="radio"/>	GO:0006970	4	response to osmotic stress	89	0.0137	8	0.0193	0.0936824	E
<input type="radio"/>	GO:0065004	6,5	protein-DNA complex assembly	74	0.0114	7	0.0169	0.0940654	E
<input type="radio"/>	GO:0022616	6	DNA strand elongation	32	0.0049	4	0.0097	0.0944347	E
<input type="radio"/>	GO:0006271	8,7	DNA strand elongation during DNA replication	32	0.0049	4	0.0097	0.0944347	E
<input type="radio"/>	GO:0031509	7,11	telomeric heterochromatin formation	60	0.0093	6	0.0145	0.0965636	E
<input type="radio"/>	GO:0006348	11,7,8,12,10	chromatin silencing at telomere	60	0.0093	6	0.0145	0.0965636	E
<input type="radio"/>	GO:0006310	6	DNA recombination	122	0.0188	10	0.0242	0.0966779	E
<input type="radio"/>	GO:0030148	7,6,8	sphingolipid biosynthetic process	20	0.0031	3	0.0072	0.0968476	E
<input type="radio"/>	GO:0006353	8,7	transcription termination	20	0.0031	3	0.0072	0.0968476	E
<input type="radio"/>	GO:0000165	7	MAPKKK cascade	20	0.0031	3	0.0072	0.0968476	E
<input type="radio"/>	GO:0006614	11,10,9,8,7	SRP-dependent cotranslational protein targeting to membrane	20	0.0031	3	0.0072	0.0968476	E
<input type="radio"/>	GO:0009451	6	RNA modification	139	0.0215	11	0.0266	0.0975132	E
<input type="radio"/>	GO:0007124	6,4,8,9	pseudohyphal growth	61	0.0094	6	0.0145	0.1002873	E
<input type="radio"/>	GO:0048522	5,4	positive regulation of cellular process	124	0.0191	10	0.0242	0.1003703	E
<input type="radio"/>	GO:0048518	4	positive regulation of biological process	124	0.0191	10	0.0242	0.1003703	E
<input type="radio"/>	GO:0007154	3	cell communication	240	0.0371	16	0.0386	0.1031320	E
<input type="radio"/>	GO:0017038	5,6,7	protein import	109	0.0168	9	0.0217	0.1033354	E
<input type="radio"/>	GO:0006357	9,8	regulation of transcription from RNA polymerase II promoter	221	0.0341	15	0.0362	0.1049521	E
<input type="radio"/>	GO:0016568	8	chromatin modification	223	0.0344	15	0.0362	0.1057689	E
<input type="radio"/>	GO:0009072	6,5,7	aromatic amino acid family metabolic process	21	0.0032	3	0.0072	0.1057958	E
<input type="radio"/>	GO:0046467	6,5,7	membrane lipid biosynthetic process	78	0.0120	7	0.0169	0.1061799	E
<input type="radio"/>	GO:0019236	4	response to pheromone	94	0.0145	8	0.0193	0.1063139	E
<input type="radio"/>	GO:0006869	4,5	lipid transport	34	0.0053	4	0.0097	0.1067825	E
<input type="radio"/>	GO:0007129	10,8,7,5,9,6,4	synapsis	10	0.0015	2	0.0048	0.1084013	E
<input type="radio"/>	GO:0007165	4	signal transduction	209	0.0323	14	0.0338	0.1097806	E

<input type="radio"/>	GO:0000086	8,5,6,7,4	G2/M transition of mitotic cell cycle	35	0.0054	4	0.0097	0.1128878	E
<input type="radio"/>	GO:0048590	3	non-developmental growth	35	0.0054	4	0.0097	0.1128878	E
<input type="radio"/>	GO:0007117	6,5,4	budding cell bud growth	35	0.0054	4	0.0097	0.1128878	E
<input type="radio"/>	GO:0006261	7	DNA-dependent DNA replication	97	0.0150	8	0.0193	0.1133215	E
<input type="radio"/>	GO:0006839	7,5,6	mitochondrial transport	65	0.0100	6	0.0145	0.1146951	E
<input type="radio"/>	GO:0030150	10,9,8,7	protein import into mitochondrial matrix	22	0.0034	3	0.0072	0.1147006	E
<input type="radio"/>	GO:0030472	6,5,10	mitotic spindle organization and biogenesis in nucleus	22	0.0034	3	0.0072	0.1147006	E
<input type="radio"/>	GO:0009893	5,4	positive regulation of metabolic process	116	0.0179	9	0.0217	0.1166147	E
<input type="radio"/>	GO:0031325	6,5	positive regulation of cellular metabolic process	116	0.0179	9	0.0217	0.1166147	E
<input type="radio"/>	GO:0006338	9	chromatin remodeling	155	0.0239	11	0.0266	0.1177728	E
<input type="radio"/>	GO:0042255	7,6	ribosome assembly	66	0.0102	6	0.0145	0.1181354	E
<input type="radio"/>	GO:0051252	7,6	regulation of RNA metabolic process	36	0.0056	4	0.0097	0.1189147	E
<input type="radio"/>	GO:0006563	7,8	L-serine metabolic process	2	0.0003	1	0.0024	0.1197015	E
<input type="radio"/>	GO:0009221	7,8	pyrimidine deoxyribonucleotide biosynthetic process	2	0.0003	1	0.0024	0.1197015	E
<input type="radio"/>	GO:0046087	8	cytidine metabolic process	2	0.0003	1	0.0024	0.1197015	E
<input type="radio"/>	GO:0018196	8	peptidyl-asparagine modification	2	0.0003	1	0.0024	0.1197015	E
<input type="radio"/>	GO:0016576	11,9,8	histone dephosphorylation	2	0.0003	1	0.0024	0.1197015	E
<input type="radio"/>	GO:0042308	8,9,11,12,10,7	negative regulation of protein import into nucleus	2	0.0003	1	0.0024	0.1197015	E
<input type="radio"/>	GO:0006451	8,7,6	translational readthrough	2	0.0003	1	0.0024	0.1197015	E
<input type="radio"/>	GO:0006661	10,9,11	phosphatidylinositol biosynthetic process	2	0.0003	1	0.0024	0.1197015	E
<input type="radio"/>	GO:0009226	5,6	nucleotide-sugar biosynthetic process	2	0.0003	1	0.0024	0.1197015	E
<input type="radio"/>	GO:0006046	8,9	N-acetylglucosamine catabolic process	2	0.0003	1	0.0024	0.1197015	E
<input type="radio"/>	GO:0032465	6,5	regulation of cytokinesis	2	0.0003	1	0.0024	0.1197015	E
<input type="radio"/>	GO:0019673	8,6,9	GDP-mannose metabolic process	2	0.0003	1	0.0024	0.1197015	E
<input type="radio"/>	GO:0046823	7,10,6,8,9	negative regulation of nucleocytoplasmic transport	2	0.0003	1	0.0024	0.1197015	E
<input type="radio"/>	GO:0042991	10,11,8,9,7	transcription factor import into nucleus	2	0.0003	1	0.0024	0.1197015	E
<input type="radio"/>	GO:0048026	10,9,12	positive regulation of nuclear mRNA splicing, via spliceosome	2	0.0003	1	0.0024	0.1197015	E
<input type="radio"/>	GO:0007128	10,8,7,9,6	meiotic prophase I	2	0.0003	1	0.0024	0.1197015	E
<input type="radio"/>	GO:0007189	9,10	G-protein signaling, adenylate cyclase activating pathway	2	0.0003	1	0.0024	0.1197015	E
<input type="radio"/>	GO:0006556	8,7,6,9,5	S-adenosylmethionine biosynthetic process	2	0.0003	1	0.0024	0.1197015	E
<input type="radio"/>	GO:0006437	9,8,10,7	tyrosyl-tRNA aminoacylation	2	0.0003	1	0.0024	0.1197015	E
<input type="radio"/>	GO:0046135	6,7	pyrimidine nucleoside catabolic process	2	0.0003	1	0.0024	0.1197015	E
<input type="radio"/>	GO:0009202	7,8	deoxyribonucleoside triphosphate biosynthetic process	2	0.0003	1	0.0024	0.1197015	E
<input type="radio"/>	GO:0042992	9,10,12,13,11,8	negative regulation of transcription factor import into nucleus	2	0.0003	1	0.0024	0.1197015	E
<input type="radio"/>	GO:0048250	8,6,9,7,10	mitochondrial iron ion transport	2	0.0003	1	0.0024	0.1197015	E
<input type="radio"/>	GO:0033260	8,7,6	DNA replication during S phase	2	0.0003	1	0.0024	0.1197015	E
<input type="radio"/>	GO:0042990	9,8,11,12,10,7	regulation of transcription factor import into nucleus	2	0.0003	1	0.0024	0.1197015	E
<input type="radio"/>	GO:0000354	7,8,6,10,12	cis assembly of pre-catalytic spliceosome	2	0.0003	1	0.0024	0.1197015	E
<input type="radio"/>	GO:0035057	11,10,13	positive regulation of nuclear mRNA splicing via U2-type spliceosome	2	0.0003	1	0.0024	0.1197015	E
<input type="radio"/>	GO:0046348	6,7	amino sugar catabolic process	2	0.0003	1	0.0024	0.1197015	E
<input type="radio"/>	GO:0018279	10,9,8	protein amino acid N-linked glycosylation via asparagine	2	0.0003	1	0.0024	0.1197015	E
<input type="radio"/>	GO:0033313	8,7	meiotic cell cycle checkpoint	2	0.0003	1	0.0024	0.1197015	E

<input type="radio"/>	GO:0046131	7	pyrimidine ribonucleoside metabolic process	2	0.0003	1	0.0024	0.1197015	E
<input type="radio"/>	GO:0045740	9,8	positive regulation of DNA replication	2	0.0003	1	0.0024	0.1197015	E
<input type="radio"/>	GO:0031055	10	chromatin remodeling at centromere	2	0.0003	1	0.0024	0.1197015	E
<input type="radio"/>	GO:0018987	6	osmoregulation	2	0.0003	1	0.0024	0.1197015	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	0.0024	0.1197015	E
<input type="radio"/>	GO:0044419	3	interspecies interaction between organisms	2	0.0003	1	0.0024	0.1197015	E
<input type="radio"/>	GO:0006564	8,9	L-serine biosynthetic process	2	0.0003	1	0.0024	0.1197015	E
<input type="radio"/>	GO:0006043	7,8	glucosamine catabolic process	2	0.0003	1	0.0024	0.1197015	E
<input type="radio"/>	GO:0050685	9,8	positive regulation of mRNA processing	2	0.0003	1	0.0024	0.1197015	E
<input type="radio"/>	GO:0035055	10,9,12	regulation of nuclear mRNA splicing via U2-type spliceosome	2	0.0003	1	0.0024	0.1197015	E
<input type="radio"/>	GO:0000078	9,11,10,8,6,7	cell morphogenesis checkpoint	2	0.0003	1	0.0024	0.1197015	E
<input type="radio"/>	GO:0043409	7,9,6	negative regulation of MAPKKK cascade	2	0.0003	1	0.0024	0.1197015	E
<input type="radio"/>	GO:0000168	10,11,8,9,7	activation of MAPKK activity during osmolarity sensing	2	0.0003	1	0.0024	0.1197015	E
<input type="radio"/>	GO:0019307	8,9	mannose biosynthetic process	2	0.0003	1	0.0024	0.1197015	E
<input type="radio"/>	GO:0051598	9,11,8,10,7	meiotic recombination checkpoint	2	0.0003	1	0.0024	0.1197015	E
<input type="radio"/>	GO:0019988	7,8,9,6	charged-tRNA modification	2	0.0003	1	0.0024	0.1197015	E
<input type="radio"/>	GO:0006032	9,10,8,7	chitin catabolic process	2	0.0003	1	0.0024	0.1197015	E
<input type="radio"/>	GO:0009133	6,7	nucleoside diphosphate biosynthetic process	2	0.0003	1	0.0024	0.1197015	E
<input type="radio"/>	GO:0009298	9,6,7,10	GDP-mannose biosynthetic process	2	0.0003	1	0.0024	0.1197015	E
<input type="radio"/>	GO:0051324	7,6,5	prophase	2	0.0003	1	0.0024	0.1197015	E
<input type="radio"/>	GO:0033262	8,9,7	regulation of DNA replication during S phase	2	0.0003	1	0.0024	0.1197015	E
<input type="radio"/>	GO:0007243	6	protein kinase cascade	23	0.0036	3	0.0072	0.1235058	E
<input type="radio"/>	GO:0006613	10,9,8,7,6	cotranslational protein targeting to membrane	23	0.0036	3	0.0072	0.1235058	E
<input type="radio"/>	GO:0051168	9,7,8	nuclear export	102	0.0158	8	0.0193	0.1237559	E
<input type="radio"/>	GO:0007109	7,6,5,4	cytokinesis, completion of separation	11	0.0017	2	0.0048	0.1240484	E
<input type="radio"/>	GO:0006276	3	plasmid maintenance	11	0.0017	2	0.0048	0.1240484	E
<input type="radio"/>	GO:0016237	4,6	microautophagy	11	0.0017	2	0.0048	0.1240484	E
<input type="radio"/>	GO:0007050	7,8,6	cell cycle arrest	11	0.0017	2	0.0048	0.1240484	E
<input type="radio"/>	GO:0031497	5,9	chromatin assembly	104	0.0161	8	0.0193	0.1274296	E
<input type="radio"/>	GO:0006643	5,6	membrane lipid metabolic process	125	0.0193	9	0.0217	0.1293192	E
<input type="radio"/>	GO:0000288	10,8,9	mRNA catabolic process, deadenylation-dependent decay	24	0.0037	3	0.0072	0.1321595	E
<input type="radio"/>	GO:0045935	7,6	positive regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	108	0.0167	8	0.0193	0.1338265	E
<input type="radio"/>	GO:0006403	4	RNA localization	90	0.0139	7	0.0169	0.1363585	E
<input type="radio"/>	GO:0007005	5	mitochondrion organization and biogenesis	110	0.0170	8	0.0193	0.1365253	E
<input type="radio"/>	GO:0007088	7,9,8,6	regulation of mitosis	55	0.0085	5	0.0121	0.1369887	E
<input type="radio"/>	GO:0006811	4,5	ion transport	115	0.0178	8	0.0193	0.1417547	E
<input type="radio"/>	GO:0006401	6	RNA catabolic process	74	0.0114	6	0.0145	0.1422814	E
<input type="radio"/>	GO:0009628	3	response to abiotic stimulus	117	0.0181	8	0.0193	0.1432317	E
<input type="radio"/>	GO:0006333	8	chromatin assembly or disassembly	119	0.0184	8	0.0193	0.1443583	E
<input type="radio"/>	GO:0006302	7,6	double-strand break repair	57	0.0088	5	0.0121	0.1445447	E
<input type="radio"/>	GO:0000749	5	response to pheromone during conjugation with cellular fusion	57	0.0088	5	0.0121	0.1445447	E
<input type="radio"/>	GO:0045814	5	negative regulation of gene expression, epigenetic	95	0.0147	7	0.0169	0.1450772	E

<input type="radio"/>	GO:0006342	10,6,7,11,9	chromatin silencing	95	0.0147	7	0.0169	0.1450772	E
<input type="radio"/>	GO:0016458	5	gene silencing	95	0.0147	7	0.0169	0.1450772	E
<input type="radio"/>	GO:0031507	6,10	heterochromatin formation	95	0.0147	7	0.0169	0.1450772	E
<input type="radio"/>	GO:0010324	5	membrane invagination	96	0.0148	7	0.0169	0.1465065	E
<input type="radio"/>	GO:0000027	9,7,8,6	ribosomal large subunit assembly and maintenance	41	0.0063	4	0.0097	0.1471213	E
<input type="radio"/>	GO:0051052	7,6	regulation of DNA metabolic process	41	0.0063	4	0.0097	0.1471213	E
<input type="radio"/>	GO:0009966	5,4	regulation of signal transduction	26	0.0040	3	0.0072	0.1488283	E
<input type="radio"/>	GO:0042274	6,5	ribosomal small subunit biogenesis and assembly	26	0.0040	3	0.0072	0.1488283	E
<input type="radio"/>	GO:0040029	4	regulation of gene expression, epigenetic	100	0.0154	7	0.0169	0.1511453	E
<input type="radio"/>	GO:0006944	5	membrane fusion	59	0.0091	5	0.0121	0.1515033	E
<input type="radio"/>	GO:0016049	5,3,7,8	cell growth	102	0.0158	7	0.0169	0.1528152	E
<input type="radio"/>	GO:0051188	5	cofactor biosynthetic process	79	0.0122	6	0.0145	0.1535796	E
<input type="radio"/>	GO:0006405	10,8,5,7,9,6	RNA export from nucleus	79	0.0122	6	0.0145	0.1535796	E
<input type="radio"/>	GO:0000920	6,4	cell separation during cytokinesis	13	0.0020	2	0.0048	0.1542137	E
<input type="radio"/>	GO:0006915	6,8	apoptosis	13	0.0020	2	0.0048	0.1542137	E
<input type="radio"/>	GO:0007103	6,7,5,8	spindle pole body duplication in nuclear envelope	13	0.0020	2	0.0048	0.1542137	E
<input type="radio"/>	GO:0008219	4,6	cell death	13	0.0020	2	0.0048	0.1542137	E
<input type="radio"/>	GO:0009082	7,8	branched chain family amino acid biosynthetic process	13	0.0020	2	0.0048	0.1542137	E
<input type="radio"/>	GO:0016265	3	death	13	0.0020	2	0.0048	0.1542137	E
<input type="radio"/>	GO:0012501	5,7	programmed cell death	13	0.0020	2	0.0048	0.1542137	E
<input type="radio"/>	GO:0050658	4,6,5,7	RNA transport	80	0.0124	6	0.0145	0.1554425	E
<input type="radio"/>	GO:0050657	5,6	nucleic acid transport	80	0.0124	6	0.0145	0.1554425	E
<input type="radio"/>	GO:0051236	3,4,5	establishment of RNA localization	80	0.0124	6	0.0145	0.1554425	E
<input type="radio"/>	GO:0030384	8,9	phosphoinositide metabolic process	43	0.0066	4	0.0097	0.1571656	E
<input type="radio"/>	GO:0006888	8,6,5,7	ER to Golgi vesicle-mediated transport	81	0.0125	6	0.0145	0.1571690	E
<input type="radio"/>	GO:0006887	8,6,5,7	exocytosis	44	0.0068	4	0.0097	0.1618637	E
<input type="radio"/>	GO:0000122	10,9	negative regulation of transcription from RNA polymerase II promoter	63	0.0097	5	0.0121	0.1634352	E
<input type="radio"/>	GO:0000054	10,11,6,8,9	ribosome export from nucleus	28	0.0043	3	0.0072	0.1643850	E
<input type="radio"/>	GO:0046489	9,8,10	phosphoinositide biosynthetic process	28	0.0043	3	0.0072	0.1643850	E
<input type="radio"/>	GO:0051204	7,6,5	protein insertion into mitochondrial membrane	3	0.0005	1	0.0024	0.1680980	E
<input type="radio"/>	GO:0007090	8,9,7,6	regulation of S phase of mitotic cell cycle	3	0.0005	1	0.0024	0.1680980	E
<input type="radio"/>	GO:0048024	9,8,11	regulation of nuclear mRNA splicing, via spliceosome	3	0.0005	1	0.0024	0.1680980	E
<input type="radio"/>	GO:0006857	5,6	oligopeptide transport	3	0.0005	1	0.0024	0.1680980	E
<input type="radio"/>	GO:0043102	6,5,7	amino acid salvage	3	0.0005	1	0.0024	0.1680980	E
<input type="radio"/>	GO:0009090	8,9	homoserine biosynthetic process	3	0.0005	1	0.0024	0.1680980	E
<input type="radio"/>	GO:0000387	5,9,11	spliceosomal snRNP biogenesis	3	0.0005	1	0.0024	0.1680980	E
<input type="radio"/>	GO:0000244	7,6,10,12	assembly of spliceosomal tri-snRNP	3	0.0005	1	0.0024	0.1680980	E
<input type="radio"/>	GO:0007030	5	Golgi organization and biogenesis	3	0.0005	1	0.0024	0.1680980	E
<input type="radio"/>	GO:0046160	7,8,6	heme a metabolic process	3	0.0005	1	0.0024	0.1680980	E
<input type="radio"/>	GO:0016093	7,8	polyprenol metabolic process	3	0.0005	1	0.0024	0.1680980	E
<input type="radio"/>	GO:0032386	6,7,5	regulation of intracellular transport	3	0.0005	1	0.0024	0.1680980	E
<input type="radio"/>	GO:0050684	8,7	regulation of mRNA processing	3	0.0005	1	0.0024	0.1680980	E
<input type="radio"/>	GO:0033157	7,8,6	regulation of intracellular protein transport	3	0.0005	1	0.0024	0.1680980	E

<input type="checkbox"/>	GO:0000186	9,10,8	activation of MAPKK activity	3	0.0005	1	0.0024	0.1680980	E
<input type="checkbox"/>	GO:0051205	6,5,4	protein insertion into membrane	3	0.0005	1	0.0024	0.1680980	E
<input type="checkbox"/>	GO:0016090	6,7	prenol metabolic process	3	0.0005	1	0.0024	0.1680980	E
<input type="checkbox"/>	GO:0016091	7,6,8	prenol biosynthetic process	3	0.0005	1	0.0024	0.1680980	E
<input type="checkbox"/>	GO:0000321	9,8,7,6	re-entry into mitotic cell cycle after pheromone arrest	3	0.0005	1	0.0024	0.1680980	E
<input type="checkbox"/>	GO:0019509	7,8,6,9	methionine salvage	3	0.0005	1	0.0024	0.1680980	E
<input type="checkbox"/>	GO:0046500	6,5	S-adenosylmethionine metabolic process	3	0.0005	1	0.0024	0.1680980	E
<input type="checkbox"/>	GO:0000320	7,6	re-entry into mitotic cell cycle	3	0.0005	1	0.0024	0.1680980	E
<input type="checkbox"/>	GO:0051668	5,4	localization within membrane	3	0.0005	1	0.0024	0.1680980	E
<input type="checkbox"/>	GO:0000917	6,4	barrier septum formation	3	0.0005	1	0.0024	0.1680980	E
<input type="checkbox"/>	GO:0043065	7,8,10,6	positive regulation of apoptosis	3	0.0005	1	0.0024	0.1680980	E
<input type="checkbox"/>	GO:0051224	7,6,8	negative regulation of protein transport	3	0.0005	1	0.0024	0.1680980	E
<input type="checkbox"/>	GO:0016094	8,7,9	polyprenol biosynthetic process	3	0.0005	1	0.0024	0.1680980	E
<input type="checkbox"/>	GO:0043068	6,7,9,5	positive regulation of programmed cell death	3	0.0005	1	0.0024	0.1680980	E
<input type="checkbox"/>	GO:0043408	6,8,5	regulation of MAPKKK cascade	3	0.0005	1	0.0024	0.1680980	E
<input type="checkbox"/>	GO:0042306	8,7,10,11,9,6	regulation of protein import into nucleus	3	0.0005	1	0.0024	0.1680980	E
<input type="checkbox"/>	GO:0006835	6,7	dicarboxylic acid transport	3	0.0005	1	0.0024	0.1680980	E
<input type="checkbox"/>	GO:0051054	8,7	positive regulation of DNA metabolic process	3	0.0005	1	0.0024	0.1680980	E
<input type="checkbox"/>	GO:0006784	8,7,9	heme a biosynthetic process	3	0.0005	1	0.0024	0.1680980	E
<input type="checkbox"/>	GO:0009132	6	nucleoside diphosphate metabolic process	3	0.0005	1	0.0024	0.1680980	E
<input type="checkbox"/>	GO:0046822	6,9,5,7,8	regulation of nucleocytoplasmic transport	3	0.0005	1	0.0024	0.1680980	E
<input type="checkbox"/>	GO:0008272	7,8	sulfate transport	3	0.0005	1	0.0024	0.1680980	E
<input type="checkbox"/>	GO:0051302	5,4	regulation of cell division	3	0.0005	1	0.0024	0.1680980	E
<input type="checkbox"/>	GO:0009263	6,7	deoxyribonucleotide biosynthetic process	3	0.0005	1	0.0024	0.1680980	E
<input type="checkbox"/>	GO:0030474	5,6,4,7	spindle pole body duplication	14	0.0022	2	0.0048	0.1684468	E
<input type="checkbox"/>	GO:0007118	7,6,5	budding cell apical bud growth	14	0.0022	2	0.0048	0.1684468	E
<input type="checkbox"/>	GO:0009108	6	coenzyme biosynthetic process	66	0.0102	5	0.0121	0.1705196	E
<input type="checkbox"/>	GO:0000041	7,8	transition metal ion transport	46	0.0071	4	0.0097	0.1705578	E
<input type="checkbox"/>	GO:0009110	5	vitamin biosynthetic process	46	0.0071	4	0.0097	0.1705578	E
<input type="checkbox"/>	GO:0042364	6	water-soluble vitamin biosynthetic process	46	0.0071	4	0.0097	0.1705578	E
<input type="checkbox"/>	GO:0007033	5	vacuole organization and biogenesis	67	0.0103	5	0.0121	0.1725135	E
<input type="checkbox"/>	GO:0006497	8,7,6	protein amino acid lipidation	48	0.0074	4	0.0097	0.1782608	E
<input type="checkbox"/>	GO:0042158	7,5	lipoprotein biosynthetic process	48	0.0074	4	0.0097	0.1782608	E
<input type="checkbox"/>	GO:0042157	6	lipoprotein metabolic process	48	0.0074	4	0.0097	0.1782608	E
<input type="checkbox"/>	GO:0043487	8,7	regulation of RNA stability	30	0.0046	3	0.0072	0.1785796	E
<input type="checkbox"/>	GO:0043488	9,8,7	regulation of mRNA stability	30	0.0046	3	0.0072	0.1785796	E
<input type="checkbox"/>	GO:0009141	6	nucleoside triphosphate metabolic process	30	0.0046	3	0.0072	0.1785796	E
<input type="checkbox"/>	GO:0006525	7,8,5,4	arginine metabolic process	15	0.0023	2	0.0048	0.1819697	E
<input type="checkbox"/>	GO:0000051	4,3	urea cycle intermediate metabolic process	15	0.0023	2	0.0048	0.1819697	E
<input type="checkbox"/>	GO:0022401	7,6	adaptation of signaling pathway	15	0.0023	2	0.0048	0.1819697	E
<input type="checkbox"/>	GO:0016073	6	snRNA metabolic process	15	0.0023	2	0.0048	0.1819697	E
<input type="checkbox"/>	GO:0000754	8,7,5	adaptation to pheromone during conjugation with cellular fusion	15	0.0023	2	0.0048	0.1819697	E
<input type="checkbox"/>	GO:0015918	5,6	sterol transport	15	0.0023	2	0.0048	0.1819697	E
<input type="checkbox"/>	GO:0009651	5	response to salt stress	15	0.0023	2	0.0048	0.1819697	E

<input type="checkbox"/>	GO:0000114	10,8,9,5,7,4	G1-specific transcription in mitotic cell cycle	15	0.0023	2	0.0048	0.1819697	E
<input type="checkbox"/>	GO:0015837	4,5	amine transport	50	0.0077	4	0.0097	0.1849267	E
<input type="checkbox"/>	GO:0006368	9,7,8	RNA elongation from RNA polymerase II promoter	53	0.0082	4	0.0097	0.1929307	E
<input type="checkbox"/>	GO:0031023	5	microtubule organizing center organization and biogenesis	16	0.0025	2	0.0048	0.1947040	E
<input type="checkbox"/>	GO:0009081	6,7	branched chain family amino acid metabolic process	16	0.0025	2	0.0048	0.1947040	E
<input type="checkbox"/>	GO:0010383	7,5,6	cell wall polysaccharide metabolic process	16	0.0025	2	0.0048	0.1947040	E
<input type="checkbox"/>	GO:0051300	5,4,6	spindle pole body organization and biogenesis	16	0.0025	2	0.0048	0.1947040	E
<input type="checkbox"/>	GO:0042257	8,7	ribosomal subunit assembly	55	0.0085	4	0.0097	0.1969335	E
<input type="checkbox"/>	GO:0006611	9,10,7,8	protein export from nucleus	56	0.0086	4	0.0097	0.1985402	E
<input type="checkbox"/>	GO:0008654	7,6,8	phospholipid biosynthetic process	58	0.0090	4	0.0097	0.2009814	E
<input type="checkbox"/>	GO:0006354	8,6,7	RNA elongation	59	0.0091	4	0.0097	0.2018252	E
<input type="checkbox"/>	GO:0006650	7,8	glycerophospholipid metabolic process	60	0.0093	4	0.0097	0.2024250	E
<input type="checkbox"/>	GO:0006402	7	mRNA catabolic process	60	0.0093	4	0.0097	0.2024250	E
<input type="checkbox"/>	GO:0030001	6,7	metal ion transport	62	0.0096	4	0.0097	0.2029178	E
<input type="checkbox"/>	GO:0043543	7	protein amino acid acylation	62	0.0096	4	0.0097	0.2029178	E
<input type="checkbox"/>	GO:0007266	8	Rho protein signal transduction	17	0.0026	2	0.0048	0.2065912	E
<input type="checkbox"/>	GO:0000742	7,5	karyogamy during conjugation with cellular fusion	17	0.0026	2	0.0048	0.2065912	E
<input type="checkbox"/>	GO:0000741	6	karyogamy	17	0.0026	2	0.0048	0.2065912	E
<input type="checkbox"/>	GO:0045132	9,7,8,6,4	meiotic chromosome segregation	17	0.0026	2	0.0048	0.2065912	E
<input type="checkbox"/>	GO:0000304	6	response to singlet oxygen	4	0.0006	1	0.0024	0.2098303	E
<input type="checkbox"/>	GO:0030037	5,4,9	actin filament reorganization during cell cycle	4	0.0006	1	0.0024	0.2098303	E
<input type="checkbox"/>	GO:0007157	5	heterophilic cell adhesion	4	0.0006	1	0.0024	0.2098303	E
<input type="checkbox"/>	GO:0000731	7,6	DNA synthesis during DNA repair	4	0.0006	1	0.0024	0.2098303	E
<input type="checkbox"/>	GO:0006278	7	RNA-dependent DNA replication	4	0.0006	1	0.0024	0.2098303	E
<input type="checkbox"/>	GO:0009891	6,5	positive regulation of biosynthetic process	4	0.0006	1	0.0024	0.2098303	E
<input type="checkbox"/>	GO:0031384	6,8,11,10,9,7,12	regulation of initiation of mating projection growth	4	0.0006	1	0.0024	0.2098303	E
<input type="checkbox"/>	GO:0031328	7,6	positive regulation of cellular biosynthetic process	4	0.0006	1	0.0024	0.2098303	E
<input type="checkbox"/>	GO:0006529	8,9	asparagine biosynthetic process	4	0.0006	1	0.0024	0.2098303	E
<input type="checkbox"/>	GO:0016036	8,7,6	cellular response to phosphate starvation	4	0.0006	1	0.0024	0.2098303	E
<input type="checkbox"/>	GO:0000771	6,4	agglutination	4	0.0006	1	0.0024	0.2098303	E
<input type="checkbox"/>	GO:0031532	8	actin cytoskeleton reorganization	4	0.0006	1	0.0024	0.2098303	E
<input type="checkbox"/>	GO:0000349	8,7,10,12	generation of catalytic spliceosome for first transesterification step	4	0.0006	1	0.0024	0.2098303	E
<input type="checkbox"/>	GO:0051051	6,5	negative regulation of transport	4	0.0006	1	0.0024	0.2098303	E
<input type="checkbox"/>	GO:0009164	5,6	nucleoside catabolic process	4	0.0006	1	0.0024	0.2098303	E
<input type="checkbox"/>	GO:0046520	8,7,9	sphingoid biosynthetic process	4	0.0006	1	0.0024	0.2098303	E
<input type="checkbox"/>	GO:0043067	5,6,8,4	regulation of programmed cell death	4	0.0006	1	0.0024	0.2098303	E
<input type="checkbox"/>	GO:0042981	6,7,9,5	regulation of apoptosis	4	0.0006	1	0.0024	0.2098303	E
<input type="checkbox"/>	GO:0030497	8,7,9,6	fatty acid elongation	4	0.0006	1	0.0024	0.2098303	E
<input type="checkbox"/>	GO:0000752	7,5,6	agglutination during conjugation with cellular fusion	4	0.0006	1	0.0024	0.2098303	E
<input type="checkbox"/>	GO:0001100	9,11,10,8	negative regulation of exit from mitosis	4	0.0006	1	0.0024	0.2098303	E
<input type="checkbox"/>	GO:0006592	8,9,6,5	ornithine biosynthetic process	4	0.0006	1	0.0024	0.2098303	E
<input type="checkbox"/>	GO:0006596	7,8	polyamine biosynthetic process	4	0.0006	1	0.0024	0.2098303	E

<input type="radio"/>	GO:0051223	6,5,7	regulation of protein transport	4	0.0006	1	0.0024	0.2098303	E
<input type="radio"/>	GO:0045943	10,9	positive regulation of transcription from RNA polymerase I promoter	4	0.0006	1	0.0024	0.2098303	E
<input type="radio"/>	GO:0045727	8,7,6	positive regulation of protein biosynthetic process	4	0.0006	1	0.0024	0.2098303	E
<input type="radio"/>	GO:0046513	9,8,10	ceramide biosynthetic process	4	0.0006	1	0.0024	0.2098303	E
<input type="radio"/>	GO:0031204	9,11,10,7,8	posttranslational protein targeting to membrane, translocation	4	0.0006	1	0.0024	0.2098303	E
<input type="radio"/>	GO:0006378	9	mRNA polyadenylation	18	0.0028	2	0.0048	0.2175900	E
<input type="radio"/>	GO:0006273	9,8	lagging strand elongation	18	0.0028	2	0.0048	0.2175900	E
<input type="radio"/>	GO:0000018	8,7	regulation of DNA recombination	18	0.0028	2	0.0048	0.2175900	E
<input type="radio"/>	GO:0007265	7	Ras protein signal transduction	39	0.0060	3	0.0072	0.2220864	E
<input type="radio"/>	GO:0046474	8,7,9	glycerophospholipid biosynthetic process	39	0.0060	3	0.0072	0.2220864	E
<input type="radio"/>	GO:0006865	5,6,7	amino acid transport	39	0.0060	3	0.0072	0.2220864	E
<input type="radio"/>	GO:0043681	6,7,8	protein import into mitochondrion	40	0.0062	3	0.0072	0.2247636	E
<input type="radio"/>	GO:0006275	8,7	regulation of DNA replication	19	0.0029	2	0.0048	0.2276742	E
<input type="radio"/>	GO:0009064	6,7	glutamine family amino acid metabolic process	43	0.0066	3	0.0072	0.2303183	E
<input type="radio"/>	GO:0007052	5,4,9	mitotic spindle organization and biogenesis	44	0.0068	3	0.0072	0.2313793	E
<input type="radio"/>	GO:0051647	6,5	nucleus localization	20	0.0031	2	0.0048	0.2368300	E
<input type="radio"/>	GO:0040023	6,7,4,5	establishment of nucleus localization	20	0.0031	2	0.0048	0.2368300	E
<input type="radio"/>	GO:0016579	9	protein deubiquitination	20	0.0031	2	0.0048	0.2368300	E
<input type="radio"/>	GO:0006308	5,6	DNA catabolic process	20	0.0031	2	0.0048	0.2368300	E
<input type="radio"/>	GO:0007097	7,8,5,6	nuclear migration	20	0.0031	2	0.0048	0.2368300	E
<input type="radio"/>	GO:0051320	7,6,5	S phase	20	0.0031	2	0.0048	0.2368300	E
<input type="radio"/>	GO:0030007	10,8	cellular potassium ion homeostasis	5	0.0008	1	0.0024	0.2455504	E
<input type="radio"/>	GO:0055075	9	potassium ion homeostasis	5	0.0008	1	0.0024	0.2455504	E
<input type="radio"/>	GO:0045991	10,8,9,6	positive regulation of transcription by carbon catabolites	5	0.0008	1	0.0024	0.2455504	E
<input type="radio"/>	GO:0007188	8,9	G-protein signaling, coupled to cAMP nucleotide second messenger	5	0.0008	1	0.0024	0.2455504	E
<input type="radio"/>	GO:0016337	4	cell-cell adhesion	5	0.0008	1	0.0024	0.2455504	E
<input type="radio"/>	GO:0000411	11,9,10,7	positive regulation of transcription by galactose	5	0.0008	1	0.0024	0.2455504	E
<input type="radio"/>	GO:0051247	6,5	positive regulation of protein metabolic process	5	0.0008	1	0.0024	0.2455504	E
<input type="radio"/>	GO:0051254	8,7	positive regulation of RNA metabolic process	5	0.0008	1	0.0024	0.2455504	E
<input type="radio"/>	GO:0043001	10,8,7,9	Golgi to plasma membrane protein transport	5	0.0008	1	0.0024	0.2455504	E
<input type="radio"/>	GO:0000101	6,7,8	sulfur amino acid transport	5	0.0008	1	0.0024	0.2455504	E
<input type="radio"/>	GO:0006221	6,7	pyrimidine nucleotide biosynthetic process	5	0.0008	1	0.0024	0.2455504	E
<input type="radio"/>	GO:0009098	8,9	leucine biosynthetic process	5	0.0008	1	0.0024	0.2455504	E
<input type="radio"/>	GO:0007023	8	post-chaperonin tubulin folding pathway	5	0.0008	1	0.0024	0.2455504	E
<input type="radio"/>	GO:0051083	8	cotranslational protein folding	5	0.0008	1	0.0024	0.2455504	E
<input type="radio"/>	GO:0000409	10,8,9,6	regulation of transcription by galactose	5	0.0008	1	0.0024	0.2455504	E
<input type="radio"/>	GO:0007187	7,8	G-protein signaling, coupled to cyclic nucleotide second messenger	5	0.0008	1	0.0024	0.2455504	E
<input type="radio"/>	GO:0006797	6	polyphosphate metabolic process	5	0.0008	1	0.0024	0.2455504	E
<input type="radio"/>	GO:0007329	11,10,7	positive regulation of transcription from RNA polymerase II promoter by pheromones	5	0.0008	1	0.0024	0.2455504	E
<input type="radio"/>	GO:0009371	10,9,6	positive regulation of transcription by pheromones	5	0.0008	1	0.0024	0.2455504	E
<input type="radio"/>	GO:0048284	5	organelle fusion	22	0.0034	2	0.0048	0.2523553	E

<input type="radio"/>	GO:0007020	8	microtubule nucleation	23	0.0036	2	0.0048	0.2587455	E
<input type="radio"/>	GO:0043044	10	ATP-dependent chromatin remodeling	23	0.0036	2	0.0048	0.2587455	E
<input type="radio"/>	GO:0007006	5,6	mitochondrial membrane organization and biogenesis	24	0.0037	2	0.0048	0.2642460	E
<input type="radio"/>	GO:0043631	8	RNA polyadenylation	24	0.0037	2	0.0048	0.2642460	E
<input type="radio"/>	GO:0006298	7,9,6	mismatch repair	25	0.0039	2	0.0048	0.2688829	E
<input type="radio"/>	GO:0045005	8,6	maintenance of fidelity during DNA-dependent DNA replication	25	0.0039	2	0.0048	0.2688829	E
<input type="radio"/>	GO:0006609	10,11,8,9,7	mRNA-binding (hnRNP) protein import into nucleus	25	0.0039	2	0.0048	0.2688829	E
<input type="radio"/>	GO:0006506	10,9,8,7,11	GPI anchor biosynthetic process	26	0.0040	2	0.0048	0.2726863	E
<input type="radio"/>	GO:0051029	5,7,6,8	rRNA transport	26	0.0040	2	0.0048	0.2726863	E
<input type="radio"/>	GO:0006407	11,9,6,8,10,7	rRNA export from nucleus	26	0.0040	2	0.0048	0.2726863	E
<input type="radio"/>	GO:0007093	8,10,9,7	mitotic cell cycle checkpoint	27	0.0042	2	0.0048	0.2756897	E
<input type="radio"/>	GO:0006505	9,10	GPI anchor metabolic process	27	0.0042	2	0.0048	0.2756897	E
<input type="radio"/>	GO:0000080	7,8,6	G1 phase of mitotic cell cycle	27	0.0042	2	0.0048	0.2756897	E
<input type="radio"/>	GO:0051318	6,7,5	G1 phase	27	0.0042	2	0.0048	0.2756897	E
<input type="radio"/>	GO:0009084	7,8	glutamine family amino acid biosynthetic process	27	0.0042	2	0.0048	0.2756897	E
<input type="radio"/>	GO:0006591	7,8,5,4	ornithine metabolic process	6	0.0009	1	0.0024	0.2758543	E
<input type="radio"/>	GO:0031383	5,7,10,9,8,6,11	regulation of mating projection biogenesis	6	0.0009	1	0.0024	0.2758543	E
<input type="radio"/>	GO:0009396	6,7,8	folic acid and derivative biosynthetic process	6	0.0009	1	0.0024	0.2758543	E
<input type="radio"/>	GO:0006771	7	riboflavin metabolic process	6	0.0009	1	0.0024	0.2758543	E
<input type="radio"/>	GO:0031344	4,6,8,7,5,9	regulation of cell projection organization and biogenesis	6	0.0009	1	0.0024	0.2758543	E
<input type="radio"/>	GO:0006013	7,8	mannose metabolic process	6	0.0009	1	0.0024	0.2758543	E
<input type="radio"/>	GO:0009231	7,8	riboflavin biosynthetic process	6	0.0009	1	0.0024	0.2758543	E
<input type="radio"/>	GO:0019795	7,8	nonprotein amino acid biosynthetic process	6	0.0009	1	0.0024	0.2758543	E
<input type="radio"/>	GO:0006409	11,9,6,8,10,7	tRNA export from nucleus	29	0.0045	2	0.0048	0.2794425	E
<input type="radio"/>	GO:0051656	6,3,5,4	establishment of organelle localization	29	0.0045	2	0.0048	0.2794425	E
<input type="radio"/>	GO:0046364	6,7	monosaccharide biosynthetic process	30	0.0046	2	0.0048	0.2802691	E
<input type="radio"/>	GO:0006893	9,7,6,8	Golgi to plasma membrane transport	30	0.0046	2	0.0048	0.2802691	E
<input type="radio"/>	GO:0051031	5,7,6,8	tRNA transport	30	0.0046	2	0.0048	0.2802691	E
<input type="radio"/>	GO:0019319	7,8	hexose biosynthetic process	30	0.0046	2	0.0048	0.2802691	E
<input type="radio"/>	GO:0007062	7,4	sister chromatid cohesion	31	0.0048	2	0.0048	0.2804490	E
<input type="radio"/>	GO:0000002	6	mitochondrial genome maintenance	31	0.0048	2	0.0048	0.2804490	E
<input type="radio"/>	GO:0006078	9,8,10	1,6-beta-glucan biosynthetic process	7	0.0011	1	0.0024	0.3012867	E
<input type="radio"/>	GO:0051348	6	negative regulation of transferase activity	7	0.0011	1	0.0024	0.3012867	E
<input type="radio"/>	GO:0000376	9	RNA splicing, via transesterification reactions with guanosine as nucleophile	7	0.0011	1	0.0024	0.3012867	E
<input type="radio"/>	GO:0000727	9,8	double-strand break repair via break-induced replication	7	0.0011	1	0.0024	0.3012867	E
<input type="radio"/>	GO:0006621	7,6,5,4	protein retention in ER	7	0.0011	1	0.0024	0.3012867	E
<input type="radio"/>	GO:0009102	6,7,8	biotin biosynthetic process	7	0.0011	1	0.0024	0.3012867	E
<input type="radio"/>	GO:0015936	7	coenzyme A metabolic process	7	0.0011	1	0.0024	0.3012867	E
<input type="radio"/>	GO:0006595	6,7	polyamine metabolic process	7	0.0011	1	0.0024	0.3012867	E
<input type="radio"/>	GO:0009225	5	nucleotide-sugar metabolic process	7	0.0011	1	0.0024	0.3012867	E
<input type="radio"/>	GO:0000372	10	Group I intron splicing	7	0.0011	1	0.0024	0.3012867	E
<input type="radio"/>	GO:0006551	7,8	leucine metabolic process	7	0.0011	1	0.0024	0.3012867	E
<input type="radio"/>	GO:0006829	8,9	zinc ion transport	7	0.0011	1	0.0024	0.3012867	E

<input type="radio"/>	GO:0045896	9,7,5,8,6,4	regulation of transcription, mitotic	7	0.0011	1	0.0024	0.3012867	E
<input type="radio"/>	GO:0045835	8,10,9,7	negative regulation of meiosis	7	0.0011	1	0.0024	0.3012867	E
<input type="radio"/>	GO:0006768	5,7,6	biotin metabolic process	7	0.0011	1	0.0024	0.3012867	E
<input type="radio"/>	GO:0006469	7,8	negative regulation of protein kinase activity	7	0.0011	1	0.0024	0.3012867	E
<input type="radio"/>	GO:0007068	10,8,6,9,7,5	negative regulation of transcription, mitotic	7	0.0011	1	0.0024	0.3012867	E
<input type="radio"/>	GO:0031382	9,8,10,7	mating projection biogenesis	7	0.0011	1	0.0024	0.3012867	E
<input type="radio"/>	GO:0006465	9,5	signal peptide processing	7	0.0011	1	0.0024	0.3012867	E
<input type="radio"/>	GO:0015937	7,8	coenzyme A biosynthetic process	7	0.0011	1	0.0024	0.3012867	E
<input type="radio"/>	GO:0009435	8,7,10,9	NAD biosynthetic process	7	0.0011	1	0.0024	0.3012867	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	1	0.0024	0.3012867	E
<input type="radio"/>	GO:0043248	8,7	proteasome assembly	7	0.0011	1	0.0024	0.3012867	E
<input type="radio"/>	GO:0007323	9	peptide pheromone maturation	8	0.0012	1	0.0024	0.3223447	E
<input type="radio"/>	GO:0048858	6,7	cell projection morphogenesis	8	0.0012	1	0.0024	0.3223447	E
<input type="radio"/>	GO:0032990	5,6	cell part morphogenesis	8	0.0012	1	0.0024	0.3223447	E
<input type="radio"/>	GO:0007119	7,6,5	budding cell isotropic bud growth	8	0.0012	1	0.0024	0.3223447	E
<input type="radio"/>	GO:0006855	5,6	multidrug transport	8	0.0012	1	0.0024	0.3223447	E
<input type="radio"/>	GO:0016973	12,10,7,9,11,8	poly(A)+ mRNA export from nucleus	8	0.0012	1	0.0024	0.3223447	E
<input type="radio"/>	GO:0042727	7	riboflavin and derivative biosynthetic process	8	0.0012	1	0.0024	0.3223447	E
<input type="radio"/>	GO:0006672	8,9	ceramide metabolic process	8	0.0012	1	0.0024	0.3223447	E
<input type="radio"/>	GO:0030031	8,7,9	cell projection biogenesis	8	0.0012	1	0.0024	0.3223447	E
<input type="radio"/>	GO:0000335	10,9,6	negative regulation of DNA transposition	8	0.0012	1	0.0024	0.3223447	E
<input type="radio"/>	GO:0042816	6	vitamin B6 metabolic process	8	0.0012	1	0.0024	0.3223447	E
<input type="radio"/>	GO:0006077	8,9	1,6-beta-glucan metabolic process	8	0.0012	1	0.0024	0.3223447	E
<input type="radio"/>	GO:0042726	6	riboflavin and derivative metabolic process	8	0.0012	1	0.0024	0.3223447	E
<input type="radio"/>	GO:0030030	7,6,8	cell projection organization and biogenesis	8	0.0012	1	0.0024	0.3223447	E
<input type="radio"/>	GO:0006356	9,8	regulation of transcription from RNA polymerase I promoter	8	0.0012	1	0.0024	0.3223447	E
<input type="radio"/>	GO:0008614	7	pyridoxine metabolic process	8	0.0012	1	0.0024	0.3223447	E
<input type="radio"/>	GO:0022610	2	biological adhesion	9	0.0014	1	0.0024	0.3394824	E
<input type="radio"/>	GO:0046470	8,9	phosphatidylcholine metabolic process	9	0.0014	1	0.0024	0.3394824	E
<input type="radio"/>	GO:0015802	6,7,8	basic amino acid transport	9	0.0014	1	0.0024	0.3394824	E
<input type="radio"/>	GO:0000393	7,6,9,11	spliceosomal conformational changes to generate catalytic conformation	9	0.0014	1	0.0024	0.3394824	E
<input type="radio"/>	GO:0006283	8,7	transcription-coupled nucleotide-excision repair	9	0.0014	1	0.0024	0.3394824	E
<input type="radio"/>	GO:0042138	11,9,8,5,6,10,7,4	meiotic DNA double-strand break formation	9	0.0014	1	0.0024	0.3394824	E
<input type="radio"/>	GO:0019933	8	cAMP-mediated signaling	9	0.0014	1	0.0024	0.3394824	E
<input type="radio"/>	GO:0019935	7	cyclic-nucleotide-mediated signaling	9	0.0014	1	0.0024	0.3394824	E
<input type="radio"/>	GO:0000128	3	flocculation	9	0.0014	1	0.0024	0.3394824	E
<input type="radio"/>	GO:0007155	3	cell adhesion	9	0.0014	1	0.0024	0.3394824	E
<input type="radio"/>	GO:0000290	11,8,9,10	deadenylation-dependent decapping	9	0.0014	1	0.0024	0.3394824	E
<input type="radio"/>	GO:0030491	7,9,10,6,8	heteroduplex formation	9	0.0014	1	0.0024	0.3394824	E
<input type="radio"/>	GO:0006528	7,8	asparagine metabolic process	9	0.0014	1	0.0024	0.3394824	E
<input type="radio"/>	GO:0019794	6,7	nonprotein amino acid metabolic process	9	0.0014	1	0.0024	0.3394824	E
<input type="radio"/>	GO:0045912	6,5	negative regulation of carbohydrate metabolic process	9	0.0014	1	0.0024	0.3394824	E
<input type="radio"/>	GO:0045721	7,9,8,10,6,11	negative regulation of gluconeogenesis	9	0.0014	1	0.0024	0.3394824	E

<input type="radio"/>	GO:0000501	4	flocculation via cell wall protein-carbohydrate interaction	9	0.0014	1	0.0024	0.3394824	E
<input type="radio"/>	GO:0051180	4,5	vitamin transport	9	0.0014	1	0.0024	0.3394824	E
<input type="radio"/>	GO:0009373	9,8,5	regulation of transcription by pheromones	10	0.0015	1	0.0024	0.3531135	E
<input type="radio"/>	GO:0046519	7,8	sphingoid metabolic process	10	0.0015	1	0.0024	0.3531135	E
<input type="radio"/>	GO:0000337	9,8,5	regulation of DNA transposition	10	0.0015	1	0.0024	0.3531135	E
<input type="radio"/>	GO:0006791	5	sulfur utilization	10	0.0015	1	0.0024	0.3531135	E
<input type="radio"/>	GO:0008298	5	intracellular mRNA localization	10	0.0015	1	0.0024	0.3531135	E
<input type="radio"/>	GO:0000103	6	sulfate assimilation	10	0.0015	1	0.0024	0.3531135	E
<input type="radio"/>	GO:0006313	7,4	transposition, DNA-mediated	10	0.0015	1	0.0024	0.3531135	E
<input type="radio"/>	GO:0019363	7,6,8	pyridine nucleotide biosynthetic process	10	0.0015	1	0.0024	0.3531135	E
<input type="radio"/>	GO:0015718	6,7	monocarboxylic acid transport	10	0.0015	1	0.0024	0.3531135	E
<input type="radio"/>	GO:0006616	9,12,11,7,10,8	SRP-dependent cotranslational protein targeting to membrane, translocation	10	0.0015	1	0.0024	0.3531135	E
<input type="radio"/>	GO:0006012	7,8	galactose metabolic process	10	0.0015	1	0.0024	0.3531135	E
<input type="radio"/>	GO:0055069	9	zinc ion homeostasis	10	0.0015	1	0.0024	0.3531135	E
<input type="radio"/>	GO:0006882	10,8	cellular zinc ion homeostasis	10	0.0015	1	0.0024	0.3531135	E
<input type="radio"/>	GO:0030846	10,9	transcription termination from Pol II promoter, RNA polymerase(A) coupled	10	0.0015	1	0.0024	0.3531135	E
<input type="radio"/>	GO:0046019	10,9,6	regulation of transcription from RNA polymerase II promoter by pheromones	10	0.0015	1	0.0024	0.3531135	E
<input type="radio"/>	GO:0006526	8,9,6,5	arginine biosynthetic process	10	0.0015	1	0.0024	0.3531135	E
<input type="radio"/>	GO:0000161	7,8,6	MAPKKK cascade during osmolarity sensing	11	0.0017	1	0.0024	0.3636151	E
<input type="radio"/>	GO:0065002	8,6,7	intracellular protein transport across a membrane	11	0.0017	1	0.0024	0.3636151	E
<input type="radio"/>	GO:0031163	5	metallo-sulfur cluster assembly	11	0.0017	1	0.0024	0.3636151	E
<input type="radio"/>	GO:0006972	5	hyperosmotic response	11	0.0017	1	0.0024	0.3636151	E
<input type="radio"/>	GO:0016226	6	iron-sulfur cluster assembly	11	0.0017	1	0.0024	0.3636151	E
<input type="radio"/>	GO:0051049	5,4	regulation of transport	11	0.0017	1	0.0024	0.3636151	E
<input type="radio"/>	GO:0006518	4	peptide metabolic process	11	0.0017	1	0.0024	0.3636151	E
<input type="radio"/>	GO:0006384	8,9,7	transcription initiation from RNA polymerase III promoter	11	0.0017	1	0.0024	0.3636151	E
<input type="radio"/>	GO:0043086	5	negative regulation of enzyme activity	11	0.0017	1	0.0024	0.3636151	E
<input type="radio"/>	GO:0051274	8,9	beta-glucan biosynthetic process	11	0.0017	1	0.0024	0.3636151	E
<input type="radio"/>	GO:0000055	11,12,7,9,10	ribosomal large subunit export from nucleus	11	0.0017	1	0.0024	0.3636151	E
<input type="radio"/>	GO:0051273	7,8	beta-glucan metabolic process	12	0.0019	1	0.0024	0.3713307	E
<input type="radio"/>	GO:0006284	7,6	base-excision repair	12	0.0019	1	0.0024	0.3713307	E
<input type="radio"/>	GO:0045910	9,8	negative regulation of DNA recombination	12	0.0019	1	0.0024	0.3713307	E
<input type="radio"/>	GO:0015914	5,6	phospholipid transport	12	0.0019	1	0.0024	0.3713307	E
<input type="radio"/>	GO:0000302	5	response to reactive oxygen species	12	0.0019	1	0.0024	0.3713307	E
<input type="radio"/>	GO:0000272	6	polysaccharide catabolic process	12	0.0019	1	0.0024	0.3713307	E
<input type="radio"/>	GO:0007007	6,7	inner mitochondrial membrane organization and biogenesis	12	0.0019	1	0.0024	0.3713307	E
<input type="radio"/>	GO:0044247	7,6	cellular polysaccharide catabolic process	12	0.0019	1	0.0024	0.3713307	E
<input type="radio"/>	GO:0033014	6	tetrapyrrole biosynthetic process	13	0.0020	1	0.0024	0.3765727	E
<input type="radio"/>	GO:0006783	7,6,8	heme biosynthetic process	13	0.0020	1	0.0024	0.3765727	E
<input type="radio"/>	GO:0031929	6	TOR signaling pathway	13	0.0020	1	0.0024	0.3765727	E
<input type="radio"/>	GO:0006633	7,6,8,5	fatty acid biosynthetic process	13	0.0020	1	0.0024	0.3765727	E
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<input type="radio"/>	GO:0006537	8,9	glutamate biosynthetic process	13	0.0020	1	0.0024	0.3765727	E

<input type="radio"/>	GO:0006779	6,7	porphyrin biosynthetic process	13	0.0020	1	0.0024	0.3765727	E
<input type="radio"/>	GO:0006450	8,7,6	regulation of translational fidelity	13	0.0020	1	0.0024	0.3765727	E
<input type="radio"/>	GO:0006334	6,7,10	nucleosome assembly	13	0.0020	1	0.0024	0.3765727	E
<input type="radio"/>	GO:0006111	8,7,9,10,6	regulation of gluconeogenesis	13	0.0020	1	0.0024	0.3765727	E
<input type="radio"/>	GO:0042168	6,7,5	heme metabolic process	14	0.0022	1	0.0024	0.3796249	E
<input type="radio"/>	GO:0045990	9,7,8,5	regulation of transcription by carbon catabolites	14	0.0022	1	0.0024	0.3796249	E
<input type="radio"/>	GO:0006778	5,6	porphyrin metabolic process	14	0.0022	1	0.0024	0.3796249	E
<input type="radio"/>	GO:0033013	5	tetrapyrrole metabolic process	14	0.0022	1	0.0024	0.3796249	E
<input type="radio"/>	GO:0007018	8,7,6	microtubule-based movement	15	0.0023	1	0.0024	0.3807453	E
<input type="radio"/>	GO:0000737	6,7	DNA catabolic process, endonucleolytic	15	0.0023	1	0.0024	0.3807453	E
<input type="radio"/>	GO:0030473	8,9,6,7	nuclear migration, microtubule-mediated	15	0.0023	1	0.0024	0.3807453	E
<input type="radio"/>	GO:0008150	1	biological process	6476	1.0000	414	1.0000	1.0000000	D
<input type="radio"/>	GO:0016050	5	vesicle organization and biogenesis	16	0.0025	1	0.0024	0.3801678	D
<input type="radio"/>	GO:0006536	7,8	glutamate metabolic process	16	0.0025	1	0.0024	0.3801678	D
<input type="radio"/>	GO:0030705	7,5,6	cytoskeleton-dependent intracellular transport	17	0.0026	1	0.0024	0.3781044	D
<input type="radio"/>	GO:0006030	8,6,7,9	chitin metabolic process	17	0.0026	1	0.0024	0.3781044	D
<input type="radio"/>	GO:0016053	5	organic acid biosynthetic process	17	0.0026	1	0.0024	0.3781044	D
<input type="radio"/>	GO:0045003	9,8	double-strand break repair via synthesis-dependent strand annealing	17	0.0026	1	0.0024	0.3781044	D
<input type="radio"/>	GO:0046394	6	carboxylic acid biosynthetic process	17	0.0026	1	0.0024	0.3781044	D
<input type="radio"/>	GO:0016571	11,9,10,8	histone methylation	18	0.0028	1	0.0024	0.3747470	D
<input type="radio"/>	GO:0000084	8,7,6	S phase of mitotic cell cycle	18	0.0028	1	0.0024	0.3747470	D
<input type="radio"/>	GO:0007584	6,4	response to nutrient	18	0.0028	1	0.0024	0.3747470	D
<input type="radio"/>	GO:0000753	7,8,6	cellular morphogenesis during conjugation with cellular fusion	18	0.0028	1	0.0024	0.3747470	D
<input type="radio"/>	GO:0009267	7,6,5	cellular response to starvation	19	0.0029	1	0.0024	0.3702691	D
<input type="radio"/>	GO:0009228	7,8	thiamin biosynthetic process	19	0.0029	1	0.0024	0.3702691	D
<input type="radio"/>	GO:0031669	6,5	cellular response to nutrient levels	19	0.0029	1	0.0024	0.3702691	D
<input type="radio"/>	GO:0042594	6,4	response to starvation	19	0.0029	1	0.0024	0.3702691	D
<input type="radio"/>	GO:0006875	9,7	cellular metal ion homeostasis	19	0.0029	1	0.0024	0.3702691	D
<input type="radio"/>	GO:0000245	7,6,9,11	spliceosome assembly	19	0.0029	1	0.0024	0.3702691	D
<input type="radio"/>	GO:0006040	5,6	amino sugar metabolic process	19	0.0029	1	0.0024	0.3702691	D
<input type="radio"/>	GO:0043255	7,6,5	regulation of carbohydrate biosynthetic process	19	0.0029	1	0.0024	0.3702691	D
<input type="radio"/>	GO:0055065	8	metal ion homeostasis	19	0.0029	1	0.0024	0.3702691	D
<input type="radio"/>	GO:0006041	6,7	glucosamine metabolic process	19	0.0029	1	0.0024	0.3702691	D
<input type="radio"/>	GO:0006044	7,8	N-acetylglucosamine metabolic process	19	0.0029	1	0.0024	0.3702691	D
<input type="radio"/>	GO:0000722	9,8	telomere maintenance via recombination	19	0.0029	1	0.0024	0.3702691	D
<input type="radio"/>	GO:0031668	5,4	cellular response to extracellular stimulus	19	0.0029	1	0.0024	0.3702691	D
<input type="radio"/>	GO:0042724	7	thiamin and derivative biosynthetic process	20	0.0031	1	0.0024	0.3648275	D
<input type="radio"/>	GO:0006772	7	thiamin metabolic process	20	0.0031	1	0.0024	0.3648275	D
<input type="radio"/>	GO:0000767	6,7	cellular morphogenesis during conjugation	20	0.0031	1	0.0024	0.3648275	D
<input type="radio"/>	GO:0051053	8,7	negative regulation of DNA metabolic process	20	0.0031	1	0.0024	0.3648275	D
<input type="radio"/>	GO:0006826	7,8,9	iron ion transport	20	0.0031	1	0.0024	0.3648275	D
<input type="radio"/>	GO:0045324	8,6,7	late endosome to vacuole transport	21	0.0032	1	0.0024	0.3585634	D
<input type="radio"/>	GO:0051716	3	cellular response to stimulus	21	0.0032	1	0.0024	0.3585634	D
<input type="radio"/>	GO:0033554	4	cellular response to stress	21	0.0032	1	0.0024	0.3585634	D

<input type="radio"/>	GO:0019674	9,8	NAD metabolic process	21	0.0032	1	0.0024	0.3585634	D
<input type="radio"/>	GO:0006891	8,6,5,7	intra-Golgi vesicle-mediated transport	21	0.0032	1	0.0024	0.3585634	D
<input type="radio"/>	GO:0042723	6	thiamin and derivative metabolic process	22	0.0034	1	0.0024	0.3516040	D
<input type="radio"/>	GO:0006311	10,8,7,5,9,6,4	meiotic gene conversion	22	0.0034	1	0.0024	0.3516040	D
<input type="radio"/>	GO:0006408	11,9,6,8,10,7	snRNA export from nucleus	23	0.0036	1	0.0024	0.3440637	D
<input type="radio"/>	GO:0006479	9,7	protein amino acid methylation	23	0.0036	1	0.0024	0.3440637	D
<input type="radio"/>	GO:0006610	10,11,8,9,7	ribosomal protein import into nucleus	23	0.0036	1	0.0024	0.3440637	D
<input type="radio"/>	GO:0006608	10,11,8,9,7	snRNP protein import into nucleus	23	0.0036	1	0.0024	0.3440637	D
<input type="radio"/>	GO:0006607	10,11,8,9,7	NLS-bearing substrate import into nucleus	23	0.0036	1	0.0024	0.3440637	D
<input type="radio"/>	GO:0051030	5,7,6,8	snRNA transport	23	0.0036	1	0.0024	0.3440637	D
<input type="radio"/>	GO:0008213	8	protein amino acid alkylation	23	0.0036	1	0.0024	0.3440637	D
<input type="radio"/>	GO:0007534	6,8,7	gene conversion at mating-type locus	23	0.0036	1	0.0024	0.3440637	D
<input type="radio"/>	GO:0006096	9,10	glycolysis	24	0.0037	1	0.0024	0.3360451	D
<input type="radio"/>	GO:0006890	8,6,5,7	retrograde vesicle-mediated transport, Golgi to ER	24	0.0037	1	0.0024	0.3360451	D
<input type="radio"/>	GO:0016575	11,9	histone deacetylation	24	0.0037	1	0.0024	0.3360451	D
<input type="radio"/>	GO:0007035	13,10,6,11	vacuolar acidification	24	0.0037	1	0.0024	0.3360451	D
<input type="radio"/>	GO:0045851	8	pH reduction	24	0.0037	1	0.0024	0.3360451	D
<input type="radio"/>	GO:0051278	8,7	chitin- and beta-glucan-containing cell wall polysaccharide biosynthetic process	24	0.0037	1	0.0024	0.3360451	D
<input type="radio"/>	GO:0051452	12,9,10	cellular pH reduction	24	0.0037	1	0.0024	0.3360451	D
<input type="radio"/>	GO:0006896	9,8,7,6	Golgi to vacuole transport	24	0.0037	1	0.0024	0.3360451	D
<input type="radio"/>	GO:0051453	11,8,9	regulation of cellular pH	25	0.0039	1	0.0024	0.3276400	D
<input type="radio"/>	GO:0009250	7,8	glucan biosynthetic process	25	0.0039	1	0.0024	0.3276400	D
<input type="radio"/>	GO:0000724	8,7	double-strand break repair via homologous recombination	25	0.0039	1	0.0024	0.3276400	D
<input type="radio"/>	GO:0030641	10,8	cellular hydrogen ion homeostasis	25	0.0039	1	0.0024	0.3276400	D
<input type="radio"/>	GO:0000001	8,7,6	mitochondrion inheritance	26	0.0040	1	0.0024	0.3189307	D
<input type="radio"/>	GO:0006476	8	protein amino acid deacetylation	26	0.0040	1	0.0024	0.3189307	D
<input type="radio"/>	GO:0048311	7,6	mitochondrion distribution	26	0.0040	1	0.0024	0.3189307	D
<input type="radio"/>	GO:0051646	6,5	mitochondrion localization	27	0.0042	1	0.0024	0.3099904	D
<input type="radio"/>	GO:0009142	6,7	nucleoside triphosphate biosynthetic process	27	0.0042	1	0.0024	0.3099904	D
<input type="radio"/>	GO:0006906	6,5	vesicle fusion	28	0.0043	1	0.0024	0.3008842	D
<input type="radio"/>	GO:0018193	7	peptidyl-amino acid modification	28	0.0043	1	0.0024	0.3008842	D
<input type="radio"/>	GO:0006094	8,9	gluconeogenesis	28	0.0043	1	0.0024	0.3008842	D
<input type="radio"/>	GO:0009636	4	response to toxin	28	0.0043	1	0.0024	0.3008842	D
<input type="radio"/>	GO:0032507	6,5,4	maintenance of cellular protein localization	29	0.0045	1	0.0024	0.2916699	D
<input type="radio"/>	GO:0006109	5,4	regulation of carbohydrate metabolic process	29	0.0045	1	0.0024	0.2916699	D
<input type="radio"/>	GO:0000725	7,6	recombinational repair	29	0.0045	1	0.0024	0.2916699	D
<input type="radio"/>	GO:0051651	5,4,3	maintenance of cellular localization	29	0.0045	1	0.0024	0.2916699	D
<input type="radio"/>	GO:0006885	7	regulation of pH	29	0.0045	1	0.0024	0.2916699	D
<input type="radio"/>	GO:0009063	6,7	amino acid catabolic process	29	0.0045	1	0.0024	0.2916699	D
<input type="radio"/>	GO:0006999	6	nuclear pore organization and biogenesis	29	0.0045	1	0.0024	0.2916699	D
<input type="radio"/>	GO:0007533	5,7,6	mating type switching	29	0.0045	1	0.0024	0.2916699	D
<input type="radio"/>	GO:0045185	5,4,3	maintenance of protein localization	30	0.0046	1	0.0024	0.2823986	D
<input type="radio"/>	GO:0051128	5,4	regulation of cellular component organization and biogenesis	30	0.0046	1	0.0024	0.2823986	D
<input type="radio"/>	GO:0006118	4	electron transport	33	0.0051	2	0.0048	0.2790301	D

<input type="radio"/>	GO:0055067	8	monovalent inorganic cation homeostasis	34	0.0053	2	0.0048	0.2775117	D
<input type="radio"/>	GO:0030004	9,7	cellular monovalent inorganic cation homeostasis	34	0.0053	2	0.0048	0.2775117	D
<input type="radio"/>	GO:0046165	5	alcohol biosynthetic process	35	0.0054	2	0.0048	0.2755065	D
<input type="radio"/>	GO:0030433	9,11,10,12	ER-associated protein catabolic process	35	0.0054	2	0.0048	0.2755065	D
<input type="radio"/>	GO:0009991	4	response to extracellular stimulus	37	0.0057	2	0.0048	0.2701895	D
<input type="radio"/>	GO:0009605	3	response to external stimulus	37	0.0057	2	0.0048	0.2701895	D
<input type="radio"/>	GO:0031667	5	response to nutrient levels	37	0.0057	2	0.0048	0.2701895	D
<input type="radio"/>	GO:0016485	8	protein processing	38	0.0059	2	0.0048	0.2669515	D
<input type="radio"/>	GO:0006515	8,9	misfolded or incompletely synthesized protein catabolic process	38	0.0059	2	0.0048	0.2669515	D
<input type="radio"/>	GO:0043039	7,8	tRNA aminoacylation	32	0.0049	1	0.0024	0.2638594	D
<input type="radio"/>	GO:0009310	5,6	amine catabolic process	32	0.0049	1	0.0024	0.2638594	D
<input type="radio"/>	GO:0019932	6	second-messenger-mediated signaling	32	0.0049	1	0.0024	0.2638594	D
<input type="radio"/>	GO:0006418	8,7,9,6	tRNA aminoacylation for protein translation	32	0.0049	1	0.0024	0.2638594	D
<input type="radio"/>	GO:0043038	6,7	amino acid activation	32	0.0049	1	0.0024	0.2638594	D
<input type="radio"/>	GO:0044270	5,4	nitrogen compound catabolic process	32	0.0049	1	0.0024	0.2638594	D
<input type="radio"/>	GO:0001302	5	replicative cell aging	39	0.0060	2	0.0048	0.2633743	D
<input type="radio"/>	GO:0016573	11,9	histone acetylation	40	0.0062	2	0.0048	0.2594916	D
<input type="radio"/>	GO:0009272	7	chitin- and beta-glucan-containing cell wall biogenesis	33	0.0051	1	0.0024	0.2546657	D
<input type="radio"/>	GO:0051235	3,2	maintenance of localization	33	0.0051	1	0.0024	0.2546657	D
<input type="radio"/>	GO:0006270	8,6	DNA replication initiation	33	0.0051	1	0.0024	0.2546657	D
<input type="radio"/>	GO:0042546	6	cell wall biogenesis	33	0.0051	1	0.0024	0.2546657	D
<input type="radio"/>	GO:0006007	8,9	glucose catabolic process	34	0.0053	1	0.0024	0.2455639	D
<input type="radio"/>	GO:0015674	6,7	di-, tri-valent inorganic cation transport	34	0.0053	1	0.0024	0.2455639	D
<input type="radio"/>	GO:0007530	4,5	sex determination	35	0.0054	1	0.0024	0.2365801	D
<input type="radio"/>	GO:0007531	4,6,5	mating type determination	35	0.0054	1	0.0024	0.2365801	D
<input type="radio"/>	GO:0003006	3,4	reproductive developmental process	35	0.0054	1	0.0024	0.2365801	D
<input type="radio"/>	GO:0006914	3	autophagy	45	0.0069	2	0.0048	0.2365715	D
<input type="radio"/>	GO:0006312	7	mitotic recombination	45	0.0069	2	0.0048	0.2365715	D
<input type="radio"/>	GO:0007051	8	spindle organization and biogenesis	47	0.0073	3	0.0072	0.2323680	D
<input type="radio"/>	GO:0006626	9,8,7,6	protein targeting to mitochondrion	52	0.0080	3	0.0072	0.2275879	D
<input type="radio"/>	GO:0048468	3,5	cell development	52	0.0080	3	0.0072	0.2275879	D
<input type="radio"/>	GO:0000075	7,6	cell cycle checkpoint	53	0.0082	3	0.0072	0.2258087	D
<input type="radio"/>	GO:0006473	8	protein amino acid acetylation	48	0.0074	2	0.0048	0.2209836	D
<input type="radio"/>	GO:0006997	5	nuclear organization and biogenesis	57	0.0088	3	0.0072	0.2164778	D
<input type="radio"/>	GO:0007569	4	cell aging	49	0.0076	2	0.0048	0.2156206	D
<input type="radio"/>	GO:0007568	3	aging	49	0.0076	2	0.0048	0.2156206	D
<input type="radio"/>	GO:0055072	9	iron ion homeostasis	38	0.0059	1	0.0024	0.2105425	D
<input type="radio"/>	GO:0006879	10,8	cellular iron ion homeostasis	38	0.0059	1	0.0024	0.2105425	D
<input type="radio"/>	GO:0006090	7	pyruvate metabolic process	38	0.0059	1	0.0024	0.2105425	D
<input type="radio"/>	GO:0008643	4,5	carbohydrate transport	38	0.0059	1	0.0024	0.2105425	D
<input type="radio"/>	GO:0001510	7	RNA methylation	60	0.0093	3	0.0072	0.2075835	D
<input type="radio"/>	GO:0007264	6	small GTPase mediated signal transduction	61	0.0094	3	0.0072	0.2043353	D
<input type="radio"/>	GO:0019320	7,8	hexose catabolic process	39	0.0060	1	0.0024	0.2022213	D
<input type="radio"/>	GO:0005976	5	polysaccharide metabolic process	65	0.0100	4	0.0097	0.2019958	D

<input type="checkbox"/>	GO:0044264	5,6	cellular polysaccharide metabolic process	65	0.0100	4	0.0097	0.2019958	D
<input type="checkbox"/>	GO:0051028	5,7,6,8	mRNA transport	66	0.0102	4	0.0097	0.2012762	D
<input type="checkbox"/>	GO:0006406	11,9,6,8,10,7	mRNA export from nucleus	66	0.0102	4	0.0097	0.2012762	D
<input type="checkbox"/>	GO:0006892	8,6,5,7	post-Golgi vesicle-mediated transport	69	0.0107	4	0.0097	0.1979963	D
<input type="checkbox"/>	GO:0048308	5	organelle inheritance	40	0.0062	1	0.0024	0.1940992	D
<input type="checkbox"/>	GO:0006006	7,8	glucose metabolic process	65	0.0100	3	0.0072	0.1902797	D
<input type="checkbox"/>	GO:0000271	6,7	polysaccharide biosynthetic process	41	0.0063	1	0.0024	0.1861849	D
<input type="checkbox"/>	GO:0045944	10,9	positive regulation of transcription from RNA polymerase II promoter	76	0.0117	4	0.0097	0.1849131	D
<input type="checkbox"/>	GO:0000226	7	microtubule cytoskeleton organization and biogenesis	81	0.0125	5	0.0121	0.1816312	D
<input type="checkbox"/>	GO:0007114	5,4	cell budding	85	0.0131	5	0.0121	0.1784987	D
<input type="checkbox"/>	GO:0019954	3	asexual reproduction	85	0.0131	5	0.0121	0.1784987	D
<input type="checkbox"/>	GO:0019318	6,7	hexose metabolic process	85	0.0131	5	0.0121	0.1784987	D
<input type="checkbox"/>	GO:0006769	8,7	nicotinamide metabolic process	42	0.0065	1	0.0024	0.1784851	D
<input type="checkbox"/>	GO:0051640	5,4	organelle localization	56	0.0086	2	0.0048	0.1775406	D
<input type="checkbox"/>	GO:0006897	6,5	endocytosis	86	0.0133	5	0.0121	0.1773888	D
<input type="checkbox"/>	GO:0016570	10,8	histone modification	91	0.0141	5	0.0121	0.1701499	D
<input type="checkbox"/>	GO:0016569	9	covalent chromatin modification	91	0.0141	5	0.0121	0.1701499	D
<input type="checkbox"/>	GO:0005996	5,6	monosaccharide metabolic process	92	0.0142	5	0.0121	0.1684030	D
<input type="checkbox"/>	GO:0006979	4	response to oxidative stress	71	0.0110	3	0.0072	0.1672812	D
<input type="checkbox"/>	GO:0045893	9,8	positive regulation of transcription, DNA-dependent	95	0.0147	6	0.0145	0.1670753	D
<input type="checkbox"/>	GO:0032259	5	methylation	83	0.0128	4	0.0097	0.1665849	D
<input type="checkbox"/>	GO:0043414	6	biopolymer methylation	83	0.0128	4	0.0097	0.1665849	D
<input type="checkbox"/>	GO:0006730	4	one-carbon compound metabolic process	97	0.0150	6	0.0145	0.1664463	D
<input type="checkbox"/>	GO:0007017	6	microtubule-based process	101	0.0156	6	0.0145	0.1638644	D
<input type="checkbox"/>	GO:0045941	8,7	positive regulation of transcription	101	0.0156	6	0.0145	0.1638644	D
<input type="checkbox"/>	GO:0006289	7,6	nucleotide-excision repair	44	0.0068	1	0.0024	0.1637480	D
<input type="checkbox"/>	GO:0046365	6,7	monosaccharide catabolic process	44	0.0068	1	0.0024	0.1637480	D
<input type="checkbox"/>	GO:0031505	6	chitin- and beta-glucan-containing cell wall organization and biogenesis	44	0.0068	1	0.0024	0.1637480	D
<input type="checkbox"/>	GO:0009060	6	aerobic respiration	84	0.0130	4	0.0097	0.1636964	D
<input type="checkbox"/>	GO:0006812	5,6	cation transport	97	0.0150	5	0.0121	0.1584752	D
<input type="checkbox"/>	GO:0006644	6,7	phospholipid metabolic process	97	0.0150	5	0.0121	0.1584752	D
<input type="checkbox"/>	GO:0019362	7,6	pyridine nucleotide metabolic process	45	0.0069	1	0.0024	0.1567163	D
<input type="checkbox"/>	GO:0000375	8	RNA splicing, via transesterification reactions	110	0.0170	6	0.0145	0.1526496	D
<input type="checkbox"/>	GO:0007015	8	actin filament organization	61	0.0094	2	0.0048	0.1514105	D
<input type="checkbox"/>	GO:0006073	6,7	glucan metabolic process	46	0.0071	1	0.0024	0.1499108	D
<input type="checkbox"/>	GO:0006468	8,7	protein amino acid phosphorylation	101	0.0156	5	0.0121	0.1494161	D
<input type="checkbox"/>	GO:0045333	5	cellular respiration	89	0.0137	4	0.0097	0.1486876	D
<input type="checkbox"/>	GO:0006767	5	water-soluble vitamin metabolic process	89	0.0137	4	0.0097	0.1486876	D
<input type="checkbox"/>	GO:0006766	4	vitamin metabolic process	89	0.0137	4	0.0097	0.1486876	D
<input type="checkbox"/>	GO:0000398	8,10	nuclear mRNA splicing, via spliceosome	102	0.0158	5	0.0121	0.1470377	D
<input type="checkbox"/>	GO:0000819	7,4	sister chromatid segregation	62	0.0096	2	0.0048	0.1464091	D
<input type="checkbox"/>	GO:0007034	7,5,6	vacuolar transport	114	0.0176	6	0.0145	0.1458225	D
<input type="checkbox"/>	GO:0000377	9	RNA splicing, via transesterification reactions with bulged adenosine as nucleophile	103	0.0159	5	0.0121	0.1446233	D

<input type="radio"/>	GO:0016051	5	carbohydrate biosynthetic process	77	0.0119	3	0.0072	0.1437882	D
<input type="radio"/>	GO:0006631	5,7,6	fatty acid metabolic process	47	0.0073	1	0.0024	0.1433317	D
<input type="radio"/>	GO:0046164	5	alcohol catabolic process	47	0.0073	1	0.0024	0.1433317	D
<input type="radio"/>	GO:0043161	10,9,11	proteasomal ubiquitin-dependent protein catabolic process	63	0.0097	2	0.0048	0.1414966	D
<input type="radio"/>	GO:0000087	7,5,6	M phase of mitotic cell cycle	129	0.0199	7	0.0169	0.1387405	D
<input type="radio"/>	GO:0030005	9,7	cellular di-, tri-valent inorganic cation homeostasis	64	0.0099	2	0.0048	0.1366774	D
<input type="radio"/>	GO:0055066	8	di-, tri-valent inorganic cation homeostasis	64	0.0099	2	0.0048	0.1366774	D
<input type="radio"/>	GO:0048878	5	chemical homeostasis	121	0.0187	6	0.0145	0.1321078	D
<input type="radio"/>	GO:0016197	7,5,6	endosome transport	49	0.0076	1	0.0024	0.1308472	D
<input type="radio"/>	GO:0006397	7	mRNA processing	157	0.0242	9	0.0217	0.1291464	D
<input type="radio"/>	GO:0048193	7,5,6	Golgi vesicle transport	166	0.0256	10	0.0242	0.1280982	D
<input type="radio"/>	GO:0007242	5	intracellular signaling cascade	137	0.0212	7	0.0169	0.1256028	D
<input type="radio"/>	GO:0016044	4	membrane organization and biogenesis	188	0.0290	12	0.0290	0.1199477	D
<input type="radio"/>	GO:0007067	8,6,7,5	mitosis	127	0.0196	6	0.0145	0.1193119	D
<input type="radio"/>	GO:0016071	6	mRNA metabolic process	210	0.0324	13	0.0314	0.1144735	D
<input type="radio"/>	GO:0055082	6,4	cellular chemical homeostasis	115	0.0178	5	0.0121	0.1143095	D
<input type="radio"/>	GO:0006873	7,5	cellular ion homeostasis	115	0.0178	5	0.0121	0.1143095	D
<input type="radio"/>	GO:0000154	7,8	rRNA modification	85	0.0131	3	0.0072	0.1141197	D
<input type="radio"/>	GO:0043623	7,6	cellular protein complex assembly	69	0.0107	2	0.0048	0.1140975	D
<input type="radio"/>	GO:0051186	4	cofactor metabolic process	170	0.0263	9	0.0217	0.1136520	D
<input type="radio"/>	GO:0007010	5	cytoskeleton organization and biogenesis	227	0.0351	14	0.0338	0.1101984	D
<input type="radio"/>	GO:0055080	7	cation homeostasis	102	0.0158	4	0.0097	0.1091439	D
<input type="radio"/>	GO:0030003	8,6	cellular cation homeostasis	102	0.0158	4	0.0097	0.1091439	D
<input type="radio"/>	GO:0006796	5	phosphate metabolic process	212	0.0327	12	0.0290	0.1079351	D
<input type="radio"/>	GO:0006793	4	phosphorus metabolic process	212	0.0327	12	0.0290	0.1079351	D
<input type="radio"/>	GO:0006323	6	DNA packaging	253	0.0391	16	0.0386	0.1044417	D
<input type="radio"/>	GO:0006325	7	establishment and/or maintenance of chromatin architecture	253	0.0391	16	0.0386	0.1044417	D
<input type="radio"/>	GO:0050801	6	ion homeostasis	119	0.0184	5	0.0121	0.1042684	D
<input type="radio"/>	GO:0042592	4	homeostatic process	134	0.0207	6	0.0145	0.1040468	D
<input type="radio"/>	GO:0006732	5	coenzyme metabolic process	136	0.0210	6	0.0145	0.0997255	D
<input type="radio"/>	GO:0030036	7	actin cytoskeleton organization and biogenesis	107	0.0165	4	0.0097	0.0950464	D
<input type="radio"/>	GO:0006733	6	oxidoreduction coenzyme metabolic process	56	0.0086	1	0.0024	0.0939171	D
<input type="radio"/>	GO:0032787	6	monocarboxylic acid metabolic process	126	0.0195	5	0.0121	0.0875149	D
<input type="radio"/>	GO:0019725	5,3	cellular homeostasis	128	0.0198	5	0.0121	0.0829846	D
<input type="radio"/>	GO:0030029	6	actin filament-based process	112	0.0173	4	0.0097	0.0820064	D
<input type="radio"/>	GO:0016192	4,5	vesicle-mediated transport	328	0.0506	18	0.0435	0.0769089	D
<input type="radio"/>	GO:0006950	3	response to stress	488	0.0754	31	0.0749	0.0767180	D
<input type="radio"/>	GO:0016052	5	carbohydrate catabolic process	80	0.0124	2	0.0048	0.0739363	D
<input type="radio"/>	GO:0044275	6	cellular carbohydrate catabolic process	80	0.0124	2	0.0048	0.0739363	D
<input type="radio"/>	GO:0006461	6,5	protein complex assembly	116	0.0179	4	0.0097	0.0724291	D
<input type="radio"/>	GO:0032446	8	protein modification by small protein conjugation	84	0.0130	2	0.0048	0.0624889	D
<input type="radio"/>	GO:0006623	9,8,7,6	protein targeting to vacuole	67	0.0103	1	0.0024	0.0540411	D
<input type="radio"/>	GO:0006512	8	ubiquitin cycle	88	0.0136	2	0.0048	0.0525626	D
<input type="radio"/>	GO:0044262	5	cellular carbohydrate metabolic process	213	0.0329	9	0.0217	0.0515452	D

<input type="checkbox"/>	GO:0009059	4	macromolecule biosynthetic process	886	0.1368	52	0.1256	0.0478860	D
<input type="checkbox"/>	GO:0043687	7	post-translational protein modification	388	0.0599	19	0.0459	0.0416726	D
<input type="checkbox"/>	GO:0043285	5	biopolymer catabolic process	277	0.0428	12	0.0290	0.0377851	D
<input type="checkbox"/>	GO:0016310	6	phosphorylation	155	0.0239	5	0.0121	0.0361452	D
<input type="checkbox"/>	GO:0005975	4	carbohydrate metabolic process	233	0.0360	9	0.0217	0.0307515	D
<input type="checkbox"/>	GO:0006091	3	generation of precursor metabolites and energy	183	0.0283	6	0.0145	0.0264252	D
<input type="checkbox"/>	GO:0015980	4	energy derivation by oxidation of organic compounds	145	0.0224	4	0.0097	0.0257601	D
<input type="checkbox"/>	GO:0044267	5	cellular protein metabolic process	1498	0.2313	86	0.2077	0.0245210	D
<input type="checkbox"/>	GO:0019538	4	protein metabolic process	1547	0.2389	89	0.2150	0.0241527	D
<input type="checkbox"/>	GO:0044260	4	cellular macromolecule metabolic process	1552	0.2397	88	0.2126	0.0197919	D
<input type="checkbox"/>	GO:0006508	6	proteolysis	178	0.0275	5	0.0121	0.0155881	D
<input type="checkbox"/>	GO:0009057	4	macromolecule catabolic process	345	0.0533	13	0.0314	0.0101318	D
<input type="checkbox"/>	GO:0019941	8,7,9	modification-dependent protein catabolic process	148	0.0229	3	0.0072	0.0090923	D
<input type="checkbox"/>	GO:0006511	9,8,10	ubiquitin-dependent protein catabolic process	148	0.0229	3	0.0072	0.0090923	D
<input type="checkbox"/>	GO:0044265	5	cellular macromolecule catabolic process	314	0.0485	11	0.0266	0.0082313	D
<input type="checkbox"/>	GO:0030163	6,5	protein catabolic process	173	0.0267	4	0.0097	0.0080288	D
<input type="checkbox"/>	GO:0051603	7,8	proteolysis involved in cellular protein catabolic process	151	0.0233	3	0.0072	0.0078974	D
<input type="checkbox"/>	GO:0032196	3	transposition	105	0.0162	1	0.0024	0.0066874	D
<input type="checkbox"/>	GO:0043632	6	modification-dependent macromolecule catabolic process	155	0.0239	3	0.0072	0.0065318	D
<input type="checkbox"/>	GO:0044257	6,7	cellular protein catabolic process	160	0.0247	3	0.0072	0.0051359	D
<input type="checkbox"/>	GO:0009056	3	catabolic process	438	0.0676	16	0.0386	0.0033836	D
<input type="checkbox"/>	GO:0044248	4	cellular catabolic process	425	0.0656	15	0.0362	0.0027762	D
<input type="checkbox"/>	GO:0006412	6,5	translation	688	0.1062	27	0.0652	0.0009539	D
<input type="checkbox"/>	GO:0006414	7,6	translational elongation	313	0.0483	1	0.0024	1.384402E-08	D
<input type="checkbox"/>	GO:0043284	5	biopolymer biosynthetic process	354	0.0547	2	0.0048	1.152161E-08	D