GO-Stats Results

Your dataset contains **799** annotated gene products.
You can download a tabulated text output file here, for use with a spreadsheet application.

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

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

GO ID	Level	GO Term	R O	R F	D O	D F	P-value	E/D
○ GO:0022613	4	ribonucleoprotein complex biogenesis and assembly	483	0.0746	215	0.2691	2.559781E-77	E
○ GO:0042254	5	ribosome biogenesis and assembly	410	0.0633	191	0.2390	4.416101E-72	E
○ GO:0009987	2	cellular process	4654	0.7187	732	0.9161	1.376118E-48	E
○ GO:0006139	4	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	1532	0.2366	357	0.4468	3.821426E-45	E
○ GO:0006396	6	RNA processing	491	0.0758	171	0.2140	3.001671E-42	E
○ GO:0006996	4	organelle organization and biogenesis	1388	0.2143	328	0.4105	8.479723E-42	E
○ GO:0016043	3	cellular component organization and biogenesis	2264	0.3496	453	0.5670	2.215428E-41	E
○ GO:0016070	5	RNA metabolic process	1058	0.1634	272	0.3404	2.394653E-40	E
○ GO:0016072	6	rRNA metabolic process	256	0.0395	108	0.1352	7.599676E-35	E
○ GO:0006364	6,7	rRNA processing	249	0.0384	104	0.1302	4.326865E-33	E
○ GO:0008152	2	metabolic process	3516	0.5429	577	0.7222	7.609584E-29	E
○ GO:0044238	3	primary metabolic process	3247	0.5014	542	0.6783	1.673549E-27	E
○ GO:0044237	3	cellular metabolic process	3403	0.5255	556	0.6959	6.379202E-26	E
○ GO:0042273	6,5	ribosomal large subunit biogenesis and assembly	64	0.0099	42	0.0526	1.319921E-23	E
○ GO:0000460	7,8	maturation of 5.8S rRNA	36	0.0056	29	0.0363	9.651079E-21	E
○ GO:0000466	8,9	maturation of 5.8S rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	34	0.0053	27	0.0338	4.335745E-19	E
○ GO:0022618	6,5	protein-RNA complex assembly	144	0.0222	58	0.0726	7.183780E-18	E
○ GO:0043283	4	biopolymer metabolic process	2230	0.3443	381	0.4768	4.855305E-17	E
○ GO:0000462	8,9	maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	45	0.0069	28	0.0350	2.974378E-15	E
○ GO:0030490	7,8	maturation of SSU-rRNA	45	0.0069	28	0.0350	2.974378E-15	E

○	GO:0043170	3	macromolecule metabolic process	2841	0.4387	452	0.5657	4.247419E-15	E
○	GO:0006399	6	tRNA metabolic process	121	0.0187	48	0.0601	1.074279E-14	E
○	GO:0006520	5,6	amino acid metabolic process	187	0.0289	60	0.0751	3.491284E-13	E
○	GO:0006519	4	amino acid and derivative metabolic process	202	0.0312	63	0.0788	3.714149E-13	E
○	GO:0008033	7	tRNA processing	84	0.0130	36	0.0451	1.571049E-12	E
○	GO:0065003	5,4	macromolecular complex assembly	328	0.0506	84	0.1051	7.078226E-12	E
○	GO:0006400	7,8	tRNA modification	52	0.0080	26	0.0325	2.927254E-11	E
○	GO:0006725	4	aromatic compound metabolic process	60	0.0093	28	0.0350	4.109200E-11	E
○	GO:0044249	4	cellular biosynthetic process	366	0.0565	88	0.1101	8.022180E-11	E
○	GO:0042255	7,6	ribosome assembly	66	0.0102	29	0.0363	1.123382E-10	E
○	GO:0000027	9,7,8,6	ribosomal large subunit assembly and maintenance	41	0.0063	22	0.0275	1.677198E-10	E
○	GO:0000479	8,9	endonucleolytic cleavage of tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	20	0.0031	15	0.0188	1.689163E-10	E
○	GO:0000478	7,8	endonucleolytic cleavages during rRNA processing	20	0.0031	15	0.0188	1.689163E-10	E
○	GO:0000447	9,10	endonucleolytic cleavage between SSU-rRNA and 5.8S rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	20	0.0031	15	0.0188	1.689163E-10	E
○	GO:0008652	6,7	amino acid biosynthetic process	106	0.0164	38	0.0476	2.171173E-10	E
○	GO:0022607	4	cellular component assembly	471	0.0727	104	0.1302	2.802574E-10	E
○	GO:0009308	4	amine metabolic process	228	0.0352	62	0.0776	3.329715E-10	E
○	GO:0009309	5,6	amine biosynthetic process	114	0.0176	39	0.0488	6.058671E-10	E
○	GO:0044271	5,4	nitrogen compound biosynthetic process	115	0.0178	39	0.0488	8.072556E-10	E
○	GO:0000470	7,8	maturation of LSU-rRNA	14	0.0022	12	0.0150	8.119470E-10	E
○	GO:0000463	8,9	maturation of LSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	14	0.0022	12	0.0150	8.119470E-10	E
○	GO:0006807	3	nitrogen compound metabolic process	251	0.0388	64	0.0801	2.851079E-09	E
○	GO:0006360	8,7	transcription from RNA polymerase I promoter	34	0.0053	18	0.0225	1.035709E-08	E
○	GO:0006413	7,6	translational initiation	49	0.0076	22	0.0275	1.216263E-08	E
○	GO:0042257	8,7	ribosomal subunit assembly	55	0.0085	23	0.0288	2.900983E-08	E
○	GO:0051169	7,5,6	nuclear transport	129	0.0199	39	0.0488	2.928389E-08	E
○	GO:0006913	8,6,7	nucleocytoplasmic transport	129	0.0199	39	0.0488	2.928389E-08	E
○	GO:0006206	6	pyrimidine base metabolic process	17	0.0026	12	0.0150	3.739429E-08	E
○	GO:0051168	9,7,8	nuclear export	102	0.0158	33	0.0413	5.649058E-08	E
○	GO:0019856	7,6	pyrimidine base biosynthetic process	15	0.0023	11	0.0138	7.701600E-08	E
○	GO:0046483	4	heterocycle metabolic process	76	0.0117	27	0.0338	1.057618E-07	E
○	GO:0009112	5	nucleobase metabolic process	31	0.0048	16	0.0200	1.090095E-07	E
								1.447128E	

○	GO:0000054	10,11,6,8,9	ribosome export from nucleus	28	0.0043	15	0.0188	1.447138E-07	E
○	GO:0006082	4	organic acid metabolic process	314	0.0485	70	0.0876	1.651573E-07	E
○	GO:0019752	5	carboxylic acid metabolic process	314	0.0485	70	0.0876	1.651573E-07	E
○	GO:0006611	9,10,7,8	protein export from nucleus	56	0.0086	22	0.0275	2.126647E-07	E
○	GO:0046112	6,5	nucleobase biosynthetic process	21	0.0032	12	0.0150	1.056153E-06	E
○	GO:0016071	6	mRNA metabolic process	210	0.0324	50	0.0626	1.274726E-06	E
○	GO:0009101	7,5	glycoprotein biosynthetic process	78	0.0120	24	0.0300	8.718913E-06	E
○	GO:0008380	7	RNA splicing	132	0.0204	34	0.0426	1.024561E-05	E
○	GO:0009100	6	glycoprotein metabolic process	79	0.0122	24	0.0300	1.100653E-05	E
○	GO:0019438	5	aromatic compound biosynthetic process	18	0.0028	10	0.0125	1.200944E-05	E
○	GO:0009451	6	RNA modification	139	0.0215	35	0.0438	1.285919E-05	E
○	GO:0030488	8,9	tRNA methylation	15	0.0023	9	0.0113	1.457798E-05	E
○	GO:0006696	7,8,9	ergosterol biosynthetic process	26	0.0040	12	0.0150	1.811052E-05	E
○	GO:0008204	6,7,8	ergosterol metabolic process	26	0.0040	12	0.0150	1.811052E-05	E
○	GO:0006220	6	pyrimidine nucleotide metabolic process	7	0.0011	6	0.0075	2.131015E-05	E
○	GO:0009123	6	nucleoside monophosphate metabolic process	19	0.0029	10	0.0125	2.225576E-05	E
○	GO:0009081	6,7	branched chain family amino acid metabolic process	16	0.0025	9	0.0113	2.924685E-05	E
○	GO:0009073	7,6,8	aromatic amino acid family biosynthetic process	16	0.0025	9	0.0113	2.924685E-05	E
○	GO:0009082	7,8	branched chain family amino acid biosynthetic process	13	0.0020	8	0.0100	3.489476E-05	E
○	GO:0006260	6	DNA replication	117	0.0181	30	0.0375	3.498851E-05	E
○	GO:0006401	6	RNA catabolic process	74	0.0114	22	0.0275	3.540103E-05	E
○	GO:0006351	7,6	transcription, DNA-dependent	522	0.0806	93	0.1164	3.874881E-05	E
○	GO:0032774	6	RNA biosynthetic process	524	0.0809	93	0.1164	4.451494E-05	E
○	GO:0006350	5	transcription	567	0.0876	99	0.1239	4.890693E-05	E
○	GO:0009066	6,7	aspartate family amino acid metabolic process	46	0.0071	16	0.0200	5.141335E-05	E
○	GO:0009124	6,7	nucleoside monophosphate biosynthetic process	17	0.0026	9	0.0113	5.454923E-05	E
○	GO:0031323	5,4	regulation of cellular metabolic process	507	0.0783	90	0.1126	5.743313E-05	E
○	GO:0016125	5,6,7	sterol metabolic process	42	0.0065	15	0.0188	6.198264E-05	E
○	GO:0009072	6,5,7	aromatic amino acid family metabolic process	21	0.0032	10	0.0125	6.547685E-05	E
○	GO:0006383	8,7	transcription from RNA polymerase III promoter	38	0.0059	14	0.0175	7.355356E-05	E
○	GO:0008202	5,6	steroid metabolic process	43	0.0066	15	0.0188	8.358876E-05	E
○	GO:0006486	8,7,6	protein amino acid glycosylation	73	0.0113	21	0.0263	8.661851E-05	E
○	GO:0043413	6	biopolymer glycosylation	73	0.0113	21	0.0263	8.661851E-05	E
○	GO:0009126	7	purine nucleoside monophosphate metabolic process	18	0.0028	9	0.0113	9.575463E-05	E
								9.575463E	

○	GO:0009116	5	nucleoside metabolic process	18	0.0028	9	0.0113	9.575463E-05	E
○	GO:0015931	4,5	nucleobase, nucleoside, nucleotide and nucleic acid transport	90	0.0139	24	0.0300	0.0001029	E
○	GO:0006261	7	DNA-dependent DNA replication	97	0.0150	25	0.0313	0.0001323	E
○	GO:0016073	6	snRNA metabolic process	15	0.0023	8	0.0100	0.0001344	E
○	GO:0043094	4	metabolic compound salvage	19	0.0029	9	0.0113	0.0001597	E
○	GO:0006397	7	mRNA processing	157	0.0242	35	0.0438	0.0001614	E
○	GO:0006694	6,5,7	steroid biosynthetic process	32	0.0049	12	0.0150	0.0001939	E
○	GO:0016126	6,7,8	sterol biosynthetic process	32	0.0049	12	0.0150	0.0001939	E
○	GO:0009262	6	deoxyribonucleotide metabolic process	9	0.0014	6	0.0075	0.0001969	E
○	GO:0018193	7	peptidyl-amino acid modification	28	0.0043	11	0.0138	0.0002230	E
○	GO:0045943	10,9	positive regulation of transcription from RNA polymerase I promoter	4	0.0006	4	0.0050	0.0002302	E
○	GO:0009127	7,8	purine nucleoside monophosphate biosynthetic process	16	0.0025	8	0.0100	0.0002359	E
○	GO:0006403	4	RNA localization	90	0.0139	23	0.0288	0.0002664	E
○	GO:0000398	8,10	nuclear mRNA splicing, via spliceosome	102	0.0158	25	0.0313	0.0002921	E
○	GO:0000377	9	RNA splicing, via transesterification reactions with bulged adenosine as nucleophile	103	0.0159	25	0.0313	0.0003389	E
○	GO:0009161	7	ribonucleoside monophosphate metabolic process	17	0.0026	8	0.0100	0.0003909	E
○	GO:0016074	6	snoRNA metabolic process	17	0.0026	8	0.0100	0.0003909	E
○	GO:0009167	8	purine ribonucleoside monophosphate metabolic process	17	0.0026	8	0.0100	0.0003909	E
○	GO:0019222	4,3	regulation of metabolic process	538	0.0831	90	0.1126	0.0003940	E
○	GO:0000375	8	RNA splicing, via transesterification reactions	110	0.0170	26	0.0325	0.0003991	E
○	GO:0019219	6,5	regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	440	0.0679	76	0.0951	0.0004151	E
○	GO:0006446	8,7,6	regulation of translational initiation	10	0.0015	6	0.0075	0.0004318	E
○	GO:0006402	7	mRNA catabolic process	60	0.0093	17	0.0213	0.0004522	E
○	GO:0040029	4	regulation of gene expression, epigenetic	100	0.0154	24	0.0300	0.0005111	E
○	GO:0007049	3	cell cycle	458	0.0707	78	0.0976	0.0005266	E
○	GO:0000105	8,9	histidine biosynthetic process	14	0.0022	7	0.0088	0.0005847	E
○	GO:0006547	7,8	histidine metabolic process	14	0.0022	7	0.0088	0.0005847	E
○	GO:0009075	6,7	histidine family amino acid metabolic process	14	0.0022	7	0.0088	0.0005847	E
○	GO:0009076	7,8	histidine family amino acid biosynthetic process	14	0.0022	7	0.0088	0.0005847	E
○	GO:0006405	10,8,5,7,9,6	RNA export from nucleus	79	0.0122	20	0.0250	0.0007018	E
○	GO:0045449	7,6	regulation of transcription	386	0.0596	67	0.0839	0.0007225	E
○	GO:0006355	8,7	regulation of transcription, DNA-dependent	359	0.0554	63	0.0788	0.0007630	E
○	GO:0006417	7,6,5	regulation of translation	47	0.0073	14	0.0175	0.0008057	E
○	GO:0051236	3,4,5	establishment of RNA localization	80	0.0124	20	0.0250	0.0008217	E
○	GO:0050658	4,6,5,7	RNA transport	80	0.0124	20	0.0250	0.0008217	E
○	GO:0050657	5,6	nucleic acid transport	80	0.0124	20	0.0250	0.0008217	E
○	GO:0046907	6,4,5	intracellular transport	545	0.0842	89	0.1114	0.0008369	E
○	GO:0031497	5,9	chromatin assembly	104	0.0161	24	0.0300	0.0008847	E
○	GO:0022402	4,3	cell cycle process	439	0.0678	74	0.0926	0.0009002	E
○	GO:0009168	8,9	purine ribonucleoside monophosphate biosynthetic process	15	0.0023	7	0.0088	0.0009620	E

○	GO:0009156	7,8	ribonucleoside monophosphate biosynthetic process	15	0.0023	7	0.0088	0.0009620	E
○	GO:0006487	9,8,7	protein amino acid N-linked glycosylation	48	0.0074	14	0.0175	0.0009986	E
○	GO:0009117	5	nucleotide metabolic process	111	0.0171	25	0.0313	0.0010003	E
○	GO:0017182	9	peptidyl-diphthamide metabolic process	5	0.0008	4	0.0050	0.0010096	E
○	GO:0017183	10,4	peptidyl-diphthamide biosynthetic process from peptidyl-histidine	5	0.0008	4	0.0050	0.0010096	E
○	GO:0006213	6	pyrimidine nucleoside metabolic process	5	0.0008	4	0.0050	0.0010096	E
○	GO:0006221	6,7	pyrimidine nucleotide biosynthetic process	5	0.0008	4	0.0050	0.0010096	E
○	GO:0018202	8	peptidyl-histidine modification	5	0.0008	4	0.0050	0.0010096	E
○	GO:0006356	9,8	regulation of transcription from RNA polymerase I promoter	8	0.0012	5	0.0063	0.0010691	E
○	GO:0051325	6,5	interphase	112	0.0173	25	0.0313	0.0011311	E
○	GO:0051329	7,5,6	interphase of mitotic cell cycle	112	0.0173	25	0.0313	0.0011311	E
○	GO:0050794	4,3	regulation of cellular process	738	0.1140	114	0.1427	0.0013012	E
○	GO:0016458	5	gene silencing	95	0.0147	22	0.0275	0.0013118	E
○	GO:0045814	5	negative regulation of gene expression, epigenetic	95	0.0147	22	0.0275	0.0013118	E
○	GO:0031507	6,10	heterochromatin formation	95	0.0147	22	0.0275	0.0013118	E
○	GO:0006342	10,6,7,11,9	chromatin silencing	95	0.0147	22	0.0275	0.0013118	E
○	GO:0033036	3	macromolecule localization	382	0.0590	65	0.0814	0.0013220	E
○	GO:0051028	5,7,6,8	mRNA transport	66	0.0102	17	0.0213	0.0013466	E
○	GO:0006406	11,9,6,8,10,7	mRNA export from nucleus	66	0.0102	17	0.0213	0.0013466	E
○	GO:0006605	8,6,7	protein targeting	258	0.0398	47	0.0588	0.0014219	E
○	GO:0006056	7	mannoprotein metabolic process	12	0.0019	6	0.0075	0.0014625	E
○	GO:0006057	8,6	mannoprotein biosynthetic process	12	0.0019	6	0.0075	0.0014625	E
○	GO:0000032	8,6,9,7	cell wall mannoprotein biosynthetic process	12	0.0019	6	0.0075	0.0014625	E
○	GO:0031506	7,5,8,6	cell wall glycoprotein biosynthetic process	12	0.0019	6	0.0075	0.0014625	E
○	GO:0006886	7,5,6	intracellular protein transport	274	0.0423	49	0.0613	0.0016682	E
○	GO:0051649	5,3,4	establishment of cellular localization	606	0.0936	95	0.1189	0.0018642	E
○	GO:0007090	8,9,7,6	regulation of S phase of mitotic cell cycle	3	0.0005	3	0.0038	0.0018719	E
○	GO:0009219	7	pyrimidine deoxyribonucleotide metabolic process	3	0.0005	3	0.0038	0.0018719	E
○	GO:0046500	6,5	S-adenosylmethionine metabolic process	3	0.0005	3	0.0038	0.0018719	E
○	GO:0043101	5	purine salvage	9	0.0014	5	0.0063	0.0021102	E
○	GO:0006379	8	mRNA cleavage	26	0.0040	9	0.0113	0.0021653	E
○	GO:0006407	11,9,6,8,10,7	rRNA export from nucleus	26	0.0040	9	0.0113	0.0021653	E
○	GO:0051029	5,7,6,8	rRNA transport	26	0.0040	9	0.0113	0.0021653	E
○	GO:0006575	5	amino acid derivative metabolic process	31	0.0048	10	0.0125	0.0022334	E
○	GO:0043412	5	biopolymer modification	664	0.1025	102	0.1277	0.0023895	E
○	GO:0015031	4,5,6	protein transport	280	0.0432	49	0.0613	0.0024691	E
○	GO:0065007	2	biological regulation	948	0.1464	139	0.1740	0.0028069	E
○	GO:0043038	6,7	amino acid activation	32	0.0049	10	0.0125	0.0028508	E
○	GO:0043039	7,8	tRNA aminoacylation	32	0.0049	10	0.0125	0.0028508	E
○	GO:0006418	8,7,9,6	tRNA aminoacylation for protein translation	32	0.0049	10	0.0125	0.0028508	E
○	GO:0050789	3	regulation of biological process	761	0.1175	114	0.1427	0.0030828	E
○	GO:0007163	6,3,7	establishment and/or maintenance of cell polarity	115	0.0178	24	0.0300	0.0031905	E
○	GO:0006259	5	DNA metabolic process	523	0.0808	82	0.1026	0.0032189	E

○	GO:0030010	7,4,8	establishment of cell polarity	103	0.0159	22	0.0275	0.0034296	E
○	GO:0009058	3	biosynthetic process	1249	0.1929	177	0.2215	0.0035486	E
○	GO:0000096	6,7,5	sulfur amino acid metabolic process	33	0.0051	10	0.0125	0.0035895	E
○	GO:0006188	9,10	IMP biosynthetic process	14	0.0022	6	0.0075	0.0036583	E
○	GO:0046040	9	IMP metabolic process	14	0.0022	6	0.0075	0.0036583	E
○	GO:0000278	4	mitotic cell cycle	266	0.0411	46	0.0576	0.0038036	E
○	GO:0022403	5,4	cell cycle phase	353	0.0545	58	0.0726	0.0041125	E
○	GO:0045184	3,4,5	establishment of protein localization	296	0.0457	50	0.0626	0.0041936	E
○	GO:0007001	6	chromosome organization and biogenesis (sensu Eukaryota)	567	0.0876	87	0.1089	0.0042376	E
○	GO:0051641	4,3	cellular localization	642	0.0991	97	0.1214	0.0042435	E
○	GO:0000245	7,6,9,11	spliceosome assembly	19	0.0029	7	0.0088	0.0044641	E
○	GO:0006333	8	chromatin assembly or disassembly	119	0.0184	24	0.0300	0.0047321	E
○	GO:0006555	7,8,6	methionine metabolic process	24	0.0037	8	0.0100	0.0047376	E
○	GO:0051276	5	chromosome organization and biogenesis	572	0.0883	87	0.1089	0.0051033	E
○	GO:0032506	5,3	cytokinetic process	88	0.0136	19	0.0238	0.0052662	E
○	GO:0000079	8,7,6	regulation of cyclin-dependent protein kinase activity	15	0.0023	6	0.0075	0.0053490	E
○	GO:0006374	9,11	nuclear mRNA splicing via U2-type spliceosome	15	0.0023	6	0.0075	0.0053490	E
○	GO:0006617	8,12,11,7,10,9	SRP-dependent cotranslational protein targeting to membrane, signal sequence recognition	7	0.0011	4	0.0050	0.0054372	E
○	GO:0040031	7	snRNA modification	7	0.0011	4	0.0050	0.0054372	E
○	GO:0031120	8	snRNA pseudouridine synthesis	7	0.0011	4	0.0050	0.0054372	E
○	GO:0042398	6,5	amino acid derivative biosynthetic process	20	0.0031	7	0.0088	0.0060254	E
○	GO:0000910	4	cytokinesis	109	0.0168	22	0.0275	0.0063017	E
○	GO:0009165	5,6	nucleotide biosynthetic process	59	0.0091	14	0.0175	0.0065632	E
○	GO:0000135	9,8	septin checkpoint	4	0.0006	3	0.0038	0.0065669	E
○	GO:0009200	7	deoxyribonucleoside triphosphate metabolic process	4	0.0006	3	0.0038	0.0065669	E
○	GO:0009147	7	pyrimidine nucleoside triphosphate metabolic process	4	0.0006	3	0.0038	0.0065669	E
○	GO:0031565	8,7	cytokinesis checkpoint	4	0.0006	3	0.0038	0.0065669	E
○	GO:0050000	6,5	chromosome localization	4	0.0006	3	0.0038	0.0065669	E
○	GO:0000731	7,6	DNA synthesis during DNA repair	4	0.0006	3	0.0038	0.0065669	E
○	GO:0032989	4,5	cellular structure morphogenesis	248	0.0383	42	0.0526	0.0069203	E
○	GO:0000902	5,6	cell morphogenesis	248	0.0383	42	0.0526	0.0069203	E
○	GO:0048856	3	anatomical structure development	248	0.0383	42	0.0526	0.0069203	E
○	GO:0009653	4,3	anatomical structure morphogenesis	248	0.0383	42	0.0526	0.0069203	E
○	GO:0006730	4	one-carbon compound metabolic process	97	0.0150	20	0.0250	0.0069383	E
○	GO:0007062	7,4	sister chromatid cohesion	31	0.0048	9	0.0113	0.0072681	E
○	GO:0030467	7,4,8	establishment and/or maintenance of cell polarity (sensu Fungi)	66	0.0102	15	0.0188	0.0074102	E
○	GO:0000282	7,9,5,6,10	cellular bud site selection	66	0.0102	15	0.0188	0.0074102	E
○	GO:0007105	6,4	cytokinesis, site selection	66	0.0102	15	0.0188	0.0074102	E
○	GO:0030468	8,5,9	establishment of cell polarity (sensu Fungi)	66	0.0102	15	0.0188	0.0074102	E
○	GO:0006348	11,7,8,12,10	chromatin silencing at telomere	60	0.0093	14	0.0175	0.0075135	E
○	GO:0031509	7,11	telomeric heterochromatin formation	60	0.0093	14	0.0175	0.0075135	E
○	GO:0008104	4	protein localization	330	0.0510	53	0.0663	0.0077929	E

○	GO:0031326	6,5	regulation of cellular biosynthetic process	67	0.0103	15	0.0188	0.0083800	E
○	GO:0042278	6	purine nucleoside metabolic process	12	0.0019	5	0.0063	0.0089533	E
○	GO:0009070	7,8	serine family amino acid biosynthetic process	12	0.0019	5	0.0063	0.0089533	E
○	GO:0006338	9	chromatin remodeling	155	0.0239	28	0.0350	0.0098018	E
○	GO:0006606	9,10,7,8,6	protein import into nucleus	50	0.0077	12	0.0150	0.0099625	E
○	GO:0051170	9,7,8	nuclear import	50	0.0077	12	0.0150	0.0099625	E
○	GO:0009889	5,4	regulation of biosynthetic process	69	0.0107	15	0.0188	0.0105824	E
○	GO:0006270	8,6	DNA replication initiation	33	0.0051	9	0.0113	0.0107042	E
○	GO:0008610	5,4,6	lipid biosynthetic process	129	0.0199	24	0.0300	0.0109813	E
○	GO:0017038	5,6,7	protein import	109	0.0168	21	0.0263	0.0113197	E
○	GO:0009119	6	ribonucleoside metabolic process	13	0.0020	5	0.0063	0.0127620	E
○	GO:0007346	7,5,6	regulation of progression through mitotic cell cycle	13	0.0020	5	0.0063	0.0127620	E
○	GO:0000097	7,8,6	sulfur amino acid biosynthetic process	13	0.0020	5	0.0063	0.0127620	E
○	GO:0051030	5,7,6,8	snRNA transport	23	0.0036	7	0.0088	0.0128668	E
○	GO:0006610	10,11,8,9,7	ribosomal protein import into nucleus	23	0.0036	7	0.0088	0.0128668	E
○	GO:0006408	11,9,6,8,10,7	snRNA export from nucleus	23	0.0036	7	0.0088	0.0128668	E
○	GO:0006607	10,11,8,9,7	NLS-bearing substrate import into nucleus	23	0.0036	7	0.0088	0.0128668	E
○	GO:0006608	10,11,8,9,7	snRNP protein import into nucleus	23	0.0036	7	0.0088	0.0128668	E
○	GO:0006273	9,8	lagging strand elongation	18	0.0028	6	0.0075	0.0133937	E
○	GO:0006999	6	nuclear pore organization and biogenesis	29	0.0045	8	0.0100	0.0143735	E
○	GO:0006409	11,9,6,8,10,7	tRNA export from nucleus	29	0.0045	8	0.0100	0.0143735	E
○	GO:0032447	9	protein urmylation	5	0.0008	3	0.0038	0.0143981	E
○	GO:0009098	8,9	leucine biosynthetic process	5	0.0008	3	0.0038	0.0143981	E
○	GO:0006279	7	premeiotic DNA synthesis	5	0.0008	3	0.0038	0.0143981	E
○	GO:0009371	10,9,6	positive regulation of transcription by pheromones	5	0.0008	3	0.0038	0.0143981	E
○	GO:0043629	9	ncRNA polyadenylation	5	0.0008	3	0.0038	0.0143981	E
○	GO:0009264	6,7	deoxyribonucleotide catabolic process	5	0.0008	3	0.0038	0.0143981	E
○	GO:0007329	11,10,7	positive regulation of transcription from RNA polymerase II promoter by pheromones	5	0.0008	3	0.0038	0.0143981	E
○	GO:0043001	10,8,7,9	Golgi to plasma membrane protein transport	5	0.0008	3	0.0038	0.0143981	E
○	GO:0016075	7	rRNA catabolic process	5	0.0008	3	0.0038	0.0143981	E
○	GO:0008655	5	pyrimidine salvage	5	0.0008	3	0.0038	0.0143981	E
○	GO:0033261	7,8,6	regulation of progression through S phase	5	0.0008	3	0.0038	0.0143981	E
○	GO:0043630	9,10	ncRNA polyadenylation during polyadenylation-dependent ncRNA catabolic process	5	0.0008	3	0.0038	0.0143981	E
○	GO:0051246	5,4	regulation of protein metabolic process	72	0.0111	15	0.0188	0.0145801	E
○	GO:0006163	6	purine nucleotide metabolic process	47	0.0073	11	0.0138	0.0151424	E
○	GO:0015855	6,7	pyrimidine transport	2	0.0003	2	0.0025	0.0152056	E
○	GO:0018195	8	peptidyl-arginine modification	2	0.0003	2	0.0025	0.0152056	E
○	GO:0006556	8,7,6,9,5	S-adenosylmethionine biosynthetic process	2	0.0003	2	0.0025	0.0152056	E
○	GO:0046516	6	hypusine metabolic process	2	0.0003	2	0.0025	0.0152056	E
○	GO:0006842	6,7	tricarboxylic acid transport	2	0.0003	2	0.0025	0.0152056	E
○	GO:0009221	7,8	pyrimidine deoxyribonucleotide biosynthetic process	2	0.0003	2	0.0025	0.0152056	E
○	GO:0010410	8,6,7	hemicellulose metabolic process	2	0.0003	2	0.0025	0.0152056	E

○	GO:0000078	9,11,10,8,6,7	cell morphogenesis checkpoint	2	0.0003	2	0.0025	0.0152056	E
○	GO:0015864	6,7	pyrimidine nucleoside transport	2	0.0003	2	0.0025	0.0152056	E
○	GO:0019988	7,8,9,6	charged-tRNA modification	2	0.0003	2	0.0025	0.0152056	E
○	GO:0046515	7,6	hypusine biosynthetic process	2	0.0003	2	0.0025	0.0152056	E
○	GO:0006080	10,8,9	substituted mannan metabolic process	2	0.0003	2	0.0025	0.0152056	E
○	GO:0019344	8,9,7	cysteine biosynthetic process	2	0.0003	2	0.0025	0.0152056	E
○	GO:0009211	8	pyrimidine deoxyribonucleoside triphosphate metabolic process	2	0.0003	2	0.0025	0.0152056	E
○	GO:0009204	7,8	deoxyribonucleoside triphosphate catabolic process	2	0.0003	2	0.0025	0.0152056	E
○	GO:0010412	9,7,8	mannan metabolic process	2	0.0003	2	0.0025	0.0152056	E
○	GO:0045740	9,8	positive regulation of DNA replication	2	0.0003	2	0.0025	0.0152056	E
○	GO:0031324	6,5	negative regulation of cellular metabolic process	198	0.0306	33	0.0413	0.0152815	E
○	GO:0016481	8,7	negative regulation of transcription	162	0.0250	28	0.0350	0.0152985	E
○	GO:0043631	8	RNA polyadenylation	24	0.0037	7	0.0088	0.0159354	E
○	GO:0009069	6,7	serine family amino acid metabolic process	24	0.0037	7	0.0088	0.0159354	E
○	GO:0030466	11,7,8,12,10	chromatin silencing at silent mating-type cassette	30	0.0046	8	0.0100	0.0171954	E
○	GO:0051031	5,7,6,8	tRNA transport	30	0.0046	8	0.0100	0.0171954	E
○	GO:0006388	9,8	tRNA splicing	14	0.0022	5	0.0063	0.0174132	E
○	GO:0000394	8	RNA splicing, via endonucleolytic cleavage and ligation	14	0.0022	5	0.0063	0.0174132	E
○	GO:0006272	9,8	leading strand elongation	14	0.0022	5	0.0063	0.0174132	E
○	GO:0045934	7,6	negative regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	179	0.0276	30	0.0375	0.0176764	E
○	GO:0045859	7	regulation of protein kinase activity	25	0.0039	7	0.0088	0.0194157	E
○	GO:0045005	8,6	maintenance of fidelity during DNA-dependent DNA replication	25	0.0039	7	0.0088	0.0194157	E
○	GO:0043549	6	regulation of kinase activity	25	0.0039	7	0.0088	0.0194157	E
○	GO:0006609	10,11,8,9,7	mRNA-binding (hnRNP) protein import into nucleus	25	0.0039	7	0.0088	0.0194157	E
○	GO:0006298	7,9,6	mismatch repair	25	0.0039	7	0.0088	0.0194157	E
○	GO:0048518	4	positive regulation of biological process	124	0.0191	22	0.0275	0.0204105	E
○	GO:0048522	5,4	positive regulation of cellular process	124	0.0191	22	0.0275	0.0204105	E
○	GO:0009067	7,8	aspartate family amino acid biosynthetic process	20	0.0031	6	0.0075	0.0215183	E
○	GO:0032259	5	methylation	83	0.0128	16	0.0200	0.0216527	E
○	GO:0043414	6	biopolymer methylation	83	0.0128	16	0.0200	0.0216527	E
○	GO:0000162	9,8,7,10	tryptophan biosynthetic process	10	0.0015	4	0.0050	0.0220119	E
○	GO:0042435	7,5	indole derivative biosynthetic process	10	0.0015	4	0.0050	0.0220119	E
○	GO:0042434	6	indole derivative metabolic process	10	0.0015	4	0.0050	0.0220119	E
○	GO:0006586	6,7	indolalkylamine metabolic process	10	0.0015	4	0.0050	0.0220119	E
○	GO:0009096	8,7,9	aromatic amino acid family biosynthetic process, anthranilate pathway	10	0.0015	4	0.0050	0.0220119	E
○	GO:0042430	5	indole and derivative metabolic process	10	0.0015	4	0.0050	0.0220119	E
○	GO:0006568	7,8,6	tryptophan metabolic process	10	0.0015	4	0.0050	0.0220119	E
○	GO:0046219	7,8,6	indolalkylamine biosynthetic process	10	0.0015	4	0.0050	0.0220119	E
○	GO:0032200	7	telomere organization and biogenesis	274	0.0423	42	0.0526	0.0225200	E
○	GO:0000723	8	telomere maintenance	274	0.0423	42	0.0526	0.0225200	E
○	GO:0006997	5	nuclear organization and biogenesis	57	0.0088	12	0.0150	0.0232476	E

○	GO:0051338	5	regulation of transferase activity	26	0.0040	7	0.0088	0.0233069	E
○	GO:0006271	8,7	DNA strand elongation during DNA replication	32	0.0049	8	0.0100	0.0237827	E
○	GO:0032984	5	macromolecular complex disassembly	32	0.0049	8	0.0100	0.0237827	E
○	GO:0022616	6	DNA strand elongation	32	0.0049	8	0.0100	0.0237827	E
○	GO:0006810	3,4	transport	981	0.1515	131	0.1640	0.0237932	E
○	GO:0009892	5,4	negative regulation of metabolic process	208	0.0321	33	0.0413	0.0243891	E
○	GO:0045892	9,8	negative regulation of transcription, DNA-dependent	156	0.0241	26	0.0325	0.0243933	E
○	GO:0006166	6,8	purine ribonucleoside salvage	6	0.0009	3	0.0038	0.0252540	E
○	GO:0043174	5	nucleoside salvage	6	0.0009	3	0.0038	0.0252540	E
○	GO:0000082	8,5,6,7,4	G1/S transition of mitotic cell cycle	52	0.0080	11	0.0138	0.0273056	E
○	GO:0000080	7,8,6	G1 phase of mitotic cell cycle	27	0.0042	7	0.0088	0.0276008	E
○	GO:0051318	6,7,5	G1 phase	27	0.0042	7	0.0088	0.0276008	E
○	GO:0051234	2,3	establishment of localization	1004	0.1550	132	0.1652	0.0285601	E
○	GO:0045935	7,6	positive regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	108	0.0167	19	0.0238	0.0287059	E
○	GO:0006493	9,8,7	protein amino acid O-linked glycosylation	16	0.0025	5	0.0063	0.0292289	E
○	GO:0006464	6	protein modification process	520	0.0803	72	0.0901	0.0297710	E
○	GO:0009893	5,4	positive regulation of metabolic process	116	0.0179	20	0.0250	0.0300542	E
○	GO:0031325	6,5	positive regulation of cellular metabolic process	116	0.0179	20	0.0250	0.0300542	E
○	GO:0007021	7	tubulin folding	11	0.0017	4	0.0050	0.0303372	E
○	GO:0046128	7	purine ribonucleoside metabolic process	11	0.0017	4	0.0050	0.0303372	E
○	GO:0000055	11,12,7,9,10	ribosomal large subunit export from nucleus	11	0.0017	4	0.0050	0.0303372	E
○	GO:0051179	2	localization	1051	0.1623	137	0.1715	0.0303508	E
○	GO:0007064	10,8,5,6,9,7,4	mitotic sister chromatid cohesion	22	0.0034	6	0.0075	0.0318710	E
○	GO:0044272	5	sulfur compound biosynthetic process	22	0.0034	6	0.0075	0.0318710	E
○	GO:0043624	7,6	cellular protein complex disassembly	28	0.0043	7	0.0088	0.0322816	E
○	GO:0043241	6,5	protein complex disassembly	28	0.0043	7	0.0088	0.0322816	E
○	GO:0051052	7,6	regulation of DNA metabolic process	41	0.0063	9	0.0113	0.0341266	E
○	GO:0006164	6,7	purine nucleotide biosynthetic process	41	0.0063	9	0.0113	0.0341266	E
○	GO:0007127	9,7,6,8,5	meiosis I	75	0.0116	14	0.0175	0.0342112	E
○	GO:0000086	8,5,6,7,4	G2/M transition of mitotic cell cycle	35	0.0054	8	0.0100	0.0359242	E
○	GO:0016053	5	organic acid biosynthetic process	17	0.0026	5	0.0063	0.0363182	E
○	GO:0007266	8	Rho protein signal transduction	17	0.0026	5	0.0063	0.0363182	E
○	GO:0046394	6	carboxylic acid biosynthetic process	17	0.0026	5	0.0063	0.0363182	E
○	GO:0000279	6,5	M phase	258	0.0398	38	0.0476	0.0364374	E
○	GO:0007131	10,8,7,5,9,6,4	meiotic recombination	55	0.0085	11	0.0138	0.0365242	E
○	GO:0032502	2	developmental process	436	0.0673	60	0.0751	0.0376146	E
○	GO:0009166	5,6	nucleotide catabolic process	7	0.0011	3	0.0038	0.0387573	E
○	GO:0043633	7	modification-dependent RNA catabolic process	7	0.0011	3	0.0038	0.0387573	E
○	GO:0006551	7,8	leucine metabolic process	7	0.0011	3	0.0038	0.0387573	E
○	GO:0043634	8	polyadenylation-dependent ncRNA catabolic process	7	0.0011	3	0.0038	0.0387573	E
○	GO:0006415	8,7,6	translational termination	7	0.0011	3	0.0038	0.0387573	E
○	GO:0000056	11,12,7,9,10	ribosomal small subunit export from nucleus	7	0.0011	3	0.0038	0.0387573	E
			establishment and/or maintenance of						

○	GO:0006325	7	establishment and/or maintenance of chromatin architecture	253	0.0391	37	0.0463	0.0395077	E
○	GO:0006323	6	DNA packaging	253	0.0391	37	0.0463	0.0395077	E
○	GO:0000074	6,5	regulation of progression through cell cycle	167	0.0258	26	0.0325	0.0397753	E
○	GO:0051726	5,4	regulation of cell cycle	167	0.0258	26	0.0325	0.0397753	E
○	GO:0000244	7,6,10,12	assembly of spliceosomal tri-snRNP	3	0.0005	2	0.0025	0.0400010	E
○	GO:0000117	10,9,6,5,7,8,4	G2/M-specific transcription in mitotic cell cycle	3	0.0005	2	0.0025	0.0400010	E
○	GO:0009120	6	deoxyribonucleoside metabolic process	3	0.0005	2	0.0025	0.0400010	E
○	GO:0000917	6,4	barrier septum formation	3	0.0005	2	0.0025	0.0400010	E
○	GO:0045787	6,7,5	positive regulation of progression through cell cycle	3	0.0005	2	0.0025	0.0400010	E
○	GO:0015858	5,6	nucleoside transport	3	0.0005	2	0.0025	0.0400010	E
○	GO:0051054	8,7	positive regulation of DNA metabolic process	3	0.0005	2	0.0025	0.0400010	E
○	GO:0009263	6,7	deoxyribonucleotide biosynthetic process	3	0.0005	2	0.0025	0.0400010	E
○	GO:0046083	7	adenine metabolic process	3	0.0005	2	0.0025	0.0400010	E
○	GO:0015851	5,6	nucleobase transport	3	0.0005	2	0.0025	0.0400010	E
○	GO:0009143	6,7	nucleoside triphosphate catabolic process	3	0.0005	2	0.0025	0.0400010	E
○	GO:0000370	8,9,7,10,11,12,13	U2-type nuclear mRNA branch site recognition	3	0.0005	2	0.0025	0.0400010	E
○	GO:0006432	9,8,10,7	phenylalanyl-tRNA aminoacylation	3	0.0005	2	0.0025	0.0400010	E
○	GO:0000387	5,9,11	spliceosomal snRNP biogenesis	3	0.0005	2	0.0025	0.0400010	E
○	GO:0006561	8,9	proline biosynthetic process	3	0.0005	2	0.0025	0.0400010	E
○	GO:0046488	9,10	phosphatidylinositol metabolic process	3	0.0005	2	0.0025	0.0400010	E
○	GO:0046125	7	pyrimidine deoxyribonucleoside metabolic process	3	0.0005	2	0.0025	0.0400010	E
○	GO:0022411	4	cellular component disassembly	36	0.0056	8	0.0100	0.0405160	E
○	GO:0016568	8	chromatin modification	223	0.0344	33	0.0413	0.0414579	E
○	GO:0048523	5,4	negative regulation of cellular process	239	0.0369	35	0.0438	0.0416029	E
○	GO:0009259	6	ribonucleotide metabolic process	43	0.0066	9	0.0113	0.0422707	E
○	GO:0042401	6,7	biogenic amine biosynthetic process	18	0.0028	5	0.0063	0.0441051	E
○	GO:0000084	8,7,6	S phase of mitotic cell cycle	18	0.0028	5	0.0063	0.0441051	E
○	GO:0048519	4	negative regulation of biological process	242	0.0374	35	0.0438	0.0450086	E
○	GO:0045045	7,5,4,6	secretory pathway	243	0.0375	35	0.0438	0.0461380	E
○	GO:0007010	5	cytoskeleton organization and biogenesis	227	0.0351	33	0.0413	0.0462814	E
○	GO:0006839	7,5,6	mitochondrial transport	65	0.0100	12	0.0150	0.0464676	E
○	GO:0051321	4	meiotic cell cycle	148	0.0229	23	0.0288	0.0467074	E
○	GO:0051327	7,5,6	M phase of meiotic cell cycle	148	0.0229	23	0.0288	0.0467074	E
○	GO:0007126	8,6,7,5	meiosis	148	0.0229	23	0.0288	0.0467074	E
○	GO:0045893	9,8	positive regulation of transcription, DNA-dependent	95	0.0147	16	0.0200	0.0481159	E
○	GO:0006357	9,8	regulation of transcription from RNA polymerase II promoter	221	0.0341	32	0.0401	0.0487969	E
○	GO:0006633	7,6,8,5	fatty acid biosynthetic process	13	0.0020	4	0.0050	0.0505577	E
○	GO:0007059	3	chromosome segregation	119	0.0184	19	0.0238	0.0507035	E
○	GO:0050790	4	regulation of catalytic activity	45	0.0069	9	0.0113	0.0511114	E
○	GO:0006275	8,7	regulation of DNA replication	19	0.0029	5	0.0063	0.0524976	E
○	GO:0006790	4	sulfur metabolic process	67	0.0103	12	0.0150	0.0532405	E
○	GO:0006366	8,7	transcription from RNA polymerase II promoter	343	0.0530	46	0.0576	0.0538089	E

○	GO:0046903	3,4	secretion	250	0.0386	35	0.0438	0.0538137	E
○	GO:0032940	6,4,5	secretion by cell	250	0.0386	35	0.0438	0.0538137	E
○	GO:0001510	7	RNA methylation	60	0.0093	11	0.0138	0.0543451	E
○	GO:0045039	10,9,7,8	protein import into mitochondrial inner membrane	8	0.0012	3	0.0038	0.0543812	E
○	GO:0015940	7,8	pantothenate biosynthetic process	8	0.0012	3	0.0038	0.0543812	E
○	GO:0006566	7,8	threonine metabolic process	8	0.0012	3	0.0038	0.0543812	E
○	GO:0015939	7	pantothenate metabolic process	8	0.0012	3	0.0038	0.0543812	E
○	GO:0043144	7	snoRNA processing	8	0.0012	3	0.0038	0.0543812	E
○	GO:0000075	7,6	cell cycle checkpoint	53	0.0082	10	0.0125	0.0552312	E
○	GO:0008361	4,6,7	regulation of cell size	129	0.0199	20	0.0250	0.0552679	E
○	GO:0065009	3	regulation of a molecular function	46	0.0071	9	0.0113	0.0557380	E
○	GO:0006310	6	DNA recombination	122	0.0188	19	0.0238	0.0571507	E
○	GO:0042274	6,5	ribosomal small subunit biogenesis and assembly	26	0.0040	6	0.0075	0.0582026	E
○	GO:0010382	6,4	cell wall metabolic process	26	0.0040	6	0.0075	0.0582026	E
○	GO:0044255	4,5	cellular lipid metabolic process	229	0.0354	32	0.0401	0.0582645	E
○	GO:0051301	3	cell division	246	0.0380	34	0.0426	0.0583775	E
○	GO:0051704	2	multi-organism process	139	0.0215	21	0.0263	0.0592600	E
○	GO:0045047	9,8,7,6,5	protein targeting to ER	33	0.0051	7	0.0088	0.0604716	E
○	GO:0043681	6,7,8	protein import into mitochondrion	40	0.0062	8	0.0100	0.0609525	E
○	GO:0009260	6,7	ribonucleotide biosynthetic process	40	0.0062	8	0.0100	0.0609525	E
○	GO:0051320	7,6,5	S phase	20	0.0031	5	0.0063	0.0613895	E
○	GO:0006144	6	purine base metabolic process	14	0.0022	4	0.0050	0.0620741	E
○	GO:0007114	5,4	cell budding	85	0.0131	14	0.0175	0.0625988	E
○	GO:0019954	3	asexual reproduction	85	0.0131	14	0.0175	0.0625988	E
○	GO:0006629	4	lipid metabolic process	242	0.0374	33	0.0413	0.0628981	E
○	GO:0065008	3	regulation of biological quality	260	0.0401	35	0.0438	0.0633573	E
○	GO:0045941	8,7	positive regulation of transcription	101	0.0156	16	0.0200	0.0635435	E
○	GO:0016311	6	dephosphorylation	41	0.0063	8	0.0100	0.0664216	E
○	GO:0009150	7	purine ribonucleotide metabolic process	41	0.0063	8	0.0100	0.0664216	E
○	GO:0016180	7	snRNA processing	4	0.0006	2	0.0025	0.0701516	E
○	GO:0016077	7	snoRNA catabolic process	4	0.0006	2	0.0025	0.0701516	E
○	GO:0006529	8,9	asparagine biosynthetic process	4	0.0006	2	0.0025	0.0701516	E
○	GO:0000301	9,7,6,8	retrograde transport, vesicle recycling within Golgi	4	0.0006	2	0.0025	0.0701516	E
○	GO:0009164	5,6	nucleoside catabolic process	4	0.0006	2	0.0025	0.0701516	E
○	GO:0006491	10,9,8	N-glycan processing	4	0.0006	2	0.0025	0.0701516	E
○	GO:0006534	7,8,6	cysteine metabolic process	4	0.0006	2	0.0025	0.0701516	E
○	GO:0016036	8,7,6	cellular response to phosphate starvation	4	0.0006	2	0.0025	0.0701516	E
○	GO:0016076	7	snRNA catabolic process	4	0.0006	2	0.0025	0.0701516	E
○	GO:0031384	6,8,11,10,9,7,12	regulation of initiation of mating projection growth	4	0.0006	2	0.0025	0.0701516	E
○	GO:0000348	7,8,6,10,12	nuclear mRNA branch site recognition	4	0.0006	2	0.0025	0.0701516	E
○	GO:0015780	5,6	nucleotide-sugar transport	4	0.0006	2	0.0025	0.0701516	E
○	GO:0006891	8,6,5,7	intra-Golgi vesicle-mediated transport	21	0.0032	5	0.0063	0.0706642	E
○	GO:0032185	6	septin cytoskeleton organization and biogenesis	9	0.0014	3	0.0038	0.0715330	E
○	GO:0006280	6	mutagenesis	9	0.0014	3	0.0038	0.0715330	E

○	GO:0042138	11,9,8,5,6,10,7,4	meiotic DNA double-strand break formation	9	0.0014	3	0.0038	0.0715330	E
○	GO:0009085	8,9	lysine biosynthetic process	9	0.0014	3	0.0038	0.0715330	E
○	GO:0006528	7,8	asparagine metabolic process	9	0.0014	3	0.0038	0.0715330	E
○	GO:0031106	7	septin ring organization	9	0.0014	3	0.0038	0.0715330	E
○	GO:0006553	7,8	lysine metabolic process	9	0.0014	3	0.0038	0.0715330	E
○	GO:0000921	8,7	septin ring assembly	9	0.0014	3	0.0038	0.0715330	E
○	GO:0048590	3	non-developmental growth	35	0.0054	7	0.0088	0.0732220	E
○	GO:0007117	6,5,4	budding cell bud growth	35	0.0054	7	0.0088	0.0732220	E
○	GO:0031365	8	N-terminal protein amino acid modification	15	0.0023	4	0.0050	0.0742328	E
○	GO:0000114	10,8,9,5,7,4	G1-specific transcription in mitotic cell cycle	15	0.0023	4	0.0050	0.0742328	E
○	GO:0018409	9	peptide or protein amino-terminal blocking	15	0.0023	4	0.0050	0.0742328	E
○	GO:0006281	6,5	DNA repair	193	0.0298	26	0.0325	0.0759350	E
○	GO:0006311	10,8,7,5,9,6,4	meiotic gene conversion	22	0.0034	5	0.0063	0.0801992	E
○	GO:0030472	6,5,10	mitotic spindle organization and biogenesis in nucleus	22	0.0034	5	0.0063	0.0801992	E
○	GO:0007120	8,6,10,7,11,5	axial cellular bud site selection	22	0.0034	5	0.0063	0.0801992	E
○	GO:0006066	4	alcohol metabolic process	163	0.0252	22	0.0275	0.0834678	E
○	GO:0000746	3	conjugation	118	0.0182	17	0.0213	0.0837643	E
○	GO:0019953	3	sexual reproduction	118	0.0182	17	0.0213	0.0837643	E
○	GO:0000747	4	conjugation with cellular fusion	118	0.0182	17	0.0213	0.0837643	E
○	GO:0048193	7,5,6	Golgi vesicle transport	166	0.0256	22	0.0275	0.0864609	E
○	GO:0015698	6,7	inorganic anion transport	16	0.0025	4	0.0050	0.0867983	E
○	GO:0031023	5	microtubule organizing center organization and biogenesis	16	0.0025	4	0.0050	0.0867983	E
○	GO:0051300	5,4,6	spindle pole body organization and biogenesis	16	0.0025	4	0.0050	0.0867983	E
○	GO:0000087	7,5,6	M phase of mitotic cell cycle	129	0.0199	18	0.0225	0.0875216	E
○	GO:0006893	9,7,6,8	Golgi to plasma membrane transport	30	0.0046	6	0.0075	0.0888080	E
○	GO:0006892	8,6,5,7	post-Golgi vesicle-mediated transport	69	0.0107	11	0.0138	0.0888571	E
○	GO:0043623	7,6	cellular protein complex assembly	69	0.0107	11	0.0138	0.0888571	E
○	GO:0009373	9,8,5	regulation of transcription by pheromones	10	0.0015	3	0.0038	0.0896118	E
○	GO:0006817	7,8	phosphate transport	10	0.0015	3	0.0038	0.0896118	E
○	GO:0008298	5	intracellular mRNA localization	10	0.0015	3	0.0038	0.0896118	E
○	GO:0046019	10,9,6	regulation of transcription from RNA polymerase II promoter by pheromones	10	0.0015	3	0.0038	0.0896118	E
○	GO:0007020	8	microtubule nucleation	23	0.0036	5	0.0063	0.0898696	E
○	GO:0008213	8	protein amino acid alkylation	23	0.0036	5	0.0063	0.0898696	E
○	GO:0006613	10,9,8,7,6	cotranslational protein targeting to membrane	23	0.0036	5	0.0063	0.0898696	E
○	GO:0006479	9,7	protein amino acid methylation	23	0.0036	5	0.0063	0.0898696	E
○	GO:0009152	7,8	purine ribonucleotide biosynthetic process	38	0.0059	7	0.0088	0.0926990	E
○	GO:0046942	5,6	carboxylic acid transport	54	0.0083	9	0.0113	0.0942116	E
○	GO:0006979	4	response to oxidative stress	71	0.0110	11	0.0138	0.0959498	E
○	GO:0006461	6,5	protein complex assembly	116	0.0179	16	0.0200	0.0964816	E
○	GO:0007067	8,6,7,5	mitosis	127	0.0196	17	0.0213	0.0980450	E
○	GO:0015849	4,5	organic acid transport	55	0.0085	9	0.0113	0.0987874	E
○	GO:0001302	5	replicative cell aging	39	0.0060	7	0.0088	0.0990785	E
○	GO:0006612	9,7,8	protein targeting to membrane	39	0.0060	7	0.0088	0.0990785	E

○	GO:0006820	5,6	anion transport	17	0.0026	4	0.0050	0.0995369	E
○	GO:0045132	9,7,8,6,4	meiotic chromosome segregation	17	0.0026	4	0.0050	0.0995369	E
○	GO:0007004	9	telomere maintenance via telomerase	17	0.0026	4	0.0050	0.0995369	E
○	GO:0006576	5,6	biogenic amine metabolic process	24	0.0037	5	0.0063	0.0995517	E
○	GO:0040007	2	growth	141	0.0218	18	0.0225	0.1001275	E
○	GO:0008283	3	cell proliferation	5	0.0008	2	0.0025	0.1025211	E
○	GO:0016078	7	tRNA catabolic process	5	0.0008	2	0.0025	0.1025211	E
○	GO:0006873	7,5	cellular ion homeostasis	115	0.0178	15	0.0188	0.1079732	E
○	GO:0055082	6,4	cellular chemical homeostasis	115	0.0178	15	0.0188	0.1079732	E
○	GO:0006098	9,10,11	pentose-phosphate shunt	11	0.0017	3	0.0038	0.1080476	E
○	GO:0016237	4,6	microautophagy	11	0.0017	3	0.0038	0.1080476	E
○	GO:0050801	6	ion homeostasis	119	0.0184	15	0.0188	0.1101641	E
○	GO:0048878	5	chemical homeostasis	121	0.0187	15	0.0188	0.1104525	E
○	GO:0016571	11,9,10,8	histone methylation	18	0.0028	4	0.0050	0.1122242	E
○	GO:0006378	9	mRNA polyadenylation	18	0.0028	4	0.0050	0.1122242	E
○	GO:0007017	6	microtubule-based process	101	0.0156	13	0.0163	0.1171576	E
○	GO:0006888	8,6,5,7	ER to Golgi vesicle-mediated transport	81	0.0125	11	0.0138	0.1221203	E
○	GO:0000226	7	microtubule cytoskeleton organization and biogenesis	81	0.0125	11	0.0138	0.1221203	E
○	GO:0009064	6,7	glutamine family amino acid metabolic process	43	0.0066	7	0.0088	0.1227560	E
○	GO:0019478	7,8	D-amino acid catabolic process	1	0.0002	1	0.0013	0.1233786	E
○	GO:0009139	7,8	pyrimidine nucleoside diphosphate biosynthetic process	1	0.0002	1	0.0013	0.1233786	E
○	GO:0009149	7,8	pyrimidine nucleoside triphosphate catabolic process	1	0.0002	1	0.0013	0.1233786	E
○	GO:0031060	7,9,12,6,10,11,8	regulation of histone methylation	1	0.0002	1	0.0013	0.1233786	E
○	GO:0009189	7,8	deoxyribonucleoside diphosphate biosynthetic process	1	0.0002	1	0.0013	0.1233786	E
○	GO:0015959	9	diadenosine polyphosphate metabolic process	1	0.0002	1	0.0013	0.1233786	E
○	GO:0015746	7,8	citrate transport	1	0.0002	1	0.0013	0.1233786	E
○	GO:0006146	8,7	adenine catabolic process	1	0.0002	1	0.0013	0.1233786	E
○	GO:0033353	7,6	S-adenosylmethionine cycle	1	0.0002	1	0.0013	0.1233786	E
○	GO:0033559	6,8,7	unsaturated fatty acid metabolic process	1	0.0002	1	0.0013	0.1233786	E
○	GO:0046075	9	dTTP metabolic process	1	0.0002	1	0.0013	0.1233786	E
○	GO:0000414	8,10,13,7,11,12,9	regulation of histone H3-K36 methylation	1	0.0002	1	0.0013	0.1233786	E
○	GO:0006843	8,6,7,9	mitochondrial citrate transport	1	0.0002	1	0.0013	0.1233786	E
○	GO:0006427	9,8,10,7	histidyl-tRNA aminoacylation	1	0.0002	1	0.0013	0.1233786	E
○	GO:0009176	8	pyrimidine deoxyribonucleoside monophosphate metabolic process	1	0.0002	1	0.0013	0.1233786	E
○	GO:0000734	7,9,8	gene conversion at mating-type locus, DNA repair synthesis	1	0.0002	1	0.0013	0.1233786	E
○	GO:0046073	9	dTMP metabolic process	1	0.0002	1	0.0013	0.1233786	E
○	GO:0031569	10,12,11,9	G2/M transition size control checkpoint	1	0.0002	1	0.0013	0.1233786	E
○	GO:0002097	8,9	tRNA wobble base modification	1	0.0002	1	0.0013	0.1233786	E
○	GO:0018008	11,12,9,10	N-terminal peptidyl-glycine N-myristoylation	1	0.0002	1	0.0013	0.1233786	E
○	GO:0009223	7,8	pyrimidine deoxyribonucleotide catabolic process	1	0.0002	1	0.0013	0.1233786	E
○	GO:0006227	9,10	dUDP biosynthetic process	1	0.0002	1	0.0013	0.1233786	E
○	GO:0006168	8,7	adenine salvage	1	0.0002	1	0.0013	0.1233786	E

○	GO:0008615	8	pyridoxine biosynthetic process	1	0.0002	1	0.0013	0.1233786	E
○	GO:0045292	10,12	nuclear mRNA cis splicing, via U2-type spliceosome	1	0.0002	1	0.0013	0.1233786	E
○	GO:0009129	7	pyrimidine nucleoside monophosphate metabolic process	1	0.0002	1	0.0013	0.1233786	E
○	GO:0009157	7,8	deoxyribonucleoside monophosphate biosynthetic process	1	0.0002	1	0.0013	0.1233786	E
○	GO:0046033	9	AMP metabolic process	1	0.0002	1	0.0013	0.1233786	E
○	GO:0046077	9	dUDP metabolic process	1	0.0002	1	0.0013	0.1233786	E
○	GO:0009446	8,9	putrescine biosynthetic process	1	0.0002	1	0.0013	0.1233786	E
○	GO:0006244	6,7	pyrimidine nucleotide catabolic process	1	0.0002	1	0.0013	0.1233786	E
○	GO:0006231	9,10	dTMP biosynthetic process	1	0.0002	1	0.0013	0.1233786	E
○	GO:0009105	7,6	lipoic acid biosynthetic process	1	0.0002	1	0.0013	0.1233786	E
○	GO:0018004	10,9	N-terminal protein formylation	1	0.0002	1	0.0013	0.1233786	E
○	GO:0046113	6,5	nucleobase catabolic process	1	0.0002	1	0.0013	0.1233786	E
○	GO:0000360	8,9,7,11,13	cis assembly of U2-type pre-catalytic spliceosome	1	0.0002	1	0.0013	0.1233786	E
○	GO:0009138	7	pyrimidine nucleoside diphosphate metabolic process	1	0.0002	1	0.0013	0.1233786	E
○	GO:0042256	8,7	mature ribosome assembly	1	0.0002	1	0.0013	0.1233786	E
○	GO:0018256	8	protein amino acid formylation	1	0.0002	1	0.0013	0.1233786	E
○	GO:0006521	7,6	regulation of amino acid metabolic process	1	0.0002	1	0.0013	0.1233786	E
○	GO:0006145	7,6	purine base catabolic process	1	0.0002	1	0.0013	0.1233786	E
○	GO:0015721	7,8	bile acid and bile salt transport	1	0.0002	1	0.0013	0.1233786	E
○	GO:0015856	7,8	cytosine transport	1	0.0002	1	0.0013	0.1233786	E
○	GO:0046072	9	dTDP metabolic process	1	0.0002	1	0.0013	0.1233786	E
○	GO:0018216	9,10,8	peptidyl-arginine methylation	1	0.0002	1	0.0013	0.1233786	E
○	GO:0001718	8,7,11,10,9	conversion of met-tRNAf to fmet-tRNA	1	0.0002	1	0.0013	0.1233786	E
○	GO:0042819	7	vitamin B6 biosynthetic process	1	0.0002	1	0.0013	0.1233786	E
○	GO:0006570	7,6,8	tyrosine metabolic process	1	0.0002	1	0.0013	0.1233786	E
○	GO:0032263	7,8	GMP salvage	1	0.0002	1	0.0013	0.1233786	E
○	GO:0046107	8,7	uracil biosynthetic process	1	0.0002	1	0.0013	0.1233786	E
○	GO:0008315	10,8,7,5,9,6,4	meiotic G2/MI transition	1	0.0002	1	0.0013	0.1233786	E
○	GO:0031567	9,11,10,8	cell size control checkpoint	1	0.0002	1	0.0013	0.1233786	E
○	GO:0006235	9,10	dTTP biosynthetic process	1	0.0002	1	0.0013	0.1233786	E
○	GO:0018201	8	peptidyl-glycine modification	1	0.0002	1	0.0013	0.1233786	E
○	GO:0019284	9,7,8,6,10	methionine biosynthetic process from S-adenosylmethionine	1	0.0002	1	0.0013	0.1233786	E
○	GO:0006425	9,8,10,7	glutaminyl-tRNA aminoacylation	1	0.0002	1	0.0013	0.1233786	E
○	GO:0000459	7,8	exonucleolytic trimming during rRNA processing	1	0.0002	1	0.0013	0.1233786	E
○	GO:0006233	9,10	dTDP biosynthetic process	1	0.0002	1	0.0013	0.1233786	E
○	GO:0043096	7,6	purine base salvage	1	0.0002	1	0.0013	0.1233786	E
○	GO:0015729	7,8	oxaloacetate transport	1	0.0002	1	0.0013	0.1233786	E
○	GO:0015772	5,6	oligosaccharide transport	1	0.0002	1	0.0013	0.1233786	E
○	GO:0009212	8,9	pyrimidine deoxyribonucleoside triphosphate biosynthetic process	1	0.0002	1	0.0013	0.1233786	E
○	GO:0009186	7	deoxyribonucleoside diphosphate metabolic process	1	0.0002	1	0.0013	0.1233786	E
○	GO:0015857	7,8	uracil transport	1	0.0002	1	0.0013	0.1233786	E
○	GO:0000415	9,11,14,8,12,13,10	negative regulation of histone H3-K36 methylation	1	0.0002	1	0.0013	0.1233786	E

○	GO:0033238	6,5	regulation of amine metabolic process	1	0.0002	1	0.0013	0.1233786	E
○	GO:0006421	9,8,10,7	asparaginyl-tRNA aminoacylation	1	0.0002	1	0.0013	0.1233786	E
○	GO:0006286	8,7	base-excision repair, base-free sugar-phosphate removal	1	0.0002	1	0.0013	0.1233786	E
○	GO:0043570	6	maintenance of DNA repeat elements	1	0.0002	1	0.0013	0.1233786	E
○	GO:0009196	8	pyrimidine deoxyribonucleoside diphosphate metabolic process	1	0.0002	1	0.0013	0.1233786	E
○	GO:0009162	7	deoxyribonucleoside monophosphate metabolic process	1	0.0002	1	0.0013	0.1233786	E
○	GO:0006831	9,10	low-affinity zinc ion transport	1	0.0002	1	0.0013	0.1233786	E
○	GO:0006438	9,8,10,7	valyl-tRNA aminoacylation	1	0.0002	1	0.0013	0.1233786	E
○	GO:0015817	7,8,9	histidine transport	1	0.0002	1	0.0013	0.1233786	E
○	GO:0008612	8,7,9	hypusine biosynthetic process from peptidyl-lysine	1	0.0002	1	0.0013	0.1233786	E
○	GO:0006167	9,10	AMP biosynthetic process	1	0.0002	1	0.0013	0.1233786	E
○	GO:0015887	5,6	pantothenate transport	1	0.0002	1	0.0013	0.1233786	E
○	GO:0031576	9,11,10,8	G2/M transition checkpoint	1	0.0002	1	0.0013	0.1233786	E
○	GO:0002098	9,10	tRNA wobble uridine modification	1	0.0002	1	0.0013	0.1233786	E
○	GO:0030259	6,7	lipid glycosylation	1	0.0002	1	0.0013	0.1233786	E
○	GO:0016259	7,8,6	selenocysteine metabolic process	1	0.0002	1	0.0013	0.1233786	E
○	GO:0000046	5,6	autophagic vacuole fusion	1	0.0002	1	0.0013	0.1233786	E
○	GO:0000351	8,7,10,11,12,13	assembly of spliceosomal tri-snRNP U4/U6.U5	1	0.0002	1	0.0013	0.1233786	E
○	GO:0048280	7,6	vesicle fusion with Golgi apparatus	1	0.0002	1	0.0013	0.1233786	E
○	GO:0006863	6,7	purine transport	1	0.0002	1	0.0013	0.1233786	E
○	GO:0009177	8,9	pyrimidine deoxyribonucleoside monophosphate biosynthetic process	1	0.0002	1	0.0013	0.1233786	E
○	GO:0019860	7	uracil metabolic process	1	0.0002	1	0.0013	0.1233786	E
○	GO:0019858	7	cytosine metabolic process	1	0.0002	1	0.0013	0.1233786	E
○	GO:0015785	7,8	UDP-galactose transport	1	0.0002	1	0.0013	0.1233786	E
○	GO:0051090	8,7	regulation of transcription factor activity	1	0.0002	1	0.0013	0.1233786	E
○	GO:0006387	8	snRNA capping	1	0.0002	1	0.0013	0.1233786	E
○	GO:0046416	6,7	D-amino acid metabolic process	1	0.0002	1	0.0013	0.1233786	E
○	GO:0000481	7,8	maturation of 5S rRNA	1	0.0002	1	0.0013	0.1233786	E
○	GO:0000115	10,9,8,5,7,4	S-phase-specific transcription in mitotic cell cycle	1	0.0002	1	0.0013	0.1233786	E
○	GO:0009148	7,8	pyrimidine nucleoside triphosphate biosynthetic process	1	0.0002	1	0.0013	0.1233786	E
○	GO:0000413	8	protein peptidyl-prolyl isomerization	1	0.0002	1	0.0013	0.1233786	E
○	GO:0009445	7,8	putrescine metabolic process	1	0.0002	1	0.0013	0.1233786	E
○	GO:0032264	7,8	IMP salvage	1	0.0002	1	0.0013	0.1233786	E
○	GO:0006636	8,7,9,6	unsaturated fatty acid biosynthetic process	1	0.0002	1	0.0013	0.1233786	E
○	GO:0043433	9,8	negative regulation of transcription factor activity	1	0.0002	1	0.0013	0.1233786	E
○	GO:0015806	7,8,9	S-methylmethionine transport	1	0.0002	1	0.0013	0.1233786	E
○	GO:0015862	7,8	uridine transport	1	0.0002	1	0.0013	0.1233786	E
○	GO:0043007	7	maintenance of rDNA	1	0.0002	1	0.0013	0.1233786	E
○	GO:0015861	7,8	cytidine transport	1	0.0002	1	0.0013	0.1233786	E
○	GO:0000412	11,9	histone peptidyl-prolyl isomerization	1	0.0002	1	0.0013	0.1233786	E
○	GO:0046498	6	S-adenosylhomocysteine metabolic process	1	0.0002	1	0.0013	0.1233786	E
○	GO:0009130	7,8	pyrimidine nucleoside monophosphate	1	0.0002	1	0.0013	0.1233786	E

○		7,8	biosynthetic process	1		1			E
○	GO:0006152	6,7	purine nucleoside catabolic process	1	0.0002	1	0.0013	0.1233786	E
○	GO:0009197	8,9	pyrimidine deoxyribonucleoside diphosphate biosynthetic process	1	0.0002	1	0.0013	0.1233786	E
○	GO:0000273	6,5	lipoic acid metabolic process	1	0.0002	1	0.0013	0.1233786	E
○	GO:0051568	12,10,11,9	histone H3-K4 methylation	1	0.0002	1	0.0013	0.1233786	E
○	GO:0009213	8,9	pyrimidine deoxyribonucleoside triphosphate catabolic process	1	0.0002	1	0.0013	0.1233786	E
○	GO:0006626	9,8,7,6	protein targeting to mitochondrion	52	0.0080	8	0.0100	0.1234574	E
○	GO:0046148	5	pigment biosynthetic process	19	0.0029	4	0.0050	0.1246515	E
○	GO:0000819	7,4	sister chromatid segregation	62	0.0096	9	0.0113	0.1256734	E
○	GO:0006457	6	protein folding	84	0.0130	11	0.0138	0.1260917	E
○	GO:0015914	5,6	phospholipid transport	12	0.0019	3	0.0038	0.1263258	E
○	GO:0006284	7,6	base-excision repair	12	0.0019	3	0.0038	0.1263258	E
○	GO:0000083	10,9,6,5,7,8,4	G1/S-specific transcription in mitotic cell cycle	12	0.0019	3	0.0038	0.1263258	E
○	GO:0007007	6,7	inner mitochondrial membrane organization and biogenesis	12	0.0019	3	0.0038	0.1263258	E
○	GO:0006970	4	response to osmotic stress	89	0.0137	11	0.0138	0.1283853	E
○	GO:0065004	6,5	protein-DNA complex assembly	74	0.0114	10	0.0125	0.1291828	E
○	GO:0045944	10,9	positive regulation of transcription from RNA polymerase II promoter	76	0.0117	10	0.0125	0.1319384	E
○	GO:0051188	5	cofactor biosynthetic process	79	0.0122	10	0.0125	0.1341848	E
○	GO:0017148	8,7,6	negative regulation of protein biosynthetic process	6	0.0009	2	0.0025	0.1348412	E
○	GO:0031327	7,6	negative regulation of cellular biosynthetic process	6	0.0009	2	0.0025	0.1348412	E
○	GO:0031383	5,7,10,9,8,6,11	regulation of mating projection biogenesis	6	0.0009	2	0.0025	0.1348412	E
○	GO:0031344	4,6,8,7,5,9	regulation of cell projection organization and biogenesis	6	0.0009	2	0.0025	0.1348412	E
○	GO:0009396	6,7,8	folic acid and derivative biosynthetic process	6	0.0009	2	0.0025	0.1348412	E
○	GO:0046489	9,8,10	phosphoinositide biosynthetic process	28	0.0043	5	0.0063	0.1361136	E
○	GO:0006614	11,10,9,8,7	SRP-dependent cotranslational protein targeting to membrane	20	0.0031	4	0.0050	0.1366301	E
○	GO:0051053	8,7	negative regulation of DNA metabolic process	20	0.0031	4	0.0050	0.1366301	E
○	GO:0042440	4	pigment metabolic process	20	0.0031	4	0.0050	0.1366301	E
○	GO:0006353	8,7	transcription termination	20	0.0031	4	0.0050	0.1366301	E
○	GO:0006308	5,6	DNA catabolic process	20	0.0031	4	0.0050	0.1366301	E
○	GO:0006334	6,7,10	nucleosome assembly	13	0.0020	3	0.0038	0.1440004	E
○	GO:0006783	7,6,8	heme biosynthetic process	13	0.0020	3	0.0038	0.1440004	E
○	GO:0006450	8,7,6	regulation of translational fidelity	13	0.0020	3	0.0038	0.1440004	E
○	GO:0007103	6,7,5,8	spindle pole body duplication in nuclear envelope	13	0.0020	3	0.0038	0.1440004	E
○	GO:0006779	6,7	porphyrin biosynthetic process	13	0.0020	3	0.0038	0.1440004	E
○	GO:0033014	6	tetrapyrrole biosynthetic process	13	0.0020	3	0.0038	0.1440004	E
○	GO:0000725	7,6	recombinational repair	29	0.0045	5	0.0063	0.1442179	E
○	GO:0006470	8,7	protein amino acid dephosphorylation	29	0.0045	5	0.0063	0.1442179	E
○	GO:0000070	9,7,5,8,6,4	mitotic sister chromatid segregation	59	0.0091	8	0.0100	0.1449395	E
○	GO:0007264	6	small GTPase mediated signal transduction	61	0.0094	8	0.0100	0.1479498	E
○	GO:0007569	4	cell aging	49	0.0076	7	0.0088	0.1487205	E
○	GO:0007568	3	aging	49	0.0076	7	0.0088	0.1487205	E

○	GO:0043543	7	protein amino acid acylation	62	0.0096	8	0.0100	0.1489227	E
○	GO:0007265	7	Ras protein signal transduction	39	0.0060	6	0.0075	0.1496079	E
○	GO:0015837	4,5	amine transport	50	0.0077	7	0.0088	0.1516206	E
○	GO:0006665	6,7	sphingolipid metabolic process	30	0.0046	5	0.0063	0.1517475	E
○	GO:0048284	5	organelle fusion	22	0.0034	4	0.0050	0.1586050	E
○	GO:0040020	7,9,8,6	regulation of meiosis	22	0.0034	4	0.0050	0.1586050	E
○	GO:0030150	10,9,8,7	protein import into mitochondrial matrix	22	0.0034	4	0.0050	0.1586050	E
○	GO:0007088	7,9,8,6	regulation of mitosis	55	0.0085	7	0.0088	0.1595465	E
○	GO:0006352	7,8,6	transcription initiation	55	0.0085	7	0.0088	0.1595465	E
○	GO:0006740	10,9	NADPH regeneration	14	0.0022	3	0.0038	0.1607009	E
○	GO:0030474	5,6,4,7	spindle pole body duplication	14	0.0022	3	0.0038	0.1607009	E
○	GO:0006778	5,6	porphyrin metabolic process	14	0.0022	3	0.0038	0.1607009	E
○	GO:0042168	6,7,5	heme metabolic process	14	0.0022	3	0.0038	0.1607009	E
○	GO:0033013	5	tetrapyrrole metabolic process	14	0.0022	3	0.0038	0.1607009	E
○	GO:0030384	8,9	phosphoinositide metabolic process	43	0.0066	6	0.0075	0.1652045	E
○	GO:0009615	4,5	response to virus	7	0.0011	2	0.0025	0.1655233	E
○	GO:0009225	5	nucleotide-sugar metabolic process	7	0.0011	2	0.0025	0.1655233	E
○	GO:0031382	9,8,10,7	mating projection biogenesis	7	0.0011	2	0.0025	0.1655233	E
○	GO:0051707	3,4	response to other organism	7	0.0011	2	0.0025	0.1655233	E
○	GO:0000710	11,9,8,6,5,10,7,4	meiotic mismatch repair	7	0.0011	2	0.0025	0.1655233	E
○	GO:0043331	4	response to dsRNA	7	0.0011	2	0.0025	0.1655233	E
○	GO:0006829	8,9	zinc ion transport	7	0.0011	2	0.0025	0.1655233	E
○	GO:0043330	5,6	response to exogenous dsRNA	7	0.0011	2	0.0025	0.1655233	E
○	GO:0006560	7,8	proline metabolic process	7	0.0011	2	0.0025	0.1655233	E
○	GO:0006367	8,9,7	transcription initiation from RNA polymerase II promoter	44	0.0068	6	0.0075	0.1677091	E
○	GO:0006289	7,6	nucleotide-excision repair	44	0.0068	6	0.0075	0.1677091	E
○	GO:0019748	3	secondary metabolic process	23	0.0036	4	0.0050	0.1683456	E
○	GO:0007051	8	spindle organization and biogenesis	47	0.0073	6	0.0075	0.1718921	E
○	GO:0042158	7,5	lipoprotein biosynthetic process	48	0.0074	6	0.0075	0.1722168	E
○	GO:0006497	8,7,6	protein amino acid lipidation	48	0.0074	6	0.0075	0.1722168	E
○	GO:0042157	6	lipoprotein metabolic process	48	0.0074	6	0.0075	0.1722168	E
○	GO:0030004	9,7	cellular monovalent inorganic cation homeostasis	34	0.0053	5	0.0063	0.1751151	E
○	GO:0006869	4,5	lipid transport	34	0.0053	5	0.0063	0.1751151	E
○	GO:0055067	8	monovalent inorganic cation homeostasis	34	0.0053	5	0.0063	0.1751151	E
○	GO:0006267	8,7	pre-replicative complex assembly	15	0.0023	3	0.0038	0.1761318	E
○	GO:0000737	6,7	DNA catabolic process, endonucleolytic	15	0.0023	3	0.0038	0.1761318	E
○	GO:0045851	8	pH reduction	24	0.0037	4	0.0050	0.1771268	E
○	GO:0000288	10,8,9	mRNA catabolic process, deadenylation-dependent decay	24	0.0037	4	0.0050	0.1771268	E
○	GO:0051452	12,9,10	cellular pH reduction	24	0.0037	4	0.0050	0.1771268	E
○	GO:0007035	13,10,6,11	vacuolar acidification	24	0.0037	4	0.0050	0.1771268	E
○	GO:0007530	4,5	sex determination	35	0.0054	5	0.0063	0.1791201	E
○	GO:0007531	4,6,5	mating type determination	35	0.0054	5	0.0063	0.1791201	E
○	GO:0003006	3,4	reproductive developmental process	35	0.0054	5	0.0063	0.1791201	E
○	GO:0051252	7,6	regulation of RNA metabolic process	36	0.0056	5	0.0063	0.1823684	E
○	GO:0030641	10,8	cellular hydrogen ion homeostasis	25	0.0039	4	0.0050	0.1848830	E

○	GO:0051453	11,8,9	regulation of cellular pH	25	0.0039	4	0.0050	0.1848830	E
○	GO:0046474	8,7,9	glycerophospholipid biosynthetic process	39	0.0060	5	0.0063	0.1876693	E
○	GO:0006865	5,6,7	amino acid transport	39	0.0060	5	0.0063	0.1876693	E
○	GO:0006506	10,9,8,7,11	GPI anchor biosynthetic process	26	0.0040	4	0.0050	0.1915711	E
○	GO:0030030	7,6,8	cell projection organization and biogenesis	8	0.0012	2	0.0025	0.1935071	E
○	GO:0000903	6,4,8,7,9	cellular morphogenesis during vegetative growth	8	0.0012	2	0.0025	0.1935071	E
○	GO:0008156	9,8	negative regulation of DNA replication	8	0.0012	2	0.0025	0.1935071	E
○	GO:0030031	8,7,9	cell projection biogenesis	8	0.0012	2	0.0025	0.1935071	E
○	GO:0000335	10,9,6	negative regulation of DNA transposition	8	0.0012	2	0.0025	0.1935071	E
○	GO:0048858	6,7	cell projection morphogenesis	8	0.0012	2	0.0025	0.1935071	E
○	GO:0009890	6,5	negative regulation of biosynthetic process	8	0.0012	2	0.0025	0.1935071	E
○	GO:0032990	5,6	cell part morphogenesis	8	0.0012	2	0.0025	0.1935071	E
○	GO:0007323	9	peptide pheromone maturation	8	0.0012	2	0.0025	0.1935071	E
○	GO:0019878	9,10	lysine biosynthetic process via aminoadipic acid	8	0.0012	2	0.0025	0.1935071	E
○	GO:0007093	8,10,9,7	mitotic cell cycle checkpoint	27	0.0042	4	0.0050	0.1971691	E
○	GO:0006505	9,10	GPI anchor metabolic process	27	0.0042	4	0.0050	0.1971691	E
○	GO:0009084	7,8	glutamine family amino acid biosynthetic process	27	0.0042	4	0.0050	0.1971691	E
○	GO:0032005	7,6	signal transduction during conjugation with cellular fusion	28	0.0043	4	0.0050	0.2016736	E
○	GO:0000750	8,7,6	pheromone-dependent signal transduction during conjugation with cellular fusion	28	0.0043	4	0.0050	0.2016736	E
○	GO:0006739	9,8	NADP metabolic process	17	0.0026	3	0.0038	0.2023607	E
○	GO:0000742	7,5	karyogamy during conjugation with cellular fusion	17	0.0026	3	0.0038	0.2023607	E
○	GO:0000741	6	karyogamy	17	0.0026	3	0.0038	0.2023607	E
○	GO:0007533	5,7,6	mating type switching	29	0.0045	4	0.0050	0.2050978	E
○	GO:0006885	7	regulation of pH	29	0.0045	4	0.0050	0.2050978	E
○	GO:0009063	6,7	amino acid catabolic process	29	0.0045	4	0.0050	0.2050978	E
○	GO:0043487	8,7	regulation of RNA stability	30	0.0046	4	0.0050	0.2074690	E
○	GO:0046999	5,4	regulation of conjugation	30	0.0046	4	0.0050	0.2074690	E
○	GO:0009141	6	nucleoside triphosphate metabolic process	30	0.0046	4	0.0050	0.2074690	E
○	GO:0031137	6,5	regulation of conjugation with cellular fusion	30	0.0046	4	0.0050	0.2074690	E
○	GO:0043488	9,8,7	regulation of mRNA stability	30	0.0046	4	0.0050	0.2074690	E
○	GO:0007121	8,6,10,7,11,5	bipolar cellular bud site selection	32	0.0049	4	0.0050	0.2092202	E
○	GO:0044270	5,4	nitrogen compound catabolic process	32	0.0049	4	0.0050	0.2092202	E
○	GO:0009310	5,6	amine catabolic process	32	0.0049	4	0.0050	0.2092202	E
○	GO:0000753	7,8,6	cellular morphogenesis during conjugation with cellular fusion	18	0.0028	3	0.0038	0.2129064	E
○	GO:0006369	9,8	transcription termination from RNA polymerase II promoter	18	0.0028	3	0.0038	0.2129064	E
○	GO:0016576	11,9,8	histone dephosphorylation	2	0.0003	1	0.0013	0.2163461	E
○	GO:0006451	8,7,6	translational readthrough	2	0.0003	1	0.0013	0.2163461	E
○	GO:0051666	5,4	actin cortical patch localization	2	0.0003	1	0.0013	0.2163461	E
○	GO:0046087	8	cytidine metabolic process	2	0.0003	1	0.0013	0.2163461	E
○	GO:0033313	8,7	meiotic cell cycle checkpoint	2	0.0003	1	0.0013	0.2163461	E
○	GO:0006429	9,8,10,7	leucyl-tRNA aminoacylation	2	0.0003	1	0.0013	0.2163461	E
○	GO:0006541	7,8	glutamine metabolic process	2	0.0003	1	0.0013	0.2163461	E

○	GO:0007580	10,6	extrachromosomal circular DNA accumulation during cell aging	2	0.0003	1	0.0013	0.2163461	E
○	GO:0006047	8,6,9	UDP-N-acetylglucosamine metabolic process	2	0.0003	1	0.0013	0.2163461	E
○	GO:0030969	8,6,7	UFP-specific transcription factor mRNA processing during unfolded protein response	2	0.0003	1	0.0013	0.2163461	E
○	GO:0009218	7	pyrimidine ribonucleotide metabolic process	2	0.0003	1	0.0013	0.2163461	E
○	GO:0046131	7	pyrimidine ribonucleoside metabolic process	2	0.0003	1	0.0013	0.2163461	E
○	GO:0045141	9,7,5,8,6,4	telomere clustering	2	0.0003	1	0.0013	0.2163461	E
○	GO:0000280	3	nuclear division	2	0.0003	1	0.0013	0.2163461	E
○	GO:0010043	6	response to zinc ion	2	0.0003	1	0.0013	0.2163461	E
○	GO:0035057	11,10,13	positive regulation of nuclear mRNA splicing via U2-type spliceosome	2	0.0003	1	0.0013	0.2163461	E
○	GO:0006824	7,8,9	cobalt ion transport	2	0.0003	1	0.0013	0.2163461	E
○	GO:0050685	9,8	positive regulation of mRNA processing	2	0.0003	1	0.0013	0.2163461	E
○	GO:0009133	6,7	nucleoside diphosphate biosynthetic process	2	0.0003	1	0.0013	0.2163461	E
○	GO:0042558	5	pteridine and derivative metabolic process	2	0.0003	1	0.0013	0.2163461	E
○	GO:0006661	10,9,11	phosphatidylinositol biosynthetic process	2	0.0003	1	0.0013	0.2163461	E
○	GO:0009298	9,6,7,10	GDP-mannose biosynthetic process	2	0.0003	1	0.0013	0.2163461	E
○	GO:0007000	6	nucleolus organization and biogenesis	2	0.0003	1	0.0013	0.2163461	E
○	GO:0046036	9	CTP metabolic process	2	0.0003	1	0.0013	0.2163461	E
○	GO:0044419	3	interspecies interaction between organisms	2	0.0003	1	0.0013	0.2163461	E
○	GO:0046135	6,7	pyrimidine nucleoside catabolic process	2	0.0003	1	0.0013	0.2163461	E
○	GO:0006282	8,7,6	regulation of DNA repair	2	0.0003	1	0.0013	0.2163461	E
○	GO:0051324	7,6,5	prophase	2	0.0003	1	0.0013	0.2163461	E
○	GO:0046656	7,8,9	folic acid biosynthetic process	2	0.0003	1	0.0013	0.2163461	E
○	GO:0048250	8,6,9,7,10	mitochondrial iron ion transport	2	0.0003	1	0.0013	0.2163461	E
○	GO:0000388	8,7,6,10,12	spliceosome conformational change to release U4 (or U4atac) and U1 (or U11)	2	0.0003	1	0.0013	0.2163461	E
○	GO:0051598	9,11,8,10,7	meiotic recombination checkpoint	2	0.0003	1	0.0013	0.2163461	E
○	GO:0019307	8,9	mannose biosynthetic process	2	0.0003	1	0.0013	0.2163461	E
○	GO:0035055	10,9,12	regulation of nuclear mRNA splicing via U2-type spliceosome	2	0.0003	1	0.0013	0.2163461	E
○	GO:0006048	9,7,10	UDP-N-acetylglucosamine biosynthetic process	2	0.0003	1	0.0013	0.2163461	E
○	GO:0006241	9,10	CTP biosynthetic process	2	0.0003	1	0.0013	0.2163461	E
○	GO:0006426	9,8,10,7	glycyl-tRNA aminoacylation	2	0.0003	1	0.0013	0.2163461	E
○	GO:0015781	6,7	pyrimidine nucleotide-sugar transport	2	0.0003	1	0.0013	0.2163461	E
○	GO:0009220	7,8	pyrimidine ribonucleotide biosynthetic process	2	0.0003	1	0.0013	0.2163461	E
○	GO:0007128	10,8,7,9,6	meiotic prophase I	2	0.0003	1	0.0013	0.2163461	E
○	GO:0009061	6	anaerobic respiration	2	0.0003	1	0.0013	0.2163461	E
○	GO:0006545	8,9	glycine biosynthetic process	2	0.0003	1	0.0013	0.2163461	E
○	GO:0009226	5,6	nucleotide-sugar biosynthetic process	2	0.0003	1	0.0013	0.2163461	E
○	GO:0009208	8	pyrimidine ribonucleoside triphosphate metabolic process	2	0.0003	1	0.0013	0.2163461	E
○	GO:0046655	6,8	folic acid metabolic process	2	0.0003	1	0.0013	0.2163461	E
○	GO:0050667	7,8,6	homocysteine metabolic process	2	0.0003	1	0.0013	0.2163461	E
○	GO:0032261	6,7	purine nucleotide salvage	2	0.0003	1	0.0013	0.2163461	E

○	GO:0000354	7,8,6,10,12	cis assembly of pre-catalytic spliceosome	2	0.0003	1	0.0013	0.2163461	E
○	GO:0031056	6,8,11,5,9,7	regulation of histone modification	2	0.0003	1	0.0013	0.2163461	E
○	GO:0048026	10,9,12	positive regulation of nuclear mRNA splicing, via spliceosome	2	0.0003	1	0.0013	0.2163461	E
○	GO:0010032	7	meiotic chromosome condensation	2	0.0003	1	0.0013	0.2163461	E
○	GO:0009209	8,9	pyrimidine ribonucleoside triphosphate biosynthetic process	2	0.0003	1	0.0013	0.2163461	E
○	GO:0006430	9,8,10,7	lysyl-tRNA aminoacylation	2	0.0003	1	0.0013	0.2163461	E
○	GO:0009202	7,8	deoxyribonucleoside triphosphate biosynthetic process	2	0.0003	1	0.0013	0.2163461	E
○	GO:0009847	5	spore germination	2	0.0003	1	0.0013	0.2163461	E
○	GO:0046037	9	GMP metabolic process	2	0.0003	1	0.0013	0.2163461	E
○	GO:0042559	6	pteridine and derivative biosynthetic process	2	0.0003	1	0.0013	0.2163461	E
○	GO:0019673	8,6,9	GDP-mannose metabolic process	2	0.0003	1	0.0013	0.2163461	E
○	GO:0006345	10,6,9	loss of chromatin silencing	9	0.0014	2	0.0025	0.2181379	E
○	GO:0007076	10,8,5,6,9,7,4	mitotic chromosome condensation	9	0.0014	2	0.0025	0.2181379	E
○	GO:0006283	8,7	transcription-coupled nucleotide-excision repair	9	0.0014	2	0.0025	0.2181379	E
○	GO:0015802	6,7,8	basic amino acid transport	9	0.0014	2	0.0025	0.2181379	E
○	GO:0006760	5,7	folic acid and derivative metabolic process	9	0.0014	2	0.0025	0.2181379	E
○	GO:0030491	7,9,10,6,8	heteroduplex formation	9	0.0014	2	0.0025	0.2181379	E
○	GO:0030847	10,9	transcription termination from Pol II promoter, RNA polymerase(A)-independent	9	0.0014	2	0.0025	0.2181379	E
○	GO:0006474	10,9	N-terminal protein amino acid acetylation	9	0.0014	2	0.0025	0.2181379	E
○	GO:0045815	5	positive regulation of gene expression, epigenetic	9	0.0014	2	0.0025	0.2181379	E
○	GO:0000767	6,7	cellular morphogenesis during conjugation	20	0.0031	3	0.0038	0.2286323	E
○	GO:0016579	9	protein deubiquitination	20	0.0031	3	0.0038	0.2286323	E
○	GO:0030148	7,6,8	sphingolipid biosynthetic process	20	0.0031	3	0.0038	0.2286323	E
○	GO:0007231	6,5	osmosensory signaling pathway	22	0.0034	3	0.0038	0.2373832	E
○	GO:0006882	10,8	cellular zinc ion homeostasis	10	0.0015	2	0.0025	0.2390679	E
○	GO:0006313	7,4	transposition, DNA-mediated	10	0.0015	2	0.0025	0.2390679	E
○	GO:0006268	8	DNA unwinding during replication	10	0.0015	2	0.0025	0.2390679	E
○	GO:0055069	9	zinc ion homeostasis	10	0.0015	2	0.0025	0.2390679	E
○	GO:0001301	9,5	progressive alteration of chromatin during cell aging	10	0.0015	2	0.0025	0.2390679	E
○	GO:0009068	7,8	aspartate family amino acid catabolic process	10	0.0015	2	0.0025	0.2390679	E
○	GO:0000337	9,8,5	regulation of DNA transposition	10	0.0015	2	0.0025	0.2390679	E
○	GO:0030174	9,7,8	regulation of DNA replication initiation	10	0.0015	2	0.0025	0.2390679	E
○	GO:0007534	6,8,7	gene conversion at mating-type locus	23	0.0036	3	0.0038	0.2393215	E
○	GO:0007006	5,6	mitochondrial membrane organization and biogenesis	24	0.0037	3	0.0038	0.2397718	E
○	GO:0043086	5	negative regulation of enzyme activity	11	0.0017	2	0.0025	0.2561782	E
○	GO:0030261	6	chromosome condensation	11	0.0017	2	0.0025	0.2561782	E
○	GO:0006488	10,9,8	dolichol-linked oligosaccharide biosynthetic process	11	0.0017	2	0.0025	0.2561782	E
○	GO:0006276	3	plasmid maintenance	11	0.0017	2	0.0025	0.2561782	E
○	GO:0045910	9,8	negative regulation of DNA recombination	12	0.0019	2	0.0025	0.2695161	E
○	GO:0000302	5	response to reactive oxygen species	12	0.0019	2	0.0025	0.2695161	E
○	GO:0006301	7,6	postreplication repair	13	0.0020	2	0.0025	0.2792462	E

○	GO:0006537	8,9	glutamate biosynthetic process	13	0.0020	2	0.0025	0.2792462	E
○	GO:0031929	6	TOR signaling pathway	13	0.0020	2	0.0025	0.2792462	E
○	GO:0048024	9,8,11	regulation of nuclear mRNA splicing, via spliceosome	3	0.0005	1	0.0013	0.2845182	E
○	GO:0006835	6,7	dicarboxylic acid transport	3	0.0005	1	0.0013	0.2845182	E
○	GO:0000912	6,5,9,4	cytokinesis, formation of actomyosin apparatus	3	0.0005	1	0.0013	0.2845182	E
○	GO:0019509	7,8,6,9	methionine salvage	3	0.0005	1	0.0013	0.2845182	E
○	GO:0006549	7,8	isoleucine metabolic process	3	0.0005	1	0.0013	0.2845182	E
○	GO:0008272	7,8	sulfate transport	3	0.0005	1	0.0013	0.2845182	E
○	GO:0000321	9,8,7,6	re-entry into mitotic cell cycle after pheromone arrest	3	0.0005	1	0.0013	0.2845182	E
○	GO:0030100	6,7,5	regulation of endocytosis	3	0.0005	1	0.0013	0.2845182	E
○	GO:0016584	6,10	nucleosome positioning	3	0.0005	1	0.0013	0.2845182	E
○	GO:0018206	8	peptidyl-methionine modification	3	0.0005	1	0.0013	0.2845182	E
○	GO:0009132	6	nucleoside diphosphate metabolic process	3	0.0005	1	0.0013	0.2845182	E
○	GO:0000160	5	two-component signal transduction system (phosphorelay)	3	0.0005	1	0.0013	0.2845182	E
○	GO:0000915	7,6,10,5	cytokinesis, contractile ring formation	3	0.0005	1	0.0013	0.2845182	E
○	GO:0051352	6	negative regulation of ligase activity	3	0.0005	1	0.0013	0.2845182	E
○	GO:0051503	7,8	adenine nucleotide transport	3	0.0005	1	0.0013	0.2845182	E
○	GO:0000320	7,6	re-entry into mitotic cell cycle	3	0.0005	1	0.0013	0.2845182	E
○	GO:0031032	8	actomyosin structure organization and biogenesis	3	0.0005	1	0.0013	0.2845182	E
○	GO:0006449	8,7,9,6	regulation of translational termination	3	0.0005	1	0.0013	0.2845182	E
○	GO:0015867	8,9	ATP transport	3	0.0005	1	0.0013	0.2845182	E
○	GO:0007030	5	Golgi organization and biogenesis	3	0.0005	1	0.0013	0.2845182	E
○	GO:0017196	11,9,10	N-terminal peptidyl-methionine acetylation	3	0.0005	1	0.0013	0.2845182	E
○	GO:0051444	7	negative regulation of ubiquitin ligase activity	3	0.0005	1	0.0013	0.2845182	E
○	GO:0006452	8,7,6	translational frameshifting	3	0.0005	1	0.0013	0.2845182	E
○	GO:0006833	5,6	water transport	3	0.0005	1	0.0013	0.2845182	E
○	GO:0006784	8,7,9	heme a biosynthetic process	3	0.0005	1	0.0013	0.2845182	E
○	GO:0046160	7,8,6	heme a metabolic process	3	0.0005	1	0.0013	0.2845182	E
○	GO:0050684	8,7	regulation of mRNA processing	3	0.0005	1	0.0013	0.2845182	E
○	GO:0019413	7,8	acetate biosynthetic process	3	0.0005	1	0.0013	0.2845182	E
○	GO:0006431	9,8,10,7	methionyl-tRNA aminoacylation	3	0.0005	1	0.0013	0.2845182	E
○	GO:0007234	7,6	osmosensory signaling pathway via two-component system	3	0.0005	1	0.0013	0.2845182	E
○	GO:0043102	6,5,7	amino acid salvage	3	0.0005	1	0.0013	0.2845182	E
○	GO:0007025	8	beta-tubulin folding	3	0.0005	1	0.0013	0.2845182	E
○	GO:0051225	5,9	spindle assembly	3	0.0005	1	0.0013	0.2845182	E
○	GO:0051436	8,6,5	negative regulation of ubiquitin ligase activity during mitotic cell cycle	3	0.0005	1	0.0013	0.2845182	E
○	GO:0006285	7,8	base-excision repair, AP site formation	3	0.0005	1	0.0013	0.2845182	E
○	GO:0042044	4,5	fluid transport	3	0.0005	1	0.0013	0.2845182	E
○	GO:0006567	8,9	threonine catabolic process	3	0.0005	1	0.0013	0.2845182	E
○	GO:0042787	10,9,11	protein ubiquitination during ubiquitin-dependent protein catabolic process	14	0.0022	2	0.0025	0.2856120	E
○	GO:0007118	7,6,5	budding cell apical bud growth	14	0.0022	2	0.0025	0.2856120	E
○	GO:0000754	8,7,5	adaptation to pheromone during conjugation with cellular fusion	15	0.0023	2	0.0025	0.2889065	E

○	GO:0015918	5,6	sterol transport	15	0.0023	2	0.0025	0.2889065	E
○	GO:0022401	7,6	adaptation of signaling pathway	15	0.0023	2	0.0025	0.2889065	E
○	GO:0016050	5	vesicle organization and biogenesis	16	0.0025	2	0.0025	0.2894495	E
○	GO:0010383	7,5,6	cell wall polysaccharide metabolic process	16	0.0025	2	0.0025	0.2894495	E
○	GO:0032508	7	DNA duplex unwinding	16	0.0025	2	0.0025	0.2894495	E
○	GO:0006536	7,8	glutamate metabolic process	16	0.0025	2	0.0025	0.2894495	E
○	GO:0032392	6	DNA geometric change	16	0.0025	2	0.0025	0.2894495	E
○	GO:0030497	8,7,9,6	fatty acid elongation	4	0.0006	1	0.0013	0.3325899	E
○	GO:0000391	8,10,12	U2-dependent spliceosome disassembly	4	0.0006	1	0.0013	0.3325899	E
○	GO:0009891	6,5	positive regulation of biosynthetic process	4	0.0006	1	0.0013	0.3325899	E
○	GO:0006278	7	RNA-dependent DNA replication	4	0.0006	1	0.0013	0.3325899	E
○	GO:0009452	7	RNA capping	4	0.0006	1	0.0013	0.3325899	E
○	GO:0045144	10,8,7,5,9,6,4	meiotic sister chromatid segregation	4	0.0006	1	0.0013	0.3325899	E
○	GO:0007135	9,7,6,8,5	meiosis II	4	0.0006	1	0.0013	0.3325899	E
○	GO:0018205	8	peptidyl-lysine modification	4	0.0006	1	0.0013	0.3325899	E
○	GO:0046686	6	response to cadmium ion	4	0.0006	1	0.0013	0.3325899	E
○	GO:0032988	6	protein-RNA complex disassembly	4	0.0006	1	0.0013	0.3325899	E
○	GO:0006596	7,8	polyamine biosynthetic process	4	0.0006	1	0.0013	0.3325899	E
○	GO:0000349	8,7,10,12	generation of catalytic spliceosome for first transesterification step	4	0.0006	1	0.0013	0.3325899	E
○	GO:0000304	6	response to singlet oxygen	4	0.0006	1	0.0013	0.3325899	E
○	GO:0042542	6	response to hydrogen peroxide	4	0.0006	1	0.0013	0.3325899	E
○	GO:0045727	8,7,6	positive regulation of protein biosynthetic process	4	0.0006	1	0.0013	0.3325899	E
○	GO:0046520	8,7,9	sphingoid biosynthetic process	4	0.0006	1	0.0013	0.3325899	E
○	GO:0000390	7,9,11	spliceosome disassembly	4	0.0006	1	0.0013	0.3325899	E
○	GO:0009083	7,8	branched chain family amino acid catabolic process	4	0.0006	1	0.0013	0.3325899	E
○	GO:0043173	5	nucleotide salvage	4	0.0006	1	0.0013	0.3325899	E
○	GO:0031119	8,9	tRNA pseudouridine synthesis	4	0.0006	1	0.0013	0.3325899	E
○	GO:0006085	7	acetyl-CoA biosynthetic process	4	0.0006	1	0.0013	0.3325899	E
○	GO:0030037	5,4,9	actin filament reorganization during cell cycle	4	0.0006	1	0.0013	0.3325899	E
○	GO:0031328	7,6	positive regulation of cellular biosynthetic process	4	0.0006	1	0.0013	0.3325899	E
○	GO:0031532	8	actin cytoskeleton reorganization	4	0.0006	1	0.0013	0.3325899	E
○	GO:0015865	6,7	purine nucleotide transport	4	0.0006	1	0.0013	0.3325899	E
○	GO:0046513	9,8,10	ceramide biosynthetic process	4	0.0006	1	0.0013	0.3325899	E
○	GO:0031578	9,11,10,8	mitotic cell cycle spindle orientation checkpoint	4	0.0006	1	0.0013	0.3325899	E
○	GO:0043137	7,10,6,9	DNA replication, removal of RNA primer	5	0.0008	1	0.0013	0.3644768	E
○	GO:0051083	8	cotranslational protein folding	5	0.0008	1	0.0013	0.3644768	E
○	GO:0030026	10,8	cellular manganese ion homeostasis	5	0.0008	1	0.0013	0.3644768	E
○	GO:0000092	8,9,10,7	mitotic anaphase B	5	0.0008	1	0.0013	0.3644768	E
○	GO:0000101	6,7,8	sulfur amino acid transport	5	0.0008	1	0.0013	0.3644768	E
○	GO:0018377	9,8,7	protein myristoylation	5	0.0008	1	0.0013	0.3644768	E
○	GO:0016562	6,11,10,8,9,7	protein import into peroxisome matrix, receptor recycling	5	0.0008	1	0.0013	0.3644768	E
○	GO:0016255	11,10,8,9,12	attachment of GPI anchor to protein	5	0.0008	1	0.0013	0.3644768	E
○	GO:0031385	6,8,11,10,9,7,12	regulation of termination of mating projection growth	5	0.0008	1	0.0013	0.3644768	E

○	GO:0006498	9,10,8,7	N-terminal protein lipidation	5	0.0008	1	0.0013	0.3644768	E
○	GO:0006862	5,6	nucleotide transport	5	0.0008	1	0.0013	0.3644768	E
○	GO:0001881	5,7	receptor recycling	5	0.0008	1	0.0013	0.3644768	E
○	GO:0007535	6,8,4,7	donor selection	5	0.0008	1	0.0013	0.3644768	E
○	GO:0000188	9,10,8	inactivation of MAPK activity	5	0.0008	1	0.0013	0.3644768	E
○	GO:0007232	7,6	osmosensory signaling pathway via Sho1 osmosensor	5	0.0008	1	0.0013	0.3644768	E
○	GO:0000076	11,9,8,10	DNA replication checkpoint	5	0.0008	1	0.0013	0.3644768	E
○	GO:0007023	8	post-chaperonin tubulin folding pathway	5	0.0008	1	0.0013	0.3644768	E
○	GO:0051254	8,7	positive regulation of RNA metabolic process	5	0.0008	1	0.0013	0.3644768	E
○	GO:0016233	9	telomere capping	5	0.0008	1	0.0013	0.3644768	E
○	GO:0055075	9	potassium ion homeostasis	5	0.0008	1	0.0013	0.3644768	E
○	GO:0051247	6,5	positive regulation of protein metabolic process	5	0.0008	1	0.0013	0.3644768	E
○	GO:0018319	10,9,8	protein amino acid myristoylation	5	0.0008	1	0.0013	0.3644768	E
○	GO:0051439	7,5,4	regulation of ubiquitin ligase activity during mitotic cell cycle	5	0.0008	1	0.0013	0.3644768	E
○	GO:0006797	6	polyphosphate metabolic process	5	0.0008	1	0.0013	0.3644768	E
○	GO:0043112	6	receptor metabolic process	5	0.0008	1	0.0013	0.3644768	E
○	GO:0006530	8,9	asparagine catabolic process	5	0.0008	1	0.0013	0.3644768	E
○	GO:0006816	7,8	calcium ion transport	5	0.0008	1	0.0013	0.3644768	E
○	GO:0055071	9	manganese ion homeostasis	5	0.0008	1	0.0013	0.3644768	E
○	GO:0000173	10,11,8,9,7	inactivation of MAPK activity during osmolarity sensing	5	0.0008	1	0.0013	0.3644768	E
○	GO:0000266	6	mitochondrial fission	5	0.0008	1	0.0013	0.3644768	E
○	GO:0006499	10,11,9,8	N-terminal protein myristoylation	5	0.0008	1	0.0013	0.3644768	E
○	GO:0043407	8,9	negative regulation of MAPK activity	5	0.0008	1	0.0013	0.3644768	E
○	GO:0030007	10,8	cellular potassium ion homeostasis	5	0.0008	1	0.0013	0.3644768	E
○	GO:0016236	4	macroautophagy	6	0.0009	1	0.0013	0.3834356	E
○	GO:0001324	5,6,7	age-dependent response to oxidative stress during chronological cell aging	6	0.0009	1	0.0013	0.3834356	E
○	GO:0006013	7,8	mannose metabolic process	6	0.0009	1	0.0013	0.3834356	E
○	GO:0006544	7,8	glycine metabolic process	6	0.0009	1	0.0013	0.3834356	E
○	GO:0008299	6,5,7	isoprenoid biosynthetic process	6	0.0009	1	0.0013	0.3834356	E
○	GO:0006376	8,7,10,12,3	mRNA splice site selection	6	0.0009	1	0.0013	0.3834356	E
○	GO:0009113	7,6	purine base biosynthetic process	6	0.0009	1	0.0013	0.3834356	E
○	GO:0045041	10,9,8,7	protein import into mitochondrial intermembrane space	6	0.0009	1	0.0013	0.3834356	E
○	GO:0046020	11,10,7	negative regulation of transcription from RNA polymerase II promoter by pheromones	6	0.0009	1	0.0013	0.3834356	E
○	GO:0006720	5,6	isoprenoid metabolic process	6	0.0009	1	0.0013	0.3834356	E
○	GO:0001323	4,5,6	age-dependent general metabolic decline during chronological cell aging	6	0.0009	1	0.0013	0.3834356	E
○	GO:0032297	10,8,9	negative regulation of DNA replication initiation	6	0.0009	1	0.0013	0.3834356	E
○	GO:0007029	5	endoplasmic reticulum organization and biogenesis	6	0.0009	1	0.0013	0.3834356	E
○	GO:0046021	10,8,5,6,9,7,4	regulation of transcription from RNA polymerase II promoter, mitotic	6	0.0009	1	0.0013	0.3834356	E
○	GO:0000090	7,8,9,6	mitotic anaphase	6	0.0009	1	0.0013	0.3834356	E
○	GO:0001306	4,5	age-dependent response to oxidative stress	6	0.0009	1	0.0013	0.3834356	E
○	GO:0043405	8	regulation of MAPK activity	6	0.0009	1	0.0013	0.3834356	E

○	GO:0007089	8,9,7,6	traversing start control point of mitotic cell cycle	6	0.0009	1	0.0013	0.3834356	E
○	GO:0051438	6	regulation of ubiquitin ligase activity	6	0.0009	1	0.0013	0.3834356	E
○	GO:0051322	6,7,5	anaphase	6	0.0009	1	0.0013	0.3834356	E
○	GO:0007130	11,9,8,6,5,10,7,4	synaptonemal complex assembly	6	0.0009	1	0.0013	0.3834356	E
○	GO:0006083	7	acetate metabolic process	6	0.0009	1	0.0013	0.3834356	E
○	GO:0051340	5	regulation of ligase activity	6	0.0009	1	0.0013	0.3834356	E
○	GO:0045143	10,8,7,5,9,6,4	homologous chromosome segregation	6	0.0009	1	0.0013	0.3834356	E
○	GO:0045996	10,9,6	negative regulation of transcription by pheromones	6	0.0009	1	0.0013	0.3834356	E
○	GO:0048285	5	organelle fission	6	0.0009	1	0.0013	0.3834356	E
○	GO:0031938	12,8,5,9,13,11	regulation of chromatin silencing at telomere	6	0.0009	1	0.0013	0.3834356	E
○	GO:0007070	11,9,6,7,10,8,5	negative regulation of transcription from RNA polymerase II promoter, mitotic	6	0.0009	1	0.0013	0.3834356	E
○	GO:0031935	11,7,4,8,12,10	regulation of chromatin silencing	6	0.0009	1	0.0013	0.3834356	E
○	GO:0001402	5,4	signal transduction during filamentous growth	7	0.0011	1	0.0013	0.3921671	E
○	GO:0007571	3,4	age-dependent general metabolic decline	7	0.0011	1	0.0013	0.3921671	E
○	GO:0009086	8,9,7	methionine biosynthetic process	7	0.0011	1	0.0013	0.3921671	E
○	GO:0000376	9	RNA splicing, via transesterification reactions with guanosine as nucleophile	7	0.0011	1	0.0013	0.3921671	E
○	GO:0043248	8,7	proteasome assembly	7	0.0011	1	0.0013	0.3921671	E
○	GO:0000372	10	Group I intron splicing	7	0.0011	1	0.0013	0.3921671	E
○	GO:0006621	7,6,5,4	protein retention in ER	7	0.0011	1	0.0013	0.3921671	E
○	GO:0009102	6,7,8	biotin biosynthetic process	7	0.0011	1	0.0013	0.3921671	E
○	GO:0007068	10,8,6,9,7,5	negative regulation of transcription, mitotic	7	0.0011	1	0.0013	0.3921671	E
○	GO:0045896	9,7,5,8,6,4	regulation of transcription, mitotic	7	0.0011	1	0.0013	0.3921671	E
○	GO:0045835	8,10,9,7	negative regulation of meiosis	7	0.0011	1	0.0013	0.3921671	E
○	GO:0045332	5,7,6,8	phospholipid translocation	7	0.0011	1	0.0013	0.3921671	E
○	GO:0006595	6,7	polyamine metabolic process	7	0.0011	1	0.0013	0.3921671	E
○	GO:0006469	7,8	negative regulation of protein kinase activity	7	0.0011	1	0.0013	0.3921671	E
○	GO:0051348	6	negative regulation of transferase activity	7	0.0011	1	0.0013	0.3921671	E
○	GO:0006998	5,6	nuclear membrane organization and biogenesis	7	0.0011	1	0.0013	0.3921671	E
○	GO:0006768	5,7,6	biotin metabolic process	7	0.0011	1	0.0013	0.3921671	E
○	GO:0033205	5,4	cytokinesis during cell cycle	7	0.0011	1	0.0013	0.3921671	E
○	GO:0009435	8,7,10,9	NAD biosynthetic process	7	0.0011	1	0.0013	0.3921671	E
○	GO:0000727	9,8	double-strand break repair via break-induced replication	7	0.0011	1	0.0013	0.3921671	E
○	GO:0006359	9,8	regulation of transcription from RNA polymerase III promoter	7	0.0011	1	0.0013	0.3921671	E
○	GO:0009092	7,8	homoserine metabolic process	7	0.0011	1	0.0013	0.3921671	E
○	GO:0015677	9,10	copper ion import	8	0.0012	1	0.0013	0.3929033	E
○	GO:0008614	7	pyridoxine metabolic process	8	0.0012	1	0.0013	0.3929033	E
○	GO:0018345	9,8,7	protein palmitoylation	8	0.0012	1	0.0013	0.3929033	E
○	GO:0018318	10,9,8	protein amino acid palmitoylation	8	0.0012	1	0.0013	0.3929033	E
○	GO:0031146	11,10,12	SCF-dependent proteasomal ubiquitin-dependent protein catabolic process	8	0.0012	1	0.0013	0.3929033	E
○	GO:0042816	6	vitamin B6 metabolic process	8	0.0012	1	0.0013	0.3929033	E
○	GO:0006620	10,9,8,7,6	posttranslational protein targeting to membrane	8	0.0012	1	0.0013	0.3929033	E

○	GO:0006828	8,9	manganese ion transport	8	0.0012	1	0.0013	0.3929033	E
○	GO:0006855	5,6	multidrug transport	8	0.0012	1	0.0013	0.3929033	E
○	GO:0030011	7,4,8	maintenance of cell polarity	8	0.0012	1	0.0013	0.3929033	E
○	GO:0007119	7,6,5	budding cell isotropic bud growth	8	0.0012	1	0.0013	0.3929033	E
○	GO:0007532	9,5,7,8,6	regulation of transcription, mating-type specific	8	0.0012	1	0.0013	0.3929033	E
○	GO:0006672	8,9	ceramide metabolic process	8	0.0012	1	0.0013	0.3929033	E
○	GO:0001308	11,7,10	loss of chromatin silencing during replicative cell aging	8	0.0012	1	0.0013	0.3929033	E
○	GO:0008150	1	biological_process	6476	1.0000	799	1.0000	1.0000000	D
○	GO:0000393	7,6,9,11	spliceosomal conformational changes to generate catalytic conformation	9	0.0014	1	0.0013	0.3874817	D
○	GO:0000128	3	flocculation	9	0.0014	1	0.0013	0.3874817	D
○	GO:0001304	10,6	progressive alteration of chromatin during replicative cell aging	9	0.0014	1	0.0013	0.3874817	D
○	GO:0006984	6	ER-nuclear signaling pathway	9	0.0014	1	0.0013	0.3874817	D
○	GO:0000501	4	flocculation via cell wall protein-carbohydrate interaction	9	0.0014	1	0.0013	0.3874817	D
○	GO:0046685	5	response to arsenic	9	0.0014	1	0.0013	0.3874817	D
○	GO:0030968	7,5,6	unfolded protein response	9	0.0014	1	0.0013	0.3874817	D
○	GO:0043486	11	histone exchange	9	0.0014	1	0.0013	0.3874817	D
○	GO:0045721	7,9,8,10,6,11	negative regulation of gluconeogenesis	9	0.0014	1	0.0013	0.3874817	D
○	GO:0046470	8,9	phosphatidylcholine metabolic process	9	0.0014	1	0.0013	0.3874817	D
○	GO:0051180	4,5	vitamin transport	9	0.0014	1	0.0013	0.3874817	D
○	GO:0045912	6,5	negative regulation of carbohydrate metabolic process	9	0.0014	1	0.0013	0.3874817	D
○	GO:0000184	8	mRNA catabolic process, nonsense-mediated decay	9	0.0014	1	0.0013	0.3874817	D
○	GO:0000290	11,8,9,10	deadenylation-dependent decapping	9	0.0014	1	0.0013	0.3874817	D
○	GO:0019363	7,6,8	pyridine nucleotide biosynthetic process	10	0.0015	1	0.0013	0.3774090	D
○	GO:0015718	6,7	monocarboxylic acid transport	10	0.0015	1	0.0013	0.3774090	D
○	GO:0030846	10,9	transcription termination from Pol II promoter, RNA polymerase(A) coupled	10	0.0015	1	0.0013	0.3774090	D
○	GO:0007129	10,8,7,5,9,6,4	synapsis	10	0.0015	1	0.0013	0.3774090	D
○	GO:0000103	6	sulfate assimilation	10	0.0015	1	0.0013	0.3774090	D
○	GO:0006791	5	sulfur utilization	10	0.0015	1	0.0013	0.3774090	D
○	GO:0046519	7,8	sphingoid metabolic process	10	0.0015	1	0.0013	0.3774090	D
○	GO:0051049	5,4	regulation of transport	11	0.0017	1	0.0013	0.3639143	D
○	GO:0006972	5	hyperosmotic response	11	0.0017	1	0.0013	0.3639143	D
○	GO:0006384	8,9,7	transcription initiation from RNA polymerase III promoter	11	0.0017	1	0.0013	0.3639143	D
○	GO:0043085	5	positive regulation of enzyme activity	11	0.0017	1	0.0013	0.3639143	D
○	GO:0000161	7,8,6	MAPKKK cascade during osmolarity sensing	11	0.0017	1	0.0013	0.3639143	D
○	GO:0007109	7,6,5,4	cytokinesis, completion of separation	11	0.0017	1	0.0013	0.3639143	D
○	GO:0031163	5	metallo-sulfur cluster assembly	11	0.0017	1	0.0013	0.3639143	D
○	GO:0016226	6	iron-sulfur cluster assembly	11	0.0017	1	0.0013	0.3639143	D
○	GO:0006116	10,9	NADH oxidation	11	0.0017	1	0.0013	0.3639143	D
○	GO:0015846	5,6	polyamine transport	12	0.0019	1	0.0013	0.3479945	D
○	GO:0008219	4,6	cell death	13	0.0020	1	0.0013	0.3304530	D
○	GO:0006895	8,9,6,7	Golgi to endosome transport	13	0.0020	1	0.0013	0.3304530	D
○	GO:0006915	6,8	apoptosis	13	0.0020	1	0.0013	0.3304530	D

○	GO:0030258	5,6	lipid modification	13	0.0020	1	0.0013	0.3304530	D
○	GO:0000920	6,4	cell separation during cytokinesis	13	0.0020	1	0.0013	0.3304530	D
○	GO:0001300	5	chronological cell aging	13	0.0020	1	0.0013	0.3304530	D
○	GO:0012501	5,7	programmed cell death	13	0.0020	1	0.0013	0.3304530	D
○	GO:0009065	7,8	glutamine family amino acid catabolic process	13	0.0020	1	0.0013	0.3304530	D
○	GO:0006111	8,7,9,10,6	regulation of gluconeogenesis	13	0.0020	1	0.0013	0.3304530	D
○	GO:0016265	3	death	13	0.0020	1	0.0013	0.3304530	D
○	GO:0045786	6,7,5	negative regulation of progression through cell cycle	13	0.0020	1	0.0013	0.3304530	D
○	GO:0015893	4,5	drug transport	13	0.0020	1	0.0013	0.3304530	D
○	GO:0000011	6	vacuole inheritance	14	0.0022	1	0.0013	0.3119322	D
○	GO:0022406	3	membrane docking	14	0.0022	1	0.0013	0.3119322	D
○	GO:0000077	9,8,6	DNA damage checkpoint	14	0.0022	1	0.0013	0.3119322	D
○	GO:0048278	4,5,6	vesicle docking	14	0.0022	1	0.0013	0.3119322	D
○	GO:0006734	9,8	NADH metabolic process	14	0.0022	1	0.0013	0.3119322	D
○	GO:0042770	5	DNA damage response, signal transduction	14	0.0022	1	0.0013	0.3119322	D
○	GO:0006749	6,5	glutathione metabolic process	14	0.0022	1	0.0013	0.3119322	D
○	GO:0006825	8,9	copper ion transport	14	0.0022	1	0.0013	0.3119322	D
○	GO:0000028	9,7,8,6	ribosomal small subunit assembly and maintenance	14	0.0022	1	0.0013	0.3119322	D
○	GO:0009651	5	response to salt stress	15	0.0023	1	0.0013	0.2929407	D
○	GO:0007018	8,7,6	microtubule-based movement	15	0.0023	1	0.0013	0.2929407	D
○	GO:0000051	4,3	urea cycle intermediate metabolic process	15	0.0023	1	0.0013	0.2929407	D
○	GO:0006525	7,8,5,4	arginine metabolic process	15	0.0023	1	0.0013	0.2929407	D
○	GO:0030473	8,9,6,7	nuclear migration, microtubule-mediated	15	0.0023	1	0.0013	0.2929407	D
○	GO:0009968	6,5	negative regulation of signal transduction	17	0.0026	2	0.0025	0.2875706	D
○	GO:0006113	5	fermentation	17	0.0026	2	0.0025	0.2875706	D
○	GO:0045003	9,8	double-strand break repair via synthesis-dependent strand annealing	17	0.0026	2	0.0025	0.2875706	D
○	GO:0051248	6,5	negative regulation of protein metabolic process	18	0.0028	2	0.0025	0.2835970	D
○	GO:0010038	5	response to metal ion	18	0.0028	2	0.0025	0.2835970	D
○	GO:0000018	8,7	regulation of DNA recombination	18	0.0028	2	0.0025	0.2835970	D
○	GO:0031570	8,7	DNA integrity checkpoint	18	0.0028	2	0.0025	0.2835970	D
○	GO:0000183	11,7,8,12,10	chromatin silencing at rDNA	18	0.0028	2	0.0025	0.2835970	D
○	GO:0042594	6,4	response to starvation	19	0.0029	2	0.0025	0.2778442	D
○	GO:0031669	6,5	cellular response to nutrient levels	19	0.0029	2	0.0025	0.2778442	D
○	GO:0031668	5,4	cellular response to extracellular stimulus	19	0.0029	2	0.0025	0.2778442	D
○	GO:0009267	7,6,5	cellular response to starvation	19	0.0029	2	0.0025	0.2778442	D
○	GO:0006826	7,8,9	iron ion transport	20	0.0031	2	0.0025	0.2706104	D
○	GO:0000209	10	protein polyubiquitination	20	0.0031	2	0.0025	0.2706104	D
○	GO:0051716	3	cellular response to stimulus	21	0.0032	2	0.0025	0.2621721	D
○	GO:0033554	4	cellular response to stress	21	0.0032	2	0.0025	0.2621721	D
○	GO:0019674	9,8	NAD metabolic process	21	0.0032	2	0.0025	0.2621721	D
○	GO:0042147	8,6,7	retrograde transport, endosome to Golgi	17	0.0026	1	0.0013	0.2550477	D
○	GO:0046349	6,7	amino sugar biosynthetic process	17	0.0026	1	0.0013	0.2550477	D
○	GO:0006045	8,9	N-acetylglucosamine biosynthetic process	17	0.0026	1	0.0013	0.2550477	D
○	GO:0006042	7,8	glucosamine biosynthetic process	17	0.0026	1	0.0013	0.2550477	D

○	GO:0016558	10,9,7,8,6	protein import into peroxisome matrix	17	0.0026	1	0.0013	0.2550477	D
○	GO:0030705	7,5,6	cytoskeleton-dependent intracellular transport	17	0.0026	1	0.0013	0.2550477	D
○	GO:0006513	10	protein monoubiquitination	22	0.0034	2	0.0025	0.2527818	D
○	GO:0007243	6	protein kinase cascade	23	0.0036	2	0.0025	0.2426675	D
○	GO:0000724	8,7	double-strand break repair via homologous recombination	25	0.0039	3	0.0038	0.2388529	D
○	GO:0009607	3	response to biotic stimulus	25	0.0039	3	0.0038	0.2388529	D
○	GO:0006986	4,5	response to unfolded protein	18	0.0028	1	0.0013	0.2366862	D
○	GO:0051789	4	response to protein stimulus	18	0.0028	1	0.0013	0.2366862	D
○	GO:0010035	4	response to inorganic substance	24	0.0037	2	0.0025	0.2320320	D
○	GO:0006896	9,8,7,6	Golgi to vacuole transport	24	0.0037	2	0.0025	0.2320320	D
○	GO:0031577	8,7	spindle checkpoint	24	0.0037	2	0.0025	0.2320320	D
○	GO:0006890	8,6,5,7	retrograde vesicle-mediated transport, Golgi to ER	24	0.0037	2	0.0025	0.2320320	D
○	GO:0007096	8,10,9,7	regulation of exit from mitosis	24	0.0037	2	0.0025	0.2320320	D
○	GO:0042144	6	vacuole fusion, non-autophagic	28	0.0043	3	0.0038	0.2291579	D
○	GO:0055065	8	metal ion homeostasis	19	0.0029	1	0.0013	0.2189639	D
○	GO:0006041	6,7	glucosamine metabolic process	19	0.0029	1	0.0013	0.2189639	D
○	GO:0000722	9,8	telomere maintenance via recombination	19	0.0029	1	0.0013	0.2189639	D
○	GO:0006044	7,8	N-acetylglucosamine metabolic process	19	0.0029	1	0.0013	0.2189639	D
○	GO:0006875	9,7	cellular metal ion homeostasis	19	0.0029	1	0.0013	0.2189639	D
○	GO:0006040	5,6	amino sugar metabolic process	19	0.0029	1	0.0013	0.2189639	D
○	GO:0043255	7,6,5	regulation of carbohydrate biosynthetic process	19	0.0029	1	0.0013	0.2189639	D
○	GO:0051128	5,4	regulation of cellular component organization and biogenesis	30	0.0046	3	0.0038	0.2182035	D
○	GO:0009966	5,4	regulation of signal transduction	26	0.0040	2	0.0025	0.2098887	D
○	GO:0007186	6	G-protein coupled receptor protein signaling pathway	34	0.0053	4	0.0050	0.2073480	D
○	GO:0015674	6,7	di-, tri-valent inorganic cation transport	34	0.0053	4	0.0050	0.2073480	D
○	GO:0006007	8,9	glucose catabolic process	34	0.0053	4	0.0050	0.2073480	D
○	GO:0006084	6	acetyl-CoA metabolic process	20	0.0031	1	0.0013	0.2020030	D
○	GO:0000022	6,5,10,8	mitotic spindle elongation	20	0.0031	1	0.0013	0.2020030	D
○	GO:0051647	6,5	nucleus localization	20	0.0031	1	0.0013	0.2020030	D
○	GO:0000165	7	MAPKKK cascade	20	0.0031	1	0.0013	0.2020030	D
○	GO:0006625	9,8,6,7	protein targeting to peroxisome	20	0.0031	1	0.0013	0.2020030	D
○	GO:0007097	7,8,5,6	nuclear migration	20	0.0031	1	0.0013	0.2020030	D
○	GO:0040023	6,7,4,5	establishment of nucleus localization	20	0.0031	1	0.0013	0.2020030	D
○	GO:0051231	5,4,9,7	spindle elongation	20	0.0031	1	0.0013	0.2020030	D
○	GO:0043574	7,5,6	peroxisomal transport	20	0.0031	1	0.0013	0.2020030	D
○	GO:0007094	9,11,10,8	mitotic cell cycle spindle assembly checkpoint	20	0.0031	1	0.0013	0.2020030	D
○	GO:0009142	6,7	nucleoside triphosphate biosynthetic process	27	0.0042	2	0.0025	0.1986699	D
○	GO:0006118	4	electron transport	33	0.0051	3	0.0038	0.1974495	D
○	GO:0055072	9	iron ion homeostasis	38	0.0059	4	0.0050	0.1948420	D
○	GO:0006879	10,8	cellular iron ion homeostasis	38	0.0059	4	0.0050	0.1948420	D
○	GO:0001522	7	pseudouridine synthesis	39	0.0060	4	0.0050	0.1902997	D
○	GO:0019320	7,8	hexose catabolic process	39	0.0060	4	0.0050	0.1902997	D
○	GO:0006906	6,5	vesicle fusion	28	0.0043	2	0.0025	0.1875109	D

○	GO:0009636	4	response to toxin	28	0.0043	2	0.0025	0.1875109	D
○	GO:0009266	4	response to temperature stimulus	28	0.0043	2	0.0025	0.1875109	D
○	GO:0006769	8,7	nicotinamide metabolic process	42	0.0065	5	0.0063	0.1867950	D
○	GO:0045324	8,6,7	late endosome to vacuole transport	21	0.0032	1	0.0013	0.1858859	D
○	GO:0006081	4	aldehyde metabolic process	21	0.0032	1	0.0013	0.1858859	D
○	GO:0007052	5,4,9	mitotic spindle organization and biogenesis	44	0.0068	5	0.0063	0.1832419	D
○	GO:0006752	6	group transfer coenzyme metabolic process	44	0.0068	5	0.0063	0.1832419	D
○	GO:0030433	9,11,10,12	ER-associated protein catabolic process	35	0.0054	3	0.0038	0.1819454	D
○	GO:0019362	7,6	pyridine nucleotide metabolic process	45	0.0069	5	0.0063	0.1806993	D
○	GO:0000041	7,8	transition metal ion transport	46	0.0071	5	0.0063	0.1777051	D
○	GO:0001403	6,4,8,9	invasive growth (sensu Saccharomyces)	42	0.0065	4	0.0050	0.1743668	D
○	GO:0006473	8	protein amino acid acetylation	48	0.0074	5	0.0063	0.1705422	D
○	GO:0048468	3,5	cell development	52	0.0080	6	0.0075	0.1687092	D
○	GO:0007166	5	cell surface receptor linked signal transduction	52	0.0080	6	0.0075	0.1687092	D
○	GO:0019319	7,8	hexose biosynthetic process	30	0.0046	2	0.0025	0.1657353	D
○	GO:0046364	6,7	monosaccharide biosynthetic process	30	0.0046	2	0.0025	0.1657353	D
○	GO:0046365	6,7	monosaccharide catabolic process	44	0.0068	4	0.0050	0.1624399	D
○	GO:0006887	8,6,5,7	exocytosis	44	0.0068	4	0.0050	0.1624399	D
○	GO:0008643	4,5	carbohydrate transport	38	0.0059	3	0.0038	0.1578598	D
○	GO:0006515	8,9	misfolded or incompletely synthesized protein catabolic process	38	0.0059	3	0.0038	0.1578598	D
○	GO:0006650	7,8	glycerophospholipid metabolic process	60	0.0093	7	0.0088	0.1571859	D
○	GO:0009408	5,4	response to heat	23	0.0036	1	0.0013	0.1563599	D
○	GO:0043044	10	ATP-dependent chromatin remodeling	23	0.0036	1	0.0013	0.1563599	D
○	GO:0006303	8,7	double-strand break repair via nonhomologous end joining	23	0.0036	1	0.0013	0.1563599	D
○	GO:0006914	3	autophagy	45	0.0069	4	0.0050	0.1562512	D
○	GO:0007124	6,4,8,9	pseudohyphal growth	61	0.0094	7	0.0088	0.1556434	D
○	GO:0000749	5	response to pheromone during conjugation with cellular fusion	57	0.0088	6	0.0075	0.1555834	D
○	GO:0000002	6	mitochondrial genome maintenance	31	0.0048	2	0.0025	0.1552602	D
○	GO:0008654	7,6,8	phospholipid biosynthetic process	58	0.0090	6	0.0075	0.1520969	D
○	GO:0042364	6	water-soluble vitamin biosynthetic process	46	0.0071	4	0.0050	0.1499769	D
○	GO:0009110	5	vitamin biosynthetic process	46	0.0071	4	0.0050	0.1499769	D
○	GO:0055066	8	di-, tri-valent inorganic cation homeostasis	64	0.0099	7	0.0088	0.1492461	D
○	GO:0030005	9,7	cellular di-, tri-valent inorganic cation homeostasis	64	0.0099	7	0.0088	0.1492461	D
○	GO:0007033	5	vacuole organization and biogenesis	67	0.0103	8	0.0100	0.1487333	D
○	GO:0005977	7,6,8	glycogen metabolic process	32	0.0049	2	0.0025	0.1451311	D
○	GO:0009108	6	coenzyme biosynthetic process	66	0.0102	7	0.0088	0.1437330	D
○	GO:0006631	5,7,6	fatty acid metabolic process	47	0.0073	4	0.0050	0.1436603	D
○	GO:0046164	5	alcohol catabolic process	47	0.0073	4	0.0050	0.1436603	D
○	GO:0009201	7,8	ribonucleoside triphosphate biosynthetic process	24	0.0037	1	0.0013	0.1429815	D
○	GO:0006096	9,10	glycolysis	24	0.0037	1	0.0013	0.1429815	D
○	GO:0016573	11,9	histone acetylation	40	0.0062	3	0.0038	0.1419863	D
○	GO:0007015	8	actin filament organization	61	0.0094	6	0.0075	0.1404627	D
○	GO:0046467	6,5,7	membrane lipid biosynthetic process	78	0.0120	9	0.0113	0.1375604	D

○	GO:0030001	6,7	metal ion transport	62	0.0096	6	0.0075	0.1362884	D
○	GO:0051640	5,4	organelle localization	56	0.0086	5	0.0063	0.1324202	D
○	GO:0006733	6	oxidoreduction coenzyme metabolic process	56	0.0086	5	0.0063	0.1324202	D
○	GO:0009199	7	ribonucleoside triphosphate metabolic process	25	0.0039	1	0.0013	0.1305179	D
○	GO:0006302	7,6	double-strand break repair	57	0.0088	5	0.0063	0.1272010	D
○	GO:0019236	4	response to pheromone	94	0.0145	11	0.0138	0.1256249	D
○	GO:0010324	5	membrane invagination	96	0.0148	11	0.0138	0.1232804	D
○	GO:0006006	7,8	glucose metabolic process	65	0.0100	6	0.0075	0.1232432	D
○	GO:0055080	7	cation homeostasis	102	0.0158	12	0.0150	0.1207305	D
○	GO:0030003	8,6	cellular cation homeostasis	102	0.0158	12	0.0150	0.1207305	D
○	GO:0048311	7,6	mitochondrion distribution	26	0.0040	1	0.0013	0.1189475	D
○	GO:0000001	8,7,6	mitochondrion inheritance	26	0.0040	1	0.0013	0.1189475	D
○	GO:0030036	7	actin cytoskeleton organization and biogenesis	107	0.0165	13	0.0163	0.1180395	D
○	GO:0046165	5	alcohol biosynthetic process	35	0.0054	2	0.0025	0.1171532	D
○	GO:0006944	5	membrane fusion	59	0.0091	5	0.0063	0.1167889	D
○	GO:0030447	3	filamentous growth	94	0.0145	10	0.0125	0.1166365	D
○	GO:0030029	6	actin filament-based process	112	0.0173	13	0.0163	0.1145696	D
○	GO:0016049	5,3,7,8	cell growth	102	0.0158	11	0.0138	0.1128780	D
○	GO:0042493	4	response to drug	121	0.0187	14	0.0175	0.1098871	D
○	GO:0051646	6,5	mitochondrion localization	27	0.0042	1	0.0013	0.1082401	D
○	GO:0009628	3	response to abiotic stimulus	117	0.0181	13	0.0163	0.1079562	D
○	GO:0019725	5,3	cellular homeostasis	128	0.0198	15	0.0188	0.1075057	D
○	GO:0006368	9,7,8	RNA elongation from RNA polymerase II promoter	53	0.0082	4	0.0050	0.1067905	D
○	GO:0006312	7	mitotic recombination	45	0.0069	3	0.0038	0.1053640	D
○	GO:0006643	5,6	membrane lipid metabolic process	125	0.0193	14	0.0175	0.1049248	D
○	GO:0000154	7,8	rRNA modification	85	0.0131	8	0.0100	0.1021300	D
○	GO:0042592	4	homeostatic process	134	0.0207	15	0.0188	0.1007969	D
○	GO:0009605	3	response to external stimulus	37	0.0057	2	0.0025	0.1006860	D
○	GO:0031667	5	response to nutrient levels	37	0.0057	2	0.0025	0.1006860	D
○	GO:0009991	4	response to extracellular stimulus	37	0.0057	2	0.0025	0.1006860	D
○	GO:0006073	6,7	glucan metabolic process	46	0.0071	3	0.0038	0.0987636	D
○	GO:0006897	6,5	endocytosis	86	0.0133	8	0.0100	0.0986681	D
○	GO:0006094	8,9	gluconeogenesis	28	0.0043	1	0.0013	0.0983593	D
○	GO:0016485	8	protein processing	38	0.0059	2	0.0025	0.0931247	D
○	GO:0006090	7	pyruvate metabolic process	38	0.0059	2	0.0025	0.0931247	D
○	GO:0051656	6,3,5,4	establishment of organelle localization	29	0.0045	1	0.0013	0.0892645	D
○	GO:0051651	5,4,3	maintenance of cellular localization	29	0.0045	1	0.0013	0.0892645	D
○	GO:0006109	5,4	regulation of carbohydrate metabolic process	29	0.0045	1	0.0013	0.0892645	D
○	GO:0032507	6,5,4	maintenance of cellular protein localization	29	0.0045	1	0.0013	0.0892645	D
○	GO:0006644	6,7	phospholipid metabolic process	97	0.0150	9	0.0113	0.0878015	D
○	GO:0005976	5	polysaccharide metabolic process	65	0.0100	5	0.0063	0.0872016	D
○	GO:0044264	5,6	cellular polysaccharide metabolic process	65	0.0100	5	0.0063	0.0872016	D
○	GO:0006112	5	energy reserve metabolic process	39	0.0060	2	0.0025	0.0860068	D

○	GO:0007242	5	intracellular signaling cascade	137	0.0212	14	0.0175	0.0831309	D
○	GO:0016570	10,8	histone modification	91	0.0141	8	0.0100	0.0816038	D
○	GO:0016569	9	covalent chromatin modification	91	0.0141	8	0.0100	0.0816038	D
○	GO:0045185	5,4,3	maintenance of protein localization	30	0.0046	1	0.0013	0.0809125	D
○	GO:0016197	7,5,6	endosome transport	49	0.0076	3	0.0038	0.0806302	D
○	GO:0006974	4	response to DNA damage stimulus	234	0.0361	28	0.0350	0.0802910	D
○	GO:0048308	5	organelle inheritance	40	0.0062	2	0.0025	0.0793241	D
○	GO:0007031	5	peroxisome organization and biogenesis	40	0.0062	2	0.0025	0.0793241	D
○	GO:0032446	8	protein modification by small protein conjugation	84	0.0130	7	0.0088	0.0775776	D
○	GO:0051186	4	cofactor metabolic process	170	0.0263	18	0.0225	0.0773977	D
○	GO:0006468	8,7	protein amino acid phosphorylation	101	0.0156	9	0.0113	0.0755946	D
○	GO:0009719	3	response to endogenous stimulus	243	0.0375	28	0.0350	0.0751803	D
○	GO:0006354	8,6,7	RNA elongation	59	0.0091	4	0.0050	0.0750948	D
○	GO:0032505	4,3	reproduction of a single-celled organism	194	0.0300	21	0.0263	0.0747409	D
○	GO:0007165	4	signal transduction	209	0.0323	23	0.0288	0.0742543	D
○	GO:0019318	6,7	hexose metabolic process	85	0.0131	7	0.0088	0.0740648	D
○	GO:0031118	8,9	rRNA pseudouridine synthesis	31	0.0048	1	0.0013	0.0732589	D
○	GO:0007005	5	mitochondrion organization and biogenesis	110	0.0170	10	0.0125	0.0730485	D
○	GO:0043285	5	biopolymer catabolic process	277	0.0428	32	0.0401	0.0701956	D
○	GO:0000003	2	reproduction	323	0.0499	39	0.0488	0.0689455	D
○	GO:0022414	3,2	reproductive process	183	0.0283	19	0.0238	0.0687498	D
○	GO:0006732	5	coenzyme metabolic process	136	0.0210	13	0.0163	0.0685230	D
○	GO:0030476	8,6,7	spore wall assembly (sensu Fungi)	42	0.0065	2	0.0025	0.0672165	D
○	GO:0042244	5,6	spore wall assembly	42	0.0065	2	0.0025	0.0672165	D
○	GO:0006512	8	ubiquitin cycle	88	0.0136	7	0.0088	0.0640481	D
○	GO:0007034	7,5,6	vacuolar transport	114	0.0176	10	0.0125	0.0624340	D
○	GO:0006767	5	water-soluble vitamin metabolic process	89	0.0137	7	0.0088	0.0608969	D
○	GO:0006766	4	vitamin metabolic process	89	0.0137	7	0.0088	0.0608969	D
○	GO:0006811	4,5	ion transport	115	0.0178	10	0.0125	0.0598998	D
○	GO:0051235	3,2	maintenance of localization	33	0.0051	1	0.0013	0.0598678	D
○	GO:0022413	5,4	reproductive process in single-celled organism	149	0.0230	14	0.0175	0.0582738	D
○	GO:0048610	3,4	reproductive cellular process	149	0.0230	14	0.0175	0.0582738	D
○	GO:0043161	10,9,11	proteasomal ubiquitin-dependent protein catabolic process	63	0.0097	4	0.0050	0.0578973	D
○	GO:0000122	10,9	negative regulation of transcription from RNA polymerase II promoter	63	0.0097	4	0.0050	0.0578973	D
○	GO:0007154	3	cell communication	240	0.0371	25	0.0313	0.0547182	D
○	GO:0045229	4	external encapsulating structure organization and biogenesis	200	0.0309	20	0.0250	0.0546346	D
○	GO:0007047	5	cell wall organization and biogenesis	200	0.0309	20	0.0250	0.0546346	D
○	GO:0005996	5,6	monosaccharide metabolic process	92	0.0142	7	0.0088	0.0520441	D
○	GO:0006796	5	phosphate metabolic process	212	0.0327	21	0.0263	0.0490406	D
○	GO:0006793	4	phosphorus metabolic process	212	0.0327	21	0.0263	0.0490406	D
○	GO:0000726	7,6	non-recombinational repair	35	0.0054	1	0.0013	0.0487404	D
○	GO:0016044	4	membrane organization and biogenesis	188	0.0290	18	0.0225	0.0479148	D
○	GO:0042221	3	response to chemical stimulus	382	0.0590	42	0.0526	0.0472127	D
○	GO:0016567	9	protein ubiquitination	66	0.0102	4	0.0050	0.0470929	D

○	GO:0016192	4,5	vesicle-mediated transport	328	0.0506	35	0.0438	0.0459080	D
○	GO:0044265	5	cellular macromolecule catabolic process	314	0.0485	33	0.0413	0.0439446	D
○	GO:0006623	9,8,7,6	protein targeting to vacuole	67	0.0103	4	0.0050	0.0438714	D
○	GO:0006950	3	response to stress	488	0.0754	54	0.0676	0.0396743	D
○	GO:0009057	4	macromolecule catabolic process	345	0.0533	36	0.0451	0.0379275	D
○	GO:0045333	5	cellular respiration	89	0.0137	6	0.0075	0.0362361	D
○	GO:0032787	6	monocarboxylic acid metabolic process	126	0.0195	10	0.0125	0.0360271	D
○	GO:0044248	4	cellular catabolic process	425	0.0656	44	0.0551	0.0274222	D
○	GO:0009060	6	aerobic respiration	84	0.0130	5	0.0063	0.0263311	D
○	GO:0009056	3	catabolic process	438	0.0676	45	0.0563	0.0244719	D
○	GO:0050896	2	response to stimulus	763	0.1178	84	0.1051	0.0236032	D
○	GO:0048869	3	cellular developmental process	173	0.0267	14	0.0175	0.0213341	D
○	GO:0030154	4	cell differentiation	173	0.0267	14	0.0175	0.0213341	D
○	GO:0006812	5,6	cation transport	97	0.0150	6	0.0075	0.0213232	D
○	GO:0030437	7,6	sporulation (sensu Fungi)	108	0.0167	7	0.0088	0.0198433	D
○	GO:0048622	6,5	reproductive sporulation	108	0.0167	7	0.0088	0.0198433	D
○	GO:0031167	8,9	rRNA methylation	44	0.0068	1	0.0013	0.0186183	D
○	GO:0016052	5	carbohydrate catabolic process	80	0.0124	4	0.0050	0.0161544	D
○	GO:0044275	6	cellular carbohydrate catabolic process	80	0.0124	4	0.0050	0.0161544	D
○	GO:0015980	4	energy derivation by oxidation of organic compounds	145	0.0224	10	0.0125	0.0123446	D
○	GO:0016051	5	carbohydrate biosynthetic process	77	0.0119	3	0.0038	0.0078319	D
○	GO:0043687	7	post-translational protein modification	388	0.0599	35	0.0438	0.0074157	D
○	GO:0006091	3	generation of precursor metabolites and energy	183	0.0283	13	0.0163	0.0073629	D
○	GO:0030435	5	sporulation	123	0.0190	7	0.0088	0.0068780	D
○	GO:0043632	6	modification-dependent macromolecule catabolic process	155	0.0239	10	0.0125	0.0064818	D
○	GO:0016310	6	phosphorylation	155	0.0239	9	0.0113	0.0031089	D
○	GO:0009059	4	macromolecule biosynthetic process	886	0.1368	87	0.1089	0.0019949	D
○	GO:0044262	5	cellular carbohydrate metabolic process	213	0.0329	13	0.0163	0.0010204	D
○	GO:0019538	4	protein metabolic process	1547	0.2389	161	0.2015	0.0009977	D
○	GO:0044267	5	cellular protein metabolic process	1498	0.2313	155	0.1940	0.0009369	D
○	GO:0019941	8,7,9	modification-dependent protein catabolic process	148	0.0229	7	0.0088	0.0009211	D
○	GO:0006511	9,8,10	ubiquitin-dependent protein catabolic process	148	0.0229	7	0.0088	0.0009211	D
○	GO:0051603	7,8	proteolysis involved in cellular protein catabolic process	151	0.0233	7	0.0088	0.0007118	D
○	GO:0006508	6	proteolysis	178	0.0275	9	0.0113	0.0005138	D
○	GO:0044260	4	cellular macromolecule metabolic process	1552	0.2397	158	0.1977	0.0003925	D
○	GO:0044257	6,7	cellular protein catabolic process	160	0.0247	7	0.0088	0.0003225	D
○	GO:0030163	6,5	protein catabolic process	173	0.0267	8	0.0100	0.0002936	D
○	GO:0005975	4	carbohydrate metabolic process	233	0.0360	13	0.0163	0.0002307	D
○	GO:0032196	3	transposition	105	0.0162	2	0.0025	9.831421E-05	D
○	GO:0006412	6,5	translation	688	0.1062	55	0.0688	3.383355E-05	D
○	GO:0006414	7,6	translational elongation	313	0.0483	3	0.0038	6.984892E-15	D
○	GO:0043284	5	biopolymer biosynthetic process	354	0.0547	3	0.0038	3.419219E-17	D