

GO-Stats Results

Your dataset contains **340** annotated gene products.

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

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

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

GO ID	Level	GO Term	RO	RF	DO	DF	P-value	E/D
<input type="radio"/> GO:0065007	2	biological regulation	948	0.1464	91	0.2676	8.754958E-10	E
<input type="radio"/> GO:0050789	3	regulation of biological process	761	0.1175	72	0.2118	1.315539E-07	E
<input type="radio"/> GO:0050794	4,3	regulation of cellular process	738	0.1140	70	0.2059	1.836888E-07	E
<input type="radio"/> GO:0006357	9,8	regulation of transcription from RNA polymerase II promoter	221	0.0341	30	0.0882	8.375781E-07	E
<input type="radio"/> GO:0007154	3	cell communication	240	0.0371	31	0.0912	1.588558E-06	E
<input type="radio"/> GO:0006366	8,7	transcription from RNA polymerase II promoter	343	0.0530	39	0.1147	1.833905E-06	E
<input type="radio"/> GO:0006350	5	transcription	567	0.0876	55	0.1618	2.186566E-06	E
<input type="radio"/> GO:0019219	6,5	regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	440	0.0679	46	0.1353	2.197185E-06	E
<input type="radio"/> GO:0019222	4,3	regulation of metabolic process	538	0.0831	52	0.1529	4.611059E-06	E
<input type="radio"/> GO:0022402	4,3	cell cycle process	439	0.0678	45	0.1324	4.700791E-06	E
<input type="radio"/> GO:0045449	7,6	regulation of transcription	386	0.0596	41	0.1206	5.346549E-06	E
<input type="radio"/> GO:0006355	8,7	regulation of transcription, DNA-dependent	359	0.0554	38	0.1118	1.258319E-05	E
<input type="radio"/> GO:0007049	3	cell cycle	458	0.0707	45	0.1324	1.348077E-05	E
<input type="radio"/> GO:0000122	10,9	negative regulation of transcription from RNA polymerase II promoter	63	0.0097	13	0.0382	1.427666E-05	E
<input type="radio"/> GO:0031323	5,4	regulation of cellular metabolic process	507	0.0783	48	0.1412	1.806293E-05	E
<input type="radio"/> GO:0006351	7,6	transcription, DNA-dependent	522	0.0806	49	0.1441	1.840677E-05	E
<input type="radio"/> GO:0032774	6	RNA biosynthetic process	524	0.0809	49	0.1441	2.026798E-05	E
<input type="radio"/> GO:0009987	2	cellular process	4654	0.7187	275	0.8088	2.376673E-05	E
<input type="radio"/> GO:0006810	3,4	transport	981	0.1515	78	0.2294	2.722256E-05	E
<input type="radio"/> GO:0051179	2	localization	1051	0.1623	81	0.2382	5.404562E-05	E
<input type="radio"/> GO:0051224	2,3	establishment of localization	1004	0.1550	78	0.2204	5.795917E-05	E

<input type="radio"/>	GO:0051254	2,3	establishment of localization	1004	0.1550	70	0.2294	05		E
<input type="radio"/>	GO:0022403	5,4	cell cycle phase	353	0.0545	35	0.1029	9.665071E-05		E
<input type="radio"/>	GO:0006139	4	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	1532	0.2366	108	0.3176	0.0001051		E
<input type="radio"/>	GO:0050896	2	response to stimulus	763	0.1178	61	0.1794	0.0001763		E
<input type="radio"/>	GO:0000433	12,10,11,8	negative regulation of transcription from RNA polymerase II promoter by glucose	7	0.0011	4	0.0118	0.0002228		E
<input type="radio"/>	GO:0045014	11,9,10,7	negative regulation of transcription by glucose	7	0.0011	4	0.0118	0.0002228		E
<input type="radio"/>	GO:0000429	10,8,9,6	regulation of transcription from RNA polymerase II promoter by carbon catabolites	7	0.0011	4	0.0118	0.0002228		E
<input type="radio"/>	GO:0000437	11,9,10,7	negative regulation of transcription from RNA polymerase II promoter by carbon catabolites	7	0.0011	4	0.0118	0.0002228		E
<input type="radio"/>	GO:0000430	11,9,10,7	regulation of transcription from RNA polymerase II promoter by glucose	7	0.0011	4	0.0118	0.0002228		E
<input type="radio"/>	GO:0000279	6,5	M phase	258	0.0398	27	0.0794	0.0002441		E
<input type="radio"/>	GO:0007165	4	signal transduction	209	0.0323	23	0.0676	0.0003354		E
<input type="radio"/>	GO:0046015	10,8,9,6	regulation of transcription by glucose	8	0.0012	4	0.0118	0.0004225		E
<input type="radio"/>	GO:0045013	10,8,9,6	negative regulation of transcription by carbon catabolites	8	0.0012	4	0.0118	0.0004225		E
<input type="radio"/>	GO:0007010	5	cytoskeleton organization and biogenesis	227	0.0351	24	0.0706	0.0004431		E
<input type="radio"/>	GO:0007126	8,6,7,5	meiosis	148	0.0229	18	0.0529	0.0004440		E
<input type="radio"/>	GO:0051321	4	meiotic cell cycle	148	0.0229	18	0.0529	0.0004440		E
<input type="radio"/>	GO:0051327	7,5,6	M phase of meiotic cell cycle	148	0.0229	18	0.0529	0.0004440		E
<input type="radio"/>	GO:0031667	5	response to nutrient levels	37	0.0057	8	0.0235	0.0004454		E
<input type="radio"/>	GO:0009605	3	response to external stimulus	37	0.0057	8	0.0235	0.0004454		E
<input type="radio"/>	GO:0009991	4	response to extracellular stimulus	37	0.0057	8	0.0235	0.0004454		E
<input type="radio"/>	GO:0045990	9,7,8,5	regulation of transcription by carbon catabolites	14	0.0022	5	0.0147	0.0004811		E
<input type="radio"/>	GO:0016192	4,5	vesicle-mediated transport	328	0.0506	31	0.0912	0.0004944		E
<input type="radio"/>	GO:0007034	7,5,6	vacuolar transport	114	0.0176	15	0.0441	0.0005702		E
<input type="radio"/>	GO:0000074	6,5	regulation of progression through cell cycle	167	0.0258	19	0.0559	0.0006923		E
<input type="radio"/>	GO:0051726	5,4	regulation of cell cycle	167	0.0258	19	0.0559	0.0006923		E
<input type="radio"/>	GO:0019933	8	cAMP-mediated signaling	9	0.0014	4	0.0118	0.0007211		E
<input type="radio"/>	GO:0019935	7	cyclic-nucleotide-mediated signaling	9	0.0014	4	0.0118	0.0007211		E
<input type="radio"/>	GO:0016071	6	mRNA metabolic process	210	0.0324	22	0.0647	0.0008185		E
<input type="radio"/>	GO:0019932	6	second-messenger-mediated signaling	32	0.0049	7	0.0206	0.0009286		E
<input type="radio"/>	GO:0043162	10,9,11	ubiquitin-dependent protein catabolic process via the multivesicular body pathway	16	0.0025	5	0.0147	0.0009437		E
<input type="radio"/>	GO:0043687	7	post-translational protein modification	388	0.0599	34	0.1000	0.0009666		E
<input type="radio"/>	GO:0006464	6	protein modification process	520	0.0803	42	0.1235	0.0012720		E
<input type="radio"/>	GO:0042710	3	biofilm formation	5	0.0008	3	0.0088	0.0012895		E
<input type="radio"/>	GO:0009268	4	response to pH	5	0.0008	3	0.0088	0.0012895		E
<input type="radio"/>	GO:0007242	5	intracellular signaling cascade	137	0.0212	16	0.0471	0.0013071		E
<input type="radio"/>	GO:0043285	5	biopolymer catabolic process	277	0.0428	26	0.0765	0.0013866		E
<input type="radio"/>	GO:0007584	6,4	response to nutrient	18	0.0028	5	0.0147	0.0016641		E
<input type="radio"/>	GO:0043283	4	biopolymer metabolic process	2230	0.3443	139	0.4088	0.0018028		E
<input type="radio"/>	GO:0048523	5,4	negative regulation of cellular process	239	0.0369	23	0.0676	0.0018125		E
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<input type="radio"/>	GO:0030163	6,5	protein catabolic process	173	0.0267	18	0.0529	0.0023413	E
<input type="radio"/>	GO:0065008	3	regulation of biological quality	260	0.0401	24	0.0706	0.0024393	E
<input type="radio"/>	GO:0055072	9	iron ion homeostasis	38	0.0059	7	0.0206	0.0025321	E
<input type="radio"/>	GO:0006879	10,8	cellular iron ion homeostasis	38	0.0059	7	0.0206	0.0025321	E
<input type="radio"/>	GO:0015804	6,7,8	neutral amino acid transport	2	0.0003	2	0.0059	0.0027487	E
<input type="radio"/>	GO:0015824	7,8,9	proline transport	2	0.0003	2	0.0059	0.0027487	E
<input type="radio"/>	GO:0016197	7,5,6	endosome transport	49	0.0076	8	0.0235	0.0027550	E
<input type="radio"/>	GO:0016070	5	RNA metabolic process	1058	0.1634	72	0.2118	0.0030892	E
<input type="radio"/>	GO:0030001	6,7	metal ion transport	62	0.0096	9	0.0265	0.0033920	E
<input type="radio"/>	GO:0051704	2	multi-organism process	139	0.0215	15	0.0441	0.0035915	E
<input type="radio"/>	GO:0016043	3	cellular component organization and biogenesis	2264	0.3496	138	0.4059	0.0039179	E
<input type="radio"/>	GO:0040007	2	growth	141	0.0218	15	0.0441	0.0040515	E
<input type="radio"/>	GO:0042221	3	response to chemical stimulus	382	0.0590	31	0.0912	0.0042035	E
<input type="radio"/>	GO:0045892	9,8	negative regulation of transcription, DNA-dependent	156	0.0241	16	0.0471	0.0043165	E
<input type="radio"/>	GO:0016049	5,3,7,8	cell growth	102	0.0158	12	0.0353	0.0043844	E
<input type="radio"/>	GO:0009628	3	response to abiotic stimulus	117	0.0181	13	0.0382	0.0049412	E
<input type="radio"/>	GO:0016481	8,7	negative regulation of transcription	162	0.0250	16	0.0471	0.0059352	E
<input type="radio"/>	GO:0016575	11,9	histone deacetylation	24	0.0037	5	0.0147	0.0059961	E
<input type="radio"/>	GO:0031577	8,7	spindle checkpoint	24	0.0037	5	0.0147	0.0059961	E
<input type="radio"/>	GO:0015674	6,7	di-, tri-valent inorganic cation transport	34	0.0053	6	0.0176	0.0061031	E
<input type="radio"/>	GO:0000751	8,9,7,6	cell cycle arrest in response to pheromone	8	0.0012	3	0.0088	0.0061507	E
<input type="radio"/>	GO:0009892	5,4	negative regulation of metabolic process	208	0.0321	19	0.0559	0.0065007	E
<input type="radio"/>	GO:0045934	7,6	negative regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	179	0.0276	17	0.0500	0.0066985	E
<input type="radio"/>	GO:0006476	8	protein amino acid deacetylation	26	0.0040	5	0.0147	0.0083410	E
<input type="radio"/>	GO:0051641	4,3	cellular localization	642	0.0991	45	0.1324	0.0085988	E
<input type="radio"/>	GO:0015891	4,5	siderophore transport	9	0.0014	3	0.0088	0.0087454	E
<input type="radio"/>	GO:0046907	6,4,5	intracellular transport	545	0.0842	39	0.1147	0.0096875	E
<input type="radio"/>	GO:0007093	8,10,9,7	mitotic cell cycle checkpoint	27	0.0042	5	0.0147	0.0097050	E
<input type="radio"/>	GO:0045941	8,7	positive regulation of transcription	101	0.0156	11	0.0324	0.0099949	E
<input type="radio"/>	GO:0007017	6	microtubule-based process	101	0.0156	11	0.0324	0.0099949	E
<input type="radio"/>	GO:0006811	4,5	ion transport	115	0.0178	12	0.0353	0.0100633	E
<input type="radio"/>	GO:0000278	4	mitotic cell cycle	266	0.0411	22	0.0647	0.0101465	E
<input type="radio"/>	GO:0015837	4,5	amine transport	50	0.0077	7	0.0206	0.0105897	E
<input type="radio"/>	GO:0031325	6,5	positive regulation of cellular metabolic process	116	0.0179	12	0.0353	0.0106457	E
<input type="radio"/>	GO:0009893	5,4	positive regulation of metabolic process	116	0.0179	12	0.0353	0.0106457	E
<input type="radio"/>	GO:0006378	9	mRNA polyadenylation	18	0.0028	4	0.0118	0.0108304	E
<input type="radio"/>	GO:0044257	6,7	cellular protein catabolic process	160	0.0247	15	0.0441	0.0108892	E
<input type="radio"/>	GO:0051649	5,3,4	establishment of cellular localization	606	0.0936	42	0.1235	0.0118120	E
<input type="radio"/>	GO:0030005	9,7	cellular di-, tri-valent inorganic cation homeostasis	64	0.0099	8	0.0235	0.0121922	E
<input type="radio"/>	GO:0055066	8	di-, tri-valent inorganic cation homeostasis	64	0.0099	8	0.0235	0.0121922	E
<input type="radio"/>	GO:0006950	3	response to stress	488	0.0754	35	0.1029	0.0123757	E
<input type="radio"/>	GO:0048610	3,4	reproductive cellular process	149	0.0230	14	0.0412	0.0129865	E
<input type="radio"/>	GO:0022413	5,4	reproductive process in single-celled organism	149	0.0230	14	0.0412	0.0129865	E

<input type="radio"/>	GO:0000075	7,6	cell cycle checkpoint	53	0.0082	7	0.0206	0.0139306	E
<input type="radio"/>	GO:0051603	7,8	proteolysis involved in cellular protein catabolic process	151	0.0233	14	0.0412	0.0142020	E
<input type="radio"/>	GO:0016567	9	protein ubiquitination	66	0.0102	8	0.0235	0.0142250	E
<input type="radio"/>	GO:0044238	3	primary metabolic process	3247	0.5014	184	0.5412	0.0142924	E
<input type="radio"/>	GO:0043487	8,7	regulation of RNA stability	30	0.0046	5	0.0147	0.0145976	E
<input type="radio"/>	GO:0043488	9,8,7	regulation of mRNA stability	30	0.0046	5	0.0147	0.0145976	E
<input type="radio"/>	GO:0031324	6,5	negative regulation of cellular metabolic process	198	0.0306	17	0.0500	0.0147669	E
<input type="radio"/>	GO:0000301	9,7,6,8	retrograde transport, vesicle recycling within Golgi	4	0.0006	2	0.0059	0.0148151	E
<input type="radio"/>	GO:0000196	8,6	MAPKKK cascade during cell wall biogenesis	4	0.0006	2	0.0059	0.0148151	E
<input type="radio"/>	GO:0006814	7,8	sodium ion transport	4	0.0006	2	0.0059	0.0148151	E
<input type="radio"/>	GO:0006562	8,9	proline catabolic process	4	0.0006	2	0.0059	0.0148151	E
<input type="radio"/>	GO:0048622	6,5	reproductive sporulation	108	0.0167	11	0.0324	0.0149687	E
<input type="radio"/>	GO:0030437	7,6	sporulation (sensu Fungi)	108	0.0167	11	0.0324	0.0149687	E
<input type="radio"/>	GO:0045935	7,6	positive regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	108	0.0167	11	0.0324	0.0149687	E
<input type="radio"/>	GO:0009057	4	macromolecule catabolic process	345	0.0533	26	0.0765	0.0152562	E
<input type="radio"/>	GO:0006623	9,8,7,6	protein targeting to vacuole	67	0.0103	8	0.0235	0.0153172	E
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<input type="radio"/>	GO:0019395	6,8,7	fatty acid oxidation	11	0.0017	3	0.0088	0.0154346	E
<input type="radio"/>	GO:0007050	7,8,6	cell cycle arrest	11	0.0017	3	0.0088	0.0154346	E
<input type="radio"/>	GO:0001403	6,4,8,9	invasive growth (sensu Saccharomyces)	42	0.0065	6	0.0176	0.0155451	E
<input type="radio"/>	GO:0000226	7	microtubule cytoskeleton organization and biogenesis	81	0.0125	9	0.0265	0.0159168	E
<input type="radio"/>	GO:0048518	4	positive regulation of biological process	124	0.0191	12	0.0353	0.0161328	E
<input type="radio"/>	GO:0048522	5,4	positive regulation of cellular process	124	0.0191	12	0.0353	0.0161328	E
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<input type="radio"/>	GO:0006891	8,6,5,7	intra-Golgi vesicle-mediated transport	21	0.0032	4	0.0118	0.0180451	E
<input type="radio"/>	GO:0045324	8,6,7	late endosome to vacuole transport	21	0.0032	4	0.0118	0.0180451	E
<input type="radio"/>	GO:0030029	6	actin filament-based process	112	0.0173	11	0.0324	0.0184156	E
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<input type="radio"/>	GO:0000083	10,9,6,5,7,8,4	G1/S-specific transcription in mitotic cell cycle	12	0.0019	3	0.0088	0.0195067	E
<input type="radio"/>	GO:0008361	4,6,7	regulation of cell size	129	0.0199	12	0.0353	0.0203284	E
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<input type="radio"/>	GO:0006897	6,5	endocytosis	86	0.0133	9	0.0265	0.0215070	E
<input type="radio"/>	GO:0032505	4,3	reproduction of a single-celled organism	194	0.0300	16	0.0471	0.0223085	E
<input type="radio"/>	GO:0031111	7,10,6	negative regulation of microtubule polymerization or depolymerization	5	0.0008	2	0.0059	0.0234023	E
<input type="radio"/>	GO:0042149	8,7,6	cellular response to glucose starvation	5	0.0008	2	0.0059	0.0234023	E
<input type="radio"/>	GO:0007188	8,9	G-protein signaling, coupled to cAMP nucleotide second messenger	5	0.0008	2	0.0059	0.0234023	E
<input type="radio"/>	GO:0000017	6,7	alpha-glucoside transport	5	0.0008	2	0.0059	0.0234023	E
<input type="radio"/>	GO:0015693	7,8	magnesium ion transport	5	0.0008	2	0.0059	0.0234023	E
<input type="radio"/>	GO:0031114	7,10,6,8	regulation of microtubule depolymerization	5	0.0008	2	0.0059	0.0234023	E
<input type="radio"/>	GO:0007187	7,8	G-protein signaling, coupled to cyclic nucleotide second messenger	5	0.0008	2	0.0059	0.0234023	E

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<input type="checkbox"/>	GO:0007026	8,7,11,9,6	negative regulation of microtubule depolymerization	5	0.0008	2	0.0059	0.0234023	E
<input type="checkbox"/>	GO:0043412	5	biopolymer modification	664	0.1025	43	0.1265	0.0234396	E
<input type="checkbox"/>	GO:0019941	8,7,9	modification-dependent protein catabolic process	148	0.0229	13	0.0382	0.0236131	E
<input type="checkbox"/>	GO:0006511	9,8,10	ubiquitin-dependent protein catabolic process	148	0.0229	13	0.0382	0.0236131	E
<input type="checkbox"/>	GO:0009408	5,4	response to heat	23	0.0036	4	0.0118	0.0239911	E
<input type="checkbox"/>	GO:0009065	7,8	glutamine family amino acid catabolic process	13	0.0020	3	0.0088	0.0240366	E
<input type="checkbox"/>	GO:0045786	6,7,5	negative regulation of progression through cell cycle	13	0.0020	3	0.0088	0.0240366	E
<input type="checkbox"/>	GO:0006402	7	mRNA catabolic process	60	0.0093	7	0.0206	0.0240405	E
<input type="checkbox"/>	GO:0006259	5	DNA metabolic process	523	0.0808	35	0.1029	0.0242998	E
<input type="checkbox"/>	GO:0007051	8	spindle organization and biogenesis	47	0.0073	6	0.0176	0.0243722	E
<input type="checkbox"/>	GO:0000746	3	conjugation	118	0.0182	11	0.0324	0.0244158	E
<input type="checkbox"/>	GO:0000747	4	conjugation with cellular fusion	118	0.0182	11	0.0324	0.0244158	E
<input type="checkbox"/>	GO:0019953	3	sexual reproduction	118	0.0182	11	0.0324	0.0244158	E
<input type="checkbox"/>	GO:0044265	5	cellular macromolecule catabolic process	314	0.0485	23	0.0676	0.0246206	E
<input type="checkbox"/>	GO:0032502	2	developmental process	436	0.0673	30	0.0882	0.0249199	E
<input type="checkbox"/>	GO:0042592	4	homeostatic process	134	0.0207	12	0.0353	0.0251093	E
<input type="checkbox"/>	GO:0050801	6	ion homeostasis	119	0.0184	11	0.0324	0.0255105	E
<input type="checkbox"/>	GO:0048193	7,5,6	Golgi vesicle transport	166	0.0256	14	0.0412	0.0255951	E
<input type="checkbox"/>	GO:0000902	5,6	cell morphogenesis	248	0.0383	19	0.0559	0.0256507	E
<input type="checkbox"/>	GO:0032989	4,5	cellular structure morphogenesis	248	0.0383	19	0.0559	0.0256507	E
<input type="checkbox"/>	GO:0048856	3	anatomical structure development	248	0.0383	19	0.0559	0.0256507	E
<input type="checkbox"/>	GO:0009653	4,3	anatomical structure morphogenesis	248	0.0383	19	0.0559	0.0256507	E
<input type="checkbox"/>	GO:0007124	6,4,8,9	pseudohyphal growth	61	0.0094	7	0.0206	0.0257473	E
<input type="checkbox"/>	GO:0009056	3	catabolic process	438	0.0676	30	0.0882	0.0258511	E
<input type="checkbox"/>	GO:0043170	3	macromolecule metabolic process	2841	0.4387	158	0.4647	0.0272610	E
<input type="checkbox"/>	GO:0000288	10,8,9	mRNA catabolic process, deadenylation-dependent decay	24	0.0037	4	0.0118	0.0272902	E
<input type="checkbox"/>	GO:0006896	9,8,7,6	Golgi to vacuole transport	24	0.0037	4	0.0118	0.0272902	E
<input type="checkbox"/>	GO:0043631	8	RNA polyadenylation	24	0.0037	4	0.0118	0.0272902	E
<input type="checkbox"/>	GO:0045944	10,9	positive regulation of transcription from RNA polymerase II promoter	76	0.0117	8	0.0235	0.0274270	E
<input type="checkbox"/>	GO:0007001	6	chromosome organization and biogenesis (sensu Eukaryota)	567	0.0876	37	0.1088	0.0276174	E
<input type="checkbox"/>	GO:0048878	5	chemical homeostasis	121	0.0187	11	0.0324	0.0277782	E
<input type="checkbox"/>	GO:0051252	7,6	regulation of RNA metabolic process	36	0.0056	5	0.0147	0.0280321	E
<input type="checkbox"/>	GO:0016569	9	covalent chromatin modification	91	0.0141	9	0.0265	0.0280936	E
<input type="checkbox"/>	GO:0016570	10,8	histone modification	91	0.0141	9	0.0265	0.0280936	E
<input type="checkbox"/>	GO:0042787	10,9,11	protein ubiquitination during ubiquitin-dependent protein catabolic process	14	0.0022	3	0.0088	0.0289969	E
<input type="checkbox"/>	GO:0030036	7	actin cytoskeleton organization and biogenesis	107	0.0165	10	0.0294	0.0294246	E
<input type="checkbox"/>	GO:0051276	5	chromosome organization and biogenesis	572	0.0883	37	0.1088	0.0296877	E
<input type="checkbox"/>	GO:0030435	5	sporulation	123	0.0190	11	0.0324	0.0301475	E
<input type="checkbox"/>	GO:0043632	6	modification-dependent macromolecule catabolic process	155	0.0239	13	0.0382	0.0304529	E
<input type="checkbox"/>	GO:0030447	3	filamentous growth	94	0.0145	9	0.0265	0.0324985	E
<input type="checkbox"/>	GO:0006397	7	mRNA processing	157	0.0242	13	0.0382	0.0325696	E

<input type="radio"/>	GO:0033214	12,10	iron assimilation by chelation and transport	6	0.0009	2	0.0059	0.0332699	E
<input type="radio"/>	GO:0007019	9,7	microtubule depolymerization	6	0.0009	2	0.0059	0.0332699	E
<input type="radio"/>	GO:0031930	6	mitochondrial signaling pathway	6	0.0009	2	0.0059	0.0332699	E
<input type="radio"/>	GO:0015892	13,11,8,9,5,10,6	siderophore-iron transport	6	0.0009	2	0.0059	0.0332699	E
<input type="radio"/>	GO:0008643	4,5	carbohydrate transport	38	0.0059	5	0.0147	0.0335408	E
<input type="radio"/>	GO:0016485	8	protein processing	38	0.0059	5	0.0147	0.0335408	E
<input type="radio"/>	GO:0045893	9,8	positive regulation of transcription, DNA-dependent	95	0.0147	9	0.0265	0.0340376	E
<input type="radio"/>	GO:0031110	6,9,5	regulation of microtubule polymerization or depolymerization	15	0.0023	3	0.0088	0.0343559	E
<input type="radio"/>	GO:0006379	8	mRNA cleavage	26	0.0040	4	0.0118	0.0345002	E
<input type="radio"/>	GO:0008152	2	metabolic process	3516	0.5429	191	0.5618	0.0346079	E
<input type="radio"/>	GO:0045045	7,5,4,6	secretory pathway	243	0.0375	18	0.0529	0.0346616	E
<input type="radio"/>	GO:0044237	3	cellular metabolic process	3403	0.5255	185	0.5441	0.0347153	E
<input type="radio"/>	GO:0007067	8,6,7,5	mitosis	127	0.0196	11	0.0324	0.0351739	E
<input type="radio"/>	GO:0010324	5	membrane invagination	96	0.0148	9	0.0265	0.0356105	E
<input type="radio"/>	GO:0006865	5,6,7	amino acid transport	39	0.0060	5	0.0147	0.0364713	E
<input type="radio"/>	GO:0019725	5,3	cellular homeostasis	128	0.0198	11	0.0324	0.0364868	E
<input type="radio"/>	GO:0051301	3	cell division	246	0.0380	18	0.0529	0.0371664	E
<input type="radio"/>	GO:0006508	6	proteolysis	178	0.0275	14	0.0412	0.0373909	E
<input type="radio"/>	GO:0000087	7,5,6	M phase of mitotic cell cycle	129	0.0199	11	0.0324	0.0378208	E
<input type="radio"/>	GO:0051646	6,5	mitochondrion localization	27	0.0042	4	0.0118	0.0383904	E
<input type="radio"/>	GO:0031109	8	microtubule polymerization or depolymerization	16	0.0025	3	0.0088	0.0400786	E
<input type="radio"/>	GO:0032940	6,4,5	secretion by cell	250	0.0386	18	0.0529	0.0406034	E
<input type="radio"/>	GO:0046903	3,4	secretion	250	0.0386	18	0.0529	0.0406034	E
<input type="radio"/>	GO:0006873	7,5	cellular ion homeostasis	115	0.0178	10	0.0294	0.0407735	E
<input type="radio"/>	GO:0055082	6,4	cellular chemical homeostasis	115	0.0178	10	0.0294	0.0407735	E
<input type="radio"/>	GO:0032446	8	protein modification by small protein conjugation	84	0.0130	8	0.0235	0.0413990	E
<input type="radio"/>	GO:0009266	4	response to temperature stimulus	28	0.0043	4	0.0118	0.0424553	E
<input type="radio"/>	GO:0007047	5	cell wall organization and biogenesis	200	0.0309	15	0.0441	0.0426892	E
<input type="radio"/>	GO:0045229	4	external encapsulating structure organization and biogenesis	200	0.0309	15	0.0441	0.0426892	E
<input type="radio"/>	GO:0022414	3,2	reproductive process	183	0.0283	14	0.0412	0.0428683	E
<input type="radio"/>	GO:0007088	7,9,8,6	regulation of mitosis	55	0.0085	6	0.0176	0.0429310	E
<input type="radio"/>	GO:0006560	7,8	proline metabolic process	7	0.0011	2	0.0059	0.0441446	E
<input type="radio"/>	GO:0045835	8,10,9,7	negative regulation of meiosis	7	0.0011	2	0.0059	0.0441446	E
<input type="radio"/>	GO:0019722	7	calcium-mediated signaling	7	0.0011	2	0.0059	0.0441446	E
<input type="radio"/>	GO:0051129	6,5	negative regulation of cell organization and biogenesis	7	0.0011	2	0.0059	0.0441446	E
<input type="radio"/>	GO:0051640	5,4	organelle localization	56	0.0086	6	0.0176	0.0455816	E
<input type="radio"/>	GO:0055080	7	cation homeostasis	102	0.0158	9	0.0265	0.0456906	E
<input type="radio"/>	GO:0030003	8,6	cellular cation homeostasis	102	0.0158	9	0.0265	0.0456906	E
<input type="radio"/>	GO:0042244	5,6	spore wall assembly	42	0.0065	5	0.0147	0.0459016	E
<input type="radio"/>	GO:0030476	8,6,7	spore wall assembly (sensu Fungi)	42	0.0065	5	0.0147	0.0459016	E
<input type="radio"/>	GO:0042147	8,6,7	retrograde transport, endosome to Golgi	17	0.0026	3	0.0088	0.0461281	E
<input type="radio"/>	GO:0016568	8	chromatin modification	223	0.0344	16	0.0471	0.0483996	E
<input type="radio"/>	GO:0044248	4	cellular catabolic process	425	0.0656	27	0.0794	0.0487415	E

<input type="checkbox"/>	GO:0006512	8	ubiquitin cycle	88	0.0136	8	0.0235	0.0493092	E
<input type="checkbox"/>	GO:0006970	4	response to osmotic stress	89	0.0137	8	0.0235	0.0513634	E
<input type="checkbox"/>	GO:0006973	6,4	intracellular accumulation of glycerol	1	0.0002	1	0.0029	0.0525015	E
<input type="checkbox"/>	GO:0032780	7	negative regulation of ATPase activity	1	0.0002	1	0.0029	0.0525015	E
<input type="checkbox"/>	GO:0006517	8	protein deglycosylation	1	0.0002	1	0.0029	0.0525015	E
<input type="checkbox"/>	GO:0045732	7,8,6	positive regulation of protein catabolic process	1	0.0002	1	0.0029	0.0525015	E
<input type="checkbox"/>	GO:0015771	6,7,8	trehalose transport	1	0.0002	1	0.0029	0.0525015	E
<input type="checkbox"/>	GO:0051754	11,9,8,6,5,10,7,4	meiotic sister chromatid cohesion, centromeric	1	0.0002	1	0.0029	0.0525015	E
<input type="checkbox"/>	GO:0006516	7	glycoprotein catabolic process	1	0.0002	1	0.0029	0.0525015	E
<input type="checkbox"/>	GO:0048228	6,9,8,5	actin cortical patch distribution	1	0.0002	1	0.0029	0.0525015	E
<input type="checkbox"/>	GO:0015700	7,8	arsenite transport	1	0.0002	1	0.0029	0.0525015	E
<input type="checkbox"/>	GO:0015685	14,12,9,10,6,11,7	ferric-enterobactin transport	1	0.0002	1	0.0029	0.0525015	E
<input type="checkbox"/>	GO:0045739	9,8,7	positive regulation of DNA repair	1	0.0002	1	0.0029	0.0525015	E
<input type="checkbox"/>	GO:0009896	6,5	positive regulation of catabolic process	1	0.0002	1	0.0029	0.0525015	E
<input type="checkbox"/>	GO:0019547	9,8,10,7,6,5	arginine catabolic process to ornithine	1	0.0002	1	0.0029	0.0525015	E
<input type="checkbox"/>	GO:0015682	8,9,10	ferric iron transport	1	0.0002	1	0.0029	0.0525015	E
<input type="checkbox"/>	GO:0006039	9,10,7,6,11,8	cell wall chitin catabolic process	1	0.0002	1	0.0029	0.0525015	E
<input type="checkbox"/>	GO:0045103	6	intermediate filament-based process	1	0.0002	1	0.0029	0.0525015	E
<input type="checkbox"/>	GO:0016998	5	cell wall catabolic process	1	0.0002	1	0.0029	0.0525015	E
<input type="checkbox"/>	GO:0046098	7	guanine metabolic process	1	0.0002	1	0.0029	0.0525015	E
<input type="checkbox"/>	GO:0042930	5,6	enterobactin transport	1	0.0002	1	0.0029	0.0525015	E
<input type="checkbox"/>	GO:0043462	6	regulation of ATPase activity	1	0.0002	1	0.0029	0.0525015	E
<input type="checkbox"/>	GO:0006367	8,9,7	transcription initiation from RNA polymerase II promoter	44	0.0068	5	0.0147	0.0526565	E
<input type="checkbox"/>	GO:0065004	6,5	protein-DNA complex assembly	74	0.0114	7	0.0206	0.0530767	E
<input type="checkbox"/>	GO:0006401	6	RNA catabolic process	74	0.0114	7	0.0206	0.0530767	E
<input type="checkbox"/>	GO:0006996	4	organelle organization and biogenesis	1388	0.2143	73	0.2147	0.0540588	E
<input type="checkbox"/>	GO:0007323	9	peptide pheromone maturation	8	0.0012	2	0.0059	0.0557841	E
<input type="checkbox"/>	GO:0033212	11,9	iron assimilation	8	0.0012	2	0.0059	0.0557841	E
<input type="checkbox"/>	GO:0031668	5,4	cellular response to extracellular stimulus	19	0.0029	3	0.0088	0.0590518	E
<input type="checkbox"/>	GO:0031669	6,5	cellular response to nutrient levels	19	0.0029	3	0.0088	0.0590518	E
<input type="checkbox"/>	GO:0009267	7,6,5	cellular response to starvation	19	0.0029	3	0.0088	0.0590518	E
<input type="checkbox"/>	GO:0042594	6,4	response to starvation	19	0.0029	3	0.0088	0.0590518	E
<input type="checkbox"/>	GO:0006325	7	establishment and/or maintenance of chromatin architecture	253	0.0391	17	0.0500	0.0602561	E
<input type="checkbox"/>	GO:0006323	6	DNA packaging	253	0.0391	17	0.0500	0.0602561	E
<input type="checkbox"/>	GO:0043543	7	protein amino acid acylation	62	0.0096	6	0.0176	0.0626253	E
<input type="checkbox"/>	GO:0006631	5,7,6	fatty acid metabolic process	47	0.0073	5	0.0147	0.0633470	E
<input type="checkbox"/>	GO:0045053	7,6,5,4	protein retention in Golgi	20	0.0031	3	0.0088	0.0658468	E
<input type="checkbox"/>	GO:0006826	7,8,9	iron ion transport	20	0.0031	3	0.0088	0.0658468	E
<input type="checkbox"/>	GO:0000209	10	protein polyubiquitination	20	0.0031	3	0.0088	0.0658468	E
<input type="checkbox"/>	GO:0006497	8,7,6	protein amino acid lipidation	48	0.0074	5	0.0147	0.0670283	E
<input type="checkbox"/>	GO:0042158	7,5	lipoprotein biosynthetic process	48	0.0074	5	0.0147	0.0670283	E
<input type="checkbox"/>	GO:0042157	6	lipoprotein metabolic process	48	0.0074	5	0.0147	0.0670283	E
<input type="checkbox"/>	GO:0006635	7,9,8	fatty acid beta-oxidation	9	0.0014	2	0.0059	0.0679744	E
<input type="checkbox"/>	GO:0000290	11,8,9,10	deadenylation-dependent decapping	9	0.0014	2	0.0059	0.0679744	E
<input type="checkbox"/>	GO:0030950	8,7	establishment and/or maintenance of actin	8	0.0014	2	0.0059	0.0679744	E

<input type="radio"/>	GO:0030930	0,1	cytoskeleton polarity	9	0.0014	2	0.0059	0.0679744	E
<input type="radio"/>	GO:0046685	5	response to arsenic	9	0.0014	2	0.0059	0.0679744	E
<input type="radio"/>	GO:0030952	6	establishment and/or maintenance of cytoskeleton polarity	9	0.0014	2	0.0059	0.0679744	E
<input type="radio"/>	GO:0009719	3	response to endogenous stimulus	243	0.0375	16	0.0471	0.0690139	E
<input type="radio"/>	GO:0016044	4	membrane organization and biogenesis	188	0.0290	13	0.0382	0.0708692	E
<input type="radio"/>	GO:0051716	3	cellular response to stimulus	21	0.0032	3	0.0088	0.0728112	E
<input type="radio"/>	GO:0033554	4	cellular response to stress	21	0.0032	3	0.0088	0.0728112	E
<input type="radio"/>	GO:0006468	8,7	protein amino acid phosphorylation	101	0.0156	8	0.0235	0.0774125	E
<input type="radio"/>	GO:0006974	4	response to DNA damage stimulus	234	0.0361	15	0.0441	0.0795260	E
<input type="radio"/>	GO:0006012	7,8	galactose metabolic process	10	0.0015	2	0.0059	0.0805271	E
<input type="radio"/>	GO:0019363	7,6,8	pyridine nucleotide biosynthetic process	10	0.0015	2	0.0059	0.0805271	E
<input type="radio"/>	GO:0051261	6	protein depolymerization	10	0.0015	2	0.0059	0.0805271	E
<input type="radio"/>	GO:0051336	5	regulation of hydrolase activity	10	0.0015	2	0.0059	0.0805271	E
<input type="radio"/>	GO:0000082	8,5,6,7,4	G1/S transition of mitotic cell cycle	52	0.0080	5	0.0147	0.0821251	E
<input type="radio"/>	GO:0006892	8,6,5,7	post-Golgi vesicle-mediated transport	69	0.0107	6	0.0176	0.0839723	E
<input type="radio"/>	GO:0043623	7,6	cellular protein complex assembly	69	0.0107	6	0.0176	0.0839723	E
<input type="radio"/>	GO:0022607	4	cellular component assembly	471	0.0727	25	0.0735	0.0847541	E
<input type="radio"/>	GO:0007243	6	protein kinase cascade	23	0.0036	3	0.0088	0.0870939	E
<input type="radio"/>	GO:0006629	4	lipid metabolic process	242	0.0374	15	0.0441	0.0871633	E
<input type="radio"/>	GO:0046942	5,6	carboxylic acid transport	54	0.0083	5	0.0147	0.0897812	E
<input type="radio"/>	GO:0032787	6	monocarboxylic acid metabolic process	126	0.0195	9	0.0265	0.0911281	E
<input type="radio"/>	GO:0006972	5	hyperosmotic response	11	0.0017	2	0.0059	0.0932772	E
<input type="radio"/>	GO:0001558	5,6,4,8,9	regulation of cell growth	11	0.0017	2	0.0059	0.0932772	E
<input type="radio"/>	GO:0006352	7,8,6	transcription initiation	55	0.0085	5	0.0147	0.0936076	E
<input type="radio"/>	GO:0015849	4,5	organic acid transport	55	0.0085	5	0.0147	0.0936076	E
<input type="radio"/>	GO:0010035	4	response to inorganic substance	24	0.0037	3	0.0088	0.0943378	E
<input type="radio"/>	GO:0001302	5	replicative cell aging	39	0.0060	4	0.0118	0.0946208	E
<input type="radio"/>	GO:0006112	5	energy reserve metabolic process	39	0.0060	4	0.0118	0.0946208	E
<input type="radio"/>	GO:0006886	7,5,6	intracellular protein transport	274	0.0423	16	0.0471	0.0950757	E
<input type="radio"/>	GO:0008104	4	protein localization	330	0.0510	18	0.0529	0.0974874	E
<input type="radio"/>	GO:0006793	4	phosphorus metabolic process	212	0.0327	13	0.0382	0.0982596	E
<input type="radio"/>	GO:0006796	5	phosphate metabolic process	212	0.0327	13	0.0382	0.0982596	E
<input type="radio"/>	GO:0015031	4,5,6	protein transport	280	0.0432	16	0.0471	0.0983903	E
<input type="radio"/>	GO:0051599	5,4	response to hydrostatic pressure	2	0.0003	1	0.0029	0.0995056	E
<input type="radio"/>	GO:0008295	8,9	spermidine biosynthetic process	2	0.0003	1	0.0029	0.0995056	E
<input type="radio"/>	GO:0015805	7,8,9	S-adenosylmethionine transport	2	0.0003	1	0.0029	0.0995056	E
<input type="radio"/>	GO:0030803	10,8,9,7	negative regulation of cyclic nucleotide biosynthetic process	2	0.0003	1	0.0029	0.0995056	E
<input type="radio"/>	GO:0008216	7,8	spermidine metabolic process	2	0.0003	1	0.0029	0.0995056	E
<input type="radio"/>	GO:0030814	9,8	regulation of cAMP metabolic process	2	0.0003	1	0.0029	0.0995056	E
<input type="radio"/>	GO:0009187	6	cyclic nucleotide metabolic process	2	0.0003	1	0.0029	0.0995056	E
<input type="radio"/>	GO:0045016	8,6,7,9	mitochondrial magnesium ion transport	2	0.0003	1	0.0029	0.0995056	E
<input type="radio"/>	GO:0015840	5,6	urea transport	2	0.0003	1	0.0029	0.0995056	E
<input type="radio"/>	GO:0030808	8,6,7,5	regulation of nucleotide biosynthetic process	2	0.0003	1	0.0029	0.0995056	E
<input type="radio"/>	GO:0031087	11,9,10	deadenylation-independent decapping	2	0.0003	1	0.0029	0.0995056	E
<input type="radio"/>	GO:0030800	0,7,8,6	negative regulation of nucleotide	2	0.0003	1	0.0029	0.0995056	E

<input type="radio"/>	GO:0030809	7,7,0,0	biosynthetic process	2	0.0003	1	0.0029	0.0995056	E
<input type="radio"/>	GO:0046058	7	cAMP metabolic process	2	0.0003	1	0.0029	0.0995056	E
<input type="radio"/>	GO:0048250	8,6,9,7,10	mitochondrial iron ion transport	2	0.0003	1	0.0029	0.0995056	E
<input type="radio"/>	GO:0030817	10,8,9,7	regulation of cAMP biosynthetic process	2	0.0003	1	0.0029	0.0995056	E
<input type="radio"/>	GO:0030815	10,9	negative regulation of cAMP metabolic process	2	0.0003	1	0.0029	0.0995056	E
<input type="radio"/>	GO:0030800	9,8	negative regulation of cyclic nucleotide metabolic process	2	0.0003	1	0.0029	0.0995056	E
<input type="radio"/>	GO:0032320	8,9,10	positive regulation of Ras GTPase activity	2	0.0003	1	0.0029	0.0995056	E
<input type="radio"/>	GO:0030799	8,7	regulation of cyclic nucleotide metabolic process	2	0.0003	1	0.0029	0.0995056	E
<input type="radio"/>	GO:0031086	10,8,9	mRNA catabolic process, deadenylation-independent decay	2	0.0003	1	0.0029	0.0995056	E
<input type="radio"/>	GO:0010286	6,5	heat acclimation	2	0.0003	1	0.0029	0.0995056	E
<input type="radio"/>	GO:0030818	11,9,10,8	negative regulation of cAMP biosynthetic process	2	0.0003	1	0.0029	0.0995056	E
<input type="radio"/>	GO:0010133	9,8,10	proline catabolic process to glutamate	2	0.0003	1	0.0029	0.0995056	E
<input type="radio"/>	GO:0006426	9,8,10,7	glycyl-tRNA aminoacylation	2	0.0003	1	0.0029	0.0995056	E
<input type="radio"/>	GO:0030802	9,7,8,6	regulation of cyclic nucleotide biosynthetic process	2	0.0003	1	0.0029	0.0995056	E
<input type="radio"/>	GO:0051865	10	protein autoubiquitination	2	0.0003	1	0.0029	0.0995056	E
<input type="radio"/>	GO:0006282	8,7,6	regulation of DNA repair	2	0.0003	1	0.0029	0.0995056	E
<input type="radio"/>	GO:0006032	9,10,8,7	chitin catabolic process	2	0.0003	1	0.0029	0.0995056	E
<input type="radio"/>	GO:0046348	6,7	amino sugar catabolic process	2	0.0003	1	0.0029	0.0995056	E
<input type="radio"/>	GO:0006043	7,8	glucosamine catabolic process	2	0.0003	1	0.0029	0.0995056	E
<input type="radio"/>	GO:0015766	5,6	disaccharide transport	2	0.0003	1	0.0029	0.0995056	E
<input type="radio"/>	GO:0006171	7,8	cAMP biosynthetic process	2	0.0003	1	0.0029	0.0995056	E
<input type="radio"/>	GO:0009190	6,7	cyclic nucleotide biosynthetic process	2	0.0003	1	0.0029	0.0995056	E
<input type="radio"/>	GO:0051177	10,8,7,5,9,6,4	meiotic sister chromatid cohesion	2	0.0003	1	0.0029	0.0995056	E
<input type="radio"/>	GO:0032318	7,8,9	regulation of Ras GTPase activity	2	0.0003	1	0.0029	0.0995056	E
<input type="radio"/>	GO:0006046	8,9	N-acetylglucosamine catabolic process	2	0.0003	1	0.0029	0.0995056	E
<input type="radio"/>	GO:0043146	9,8,12,10,7	spindle stabilization	2	0.0003	1	0.0029	0.0995056	E
<input type="radio"/>	GO:0031279	5	regulation of cyclase activity	2	0.0003	1	0.0029	0.0995056	E
<input type="radio"/>	GO:0006140	7,6	regulation of nucleotide metabolic process	2	0.0003	1	0.0029	0.0995056	E
<input type="radio"/>	GO:0009415	4	response to water	2	0.0003	1	0.0029	0.0995056	E
<input type="radio"/>	GO:0051666	5,4	actin cortical patch localization	2	0.0003	1	0.0029	0.0995056	E
<input type="radio"/>	GO:0015757	7,8	galactose transport	2	0.0003	1	0.0029	0.0995056	E
<input type="radio"/>	GO:0006527	8,9,6,5	arginine catabolic process	2	0.0003	1	0.0029	0.0995056	E
<input type="radio"/>	GO:0051292	8,7	nuclear pore complex assembly	2	0.0003	1	0.0029	0.0995056	E
<input type="radio"/>	GO:0043148	10,9,6,5,4,13,11,8	mitotic spindle stabilization	2	0.0003	1	0.0029	0.0995056	E
<input type="radio"/>	GO:0050826	6,5	response to freezing	2	0.0003	1	0.0029	0.0995056	E
<input type="radio"/>	GO:0042886	4,5	amide transport	2	0.0003	1	0.0029	0.0995056	E
<input type="radio"/>	GO:0051339	5	regulation of lyase activity	2	0.0003	1	0.0029	0.0995056	E
<input type="radio"/>	GO:0045980	8,7	negative regulation of nucleotide metabolic process	2	0.0003	1	0.0029	0.0995056	E
<input type="radio"/>	GO:0045761	6,9,10	regulation of adenylate cyclase activity	2	0.0003	1	0.0029	0.0995056	E
<input type="radio"/>	GO:0048308	5	organelle inheritance	40	0.0062	4	0.0118	0.0996464	E
<input type="radio"/>	GO:0007031	5	peroxisome organization and biogenesis	40	0.0062	4	0.0118	0.0996464	E
<input type="radio"/>	GO:0006281	6,5	DNA repair	193	0.0298	12	0.0353	0.1006640	E
<input type="radio"/>	GO:0051325	6,5	interphase	112	0.0173	8	0.0235	0.1010851	E
<input type="radio"/>	GO:0051329	7,5,6	interphase of mitotic cell cycle	112	0.0173	8	0.0235	0.1010851	E

<input type="radio"/>	GO:0030154	4	cell differentiation	173	0.0267	11	0.0324	0.1019834	E
<input type="radio"/>	GO:0048869	3	cellular developmental process	173	0.0267	11	0.0324	0.1019834	E
<input type="radio"/>	GO:0019236	4	response to pheromone	94	0.0145	7	0.0206	0.1035568	E
<input type="radio"/>	GO:0045184	3,4,5	establishment of protein localization	296	0.0457	16	0.0471	0.1037189	E
<input type="radio"/>	GO:0016310	6	phosphorylation	155	0.0239	10	0.0294	0.1057860	E
<input type="radio"/>	GO:0015846	5,6	polyamine transport	12	0.0019	2	0.0059	0.1060806	E
<input type="radio"/>	GO:0008054	7,6,11,10,12	cyclin catabolic process	12	0.0019	2	0.0059	0.1060806	E
<input type="radio"/>	GO:0000001	8,7,6	mitochondrion inheritance	26	0.0040	3	0.0088	0.1088551	E
<input type="radio"/>	GO:0008645	6,7	hexose transport	26	0.0040	3	0.0088	0.1088551	E
<input type="radio"/>	GO:0048311	7,6	mitochondrion distribution	26	0.0040	3	0.0088	0.1088551	E
<input type="radio"/>	GO:0015749	5,6	monosaccharide transport	26	0.0040	3	0.0088	0.1088551	E
<input type="radio"/>	GO:0006506	10,9,8,7,11	GPI anchor biosynthetic process	26	0.0040	3	0.0088	0.1088551	E
<input type="radio"/>	GO:0006461	6,5	protein complex assembly	116	0.0179	8	0.0235	0.1089998	E
<input type="radio"/>	GO:0044255	4,5	cellular lipid metabolic process	229	0.0354	13	0.0382	0.1106219	E
<input type="radio"/>	GO:0006644	6,7	phospholipid metabolic process	97	0.0150	7	0.0206	0.1106622	E
<input type="radio"/>	GO:0007015	8	actin filament organization	61	0.0094	5	0.0147	0.1160542	E
<input type="radio"/>	GO:0006505	9,10	GPI anchor metabolic process	27	0.0042	3	0.0088	0.1160636	E
<input type="radio"/>	GO:0006334	6,7,10	nucleosome assembly	13	0.0020	2	0.0059	0.1188126	E
<input type="radio"/>	GO:0031929	6	TOR signaling pathway	13	0.0020	2	0.0059	0.1188126	E
<input type="radio"/>	GO:0040008	4,3	regulation of growth	13	0.0020	2	0.0059	0.1188126	E
<input type="radio"/>	GO:0043161	10,9,11	proteasomal ubiquitin-dependent protein catabolic process	63	0.0097	5	0.0147	0.1231687	E
<input type="radio"/>	GO:0046489	9,8,10	phosphoinositide biosynthetic process	28	0.0043	3	0.0088	0.1231984	E
<input type="radio"/>	GO:0006643	5,6	membrane lipid metabolic process	125	0.0193	8	0.0235	0.1245169	E
<input type="radio"/>	GO:0000041	7,8	transition metal ion transport	46	0.0071	4	0.0118	0.1289645	E
<input type="radio"/>	GO:0006091	3	generation of precursor metabolites and energy	183	0.0283	10	0.0294	0.1294846	E
<input type="radio"/>	GO:0006109	5,4	regulation of carbohydrate metabolic process	29	0.0045	3	0.0088	0.1302318	E
<input type="radio"/>	GO:0051651	5,4,3	maintenance of cellular localization	29	0.0045	3	0.0088	0.1302318	E
<input type="radio"/>	GO:0009063	6,7	amino acid catabolic process	29	0.0045	3	0.0088	0.1302318	E
<input type="radio"/>	GO:0006999	6	nuclear pore organization and biogenesis	29	0.0045	3	0.0088	0.1302318	E
<input type="radio"/>	GO:0006470	8,7	protein amino acid dephosphorylation	29	0.0045	3	0.0088	0.1302318	E
<input type="radio"/>	GO:0032507	6,5,4	maintenance of cellular protein localization	29	0.0045	3	0.0088	0.1302318	E
<input type="radio"/>	GO:0007005	5	mitochondrion organization and biogenesis	110	0.0170	7	0.0206	0.1364448	E
<input type="radio"/>	GO:0007033	5	vacuole organization and biogenesis	67	0.0103	5	0.0147	0.1365410	E
<input type="radio"/>	GO:0051128	5,4	regulation of cellular component organization and biogenesis	30	0.0046	3	0.0088	0.1371381	E
<input type="radio"/>	GO:0045185	5,4,3	maintenance of protein localization	30	0.0046	3	0.0088	0.1371381	E
<input type="radio"/>	GO:0006473	8	protein amino acid acetylation	48	0.0074	4	0.0118	0.1381234	E
<input type="radio"/>	GO:0006766	4	vitamin metabolic process	89	0.0137	6	0.0176	0.1392887	E
<input type="radio"/>	GO:0006767	5	water-soluble vitamin metabolic process	89	0.0137	6	0.0176	0.1392887	E
<input type="radio"/>	GO:0006741	8,7,10,9	NADP biosynthetic process	3	0.0005	1	0.0029	0.1414428	E
<input type="radio"/>	GO:0043200	5,4	response to amino acid stimulus	3	0.0005	1	0.0029	0.1414428	E
<input type="radio"/>	GO:0031647	6	regulation of protein stability	3	0.0005	1	0.0029	0.1414428	E
<input type="radio"/>	GO:0007234	7,6	osmosensory signaling pathway via two-component system	3	0.0005	1	0.0029	0.1414428	E
<input type="radio"/>	GO:0009303	8,7	rRNA transcription	3	0.0005	1	0.0029	0.1414428	E
<input type="radio"/>	GO:0051054	8,7	positive regulation of DNA metabolic	3	0.0005	1	0.0029	0.1414428	E

<input type="checkbox"/>	GO:0051054	0,1	process	3	0.0005	1	0.0029	0.1414428	E
<input type="checkbox"/>	GO:0000160	5	two-component signal transduction system (phosphorelay)	3	0.0005	1	0.0029	0.1414428	E
<input type="checkbox"/>	GO:0006370	8	mRNA capping	3	0.0005	1	0.0029	0.1414428	E
<input type="checkbox"/>	GO:0009437	6,7	carnitine metabolic process	3	0.0005	1	0.0029	0.1414428	E
<input type="checkbox"/>	GO:0030242	4,6	peroxisome degradation	3	0.0005	1	0.0029	0.1414428	E
<input type="checkbox"/>	GO:0016584	6,10	nucleosome positioning	3	0.0005	1	0.0029	0.1414428	E
<input type="checkbox"/>	GO:0050821	7	protein stabilization	3	0.0005	1	0.0029	0.1414428	E
<input type="checkbox"/>	GO:0007568	3	aging	49	0.0076	4	0.0118	0.1425394	E
<input type="checkbox"/>	GO:0007569	4	cell aging	49	0.0076	4	0.0118	0.1425394	E
<input type="checkbox"/>	GO:0030473	8,9,6,7	nuclear migration, microtubule-mediated	15	0.0023	2	0.0059	0.1436472	E
<input type="checkbox"/>	GO:0015918	5,6	sterol transport	15	0.0023	2	0.0059	0.1436472	E
<input type="checkbox"/>	GO:0031145	11,10,12	anaphase-promoting complex-dependent proteasomal ubiquitin-dependent protein catabolic process	15	0.0023	2	0.0059	0.1436472	E
<input type="checkbox"/>	GO:0031365	8	N-terminal protein amino acid modification	15	0.0023	2	0.0059	0.1436472	E
<input type="checkbox"/>	GO:0009651	5	response to salt stress	15	0.0023	2	0.0059	0.1436472	E
<input type="checkbox"/>	GO:0007091	9,7,5,8,6,4	mitotic metaphase/anaphase transition	15	0.0023	2	0.0059	0.1436472	E
<input type="checkbox"/>	GO:0007018	8,7,6	microtubule-based movement	15	0.0023	2	0.0059	0.1436472	E
<input type="checkbox"/>	GO:0005978	8,7,9	glycogen biosynthetic process	15	0.0023	2	0.0059	0.1436472	E
<input type="checkbox"/>	GO:0018409	9	peptide or protein amino-terminal blocking	15	0.0023	2	0.0059	0.1436472	E
<input type="checkbox"/>	GO:0015980	4	energy derivation by oxidation of organic compounds	145	0.0224	8	0.0235	0.1437998	E
<input type="checkbox"/>	GO:0006979	4	response to oxidative stress	71	0.0110	5	0.0147	0.1484962	E
<input type="checkbox"/>	GO:0044270	5,4	nitrogen compound catabolic process	32	0.0049	3	0.0088	0.1504768	E
<input type="checkbox"/>	GO:0015672	6,7	monovalent inorganic cation transport	32	0.0049	3	0.0088	0.1504768	E
<input type="checkbox"/>	GO:0005977	7,6,8	glycogen metabolic process	32	0.0049	3	0.0088	0.1504768	E
<input type="checkbox"/>	GO:0009310	5,6	amine catabolic process	32	0.0049	3	0.0088	0.1504768	E
<input type="checkbox"/>	GO:0006310	6	DNA recombination	122	0.0188	7	0.0206	0.1506442	E
<input type="checkbox"/>	GO:0051246	5,4	regulation of protein metabolic process	72	0.0111	5	0.0147	0.1512316	E
<input type="checkbox"/>	GO:0008380	7	RNA splicing	132	0.0204	7	0.0206	0.1546534	E
<input type="checkbox"/>	GO:0030865	6	cortical cytoskeleton organization and biogenesis	16	0.0025	2	0.0059	0.1555800	E
<input type="checkbox"/>	GO:0030866	8,7	cortical actin cytoskeleton organization and biogenesis	16	0.0025	2	0.0059	0.1555800	E
<input type="checkbox"/>	GO:0051235	3,2	maintenance of localization	33	0.0051	3	0.0088	0.1568681	E
<input type="checkbox"/>	GO:0007127	9,7,6,8,5	meiosis I	75	0.0116	5	0.0147	0.1587774	E
<input type="checkbox"/>	GO:0000398	8,10	nuclear mRNA splicing, via spliceosome	102	0.0158	6	0.0176	0.1604530	E
<input type="checkbox"/>	GO:0000377	9	RNA splicing, via transesterification reactions with bulged adenosine as nucleophile	103	0.0159	6	0.0176	0.1614500	E
<input type="checkbox"/>	GO:0000910	4	cytokinesis	109	0.0168	6	0.0176	0.1655201	E
<input type="checkbox"/>	GO:0000375	8	RNA splicing, via transesterification reactions	110	0.0170	6	0.0176	0.1658855	E
<input type="checkbox"/>	GO:0030705	7,5,6	cytoskeleton-dependent intracellular transport	17	0.0026	2	0.0059	0.1670983	E
<input type="checkbox"/>	GO:0048590	3	non-developmental growth	35	0.0054	3	0.0088	0.1690066	E
<input type="checkbox"/>	GO:0007117	6,5,4	budding cell bud growth	35	0.0054	3	0.0088	0.1690066	E
<input type="checkbox"/>	GO:0006888	8,6,5,7	ER to Golgi vesicle-mediated transport	81	0.0125	5	0.0147	0.1707028	E
<input type="checkbox"/>	GO:0008654	7,6,8	phospholipid biosynthetic process	58	0.0090	4	0.0118	0.1759884	E
<input type="checkbox"/>	GO:0007114	5,4	cell budding	85	0.0131	5	0.0147	0.1762114	E
<input type="checkbox"/>	GO:0019954	3	asexual reproduction	85	0.0131	5	0.0147	0.1762114	E

<input type="radio"/>	GO:0051248	6,5	negative regulation of protein metabolic process	18	0.0028	2	0.0059	0.1781483	E
<input type="radio"/>	GO:0006369	9,8	transcription termination from RNA polymerase II promoter	18	0.0028	2	0.0059	0.1781483	E
<input type="radio"/>	GO:0006097	6,8	glyoxylate cycle	4	0.0006	1	0.0029	0.1787136	E
<input type="radio"/>	GO:0045722	7,9,8,10,6,11	positive regulation of gluconeogenesis	4	0.0006	1	0.0029	0.1787136	E
<input type="radio"/>	GO:0043620	8,7,5	regulation of transcription in response to stress	4	0.0006	1	0.0029	0.1787136	E
<input type="radio"/>	GO:0043618	9,10,8,6	regulation of transcription from RNA polymerase II promoter in response to stress	4	0.0006	1	0.0029	0.1787136	E
<input type="radio"/>	GO:0006482	9	protein amino acid demethylation	4	0.0006	1	0.0029	0.1787136	E
<input type="radio"/>	GO:0009452	7	RNA capping	4	0.0006	1	0.0029	0.1787136	E
<input type="radio"/>	GO:0042542	6	response to hydrogen peroxide	4	0.0006	1	0.0029	0.1787136	E
<input type="radio"/>	GO:0006596	7,8	polyamine biosynthetic process	4	0.0006	1	0.0029	0.1787136	E
<input type="radio"/>	GO:0000916	6,5,4	cytokinesis, contractile ring contraction	4	0.0006	1	0.0029	0.1787136	E
<input type="radio"/>	GO:0008214	8	protein amino acid dealkylation	4	0.0006	1	0.0029	0.1787136	E
<input type="radio"/>	GO:0031321	4,8,6,7	prospore formation	4	0.0006	1	0.0029	0.1787136	E
<input type="radio"/>	GO:0015793	5,6	glycerol transport	4	0.0006	1	0.0029	0.1787136	E
<input type="radio"/>	GO:0016577	11,9,10	histone demethylation	4	0.0006	1	0.0029	0.1787136	E
<input type="radio"/>	GO:0050000	6,5	chromosome localization	4	0.0006	1	0.0029	0.1787136	E
<input type="radio"/>	GO:0031578	9,11,10,8	mitotic cell cycle spindle orientation checkpoint	4	0.0006	1	0.0029	0.1787136	E
<input type="radio"/>	GO:0009165	5,6	nucleotide biosynthetic process	59	0.0091	4	0.0118	0.1789040	E
<input type="radio"/>	GO:0000070	9,7,5,8,6,4	mitotic sister chromatid segregation	59	0.0091	4	0.0118	0.1789040	E
<input type="radio"/>	GO:0032506	5,3	cytokinetic process	88	0.0136	5	0.0147	0.1790595	E
<input type="radio"/>	GO:0007264	6	small GTPase mediated signal transduction	61	0.0094	4	0.0118	0.1842130	E
<input type="radio"/>	GO:0006515	8,9	misfolded or incompletely synthesized protein catabolic process	38	0.0059	3	0.0088	0.1853972	E
<input type="radio"/>	GO:0000819	7,4	sister chromatid segregation	62	0.0096	4	0.0118	0.1866034	E
<input type="radio"/>	GO:0043255	7,6,5	regulation of carbohydrate biosynthetic process	19	0.0029	2	0.0059	0.1886861	E
<input type="radio"/>	GO:0007265	7	Ras protein signal transduction	39	0.0060	3	0.0088	0.1903335	E
<input type="radio"/>	GO:0046474	8,7,9	glycerophospholipid biosynthetic process	39	0.0060	3	0.0088	0.1903335	E
<input type="radio"/>	GO:0005976	5	polysaccharide metabolic process	65	0.0100	4	0.0118	0.1927100	E
<input type="radio"/>	GO:0044264	5,6	cellular polysaccharide metabolic process	65	0.0100	4	0.0118	0.1927100	E
<input type="radio"/>	GO:0009108	6	coenzyme biosynthetic process	66	0.0102	4	0.0118	0.1943914	E
<input type="radio"/>	GO:0016573	11,9	histone acetylation	40	0.0062	3	0.0088	0.1949934	E
<input type="radio"/>	GO:0009889	5,4	regulation of biosynthetic process	69	0.0107	4	0.0118	0.1983878	E
<input type="radio"/>	GO:0006353	8,7	transcription termination	20	0.0031	2	0.0059	0.1986767	E
<input type="radio"/>	GO:0051647	6,5	nucleus localization	20	0.0031	2	0.0059	0.1986767	E
<input type="radio"/>	GO:0007097	7,8,5,6	nuclear migration	20	0.0031	2	0.0059	0.1986767	E
<input type="radio"/>	GO:0040023	6,7,4,5	establishment of nucleus localization	20	0.0031	2	0.0059	0.1986767	E
<input type="radio"/>	GO:0000022	6,5,10,8	mitotic spindle elongation	20	0.0031	2	0.0059	0.1986767	E
<input type="radio"/>	GO:0051231	5,4,9,7	spindle elongation	20	0.0031	2	0.0059	0.1986767	E
<input type="radio"/>	GO:0000165	7	MAPKKK cascade	20	0.0031	2	0.0059	0.1986767	E
<input type="radio"/>	GO:0016311	6	dephosphorylation	41	0.0063	3	0.0088	0.1993713	E
<input type="radio"/>	GO:0046483	4	heterocycle metabolic process	76	0.0117	4	0.0118	0.2018959	E
<input type="radio"/>	GO:0006769	8,7	nicotinamide metabolic process	42	0.0065	3	0.0088	0.2034634	E
<input type="radio"/>	GO:0009064	6,7	glutamine family amino acid metabolic process	43	0.0066	3	0.0088	0.2072668	E

<input type="checkbox"/>	GO:0030384	8,9	phosphoinositide metabolic process	43	0.0066	3	0.0088	0.2072668	E
<input type="checkbox"/>	GO:0019674	9,8	NAD metabolic process	21	0.0032	2	0.0059	0.2080936	E
<input type="checkbox"/>	GO:0006289	7,6	nucleotide-excision repair	44	0.0068	3	0.0088	0.2107803	E
<input type="checkbox"/>	GO:0045991	10,8,9,6	positive regulation of transcription by carbon catabolites	5	0.0008	1	0.0029	0.2116909	E
<input type="checkbox"/>	GO:0046688	6	response to copper ion	5	0.0008	1	0.0029	0.2116909	E
<input type="checkbox"/>	GO:0051017	9	actin filament bundle formation	5	0.0008	1	0.0029	0.2116909	E
<input type="checkbox"/>	GO:0018319	10,9,8	protein amino acid myristoylation	5	0.0008	1	0.0029	0.2116909	E
<input type="checkbox"/>	GO:0051247	6,5	positive regulation of protein metabolic process	5	0.0008	1	0.0029	0.2116909	E
<input type="checkbox"/>	GO:0006816	7,8	calcium ion transport	5	0.0008	1	0.0029	0.2116909	E
<input type="checkbox"/>	GO:0006499	10,11,9,8	N-terminal protein myristoylation	5	0.0008	1	0.0029	0.2116909	E
<input type="checkbox"/>	GO:0000266	6	mitochondrial fission	5	0.0008	1	0.0029	0.2116909	E
<input type="checkbox"/>	GO:0000411	11,9,10,7	positive regulation of transcription by galactose	5	0.0008	1	0.0029	0.2116909	E
<input type="checkbox"/>	GO:0000338	8	protein deneeddylation	5	0.0008	1	0.0029	0.2116909	E
<input type="checkbox"/>	GO:0006498	9,10,8,7	N-terminal protein lipidation	5	0.0008	1	0.0029	0.2116909	E
<input type="checkbox"/>	GO:0018377	9,8,7	protein myristoylation	5	0.0008	1	0.0029	0.2116909	E
<input type="checkbox"/>	GO:0006813	7,8	potassium ion transport	5	0.0008	1	0.0029	0.2116909	E
<input type="checkbox"/>	GO:0045816	11,10	negative regulation of global transcription from RNA polymerase II promoter	5	0.0008	1	0.0029	0.2116909	E
<input type="checkbox"/>	GO:0000409	10,8,9,6	regulation of transcription by galactose	5	0.0008	1	0.0029	0.2116909	E
<input type="checkbox"/>	GO:0046487	5,7	glyoxylate metabolic process	5	0.0008	1	0.0029	0.2116909	E
<input type="checkbox"/>	GO:0045011	10	actin cable formation	5	0.0008	1	0.0029	0.2116909	E
<input type="checkbox"/>	GO:0042176	6,7,5	regulation of protein catabolic process	5	0.0008	1	0.0029	0.2116909	E
<input type="checkbox"/>	GO:0016560	8,11,10,7,9	protein import into peroxisome matrix, docking	5	0.0008	1	0.0029	0.2116909	E
<input type="checkbox"/>	GO:0006336	7,8,11	DNA replication-independent nucleosome assembly	5	0.0008	1	0.0029	0.2116909	E
<input type="checkbox"/>	GO:0000101	6,7,8	sulfur amino acid transport	5	0.0008	1	0.0029	0.2116909	E
<input type="checkbox"/>	GO:0043087	6	regulation of GTPase activity	5	0.0008	1	0.0029	0.2116909	E
<input type="checkbox"/>	GO:0006914	3	autophagy	45	0.0069	3	0.0088	0.2140035	E
<input type="checkbox"/>	GO:0019362	7,6	pyridine nucleotide metabolic process	45	0.0069	3	0.0088	0.2140035	E
<input type="checkbox"/>	GO:0006513	10	protein monoubiquitination	22	0.0034	2	0.0059	0.2169170	E
<input type="checkbox"/>	GO:0030472	6,5,10	mitotic spindle organization and biogenesis in nucleus	22	0.0034	2	0.0059	0.2169170	E
<input type="checkbox"/>	GO:0009110	5	vitamin biosynthetic process	46	0.0071	3	0.0088	0.2169373	E
<input type="checkbox"/>	GO:0006073	6,7	glucan metabolic process	46	0.0071	3	0.0088	0.2169373	E
<input type="checkbox"/>	GO:0042364	6	water-soluble vitamin biosynthetic process	46	0.0071	3	0.0088	0.2169373	E
<input type="checkbox"/>	GO:0007020	8	microtubule nucleation	23	0.0036	2	0.0059	0.2251338	E
<input type="checkbox"/>	GO:0007166	5	cell surface receptor linked signal transduction	52	0.0080	3	0.0088	0.2286230	E
<input type="checkbox"/>	GO:0006368	9,7,8	RNA elongation from RNA polymerase II promoter	53	0.0082	3	0.0088	0.2296273	E
<input type="checkbox"/>	GO:0007131	10,8,7,5,9,6,4	meiotic recombination	55	0.0085	3	0.0088	0.2308824	E
<input type="checkbox"/>	GO:0006733	6	oxidoreduction coenzyme metabolic process	56	0.0086	3	0.0088	0.2311477	E
<input type="checkbox"/>	GO:0000749	5	response to pheromone during conjugation with cellular fusion	57	0.0088	3	0.0088	0.2311817	E
<input type="checkbox"/>	GO:0006997	5	nuclear organization and biogenesis	57	0.0088	3	0.0088	0.2311817	E
<input type="checkbox"/>	GO:0007096	8,10,9,7	regulation of exit from mitosis	24	0.0037	2	0.0059	0.2327362	E
<input type="checkbox"/>	GO:0006576	5,6	biogenic amine metabolic process	24	0.0037	2	0.0059	0.2327362	E
<input type="checkbox"/>	GO:0009607	3	response to biotic stimulus	25	0.0039	2	0.0059	0.2397216	E

<input type="radio"/>	GO:0009250	7,8	glucan biosynthetic process	25	0.0039	2	0.0059	0.2397216	E
<input type="radio"/>	GO:0000717	8,7	nucleotide-excision repair, DNA duplex unwinding	6	0.0009	1	0.0029	0.2407211	E
<input type="radio"/>	GO:0048285	5	organelle fission	6	0.0009	1	0.0029	0.2407211	E
<input type="radio"/>	GO:0046578	7,8,6	regulation of Ras protein signal transduction	6	0.0009	1	0.0029	0.2407211	E
<input type="radio"/>	GO:0046021	10,8,5,6,9,7,4	regulation of transcription from RNA polymerase II promoter, mitotic	6	0.0009	1	0.0029	0.2407211	E
<input type="radio"/>	GO:0006591	7,8,5,4	ornithine metabolic process	6	0.0009	1	0.0029	0.2407211	E
<input type="radio"/>	GO:0007089	8,9,7,6	traversing start control point of mitotic cell cycle	6	0.0009	1	0.0029	0.2407211	E
<input type="radio"/>	GO:0001324	5,6,7	age-dependent response to oxidative stress during chronological cell aging	6	0.0009	1	0.0029	0.2407211	E
<input type="radio"/>	GO:0007070	11,9,6,7,10,8,5	negative regulation of transcription from RNA polymerase II promoter, mitotic	6	0.0009	1	0.0029	0.2407211	E
<input type="radio"/>	GO:0043254	6,7,5	regulation of protein complex assembly	6	0.0009	1	0.0029	0.2407211	E
<input type="radio"/>	GO:0046020	11,10,7	negative regulation of transcription from RNA polymerase II promoter by pheromones	6	0.0009	1	0.0029	0.2407211	E
<input type="radio"/>	GO:0051058	7,8,6	negative regulation of small GTPase mediated signal transduction	6	0.0009	1	0.0029	0.2407211	E
<input type="radio"/>	GO:0001306	4,5	age-dependent response to oxidative stress	6	0.0009	1	0.0029	0.2407211	E
<input type="radio"/>	GO:0015791	4,5	polyol transport	6	0.0009	1	0.0029	0.2407211	E
<input type="radio"/>	GO:0045040	10,9,7,8	protein import into mitochondrial outer membrane	6	0.0009	1	0.0029	0.2407211	E
<input type="radio"/>	GO:0045996	10,9,6	negative regulation of transcription by pheromones	6	0.0009	1	0.0029	0.2407211	E
<input type="radio"/>	GO:0006358	10,9	regulation of global transcription from RNA polymerase II promoter	6	0.0009	1	0.0029	0.2407211	E
<input type="radio"/>	GO:0005979	8,7,9,10,6	regulation of glycogen biosynthetic process	6	0.0009	1	0.0029	0.2407211	E
<input type="radio"/>	GO:0001323	4,5,6	age-dependent general metabolic decline during chronological cell aging	6	0.0009	1	0.0029	0.2407211	E
<input type="radio"/>	GO:0051056	6,7,5	regulation of small GTPase mediated signal transduction	6	0.0009	1	0.0029	0.2407211	E
<input type="radio"/>	GO:0046580	8,9,7	negative regulation of Ras protein signal transduction	6	0.0009	1	0.0029	0.2407211	E
<input type="radio"/>	GO:0015758	7,8	glucose transport	6	0.0009	1	0.0029	0.2407211	E
<input type="radio"/>	GO:0009966	5,4	regulation of signal transduction	26	0.0040	2	0.0059	0.2460915	E
<input type="radio"/>	GO:0051318	6,7,5	G1 phase	27	0.0042	2	0.0059	0.2518512	E
<input type="radio"/>	GO:0000080	7,8,6	G1 phase of mitotic cell cycle	27	0.0042	2	0.0059	0.2518512	E
<input type="radio"/>	GO:0009636	4	response to toxin	28	0.0043	2	0.0059	0.2570092	E
<input type="radio"/>	GO:0042144	6	vacuole fusion, non-autophagic	28	0.0043	2	0.0059	0.2570092	E
<input type="radio"/>	GO:0043241	6,5	protein complex disassembly	28	0.0043	2	0.0059	0.2570092	E
<input type="radio"/>	GO:0043624	7,6	cellular protein complex disassembly	28	0.0043	2	0.0059	0.2570092	E
<input type="radio"/>	GO:0018193	7	peptidyl-amino acid modification	28	0.0043	2	0.0059	0.2570092	E
<input type="radio"/>	GO:0051656	6,3,5,4	establishment of organelle localization	29	0.0045	2	0.0059	0.2615767	E
<input type="radio"/>	GO:0006409	11,9,6,8,10,7	tRNA export from nucleus	29	0.0045	2	0.0059	0.2615767	E
<input type="radio"/>	GO:0051031	5,7,6,8	tRNA transport	30	0.0046	2	0.0059	0.2655674	E
<input type="radio"/>	GO:0030466	11,7,8,12,10	chromatin silencing at silent mating-type cassette	30	0.0046	2	0.0059	0.2655674	E
<input type="radio"/>	GO:0000715	7,8	nucleotide-excision repair, DNA damage recognition	7	0.0011	1	0.0029	0.2661264	E
<input type="radio"/>	GO:0007571	3,4	age-dependent general metabolic decline	7	0.0011	1	0.0029	0.2661264	E
<input type="radio"/>	GO:0007008	6,7	outer mitochondrial membrane organization and biogenesis	7	0.0011	1	0.0029	0.2661264	E
<input type="radio"/>	GO:0005992	7,8	trehalose biosynthetic process	7	0.0011	1	0.0029	0.2661264	E
<input type="radio"/>	GO:0009409	5,4	response to cold	7	0.0011	1	0.0029	0.2661264	E

<input type="radio"/>	GO:0046351	6,7	disaccharide biosynthetic process	7	0.0011	1	0.0029	0.2661264	E
<input type="radio"/>	GO:0006998	5,6	nuclear membrane organization and biogenesis	7	0.0011	1	0.0029	0.2661264	E
<input type="radio"/>	GO:0000256	6	allantoin catabolic process	7	0.0011	1	0.0029	0.2661264	E
<input type="radio"/>	GO:0007068	10,8,6,9,7,5	negative regulation of transcription, mitotic	7	0.0011	1	0.0029	0.2661264	E
<input type="radio"/>	GO:0043248	8,7	proteasome assembly	7	0.0011	1	0.0029	0.2661264	E
<input type="radio"/>	GO:0009410	4	response to xenobiotic stimulus	7	0.0011	1	0.0029	0.2661264	E
<input type="radio"/>	GO:0043330	5,6	response to exogenous dsRNA	7	0.0011	1	0.0029	0.2661264	E
<input type="radio"/>	GO:0009102	6,7,8	biotin biosynthetic process	7	0.0011	1	0.0029	0.2661264	E
<input type="radio"/>	GO:0000289	11,9,10	poly(A) tail shortening	7	0.0011	1	0.0029	0.2661264	E
<input type="radio"/>	GO:0009615	4,5	response to virus	7	0.0011	1	0.0029	0.2661264	E
<input type="radio"/>	GO:0046700	5	heterocycle catabolic process	7	0.0011	1	0.0029	0.2661264	E
<input type="radio"/>	GO:0009435	8,7,10,9	NAD biosynthetic process	7	0.0011	1	0.0029	0.2661264	E
<input type="radio"/>	GO:0045896	9,7,5,8,6,4	regulation of transcription, mitotic	7	0.0011	1	0.0029	0.2661264	E
<input type="radio"/>	GO:0006595	6,7	polyamine metabolic process	7	0.0011	1	0.0029	0.2661264	E
<input type="radio"/>	GO:0033205	5,4	cytokinesis during cell cycle	7	0.0011	1	0.0029	0.2661264	E
<input type="radio"/>	GO:0043331	4	response to dsRNA	7	0.0011	1	0.0029	0.2661264	E
<input type="radio"/>	GO:0006768	5,7,6	biotin metabolic process	7	0.0011	1	0.0029	0.2661264	E
<input type="radio"/>	GO:0045913	6,5	positive regulation of carbohydrate metabolic process	7	0.0011	1	0.0029	0.2661264	E
<input type="radio"/>	GO:0000255	5	allantoin metabolic process	7	0.0011	1	0.0029	0.2661264	E
<input type="radio"/>	GO:0051707	3,4	response to other organism	7	0.0011	1	0.0029	0.2661264	E
<input type="radio"/>	GO:0009112	5	nucleobase metabolic process	31	0.0048	2	0.0059	0.2689968	E
<input type="radio"/>	GO:0007062	7,4	sister chromatid cohesion	31	0.0048	2	0.0059	0.2689968	E
<input type="radio"/>	GO:0006575	5	amino acid derivative metabolic process	31	0.0048	2	0.0059	0.2689968	E
<input type="radio"/>	GO:0000002	6	mitochondrial genome maintenance	31	0.0048	2	0.0059	0.2689968	E
<input type="radio"/>	GO:0032984	5	macromolecular complex disassembly	32	0.0049	2	0.0059	0.2718823	E
<input type="radio"/>	GO:0006869	4,5	lipid transport	34	0.0053	2	0.0059	0.2760965	E
<input type="radio"/>	GO:0007186	6	G-protein coupled receptor protein signaling pathway	34	0.0053	2	0.0059	0.2760965	E
<input type="radio"/>	GO:0030433	9,11,10,12	ER-associated protein catabolic process	35	0.0054	2	0.0059	0.2774654	E
<input type="radio"/>	GO:0000086	8,5,6,7,4	G2/M transition of mitotic cell cycle	35	0.0054	2	0.0059	0.2774654	E
<input type="radio"/>	GO:0022411	4	cellular component disassembly	36	0.0056	2	0.0059	0.2783700	E
<input type="radio"/>	GO:0009890	6,5	negative regulation of biosynthetic process	8	0.0012	1	0.0029	0.2882061	E
<input type="radio"/>	GO:0031146	11,10,12	SCF-dependent proteasomal ubiquitin-dependent protein catabolic process	8	0.0012	1	0.0029	0.2882061	E
<input type="radio"/>	GO:0015939	7	pantothenate metabolic process	8	0.0012	1	0.0029	0.2882061	E
<input type="radio"/>	GO:0000903	6,4,8,7,9	cellular morphogenesis during vegetative growth	8	0.0012	1	0.0029	0.2882061	E
<input type="radio"/>	GO:0008614	7	pyridoxine metabolic process	8	0.0012	1	0.0029	0.2882061	E
<input type="radio"/>	GO:0015940	7,8	pantothenate biosynthetic process	8	0.0012	1	0.0029	0.2882061	E
<input type="radio"/>	GO:0018318	10,9,8	protein amino acid palmitoylation	8	0.0012	1	0.0029	0.2882061	E
<input type="radio"/>	GO:0030011	7,4,8	maintenance of cell polarity	8	0.0012	1	0.0029	0.2882061	E
<input type="radio"/>	GO:0042816	6	vitamin B6 metabolic process	8	0.0012	1	0.0029	0.2882061	E
<input type="radio"/>	GO:0018345	9,8,7	protein palmitoylation	8	0.0012	1	0.0029	0.2882061	E
<input type="radio"/>	GO:0000501	4	flocculation via cell wall protein-carbohydrate interaction	9	0.0014	1	0.0029	0.3072383	E
<input type="radio"/>	GO:0006874	10,8	cellular calcium ion homeostasis	9	0.0014	1	0.0029	0.3072383	E
<input type="radio"/>	GO:0019794	6,7	nonprotein amino acid metabolic process	9	0.0014	1	0.0029	0.3072383	E

<input type="checkbox"/>	GO:0006280	6	mutagenesis	9	0.0014	1	0.0029	0.3072383	E
<input type="checkbox"/>	GO:0000128	3	flocculation	9	0.0014	1	0.0029	0.3072383	E
<input type="checkbox"/>	GO:0006474	10,9	N-terminal protein amino acid acetylation	9	0.0014	1	0.0029	0.3072383	E
<input type="checkbox"/>	GO:0032185	6	septin cytoskeleton organization and biogenesis	9	0.0014	1	0.0029	0.3072383	E
<input type="checkbox"/>	GO:0008535	8,7	cytochrome c oxidase complex assembly	9	0.0014	1	0.0029	0.3072383	E
<input type="checkbox"/>	GO:0006283	8,7	transcription-coupled nucleotide-excision repair	9	0.0014	1	0.0029	0.3072383	E
<input type="checkbox"/>	GO:0055074	9	calcium ion homeostasis	9	0.0014	1	0.0029	0.3072383	E
<input type="checkbox"/>	GO:0000921	8,7	septin ring assembly	9	0.0014	1	0.0029	0.3072383	E
<input type="checkbox"/>	GO:0031106	7	septin ring organization	9	0.0014	1	0.0029	0.3072383	E
<input type="checkbox"/>	GO:0006616	9,12,11,7,10,8	SRP-dependent cotranslational protein targeting to membrane, translocation	10	0.0015	1	0.0029	0.3234810	E
<input type="checkbox"/>	GO:0010033	4	response to organic substance	10	0.0015	1	0.0029	0.3234810	E
<input type="checkbox"/>	GO:0046019	10,9,6	regulation of transcription from RNA polymerase II promoter by pheromones	10	0.0015	1	0.0029	0.3234810	E
<input type="checkbox"/>	GO:0006123	10,7,5	mitochondrial electron transport, cytochrome c to oxygen	10	0.0015	1	0.0029	0.3234810	E
<input type="checkbox"/>	GO:0005991	6,7	trehalose metabolic process	10	0.0015	1	0.0029	0.3234810	E
<input type="checkbox"/>	GO:0009373	9,8,5	regulation of transcription by pheromones	10	0.0015	1	0.0029	0.3234810	E
<input type="checkbox"/>	GO:0001101	4	response to acid	11	0.0017	1	0.0029	0.3371736	E
<input type="checkbox"/>	GO:0006116	10,9	NADH oxidation	11	0.0017	1	0.0029	0.3371736	E
<input type="checkbox"/>	GO:0007039	7,8	vacuolar protein catabolic process	11	0.0017	1	0.0029	0.3371736	E
<input type="checkbox"/>	GO:0007109	7,6,5,4	cytokinesis, completion of separation	11	0.0017	1	0.0029	0.3371736	E
<input type="checkbox"/>	GO:0065002	8,6,7	intracellular protein transport across a membrane	11	0.0017	1	0.0029	0.3371736	E
<input type="checkbox"/>	GO:0000272	6	polysaccharide catabolic process	12	0.0019	1	0.0029	0.3485384	E
<input type="checkbox"/>	GO:0000302	5	response to reactive oxygen species	12	0.0019	1	0.0029	0.3485384	E
<input type="checkbox"/>	GO:0044247	7,6	cellular polysaccharide catabolic process	12	0.0019	1	0.0029	0.3485384	E
<input type="checkbox"/>	GO:0006067	5	ethanol metabolic process	12	0.0019	1	0.0029	0.3485384	E
<input type="checkbox"/>	GO:0007103	6,7,5,8	spindle pole body duplication in nuclear envelope	13	0.0020	1	0.0029	0.3577812	E
<input type="checkbox"/>	GO:0006111	8,7,9,10,6	regulation of gluconeogenesis	13	0.0020	1	0.0029	0.3577812	E
<input type="checkbox"/>	GO:0006895	8,9,6,7	Golgi to endosome transport	13	0.0020	1	0.0029	0.3577812	E
<input type="checkbox"/>	GO:0006537	8,9	glutamate biosynthetic process	13	0.0020	1	0.0029	0.3577812	E
<input type="checkbox"/>	GO:0001300	5	chronological cell aging	13	0.0020	1	0.0029	0.3577812	E
<input type="checkbox"/>	GO:0006633	7,6,8,5	fatty acid biosynthetic process	13	0.0020	1	0.0029	0.3577812	E
<input type="checkbox"/>	GO:0000920	6,4	cell separation during cytokinesis	13	0.0020	1	0.0029	0.3577812	E
<input type="checkbox"/>	GO:0007346	7,5,6	regulation of progression through mitotic cell cycle	13	0.0020	1	0.0029	0.3577812	E
<input type="checkbox"/>	GO:0000011	6	vacuole inheritance	14	0.0022	1	0.0029	0.3650928	E
<input type="checkbox"/>	GO:0006144	6	purine base metabolic process	14	0.0022	1	0.0029	0.3650928	E
<input type="checkbox"/>	GO:0006734	9,8	NADH metabolic process	14	0.0022	1	0.0029	0.3650928	E
<input type="checkbox"/>	GO:0007118	7,6,5	budding cell apical bud growth	14	0.0022	1	0.0029	0.3650928	E
<input type="checkbox"/>	GO:0000147	5,9,8	actin cortical patch assembly	14	0.0022	1	0.0029	0.3650928	E
<input type="checkbox"/>	GO:0042770	5	DNA damage response, signal transduction	14	0.0022	1	0.0029	0.3650928	E
<input type="checkbox"/>	GO:0000077	9,8,6	DNA damage checkpoint	14	0.0022	1	0.0029	0.3650928	E
<input type="checkbox"/>	GO:0030474	5,6,4,7	spindle pole body duplication	14	0.0022	1	0.0029	0.3650928	E
<input type="checkbox"/>	GO:0006825	8,9	copper ion transport	14	0.0022	1	0.0029	0.3650928	E
<input type="checkbox"/>	GO:0006037	8,9,6,7,10	cell wall chitin metabolic process	14	0.0022	1	0.0029	0.3650928	E
<input type="checkbox"/>	GO:0022401	7,6	adaptation of signaling pathway	15	0.0023	1	0.0029	0.3706498	E

<input type="radio"/>	GO:0019856	7,6	pyrimidine base biosynthetic process	15	0.0023	1	0.0029	0.3706498	E
<input type="radio"/>	GO:0000051	4,3	urea cycle intermediate metabolic process	15	0.0023	1	0.0029	0.3706498	E
<input type="radio"/>	GO:0000754	8,7,5	adaptation to pheromone during conjugation with cellular fusion	15	0.0023	1	0.0029	0.3706498	E
<input type="radio"/>	GO:0000114	10,8,9,5,7,4	G1-specific transcription in mitotic cell cycle	15	0.0023	1	0.0029	0.3706498	E
<input type="radio"/>	GO:0009894	5,4	regulation of catabolic process	15	0.0023	1	0.0029	0.3706498	E
<input type="radio"/>	GO:0006267	8,7	pre-replicative complex assembly	15	0.0023	1	0.0029	0.3706498	E
<input type="radio"/>	GO:0006525	7,8,5,4	arginine metabolic process	15	0.0023	1	0.0029	0.3706498	E
<input type="radio"/>	GO:0015698	6,7	inorganic anion transport	16	0.0025	1	0.0029	0.3746158	E
<input type="radio"/>	GO:0006536	7,8	glutamate metabolic process	16	0.0025	1	0.0029	0.3746158	E
<input type="radio"/>	GO:0051300	5,4,6	spindle pole body organization and biogenesis	16	0.0025	1	0.0029	0.3746158	E
<input type="radio"/>	GO:0032508	7	DNA duplex unwinding	16	0.0025	1	0.0029	0.3746158	E
<input type="radio"/>	GO:0031023	5	microtubule organizing center organization and biogenesis	16	0.0025	1	0.0029	0.3746158	E
<input type="radio"/>	GO:0048017	8	inositol lipid-mediated signaling	16	0.0025	1	0.0029	0.3746158	E
<input type="radio"/>	GO:0010383	7,5,6	cell wall polysaccharide metabolic process	16	0.0025	1	0.0029	0.3746158	E
<input type="radio"/>	GO:0016050	5	vesicle organization and biogenesis	16	0.0025	1	0.0029	0.3746158	E
<input type="radio"/>	GO:0048015	7	phosphoinositide-mediated signaling	16	0.0025	1	0.0029	0.3746158	E
<input type="radio"/>	GO:0032392	6	DNA geometric change	16	0.0025	1	0.0029	0.3746158	E
<input type="radio"/>	GO:0016053	5	organic acid biosynthetic process	17	0.0026	1	0.0029	0.3771420	E
<input type="radio"/>	GO:0007266	8	Rho protein signal transduction	17	0.0026	1	0.0029	0.3771420	E
<input type="radio"/>	GO:0007004	9	telomere maintenance via telomerase	17	0.0026	1	0.0029	0.3771420	E
<input type="radio"/>	GO:0006206	6	pyrimidine base metabolic process	17	0.0026	1	0.0029	0.3771420	E
<input type="radio"/>	GO:0006820	5,6	anion transport	17	0.0026	1	0.0029	0.3771420	E
<input type="radio"/>	GO:0046394	6	carboxylic acid biosynthetic process	17	0.0026	1	0.0029	0.3771420	E
<input type="radio"/>	GO:0009968	6,5	negative regulation of signal transduction	17	0.0026	1	0.0029	0.3771420	E
<input type="radio"/>	GO:0016558	10,9,7,8,6	protein import into peroxisome matrix	17	0.0026	1	0.0029	0.3771420	E
<input type="radio"/>	GO:0045132	9,7,8,6,4	meiotic chromosome segregation	17	0.0026	1	0.0029	0.3771420	E
<input type="radio"/>	GO:0006739	9,8	NADP metabolic process	17	0.0026	1	0.0029	0.3771420	E
<input type="radio"/>	GO:0006030	8,6,7,9	chitin metabolic process	17	0.0026	1	0.0029	0.3771420	E
<input type="radio"/>	GO:0042401	6,7	biogenic amine biosynthetic process	18	0.0028	1	0.0029	0.3783681	E
<input type="radio"/>	GO:0006273	9,8	lagging strand elongation	18	0.0028	1	0.0029	0.3783681	E
<input type="radio"/>	GO:0006986	4,5	response to unfolded protein	18	0.0028	1	0.0029	0.3783681	E
<input type="radio"/>	GO:0010038	5	response to metal ion	18	0.0028	1	0.0029	0.3783681	E
<input type="radio"/>	GO:0051789	4	response to protein stimulus	18	0.0028	1	0.0029	0.3783681	E
<input type="radio"/>	GO:0000183	11,7,8,12,10	chromatin silencing at rDNA	18	0.0028	1	0.0029	0.3783681	E
<input type="radio"/>	GO:0031570	8,7	DNA integrity checkpoint	18	0.0028	1	0.0029	0.3783681	E
<input type="radio"/>	GO:0006044	7,8	N-acetylglucosamine metabolic process	19	0.0029	1	0.0029	0.3784235	E
<input type="radio"/>	GO:0006041	6,7	glucosamine metabolic process	19	0.0029	1	0.0029	0.3784235	E
<input type="radio"/>	GO:0006040	5,6	amino sugar metabolic process	19	0.0029	1	0.0029	0.3784235	E
<input type="radio"/>	GO:0006875	9,7	cellular metal ion homeostasis	19	0.0029	1	0.0029	0.3784235	E
<input type="radio"/>	GO:0055065	8	metal ion homeostasis	19	0.0029	1	0.0029	0.3784235	E
<input type="radio"/>	GO:0008150	1	biological process	6476	1.0000	340	1.0000	1.0000000	D
<input type="radio"/>	GO:0006614	11,10,9,8,7	SRP-dependent cotranslational protein targeting to membrane	20	0.0031	1	0.0029	0.3774272	D
<input type="radio"/>	GO:0006753	7	nucleoside phosphate metabolic process	20	0.0031	1	0.0029	0.3774272	D
<input type="radio"/>	GO:0015986	8,10,7,9,11,5	ATP synthesis coupled proton transport	20	0.0031	1	0.0029	0.3774272	D

<input type="checkbox"/>	GO:0006754	7,9,6,8,10	ATP biosynthetic process	20	0.0031	1	0.0029	0.3774272	D
<input type="checkbox"/>	GO:0043574	7,5,6	peroxisomal transport	20	0.0031	1	0.0029	0.3774272	D
<input type="checkbox"/>	GO:0042398	6,5	amino acid derivative biosynthetic process	20	0.0031	1	0.0029	0.3774272	D
<input type="checkbox"/>	GO:0006625	9,8,6,7	protein targeting to peroxisome	20	0.0031	1	0.0029	0.3774272	D
<input type="checkbox"/>	GO:0015985	6,8,7,9	energy coupled proton transport, down electrochemical gradient	20	0.0031	1	0.0029	0.3774272	D
<input type="checkbox"/>	GO:0046112	6,5	nucleobase biosynthetic process	21	0.0032	1	0.0029	0.3754892	D
<input type="checkbox"/>	GO:0006081	4	aldehyde metabolic process	21	0.0032	1	0.0029	0.3754892	D
<input type="checkbox"/>	GO:0046034	5,9	ATP metabolic process	21	0.0032	1	0.0029	0.3754892	D
<input type="checkbox"/>	GO:0007231	6,5	osmosensory signaling pathway	22	0.0034	1	0.0029	0.3727108	D
<input type="checkbox"/>	GO:0007064	10,8,5,6,9,7,4	mitotic sister chromatid cohesion	22	0.0034	1	0.0029	0.3727108	D
<input type="checkbox"/>	GO:0044272	5	sulfur compound biosynthetic process	22	0.0034	1	0.0029	0.3727108	D
<input type="checkbox"/>	GO:0009145	7,8	purine nucleoside triphosphate biosynthetic process	22	0.0034	1	0.0029	0.3727108	D
<input type="checkbox"/>	GO:0007120	8,6,10,7,11,5	axial cellular bud site selection	22	0.0034	1	0.0029	0.3727108	D
<input type="checkbox"/>	GO:0009206	8,9	purine ribonucleoside triphosphate biosynthetic process	22	0.0034	1	0.0029	0.3727108	D
<input type="checkbox"/>	GO:0006613	10,9,8,7,6	cotranslational protein targeting to membrane	23	0.0036	1	0.0029	0.3691855	D
<input type="checkbox"/>	GO:0006607	10,11,8,9,7	NLS-bearing substrate import into nucleus	23	0.0036	1	0.0029	0.3691855	D
<input type="checkbox"/>	GO:0006408	11,9,6,8,10,7	snRNA export from nucleus	23	0.0036	1	0.0029	0.3691855	D
<input type="checkbox"/>	GO:0051030	5,7,6,8	snRNA transport	23	0.0036	1	0.0029	0.3691855	D
<input type="checkbox"/>	GO:0009205	8	purine ribonucleoside triphosphate metabolic process	23	0.0036	1	0.0029	0.3691855	D
<input type="checkbox"/>	GO:0006608	10,11,8,9,7	snRNP protein import into nucleus	23	0.0036	1	0.0029	0.3691855	D
<input type="checkbox"/>	GO:0009144	7	purine nucleoside triphosphate metabolic process	23	0.0036	1	0.0029	0.3691855	D
<input type="checkbox"/>	GO:0006610	10,11,8,9,7	ribosomal protein import into nucleus	23	0.0036	1	0.0029	0.3691855	D
<input type="checkbox"/>	GO:0006890	8,6,5,7	retrograde vesicle-mediated transport, Golgi to ER	24	0.0037	1	0.0029	0.3649992	D
<input type="checkbox"/>	GO:0006818	4,5	hydrogen transport	24	0.0037	1	0.0029	0.3649992	D
<input type="checkbox"/>	GO:0007006	5,6	mitochondrial membrane organization and biogenesis	24	0.0037	1	0.0029	0.3649992	D
<input type="checkbox"/>	GO:0006555	7,8,6	methionine metabolic process	24	0.0037	1	0.0029	0.3649992	D
<input type="checkbox"/>	GO:0015992	5,7,6,8	proton transport	24	0.0037	1	0.0029	0.3649992	D
<input type="checkbox"/>	GO:0009201	7,8	ribonucleoside triphosphate biosynthetic process	24	0.0037	1	0.0029	0.3649992	D
<input type="checkbox"/>	GO:0042775	9,6	organelle ATP synthesis coupled electron transport	25	0.0039	1	0.0029	0.3602307	D
<input type="checkbox"/>	GO:0006609	10,11,8,9,7	mRNA-binding (hnRNP) protein import into nucleus	25	0.0039	1	0.0029	0.3602307	D
<input type="checkbox"/>	GO:0045005	8,6	maintenance of fidelity during DNA-dependent DNA replication	25	0.0039	1	0.0029	0.3602307	D
<input type="checkbox"/>	GO:0009199	7	ribonucleoside triphosphate metabolic process	25	0.0039	1	0.0029	0.3602307	D
<input type="checkbox"/>	GO:0042773	8,5	ATP synthesis coupled electron transport	25	0.0039	1	0.0029	0.3602307	D
<input type="checkbox"/>	GO:0006298	7,9,6	mismatch repair	25	0.0039	1	0.0029	0.3602307	D
<input type="checkbox"/>	GO:0051029	5,7,6,8	rRNA transport	26	0.0040	1	0.0029	0.3549526	D
<input type="checkbox"/>	GO:0006407	11,9,6,8,10,7	rRNA export from nucleus	26	0.0040	1	0.0029	0.3549526	D
<input type="checkbox"/>	GO:0010382	6,4	cell wall metabolic process	26	0.0040	1	0.0029	0.3549526	D
<input type="checkbox"/>	GO:0042274	6,5	ribosomal small subunit biogenesis and assembly	26	0.0040	1	0.0029	0.3549526	D
<input type="checkbox"/>	GO:0009142	6,7	nucleoside triphosphate biosynthetic process	27	0.0042	1	0.0029	0.3492314	D
<input type="checkbox"/>	GO:0009084	7,8	glutamine family amino acid biosynthetic process	27	0.0042	1	0.0029	0.3492314	D

<input type="checkbox"/>	GO:0006094	8,9	gluconeogenesis	28	0.0043	1	0.0029	0.3431282	D
<input type="checkbox"/>	GO:0006906	6,5	vesicle fusion	28	0.0043	1	0.0029	0.3431282	D
<input type="checkbox"/>	GO:0000725	7,6	recombinational repair	29	0.0045	1	0.0029	0.3366987	D
<input type="checkbox"/>	GO:0006885	7	regulation of pH	29	0.0045	1	0.0029	0.3366987	D
<input type="checkbox"/>	GO:0006665	6,7	sphingolipid metabolic process	30	0.0046	1	0.0029	0.3299940	D
<input type="checkbox"/>	GO:0006893	9,7,6,8	Golgi to plasma membrane transport	30	0.0046	1	0.0029	0.3299940	D
<input type="checkbox"/>	GO:0009141	6	nucleoside triphosphate metabolic process	30	0.0046	1	0.0029	0.3299940	D
<input type="checkbox"/>	GO:0046364	6,7	monosaccharide biosynthetic process	30	0.0046	1	0.0029	0.3299940	D
<input type="checkbox"/>	GO:0019319	7,8	hexose biosynthetic process	30	0.0046	1	0.0029	0.3299940	D
<input type="checkbox"/>	GO:0005984	6	disaccharide metabolic process	31	0.0048	1	0.0029	0.3230607	D
<input type="checkbox"/>	GO:0043039	7,8	tRNA aminoacylation	32	0.0049	1	0.0029	0.3159412	D
<input type="checkbox"/>	GO:0006418	8,7,9,6	tRNA aminoacylation for protein translation	32	0.0049	1	0.0029	0.3159412	D
<input type="checkbox"/>	GO:0022616	6	DNA strand elongation	32	0.0049	1	0.0029	0.3159412	D
<input type="checkbox"/>	GO:0006271	8,7	DNA strand elongation during DNA replication	32	0.0049	1	0.0029	0.3159412	D
<input type="checkbox"/>	GO:0043038	6,7	amino acid activation	32	0.0049	1	0.0029	0.3159412	D
<input type="checkbox"/>	GO:0007121	8,6,10,7,11,5	bipolar cellular bud site selection	32	0.0049	1	0.0029	0.3159412	D
<input type="checkbox"/>	GO:0042546	6	cell wall biogenesis	33	0.0051	1	0.0029	0.3086742	D
<input type="checkbox"/>	GO:0045047	9,8,7,6,5	protein targeting to ER	33	0.0051	1	0.0029	0.3086742	D
<input type="checkbox"/>	GO:0006270	8,6	DNA replication initiation	33	0.0051	1	0.0029	0.3086742	D
<input type="checkbox"/>	GO:0009272	7	chitin- and beta-glucan-containing cell wall biogenesis	33	0.0051	1	0.0029	0.3086742	D
<input type="checkbox"/>	GO:0000096	6,7,5	sulfur amino acid metabolic process	33	0.0051	1	0.0029	0.3086742	D
<input type="checkbox"/>	GO:0006118	4	electron transport	33	0.0051	1	0.0029	0.3086742	D
<input type="checkbox"/>	GO:0006360	8,7	transcription from RNA polymerase I promoter	34	0.0053	1	0.0029	0.3012949	D
<input type="checkbox"/>	GO:0046165	5	alcohol biosynthetic process	35	0.0054	1	0.0029	0.2938350	D
<input type="checkbox"/>	GO:0006612	9,7,8	protein targeting to membrane	39	0.0060	2	0.0059	0.2785146	D
<input type="checkbox"/>	GO:0000271	6,7	polysaccharide biosynthetic process	41	0.0063	2	0.0059	0.2766878	D
<input type="checkbox"/>	GO:0006752	6	group transfer coenzyme metabolic process	44	0.0068	2	0.0059	0.2714933	D
<input type="checkbox"/>	GO:0031505	6	chitin- and beta-glucan-containing cell wall organization and biogenesis	44	0.0068	2	0.0059	0.2714933	D
<input type="checkbox"/>	GO:0009152	7,8	purine ribonucleotide biosynthetic process	38	0.0059	1	0.0029	0.2712468	D
<input type="checkbox"/>	GO:0006090	7	pyruvate metabolic process	38	0.0059	1	0.0029	0.2712468	D
<input type="checkbox"/>	GO:0050790	4	regulation of catalytic activity	45	0.0069	2	0.0059	0.2691904	D
<input type="checkbox"/>	GO:0065009	3	regulation of a molecular function	46	0.0071	2	0.0059	0.2666351	D
<input type="checkbox"/>	GO:0006119	7,4	oxidative phosphorylation	46	0.0071	2	0.0059	0.2666351	D
<input type="checkbox"/>	GO:0006413	7,6	translational initiation	49	0.0076	2	0.0059	0.2576439	D
<input type="checkbox"/>	GO:0043681	6,7,8	protein import into mitochondrion	40	0.0062	1	0.0029	0.2562433	D
<input type="checkbox"/>	GO:0009260	6,7	ribonucleotide biosynthetic process	40	0.0062	1	0.0029	0.2562433	D
<input type="checkbox"/>	GO:0009150	7	purine ribonucleotide metabolic process	41	0.0063	1	0.0029	0.2488150	D
<input type="checkbox"/>	GO:0051052	7,6	regulation of DNA metabolic process	41	0.0063	1	0.0029	0.2488150	D
<input type="checkbox"/>	GO:0006164	6,7	purine nucleotide biosynthetic process	41	0.0063	1	0.0029	0.2488150	D
<input type="checkbox"/>	GO:0009259	6	ribonucleotide metabolic process	43	0.0066	1	0.0029	0.2341802	D
<input type="checkbox"/>	GO:0006354	8,6,7	RNA elongation	59	0.0091	3	0.0088	0.2305882	D
<input type="checkbox"/>	GO:0006650	7,8	glycerophospholipid metabolic process	60	0.0093	3	0.0088	0.2299773	D
<input type="checkbox"/>	GO:0006887	8,6,5,7	exocytosis	44	0.0068	1	0.0029	0.2269987	D
<input type="checkbox"/>	GO:0006839	7,5,6	mitochondrial transport	65	0.0100	3	0.0088	0.2241243	D

<input type="radio"/>	GO:0030468	8,5,9	establishment of cell polarity (sensu Funqi)	66	0.0102	3	0.0088	0.2224546	D
<input type="radio"/>	GO:0030467	7,4,8	establishment and/or maintenance of cell polarity (sensu Funqi)	66	0.0102	3	0.0088	0.2224546	D
<input type="radio"/>	GO:0000282	7,9,5,6,10	cellular bud site selection	66	0.0102	3	0.0088	0.2224546	D
<input type="radio"/>	GO:0007105	6,4	cytokinesis, site selection	66	0.0102	3	0.0088	0.2224546	D
<input type="radio"/>	GO:0031326	6,5	regulation of cellular biosynthetic process	67	0.0103	3	0.0088	0.2206386	D
<input type="radio"/>	GO:0006944	5	membrane fusion	59	0.0091	2	0.0059	0.2183083	D
<input type="radio"/>	GO:0006725	4	aromatic compound metabolic process	60	0.0093	2	0.0059	0.2139408	D
<input type="radio"/>	GO:0009066	6,7	aspartate family amino acid metabolic process	46	0.0071	1	0.0029	0.2129585	D
<input type="radio"/>	GO:0006417	7,6,5	regulation of translation	47	0.0073	1	0.0029	0.2061165	D
<input type="radio"/>	GO:0006163	6	purine nucleotide metabolic process	47	0.0073	1	0.0029	0.2061165	D
<input type="radio"/>	GO:0016051	5	carbohydrate biosynthetic process	77	0.0119	4	0.0118	0.2017783	D
<input type="radio"/>	GO:0046467	6,5,7	membrane lipid biosynthetic process	78	0.0120	4	0.0118	0.2015175	D
<input type="radio"/>	GO:0051188	5	cofactor biosynthetic process	79	0.0122	4	0.0118	0.2011177	D
<input type="radio"/>	GO:0008033	7	tRNA processing	84	0.0130	4	0.0118	0.1971890	D
<input type="radio"/>	GO:0006457	6	protein folding	84	0.0130	4	0.0118	0.1971890	D
<input type="radio"/>	GO:0009060	6	aerobic respiration	84	0.0130	4	0.0118	0.1971890	D
<input type="radio"/>	GO:0019318	6,7	hexose metabolic process	85	0.0131	4	0.0118	0.1960494	D
<input type="radio"/>	GO:0006006	7,8	glucose metabolic process	65	0.0100	2	0.0059	0.1917908	D
<input type="radio"/>	GO:0045333	5	cellular respiration	89	0.0137	4	0.0118	0.1904691	D
<input type="radio"/>	GO:0006405	10,8,5,7,9,6	RNA export from nucleus	79	0.0122	3	0.0088	0.1903755	D
<input type="radio"/>	GO:0051236	3,4,5	establishment of RNA localization	80	0.0124	3	0.0088	0.1873729	D
<input type="radio"/>	GO:0050658	4,6,5,7	RNA transport	80	0.0124	3	0.0088	0.1873729	D
<input type="radio"/>	GO:0050657	5,6	nucleic acid transport	80	0.0124	3	0.0088	0.1873729	D
<input type="radio"/>	GO:0006406	11,9,6,8,10,7	mRNA export from nucleus	66	0.0102	2	0.0059	0.1873567	D
<input type="radio"/>	GO:0051028	5,7,6,8	mRNA transport	66	0.0102	2	0.0059	0.1873567	D
<input type="radio"/>	GO:0006606	9,10,7,8,6	protein import into nucleus	50	0.0077	1	0.0029	0.1863782	D
<input type="radio"/>	GO:0051170	9,7,8	nuclear import	50	0.0077	1	0.0029	0.1863782	D
<input type="radio"/>	GO:0005996	5,6	monosaccharide metabolic process	92	0.0142	4	0.0118	0.1853426	D
<input type="radio"/>	GO:0006790	4	sulfur metabolic process	67	0.0103	2	0.0059	0.1829382	D
<input type="radio"/>	GO:0006342	10,6,7,11,9	chromatin silencing	95	0.0147	4	0.0118	0.1795482	D
<input type="radio"/>	GO:0016458	5	gene silencing	95	0.0147	4	0.0118	0.1795482	D
<input type="radio"/>	GO:0031507	6,10	heterochromatin formation	95	0.0147	4	0.0118	0.1795482	D
<input type="radio"/>	GO:0045814	5	negative regulation of gene expression, epigenetic	95	0.0147	4	0.0118	0.1795482	D
<input type="radio"/>	GO:0030010	7,4,8	establishment of cell polarity	103	0.0159	5	0.0147	0.1781901	D
<input type="radio"/>	GO:0031497	5,9	chromatin assembly	104	0.0161	5	0.0147	0.1773499	D
<input type="radio"/>	GO:0006261	7	DNA-dependent DNA replication	97	0.0150	4	0.0118	0.1753738	D
<input type="radio"/>	GO:0048468	3,5	cell development	52	0.0080	1	0.0029	0.1739201	D
<input type="radio"/>	GO:0006626	9,8,7,6	protein targeting to mitochondrion	52	0.0080	1	0.0029	0.1739201	D
<input type="radio"/>	GO:0006400	7,8	tRNA modification	52	0.0080	1	0.0029	0.1739201	D
<input type="radio"/>	GO:0009117	5	nucleotide metabolic process	111	0.0171	5	0.0147	0.1693272	D
<input type="radio"/>	GO:0040029	4	regulation of gene expression, epigenetic	100	0.0154	4	0.0118	0.1687298	D
<input type="radio"/>	GO:0007163	6,3,7	establishment and/or maintenance of cell polarity	115	0.0178	6	0.0176	0.1664321	D
<input type="radio"/>	GO:0007059	3	chromosome segregation	119	0.0184	6	0.0176	0.1654163	D
<input type="radio"/>	GO:0006260	6	DNA replication	117	0.0181	5	0.0147	0.1600142	D

<input type="radio"/>	GO:0006333	8	chromatin assembly or disassembly	119	0.0184	5	0.0147	0.1565283	D
<input type="radio"/>	GO:0015931	4,5	nucleobase, nucleoside, nucleotide and nucleic acid transport	90	0.0139	3	0.0088	0.1558709	D
<input type="radio"/>	GO:0006403	4	RNA localization	90	0.0139	3	0.0088	0.1558709	D
<input type="radio"/>	GO:0006399	6	tRNA metabolic process	121	0.0187	5	0.0147	0.1528892	D
<input type="radio"/>	GO:0042493	4	response to drug	121	0.0187	5	0.0147	0.1528892	D
<input type="radio"/>	GO:0006611	9,10,7,8	protein export from nucleus	56	0.0086	1	0.0029	0.1507760	D
<input type="radio"/>	GO:0006302	7,6	double-strand break repair	57	0.0088	1	0.0029	0.1453647	D
<input type="radio"/>	GO:0006338	9	chromatin remodeling	155	0.0239	8	0.0235	0.1448640	D
<input type="radio"/>	GO:0008610	5,4,6	lipid biosynthetic process	129	0.0199	5	0.0147	0.1372209	D
<input type="radio"/>	GO:0009100	6	glycoprotein metabolic process	79	0.0122	2	0.0059	0.1329835	D
<input type="radio"/>	GO:0006348	11,7,8,12,10	chromatin silencing at telomere	60	0.0093	1	0.0029	0.1300267	D
<input type="radio"/>	GO:0031509	7,11	telomeric heterochromatin formation	60	0.0093	1	0.0029	0.1300267	D
<input type="radio"/>	GO:0006732	5	coenzyme metabolic process	136	0.0210	5	0.0147	0.1227475	D
<input type="radio"/>	GO:0044262	5	cellular carbohydrate metabolic process	213	0.0329	10	0.0294	0.1212251	D
<input type="radio"/>	GO:0051168	9,7,8	nuclear export	102	0.0158	3	0.0088	0.1187892	D
<input type="radio"/>	GO:0005975	4	carbohydrate metabolic process	233	0.0360	11	0.0324	0.1159076	D
<input type="radio"/>	GO:0000723	8	telomere maintenance	274	0.0423	14	0.0412	0.1104821	D
<input type="radio"/>	GO:0032200	7	telomere organization and biogenesis	274	0.0423	14	0.0412	0.1104821	D
<input type="radio"/>	GO:0006605	8,6,7	protein targeting	258	0.0398	12	0.0353	0.1078630	D
<input type="radio"/>	GO:0006066	4	alcohol metabolic process	163	0.0252	6	0.0176	0.1043935	D
<input type="radio"/>	GO:0065003	5,4	macromolecular complex assembly	328	0.0506	17	0.0500	0.1012894	D
<input type="radio"/>	GO:0017038	5,6,7	protein import	109	0.0168	3	0.0088	0.0992827	D
<input type="radio"/>	GO:0033036	3	macromolecule localization	382	0.0590	20	0.0588	0.0940546	D
<input type="radio"/>	GO:0051186	4	cofactor metabolic process	170	0.0263	6	0.0176	0.0921707	D
<input type="radio"/>	GO:0019752	5	carboxylic acid metabolic process	314	0.0485	14	0.0412	0.0890668	D
<input type="radio"/>	GO:0006082	4	organic acid metabolic process	314	0.0485	14	0.0412	0.0890668	D
<input type="radio"/>	GO:0009308	4	amine metabolic process	228	0.0352	9	0.0265	0.0879502	D
<input type="radio"/>	GO:0043413	6	biopolymer glycosylation	73	0.0113	1	0.0029	0.0780608	D
<input type="radio"/>	GO:0006486	8,7,6	protein amino acid glycosylation	73	0.0113	1	0.0029	0.0780608	D
<input type="radio"/>	GO:0006519	4	amino acid and derivative metabolic process	202	0.0312	7	0.0206	0.0722829	D
<input type="radio"/>	GO:0009101	7,5	glycoprotein biosynthetic process	78	0.0120	1	0.0029	0.0635397	D
<input type="radio"/>	GO:0006807	3	nitrogen compound metabolic process	251	0.0388	9	0.0265	0.0604825	D
<input type="radio"/>	GO:0016052	5	carbohydrate catabolic process	80	0.0124	1	0.0029	0.0584454	D
<input type="radio"/>	GO:0044275	6	cellular carbohydrate catabolic process	80	0.0124	1	0.0029	0.0584454	D
<input type="radio"/>	GO:0051169	7,5,6	nuclear transport	129	0.0199	3	0.0088	0.0556117	D
<input type="radio"/>	GO:0006913	8,6,7	nucleocytoplasmic transport	129	0.0199	3	0.0088	0.0556117	D
<input type="radio"/>	GO:0044260	4	cellular macromolecule metabolic process	1552	0.2397	78	0.2294	0.0475368	D
<input type="radio"/>	GO:0044267	5	cellular protein metabolic process	1498	0.2313	74	0.2176	0.0443927	D
<input type="radio"/>	GO:0019538	4	protein metabolic process	1547	0.2389	76	0.2235	0.0420381	D
<input type="radio"/>	GO:0009309	5,6	amine biosynthetic process	114	0.0176	2	0.0059	0.0413674	D
<input type="radio"/>	GO:0044271	5,4	nitrogen compound biosynthetic process	115	0.0178	2	0.0059	0.0398629	D
<input type="radio"/>	GO:0006520	5,6	amino acid metabolic process	187	0.0289	5	0.0147	0.0382047	D
<input type="radio"/>	GO:0044249	4	cellular biosynthetic process	366	0.0565	12	0.0353	0.0210998	D
<input type="radio"/>	GO:0008652	6,7	amino acid biosynthetic process	106	0.0164	1	0.0029	0.0187415	D
<input type="radio"/>	GO:0006396	6	RNA processing	491	0.0758	17	0.0500	0.0148781	D

<input type="radio"/>	GO:0022618	6,5	protein-RNA complex assembly	144	0.0222	2	0.0059	0.0128068	D
<input type="radio"/>	GO:0009451	6	RNA modification	139	0.0215	1	0.0029	0.0040247	D
<input type="radio"/>	GO:0009059	4	macromolecule biosynthetic process	886	0.1368	21	0.0618	2.936626E-06	D
<input type="radio"/>	GO:0043284	5	biopolymer biosynthetic process	354	0.0547	2	0.0059	6.318227E-07	D
<input type="radio"/>	GO:0006412	6,5	translation	688	0.1062	11	0.0324	1.538368E-07	D
<input type="radio"/>	GO:0009058	3	biosynthetic process	1249	0.1929	31	0.0912	5.951122E-08	D
<input type="radio"/>	GO:0022613	4	ribonucleoprotein complex biogenesis and assembly	483	0.0746	3	0.0088	6.850555E-09	D
<input type="radio"/>	GO:0042254	5	ribosome biogenesis and assembly	410	0.0633	1	0.0029	2.869248E-09	D