

GO-Stats Results

Your dataset contains **269** 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:0006082	4	organic acid metabolic process	314	0.0485	35	0.1301	4.158496E-08	E
<input type="radio"/> GO:0019752	5	carboxylic acid metabolic process	314	0.0485	35	0.1301	4.158496E-08	E
<input type="radio"/> GO:0006807	3	nitrogen compound metabolic process	251	0.0388	30	0.1115	8.805989E-08	E
<input type="radio"/> GO:0044249	4	cellular biosynthetic process	366	0.0565	37	0.1375	2.031378E-07	E
<input type="radio"/> GO:0009308	4	amine metabolic process	228	0.0352	26	0.0967	1.558918E-06	E
<input type="radio"/> GO:0006519	4	amino acid and derivative metabolic process	202	0.0312	21	0.0781	5.829505E-05	E
<input type="radio"/> GO:0006520	5,6	amino acid metabolic process	187	0.0289	20	0.0743	5.884959E-05	E
<input type="radio"/> GO:0008652	6,7	amino acid biosynthetic process	106	0.0164	14	0.0520	8.293014E-05	E
<input type="radio"/> GO:0006100	6	tricarboxylic acid cycle intermediate metabolic process	20	0.0031	6	0.0223	0.0001055	E
<input type="radio"/> GO:0009309	5,6	amine biosynthetic process	114	0.0176	14	0.0520	0.0001768	E
<input type="radio"/> GO:0044271	5,4	nitrogen compound biosynthetic process	115	0.0178	14	0.0520	0.0001933	E
<input type="radio"/> GO:0006950	3	response to stress	488	0.0754	36	0.1338	0.0002367	E
<input type="radio"/> GO:0006546	8,9	glycine catabolic process	4	0.0006	3	0.0112	0.0002720	E
<input type="radio"/> GO:0046470	8,9	phosphatidylcholine metabolic process	9	0.0014	4	0.0149	0.0002979	E
<input type="radio"/> GO:0009987	2	cellular process	4654	0.7187	216	0.8030	0.0003142	E
<input type="radio"/> GO:0005975	4	carbohydrate metabolic process	233	0.0360	21	0.0781	0.0003869	E
<input type="radio"/> GO:0046165	5	alcohol biosynthetic process	35	0.0054	7	0.0260	0.0004170	E
<input type="radio"/> GO:0032787	6	monocarboxylic acid metabolic process	126	0.0195	14	0.0520	0.0004770	E
<input type="radio"/> GO:0009084	7,8	glutamine family amino acid biosynthetic process	27	0.0042	6	0.0223	0.0006019	E
<input type="radio"/> GO:0015980	4	energy derivation by oxidation of organic compounds	145	0.0224	15	0.0558	0.0006336	E
<input type="radio"/> GO:0009071	7,8	serine family amino acid catabolic process	5	0.0008	3	0.0112	0.0006520	E
<input type="radio"/> GO:0006102	6,7	isocitrate metabolic process	5	0.0008	3	0.0112	0.0006520	E
<input type="radio"/> GO:0051234	2,3	establishment of localization	1004	0.1550	60	0.2230	0.0006722	E
<input type="radio"/> GO:0006090	7	pyruvate metabolic process	38	0.0059	7	0.0260	0.0006910	E
<input type="radio"/> GO:0045454	6,4	cell redox homeostasis	11	0.0017	4	0.0149	0.0007175	E

<input type="radio"/>	GO:0030503	5,7,4	regulation of cell redox homeostasis	11	0.0017	4	0.0149	0.0007175	E
<input type="radio"/>	GO:0006094	8,9	gluconeogenesis	28	0.0043	6	0.0223	0.0007348	E
<input type="radio"/>	GO:0051179	2	localization	1051	0.1623	62	0.2305	0.0007485	E
<input type="radio"/>	GO:0044262	5	cellular carbohydrate metabolic process	213	0.0329	19	0.0706	0.0007862	E
<input type="radio"/>	GO:0016051	5	carbohydrate biosynthetic process	77	0.0119	10	0.0372	0.0009087	E
<input type="radio"/>	GO:0006732	5	coenzyme metabolic process	136	0.0210	14	0.0520	0.0009761	E
<input type="radio"/>	GO:0009109	6	coenzyme catabolic process	20	0.0031	5	0.0186	0.0009896	E
<input type="radio"/>	GO:0006810	3,4	transport	981	0.1515	58	0.2156	0.0010275	E
<input type="radio"/>	GO:0046364	6,7	monosaccharide biosynthetic process	30	0.0046	6	0.0223	0.0010656	E
<input type="radio"/>	GO:0019319	7,8	hexose biosynthetic process	30	0.0046	6	0.0223	0.0010656	E
<input type="radio"/>	GO:0051187	5	cofactor catabolic process	21	0.0032	5	0.0186	0.0012457	E
<input type="radio"/>	GO:0006544	7,8	glycine metabolic process	6	0.0009	3	0.0112	0.0012503	E
<input type="radio"/>	GO:0050896	2	response to stimulus	763	0.1178	47	0.1747	0.0013335	E
<input type="radio"/>	GO:0010324	5	membrane invagination	96	0.0148	11	0.0409	0.0014080	E
<input type="radio"/>	GO:0009064	6,7	glutamine family amino acid metabolic process	43	0.0066	7	0.0260	0.0014333	E
<input type="radio"/>	GO:0009060	6	aerobic respiration	84	0.0130	10	0.0372	0.0017124	E
<input type="radio"/>	GO:0051093	5,4	negative regulation of developmental process	2	0.0003	2	0.0074	0.0017193	E
<input type="radio"/>	GO:0045017	6,5,7	glycerolipid biosynthetic process	2	0.0003	2	0.0074	0.0017193	E
<input type="radio"/>	GO:0045596	6,5	negative regulation of cell differentiation	2	0.0003	2	0.0074	0.0017193	E
<input type="radio"/>	GO:0019915	5	sequestering of lipid	2	0.0003	2	0.0074	0.0017193	E
<input type="radio"/>	GO:0046463	6,7,8	acylglycerol biosynthetic process	2	0.0003	2	0.0074	0.0017193	E
<input type="radio"/>	GO:0046504	5	glycerol ether biosynthetic process	2	0.0003	2	0.0074	0.0017193	E
<input type="radio"/>	GO:0019432	7,8,9	triacylglycerol biosynthetic process	2	0.0003	2	0.0074	0.0017193	E
<input type="radio"/>	GO:0042174	7,6	negative regulation of sporulation	2	0.0003	2	0.0074	0.0017193	E
<input type="radio"/>	GO:0046460	6,5,7	neutral lipid biosynthetic process	2	0.0003	2	0.0074	0.0017193	E
<input type="radio"/>	GO:0006897	6,5	endocytosis	86	0.0133	10	0.0372	0.0020217	E
<input type="radio"/>	GO:0006656	9,8,10	phosphatidylcholine biosynthetic process	7	0.0011	3	0.0112	0.0020981	E
<input type="radio"/>	GO:0009628	3	response to abiotic stimulus	117	0.0181	12	0.0446	0.0021713	E
<input type="radio"/>	GO:0006099	8,7,6	tricarboxylic acid cycle	15	0.0023	4	0.0149	0.0025102	E
<input type="radio"/>	GO:0006525	7,8,5,4	arginine metabolic process	15	0.0023	4	0.0149	0.0025102	E
<input type="radio"/>	GO:0000051	4,3	urea cycle intermediate metabolic process	15	0.0023	4	0.0149	0.0025102	E
<input type="radio"/>	GO:0046356	7	acetyl-CoA catabolic process	15	0.0023	4	0.0149	0.0025102	E
<input type="radio"/>	GO:0045333	5	cellular respiration	89	0.0137	10	0.0372	0.0025643	E
<input type="radio"/>	GO:0051186	4	cofactor metabolic process	170	0.0263	15	0.0558	0.0027666	E
<input type="radio"/>	GO:0042221	3	response to chemical stimulus	382	0.0590	26	0.0967	0.0039708	E
<input type="radio"/>	GO:0030242	4,6	peroxisome degradation	3	0.0005	2	0.0074	0.0049451	E
<input type="radio"/>	GO:0006091	3	generation of precursor metabolites and energy	183	0.0283	15	0.0558	0.0051263	E
<input type="radio"/>	GO:0009063	6,7	amino acid catabolic process	29	0.0045	5	0.0186	0.0052044	E
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<input type="radio"/>	GO:0051293	6,7,8,4,5	establishment of spindle localization	10	0.0015	3	0.0112	0.0063421	E

<input type="checkbox"/>	GO:0051294	7,8,9,5,6	establishment of spindle orientation	10	0.0015	3	0.0112	0.0063421	E
<input type="checkbox"/>	GO:0016044	4	membrane organization and biogenesis	188	0.0290	15	0.0558	0.0063519	E
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<input type="checkbox"/>	GO:0044248	4	cellular catabolic process	425	0.0656	27	0.1004	0.0074284	E
<input type="checkbox"/>	GO:0044255	4,5	cellular lipid metabolic process	229	0.0354	17	0.0632	0.0074769	E
<input type="checkbox"/>	GO:0006766	4	vitamin metabolic process	89	0.0137	9	0.0335	0.0075549	E
<input type="checkbox"/>	GO:0006767	5	water-soluble vitamin metabolic process	89	0.0137	9	0.0335	0.0075549	E
<input type="checkbox"/>	GO:0006970	4	response to osmotic stress	89	0.0137	9	0.0335	0.0075549	E
<input type="checkbox"/>	GO:0044270	5,4	nitrogen compound catabolic process	32	0.0049	5	0.0186	0.0077848	E
<input type="checkbox"/>	GO:0009310	5,6	amine catabolic process	32	0.0049	5	0.0186	0.0077848	E
<input type="checkbox"/>	GO:0006914	3	autophagy	45	0.0069	6	0.0223	0.0078198	E
<input type="checkbox"/>	GO:0032505	4,3	reproduction of a single-celled organism	194	0.0300	15	0.0558	0.0080906	E
<input type="checkbox"/>	GO:0016192	4,5	vesicle-mediated transport	328	0.0506	22	0.0818	0.0081044	E
<input type="checkbox"/>	GO:0001101	4	response to acid	11	0.0017	3	0.0112	0.0083616	E
<input type="checkbox"/>	GO:0006518	4	peptide metabolic process	11	0.0017	3	0.0112	0.0083616	E
<input type="checkbox"/>	GO:0007039	7,8	vacuolar protein catabolic process	11	0.0017	3	0.0112	0.0083616	E
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<input type="checkbox"/>	GO:0007015	8	actin filament organization	61	0.0094	7	0.0260	0.0091713	E
<input type="checkbox"/>	GO:0006624	9	vacuolar protein processing	4	0.0006	2	0.0074	0.0094822	E
<input type="checkbox"/>	GO:0032258	10,9,8,7	CVT pathway	4	0.0006	2	0.0074	0.0094822	E
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<input type="checkbox"/>	GO:0045595	5,4	regulation of cell differentiation	4	0.0006	2	0.0074	0.0094822	E
<input type="checkbox"/>	GO:0006066	4	alcohol metabolic process	163	0.0252	13	0.0483	0.0100828	E
<input type="checkbox"/>	GO:0045229	4	external encapsulating structure organization and biogenesis	200	0.0309	15	0.0558	0.0101445	E
<input type="checkbox"/>	GO:0007047	5	cell wall organization and biogenesis	200	0.0309	15	0.0558	0.0101445	E
<input type="checkbox"/>	GO:0022414	3,2	reproductive process	183	0.0283	14	0.0520	0.0107753	E
<input type="checkbox"/>	GO:0008610	5,4,6	lipid biosynthetic process	129	0.0199	11	0.0409	0.0108389	E
<input type="checkbox"/>	GO:0030029	6	actin filament-based process	112	0.0173	10	0.0372	0.0109958	E
<input type="checkbox"/>	GO:0006629	4	lipid metabolic process	242	0.0374	17	0.0632	0.0115671	E
<input type="checkbox"/>	GO:0009408	5,4	response to heat	23	0.0036	4	0.0149	0.0116459	E
<input type="checkbox"/>	GO:0022413	5,4	reproductive process in single-celled organism	149	0.0230	12	0.0446	0.0119637	E
<input type="checkbox"/>	GO:0048610	3,4	reproductive cellular process	149	0.0230	12	0.0446	0.0119637	E
<input type="checkbox"/>	GO:0006644	6,7	phospholipid metabolic process	97	0.0150	9	0.0335	0.0121795	E
<input type="checkbox"/>	GO:0006537	8,9	glutamate biosynthetic process	13	0.0020	3	0.0112	0.0133253	E
<input type="checkbox"/>	GO:0009082	7,8	branched chain family amino acid biosynthetic process	13	0.0020	3	0.0112	0.0133253	E
<input type="checkbox"/>	GO:0006790	4	sulfur metabolic process	67	0.0103	7	0.0260	0.0142337	E
<input type="checkbox"/>	GO:0048869	3	cellular developmental process	173	0.0267	13	0.0483	0.0148755	E
<input type="checkbox"/>	GO:0030154	4	cell differentiation	173	0.0267	13	0.0483	0.0148755	E
<input type="checkbox"/>	GO:0006639	6,5,7	acylglycerol metabolic process	5	0.0008	2	0.0074	0.0151516	E
<input type="checkbox"/>	GO:0006638	5,6	neutral lipid metabolic process	5	0.0008	2	0.0074	0.0151516	E
<input type="checkbox"/>	GO:0006641	7,6,8	triacylglycerol metabolic process	5	0.0008	2	0.0074	0.0151516	E
<input type="checkbox"/>	GO:0006662	4	glycerol ether metabolic process	5	0.0008	2	0.0074	0.0151516	E

<input type="radio"/>	GO:0046486	5,6	glycerolipid metabolic process	5	0.0008	2	0.0074	0.0151516	E
<input type="radio"/>	GO:0000338	8	protein deneedylation	5	0.0008	2	0.0074	0.0151516	E
<input type="radio"/>	GO:0009098	8,9	leucine biosynthetic process	5	0.0008	2	0.0074	0.0151516	E
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<input type="radio"/>	GO:0006749	6,5	glutathione metabolic process	14	0.0022	3	0.0112	0.0162615	E
<input type="radio"/>	GO:0046474	8,7,9	glycerophospholipid biosynthetic process	39	0.0060	5	0.0186	0.0166053	E
<input type="radio"/>	GO:0009058	3	biosynthetic process	1249	0.1929	62	0.2305	0.0174322	E
<input type="radio"/>	GO:0006979	4	response to oxidative stress	71	0.0110	7	0.0260	0.0184190	E
<input type="radio"/>	GO:0030435	5	sporulation	123	0.0190	10	0.0372	0.0184481	E
<input type="radio"/>	GO:0006733	6	oxidoreduction coenzyme metabolic process	56	0.0086	6	0.0223	0.0196846	E
<input type="radio"/>	GO:0006643	5,6	membrane lipid metabolic process	125	0.0193	10	0.0372	0.0200689	E
<input type="radio"/>	GO:0006769	8,7	nicotinamide metabolic process	42	0.0065	5	0.0186	0.0216370	E
<input type="radio"/>	GO:0015791	4,5	polyol transport	6	0.0009	2	0.0074	0.0217897	E
<input type="radio"/>	GO:0006591	7,8,5,4	ornithine metabolic process	6	0.0009	2	0.0074	0.0217897	E
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<input type="radio"/>	GO:0030865	6	cortical cytoskeleton organization and biogenesis	16	0.0025	3	0.0112	0.0230002	E
<input type="radio"/>	GO:0009081	6,7	branched chain family amino acid metabolic process	16	0.0025	3	0.0112	0.0230002	E
<input type="radio"/>	GO:0030866	8,7	cortical actin cytoskeleton organization and biogenesis	16	0.0025	3	0.0112	0.0230002	E
<input type="radio"/>	GO:0007005	5	mitochondrion organization and biogenesis	110	0.0170	9	0.0335	0.0230261	E
<input type="radio"/>	GO:0009117	5	nucleotide metabolic process	111	0.0171	9	0.0335	0.0240344	E
<input type="radio"/>	GO:0006042	7,8	glucosamine biosynthetic process	17	0.0026	3	0.0112	0.0267788	E
<input type="radio"/>	GO:0006113	5	fermentation	17	0.0026	3	0.0112	0.0267788	E
<input type="radio"/>	GO:0046349	6,7	amino sugar biosynthetic process	17	0.0026	3	0.0112	0.0267788	E
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<input type="radio"/>	GO:0044237	3	cellular metabolic process	3403	0.5255	150	0.5576	0.0278935	E
<input type="radio"/>	GO:0009435	8,7,10,9	NAD biosynthetic process	7	0.0011	2	0.0074	0.0292467	E
<input type="radio"/>	GO:0006551	7,8	leucine metabolic process	7	0.0011	2	0.0074	0.0292467	E
<input type="radio"/>	GO:0050793	4,3	regulation of developmental process	7	0.0011	2	0.0074	0.0292467	E
<input type="radio"/>	GO:0009110	5	vitamin biosynthetic process	46	0.0071	5	0.0186	0.0294846	E
<input type="radio"/>	GO:0042364	6	water-soluble vitamin biosynthetic process	46	0.0071	5	0.0186	0.0294846	E
<input type="radio"/>	GO:0000002	6	mitochondrial genome maintenance	31	0.0048	4	0.0149	0.0295830	E
<input type="radio"/>	GO:0006986	4,5	response to unfolded protein	18	0.0028	3	0.0112	0.0308112	E
<input type="radio"/>	GO:0051789	4	response to protein stimulus	18	0.0028	3	0.0112	0.0308112	E
<input type="radio"/>	GO:0007121	8,6,10,7,11,5	bipolar cellular bud site selection	32	0.0049	4	0.0149	0.0324190	E
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<input type="radio"/>	GO:0006839	7,5,6	mitochondrial transport	65	0.0100	6	0.0223	0.0343592	E
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<input type="radio"/>	GO:0006041	6,7	glucosamine metabolic process	19	0.0029	3	0.0112	0.0350813	E
<input type="radio"/>	GO:0009228	7,8	thiamin biosynthetic process	19	0.0029	3	0.0112	0.0350813	E

<input type="radio"/>	GO:0006040	5,6	amino sugar metabolic process	19	0.0029	3	0.0112	0.0350813	E
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<input type="radio"/>	GO:0051301	3	cell division	246	0.0380	15	0.0558	0.0372418	E
<input type="radio"/>	GO:0019318	6,7	hexose metabolic process	85	0.0131	7	0.0260	0.0380721	E
<input type="radio"/>	GO:0006623	9,8,7,6	protein targeting to vacuole	67	0.0103	6	0.0223	0.0381763	E
<input type="radio"/>	GO:0007010	5	cytoskeleton organization and biogenesis	227	0.0351	14	0.0520	0.0391815	E
<input type="radio"/>	GO:0042724	7	thiamin and derivative biosynthetic process	20	0.0031	3	0.0112	0.0395719	E
<input type="radio"/>	GO:0016579	9	protein deubiquitination	20	0.0031	3	0.0112	0.0395719	E
<input type="radio"/>	GO:0000767	6,7	cellular morphogenesis during conjugation	20	0.0031	3	0.0112	0.0395719	E
<input type="radio"/>	GO:0006772	7	thiamin metabolic process	20	0.0031	3	0.0112	0.0395719	E
<input type="radio"/>	GO:0000209	10	protein polyubiquitination	20	0.0031	3	0.0112	0.0395719	E
<input type="radio"/>	GO:0006217	8,9	deoxycytidine catabolic process	1	0.0002	1	0.0037	0.0415380	E
<input type="radio"/>	GO:0045920	7,10,6,8,9	negative regulation of exocytosis	1	0.0002	1	0.0037	0.0415380	E
<input type="radio"/>	GO:0042454	6,7	ribonucleoside catabolic process	1	0.0002	1	0.0037	0.0415380	E
<input type="radio"/>	GO:0006216	8,9	cytidine catabolic process	1	0.0002	1	0.0037	0.0415380	E
<input type="radio"/>	GO:0017158	7,10,6,8,9	regulation of calcium ion-dependent exocytosis	1	0.0002	1	0.0037	0.0415380	E
<input type="radio"/>	GO:0030397	5	membrane disassembly	1	0.0002	1	0.0037	0.0415380	E
<input type="radio"/>	GO:0046092	8	deoxycytidine metabolic process	1	0.0002	1	0.0037	0.0415380	E
<input type="radio"/>	GO:0046482	5,6,8	para-aminobenzoic acid metabolic process	1	0.0002	1	0.0037	0.0415380	E
<input type="radio"/>	GO:0042148	7,9,10,6,8	strand invasion	1	0.0002	1	0.0037	0.0415380	E
<input type="radio"/>	GO:0015976	3	carbon utilization	1	0.0002	1	0.0037	0.0415380	E
<input type="radio"/>	GO:0015978	4	carbon utilization by utilization of organic compounds	1	0.0002	1	0.0037	0.0415380	E
<input type="radio"/>	GO:0046133	7,8	pyrimidine ribonucleoside catabolic process	1	0.0002	1	0.0037	0.0415380	E
<input type="radio"/>	GO:0045022	8,6,7	early endosome to late endosome transport	1	0.0002	1	0.0037	0.0415380	E
<input type="radio"/>	GO:0015719	7,8	allantoate transport	1	0.0002	1	0.0037	0.0415380	E
<input type="radio"/>	GO:0019650	7	glucose catabolic process to butanediol	1	0.0002	1	0.0037	0.0415380	E
<input type="radio"/>	GO:0046939	6,7	nucleotide phosphorylation	1	0.0002	1	0.0037	0.0415380	E
<input type="radio"/>	GO:0006980	5	redox signal response	1	0.0002	1	0.0037	0.0415380	E
<input type="radio"/>	GO:0046127	7,8	pyrimidine deoxyribonucleoside catabolic process	1	0.0002	1	0.0037	0.0415380	E
<input type="radio"/>	GO:0033037	4	polysaccharide localization	1	0.0002	1	0.0037	0.0415380	E
<input type="radio"/>	GO:0051775	4	response to redox state	1	0.0002	1	0.0037	0.0415380	E
<input type="radio"/>	GO:0017156	9,7,6,8	calcium ion-dependent exocytosis	1	0.0002	1	0.0037	0.0415380	E
<input type="radio"/>	GO:0009313	6	oligosaccharide catabolic process	1	0.0002	1	0.0037	0.0415380	E
<input type="radio"/>	GO:0006033	5	chitin localization	1	0.0002	1	0.0037	0.0415380	E
<input type="radio"/>	GO:0046121	6,7	deoxyribonucleoside catabolic process	1	0.0002	1	0.0037	0.0415380	E
<input type="radio"/>	GO:0006106	7	fumarate metabolic process	1	0.0002	1	0.0037	0.0415380	E
<input type="radio"/>	GO:0006165	7,8	nucleoside diphosphate phosphorylation	1	0.0002	1	0.0037	0.0415380	E
<input type="radio"/>	GO:0045955	8,11,7,9,10	negative regulation of calcium ion-dependent exocytosis	1	0.0002	1	0.0037	0.0415380	E
<input type="radio"/>	GO:0006512	8	ubiquitin cycle	88	0.0136	7	0.0260	0.0431875	E
<input type="radio"/>	GO:0043687	7	post-translational protein modification	388	0.0599	21	0.0781	0.0435631	E
<input type="radio"/>	GO:0006081	4	aldehyde metabolic process	21	0.0032	3	0.0112	0.0442650	E
<input type="radio"/>	GO:0019674	9,8	NAD metabolic process	21	0.0032	3	0.0112	0.0442650	E
<input type="radio"/>	GO:0030437	7,6	sporulation (sensu Fungi)	108	0.0167	8	0.0297	0.0444052	E
<input type="radio"/>	GO:0048622	6,5	reproductive sporulation	108	0.0167	8	0.0297	0.0444052	E

<input type="checkbox"/>	GO:0019725	5,3	cellular homeostasis	128	0.0198	9	0.0335	0.0445813	E
<input type="checkbox"/>	GO:0000003	2	reproduction	323	0.0499	18	0.0669	0.0455265	E
<input type="checkbox"/>	GO:0030491	7,9,10,6,8	heteroduplex formation	9	0.0014	2	0.0074	0.0460835	E
<input type="checkbox"/>	GO:0006071	6	glycerol metabolic process	9	0.0014	2	0.0074	0.0460835	E
<input type="checkbox"/>	GO:0043648	6	dicarboxylic acid metabolic process	9	0.0014	2	0.0074	0.0460835	E
<input type="checkbox"/>	GO:0019751	5	polyol metabolic process	9	0.0014	2	0.0074	0.0460835	E
<input type="checkbox"/>	GO:0019794	6,7	nonprotein amino acid metabolic process	9	0.0014	2	0.0074	0.0460835	E
<input type="checkbox"/>	GO:0046942	5,6	carboxylic acid transport	54	0.0083	5	0.0186	0.0486326	E
<input type="checkbox"/>	GO:0065008	3	regulation of biological quality	260	0.0401	15	0.0558	0.0488236	E
<input type="checkbox"/>	GO:0042723	6	thiamin and derivative metabolic process	22	0.0034	3	0.0112	0.0491421	E
<input type="checkbox"/>	GO:0044238	3	primary metabolic process	3247	0.5014	136	0.5056	0.0491616	E
<input type="checkbox"/>	GO:0005996	5,6	monosaccharide metabolic process	92	0.0142	7	0.0260	0.0504035	E
<input type="checkbox"/>	GO:0015849	4,5	organic acid transport	55	0.0085	5	0.0186	0.0512967	E
<input type="checkbox"/>	GO:0006464	6	protein modification process	520	0.0803	26	0.0967	0.0520150	E
<input type="checkbox"/>	GO:0042592	4	homeostatic process	134	0.0207	9	0.0335	0.0530770	E
<input type="checkbox"/>	GO:0007034	7,5,6	vacuolar transport	114	0.0176	8	0.0297	0.0540003	E
<input type="checkbox"/>	GO:0007534	6,8,7	gene conversion at mating-type locus	23	0.0036	3	0.0112	0.0541842	E
<input type="checkbox"/>	GO:0019363	7,6,8	pyridine nucleotide biosynthetic process	10	0.0015	2	0.0074	0.0552261	E
<input type="checkbox"/>	GO:0000103	6	sulfate assimilation	10	0.0015	2	0.0074	0.0552261	E
<input type="checkbox"/>	GO:0006791	5	sulfur utilization	10	0.0015	2	0.0074	0.0552261	E
<input type="checkbox"/>	GO:0006890	8,6,5,7	retrograde vesicle-mediated transport, Golgi to ER	24	0.0037	3	0.0112	0.0593722	E
<input type="checkbox"/>	GO:0009069	6,7	serine family amino acid metabolic process	24	0.0037	3	0.0112	0.0593722	E
<input type="checkbox"/>	GO:0006730	4	one-carbon compound metabolic process	97	0.0150	7	0.0260	0.0599347	E
<input type="checkbox"/>	GO:0009165	5,6	nucleotide biosynthetic process	59	0.0091	5	0.0186	0.0624076	E
<input type="checkbox"/>	GO:0009607	3	response to biotic stimulus	25	0.0039	3	0.0112	0.0646869	E
<input type="checkbox"/>	GO:0042244	5,6	spore wall assembly	42	0.0065	4	0.0149	0.0662861	E
<input type="checkbox"/>	GO:0030476	8,6,7	spore wall assembly (sensu Fungi)	42	0.0065	4	0.0149	0.0662861	E
<input type="checkbox"/>	GO:0051649	5,3,4	establishment of cellular localization	606	0.0936	28	0.1041	0.0680855	E
<input type="checkbox"/>	GO:0007124	6,4,8,9	pseudohyphal growth	61	0.0094	5	0.0186	0.0681828	E
<input type="checkbox"/>	GO:0000074	6,5	regulation of progression through cell cycle	167	0.0258	10	0.0372	0.0691473	E
<input type="checkbox"/>	GO:0051726	5,4	regulation of cell cycle	167	0.0258	10	0.0372	0.0691473	E
<input type="checkbox"/>	GO:0030001	6,7	metal ion transport	62	0.0096	5	0.0186	0.0711116	E
<input type="checkbox"/>	GO:0051641	4,3	cellular localization	642	0.0991	29	0.1078	0.0712966	E
<input type="checkbox"/>	GO:0006284	7,6	base-excision repair	12	0.0019	2	0.0074	0.0744466	E
<input type="checkbox"/>	GO:0046907	6,4,5	intracellular transport	545	0.0842	25	0.0929	0.0745692	E
<input type="checkbox"/>	GO:0050789	3	regulation of biological process	761	0.1175	32	0.1190	0.0763432	E
<input type="checkbox"/>	GO:0030163	6,5	protein catabolic process	173	0.0267	10	0.0372	0.0772704	E
<input type="checkbox"/>	GO:0050794	4,3	regulation of cellular process	738	0.1140	31	0.1152	0.0774364	E
<input type="checkbox"/>	GO:0019954	3	asexual reproduction	85	0.0131	6	0.0223	0.0786161	E
<input type="checkbox"/>	GO:0007114	5,4	cell budding	85	0.0131	6	0.0223	0.0786161	E
<input type="checkbox"/>	GO:0043043	5	peptide biosynthetic process	2	0.0003	1	0.0037	0.0796375	E
<input type="checkbox"/>	GO:0032204	6,9,5	regulation of telomere maintenance	2	0.0003	1	0.0037	0.0796375	E
<input type="checkbox"/>	GO:0033260	8,7,6	DNA replication during S phase	2	0.0003	1	0.0037	0.0796375	E
<input type="checkbox"/>	GO:0006047	8,6,9	UDP-N-acetylglucosamine metabolic process	2	0.0003	1	0.0037	0.0796375	E
<input type="checkbox"/>	GO:0009218	7	pyrimidine ribonucleotide metabolic process	2	0.0003	1	0.0037	0.0796375	E

<input type="radio"/>	GO:0046937	5	phytochelatin metabolic process	2	0.0003	1	0.0037	0.0796375	E
<input type="radio"/>	GO:0019627	5	urea metabolic process	2	0.0003	1	0.0037	0.0796375	E
<input type="radio"/>	GO:0015848	6,7	spermidine transport	2	0.0003	1	0.0037	0.0796375	E
<input type="radio"/>	GO:0043419	6	urea catabolic process	2	0.0003	1	0.0037	0.0796375	E
<input type="radio"/>	GO:0006104	6,7	succinyl-CoA metabolic process	2	0.0003	1	0.0037	0.0796375	E
<input type="radio"/>	GO:0046036	9	CTP metabolic process	2	0.0003	1	0.0037	0.0796375	E
<input type="radio"/>	GO:0000709	11,9,8,5,6,10,7,4	meiotic joint molecule formation	2	0.0003	1	0.0037	0.0796375	E
<input type="radio"/>	GO:0006241	9,10	CTP biosynthetic process	2	0.0003	1	0.0037	0.0796375	E
<input type="radio"/>	GO:0015840	5,6	urea transport	2	0.0003	1	0.0037	0.0796375	E
<input type="radio"/>	GO:0043605	5	amide catabolic process	2	0.0003	1	0.0037	0.0796375	E
<input type="radio"/>	GO:0006343	11,7,8,12,10	establishment of chromatin silencing	2	0.0003	1	0.0037	0.0796375	E
<input type="radio"/>	GO:0046131	7	pyrimidine ribonucleoside metabolic process	2	0.0003	1	0.0037	0.0796375	E
<input type="radio"/>	GO:0046938	6	phytochelatin biosynthetic process	2	0.0003	1	0.0037	0.0796375	E
<input type="radio"/>	GO:0042938	5,6	dipeptide transport	2	0.0003	1	0.0037	0.0796375	E
<input type="radio"/>	GO:0046135	6,7	pyrimidine nucleoside catabolic process	2	0.0003	1	0.0037	0.0796375	E
<input type="radio"/>	GO:0042886	4,5	amide transport	2	0.0003	1	0.0037	0.0796375	E
<input type="radio"/>	GO:0009209	8,9	pyrimidine ribonucleoside triphosphate biosynthetic process	2	0.0003	1	0.0037	0.0796375	E
<input type="radio"/>	GO:0046087	8	cytidine metabolic process	2	0.0003	1	0.0037	0.0796375	E
<input type="radio"/>	GO:0006048	9,7,10	UDP-N-acetylglucosamine biosynthetic process	2	0.0003	1	0.0037	0.0796375	E
<input type="radio"/>	GO:0009208	8	pyrimidine ribonucleoside triphosphate metabolic process	2	0.0003	1	0.0037	0.0796375	E
<input type="radio"/>	GO:0009220	7,8	pyrimidine ribonucleotide biosynthetic process	2	0.0003	1	0.0037	0.0796375	E
<input type="radio"/>	GO:0015809	7,8,9	arginine transport	2	0.0003	1	0.0037	0.0796375	E
<input type="radio"/>	GO:0033262	8,9,7	regulation of DNA replication during S phase	2	0.0003	1	0.0037	0.0796375	E
<input type="radio"/>	GO:0043603	4	amide metabolic process	2	0.0003	1	0.0037	0.0796375	E
<input type="radio"/>	GO:0015798	5,6	myo-inositol transport	2	0.0003	1	0.0037	0.0796375	E
<input type="radio"/>	GO:0032210	7,10,6	regulation of telomere maintenance via telomerase	2	0.0003	1	0.0037	0.0796375	E
<input type="radio"/>	GO:0006436	9,8,10,7	tryptophanyl-tRNA aminoacylation	2	0.0003	1	0.0037	0.0796375	E
<input type="radio"/>	GO:0043412	5	biopolymer modification	664	0.1025	28	0.1041	0.0808405	E
<input type="radio"/>	GO:0000750	8,7,6	pheromone-dependent signal transduction during conjugation with cellular fusion	28	0.0043	3	0.0112	0.0812010	E
<input type="radio"/>	GO:0009636	4	response to toxin	28	0.0043	3	0.0112	0.0812010	E
<input type="radio"/>	GO:0032005	7,6	signal transduction during conjugation with cellular fusion	28	0.0043	3	0.0112	0.0812010	E
<input type="radio"/>	GO:0000041	7,8	transition metal ion transport	46	0.0071	4	0.0149	0.0816721	E
<input type="radio"/>	GO:0006886	7,5,6	intracellular protein transport	274	0.0423	14	0.0520	0.0821483	E
<input type="radio"/>	GO:0006508	6	proteolysis	178	0.0275	10	0.0372	0.0839269	E
<input type="radio"/>	GO:0015893	4,5	drug transport	13	0.0020	2	0.0074	0.0843482	E
<input type="radio"/>	GO:0006633	7,6,8,5	fatty acid biosynthetic process	13	0.0020	2	0.0074	0.0843482	E
<input type="radio"/>	GO:0051656	6,3,5,4	establishment of organelle localization	29	0.0045	3	0.0112	0.0868341	E
<input type="radio"/>	GO:0007533	5,7,6	mating type switching	29	0.0045	3	0.0112	0.0868341	E
<input type="radio"/>	GO:0000725	7,6	recombinational repair	29	0.0045	3	0.0112	0.0868341	E
<input type="radio"/>	GO:0015031	4,5,6	protein transport	280	0.0432	14	0.0520	0.0871065	E
<input type="radio"/>	GO:0006605	8,6,7	protein targeting	258	0.0398	13	0.0483	0.0901628	E
<input type="radio"/>	GO:0006974	4	response to DNA damage stimulus	234	0.0361	12	0.0446	0.0916098	E
<input type="radio"/>	GO:0044257	6,7	cellular protein catabolic process	160	0.0247	9	0.0335	0.0920755	E

<input type="radio"/>	GO:0031137	6,5	regulation of conjugation with cellular fusion	30	0.0046	3	0.0112	0.0925015	E
<input type="radio"/>	GO:0046999	5,4	regulation of conjugation	30	0.0046	3	0.0112	0.0925015	E
<input type="radio"/>	GO:0022607	4	cellular component assembly	471	0.0727	20	0.0743	0.0938424	E
<input type="radio"/>	GO:0000105	8,9	histidine biosynthetic process	14	0.0022	2	0.0074	0.0943408	E
<input type="radio"/>	GO:0009076	7,8	histidine family amino acid biosynthetic process	14	0.0022	2	0.0074	0.0943408	E
<input type="radio"/>	GO:0006547	7,8	histidine metabolic process	14	0.0022	2	0.0074	0.0943408	E
<input type="radio"/>	GO:0006825	8,9	copper ion transport	14	0.0022	2	0.0074	0.0943408	E
<input type="radio"/>	GO:0007118	7,6,5	budding cell apical bud growth	14	0.0022	2	0.0074	0.0943408	E
<input type="radio"/>	GO:0006740	10,9	NADPH regeneration	14	0.0022	2	0.0074	0.0943408	E
<input type="radio"/>	GO:0045002	8,7	double-strand break repair via single-strand annealing	14	0.0022	2	0.0074	0.0943408	E
<input type="radio"/>	GO:0009075	6,7	histidine family amino acid metabolic process	14	0.0022	2	0.0074	0.0943408	E
<input type="radio"/>	GO:0007163	6,3,7	establishment and/or maintenance of cell polarity	115	0.0178	7	0.0260	0.0959869	E
<input type="radio"/>	GO:0006811	4,5	ion transport	115	0.0178	7	0.0260	0.0959869	E
<input type="radio"/>	GO:0033036	3	macromolecule localization	382	0.0590	17	0.0632	0.0973875	E
<input type="radio"/>	GO:0015837	4,5	amine transport	50	0.0077	4	0.0149	0.0973999	E
<input type="radio"/>	GO:0045184	3,4,5	establishment of protein localization	296	0.0457	14	0.0520	0.0984934	E
<input type="radio"/>	GO:0009719	3	response to endogenous stimulus	243	0.0375	12	0.0446	0.0997403	E
<input type="radio"/>	GO:0040007	2	growth	141	0.0218	8	0.0297	0.0999896	E
<input type="radio"/>	GO:0030447	3	filamentous growth	94	0.0145	6	0.0223	0.1002451	E
<input type="radio"/>	GO:0008104	4	protein localization	330	0.0510	15	0.0558	0.1010767	E
<input type="radio"/>	GO:0006281	6,5	DNA repair	193	0.0298	10	0.0372	0.1023848	E
<input type="radio"/>	GO:0009653	4,3	anatomical structure morphogenesis	248	0.0383	12	0.0446	0.1037548	E
<input type="radio"/>	GO:0032989	4,5	cellular structure morphogenesis	248	0.0383	12	0.0446	0.1037548	E
<input type="radio"/>	GO:0000902	5,6	cell morphogenesis	248	0.0383	12	0.0446	0.1037548	E
<input type="radio"/>	GO:0048856	3	anatomical structure development	248	0.0383	12	0.0446	0.1037548	E
<input type="radio"/>	GO:0006031	9,7,8,10	chitin biosynthetic process	15	0.0023	2	0.0074	0.1043571	E
<input type="radio"/>	GO:0006626	9,8,7,6	protein targeting to mitochondrion	52	0.0080	4	0.0149	0.1052473	E
<input type="radio"/>	GO:0007166	5	cell surface receptor linked signal transduction	52	0.0080	4	0.0149	0.1052473	E
<input type="radio"/>	GO:0043162	10,9,11	ubiquitin-dependent protein catabolic process via the multivesicular body pathway	16	0.0025	2	0.0074	0.1143366	E
<input type="radio"/>	GO:0051791	6,8,7	medium-chain fatty acid metabolic process	3	0.0005	1	0.0037	0.1145111	E
<input type="radio"/>	GO:0045010	8	actin nucleation	3	0.0005	1	0.0037	0.1145111	E
<input type="radio"/>	GO:0005993	8,7	trehalose catabolic process	3	0.0005	1	0.0037	0.1145111	E
<input type="radio"/>	GO:0018022	9,10,8	peptidyl-lysine methylation	3	0.0005	1	0.0037	0.1145111	E
<input type="radio"/>	GO:0046125	7	pyrimidine deoxyribonucleoside metabolic process	3	0.0005	1	0.0037	0.1145111	E
<input type="radio"/>	GO:0046174	6	polyol catabolic process	3	0.0005	1	0.0037	0.1145111	E
<input type="radio"/>	GO:0009437	6,7	carnitine metabolic process	3	0.0005	1	0.0037	0.1145111	E
<input type="radio"/>	GO:0015847	6,7	putrescine transport	3	0.0005	1	0.0037	0.1145111	E
<input type="radio"/>	GO:0051596	6	methylglyoxal catabolic process	3	0.0005	1	0.0037	0.1145111	E
<input type="radio"/>	GO:0006114	7,6	glycerol biosynthetic process	3	0.0005	1	0.0037	0.1145111	E
<input type="radio"/>	GO:0019563	7	glycerol catabolic process	3	0.0005	1	0.0037	0.1145111	E
<input type="radio"/>	GO:0051595	5	response to methylglyoxal	3	0.0005	1	0.0037	0.1145111	E
<input type="radio"/>	GO:0032973	6,7,8	amino acid export	3	0.0005	1	0.0037	0.1145111	E
<input type="radio"/>	GO:0006285	7,8	base-excision repair, AP site formation	3	0.0005	1	0.0037	0.1145111	E

<input type="radio"/>	GO:0008272	7,8	sulfate transport	3	0.0005	1	0.0037	0.1145111	E
<input type="radio"/>	GO:0046160	7,8,6	heme a metabolic process	3	0.0005	1	0.0037	0.1145111	E
<input type="radio"/>	GO:0009438	5	methylglyoxal metabolic process	3	0.0005	1	0.0037	0.1145111	E
<input type="radio"/>	GO:0006784	8,7,9	heme a biosynthetic process	3	0.0005	1	0.0037	0.1145111	E
<input type="radio"/>	GO:0017157	6,9,5,7,8	regulation of exocytosis	3	0.0005	1	0.0037	0.1145111	E
<input type="radio"/>	GO:0006307	7,6	DNA dealkylation	3	0.0005	1	0.0037	0.1145111	E
<input type="radio"/>	GO:0032974	8,6,7,9	amino acid export from vacuole	3	0.0005	1	0.0037	0.1145111	E
<input type="radio"/>	GO:0006835	6,7	dicarboxylic acid transport	3	0.0005	1	0.0037	0.1145111	E
<input type="radio"/>	GO:0006108	7	malate metabolic process	3	0.0005	1	0.0037	0.1145111	E
<input type="radio"/>	GO:0019243	7,8,6	methylglyoxal catabolic process to D-lactate	3	0.0005	1	0.0037	0.1145111	E
<input type="radio"/>	GO:0009132	6	nucleoside diphosphate metabolic process	3	0.0005	1	0.0037	0.1145111	E
<input type="radio"/>	GO:0009120	6	deoxyribonucleoside metabolic process	3	0.0005	1	0.0037	0.1145111	E
<input type="radio"/>	GO:0046173	6	polyol biosynthetic process	3	0.0005	1	0.0037	0.1145111	E
<input type="radio"/>	GO:0007186	6	G-protein coupled receptor protein signaling pathway	34	0.0053	3	0.0112	0.1151833	E
<input type="radio"/>	GO:0016049	5,3,7,8	cell growth	102	0.0158	6	0.0223	0.1183729	E
<input type="radio"/>	GO:0030010	7,4,8	establishment of cell polarity	103	0.0159	6	0.0223	0.1205086	E
<input type="radio"/>	GO:0051640	5,4	organelle localization	56	0.0086	4	0.0149	0.1206404	E
<input type="radio"/>	GO:0003006	3,4	reproductive developmental process	35	0.0054	3	0.0112	0.1207798	E
<input type="radio"/>	GO:0007117	6,5,4	budding cell bud growth	35	0.0054	3	0.0112	0.1207798	E
<input type="radio"/>	GO:0007531	4,6,5	mating type determination	35	0.0054	3	0.0112	0.1207798	E
<input type="radio"/>	GO:0007530	4,5	sex determination	35	0.0054	3	0.0112	0.1207798	E
<input type="radio"/>	GO:0048590	3	non-developmental growth	35	0.0054	3	0.0112	0.1207798	E
<input type="radio"/>	GO:0000726	7,6	non-recombinational repair	35	0.0054	3	0.0112	0.1207798	E
<input type="radio"/>	GO:0045003	9,8	double-strand break repair via synthesis-dependent strand annealing	17	0.0026	2	0.0074	0.1242258	E
<input type="radio"/>	GO:0007266	8	Rho protein signal transduction	17	0.0026	2	0.0074	0.1242258	E
<input type="radio"/>	GO:0016053	5	organic acid biosynthetic process	17	0.0026	2	0.0074	0.1242258	E
<input type="radio"/>	GO:0006739	9,8	NADP metabolic process	17	0.0026	2	0.0074	0.1242258	E
<input type="radio"/>	GO:0006030	8,6,7,9	chitin metabolic process	17	0.0026	2	0.0074	0.1242258	E
<input type="radio"/>	GO:0046394	6	carboxylic acid biosynthetic process	17	0.0026	2	0.0074	0.1242258	E
<input type="radio"/>	GO:0019740	4	nitrogen utilization	17	0.0026	2	0.0074	0.1242258	E
<input type="radio"/>	GO:0007154	3	cell communication	240	0.0371	10	0.0372	0.1302341	E
<input type="radio"/>	GO:0031570	8,7	DNA integrity checkpoint	18	0.0028	2	0.0074	0.1339769	E
<input type="radio"/>	GO:0000753	7,8,6	cellular morphogenesis during conjugation with cellular fusion	18	0.0028	2	0.0074	0.1339769	E
<input type="radio"/>	GO:0016485	8	protein processing	38	0.0059	3	0.0112	0.1371714	E
<input type="radio"/>	GO:0007264	6	small GTPase mediated signal transduction	61	0.0094	4	0.0149	0.1388256	E
<input type="radio"/>	GO:0006865	5,6,7	amino acid transport	39	0.0060	3	0.0112	0.1424625	E
<input type="radio"/>	GO:0007265	7	Ras protein signal transduction	39	0.0060	3	0.0112	0.1424625	E
<input type="radio"/>	GO:0006275	8,7	regulation of DNA replication	19	0.0029	2	0.0074	0.1435481	E
<input type="radio"/>	GO:0006501	9,8,7	C-terminal protein lipidation	4	0.0006	1	0.0037	0.1463601	E
<input type="radio"/>	GO:0031119	8,9	tRNA pseudouridine synthesis	4	0.0006	1	0.0037	0.1463601	E
<input type="radio"/>	GO:0018205	8	peptidyl-lysine modification	4	0.0006	1	0.0037	0.1463601	E
<input type="radio"/>	GO:0030037	5,4,9	actin filament reorganization during cell cycle	4	0.0006	1	0.0037	0.1463601	E
<input type="radio"/>	GO:0031328	7,6	positive regulation of cellular biosynthetic process	4	0.0006	1	0.0037	0.1463601	E
<input type="radio"/>	GO:0045021	7,6	error-free DNA repair	4	0.0006	1	0.0037	0.1463601	E

<input type="radio"/>	GO:0031532	8	actin cytoskeleton reorganization	4	0.0006	1	0.0037	0.1463601	E
<input type="radio"/>	GO:0045727	8,7,6	positive regulation of protein biosynthetic process	4	0.0006	1	0.0037	0.1463601	E
<input type="radio"/>	GO:0009164	5,6	nucleoside catabolic process	4	0.0006	1	0.0037	0.1463601	E
<input type="radio"/>	GO:0031384	6,8,11,10,9,7,12	regulation of initiation of mating projection growth	4	0.0006	1	0.0037	0.1463601	E
<input type="radio"/>	GO:0006592	8,9,6,5	ornithine biosynthetic process	4	0.0006	1	0.0037	0.1463601	E
<input type="radio"/>	GO:0009891	6,5	positive regulation of biosynthetic process	4	0.0006	1	0.0037	0.1463601	E
<input type="radio"/>	GO:0000045	5	autophagic vacuole formation	4	0.0006	1	0.0037	0.1463601	E
<input type="radio"/>	GO:0008053	6	mitochondrial fusion	4	0.0006	1	0.0037	0.1463601	E
<input type="radio"/>	GO:0009147	7	pyrimidine nucleoside triphosphate metabolic process	4	0.0006	1	0.0037	0.1463601	E
<input type="radio"/>	GO:0051051	6,5	negative regulation of transport	4	0.0006	1	0.0037	0.1463601	E
<input type="radio"/>	GO:0015793	5,6	glycerol transport	4	0.0006	1	0.0037	0.1463601	E
<input type="radio"/>	GO:0006751	7,6	glutathione catabolic process	4	0.0006	1	0.0037	0.1463601	E
<input type="radio"/>	GO:0006827	8,9,10	high affinity iron ion transport	4	0.0006	1	0.0037	0.1463601	E
<input type="radio"/>	GO:0009083	7,8	branched chain family amino acid catabolic process	4	0.0006	1	0.0037	0.1463601	E
<input type="radio"/>	GO:0006097	6,8	glyoxylate cycle	4	0.0006	1	0.0037	0.1463601	E
<input type="radio"/>	GO:0007031	5	peroxisome organization and biogenesis	40	0.0062	3	0.0112	0.1476491	E
<input type="radio"/>	GO:0043681	6,7,8	protein import into mitochondrion	40	0.0062	3	0.0112	0.1476491	E
<input type="radio"/>	GO:0005976	5	polysaccharide metabolic process	65	0.0100	4	0.0149	0.1521355	E
<input type="radio"/>	GO:0044264	5,6	cellular polysaccharide metabolic process	65	0.0100	4	0.0149	0.1521355	E
<input type="radio"/>	GO:0000271	6,7	polysaccharide biosynthetic process	41	0.0063	3	0.0112	0.1527215	E
<input type="radio"/>	GO:0051320	7,6,5	S phase	20	0.0031	2	0.0074	0.1529025	E
<input type="radio"/>	GO:0009067	7,8	aspartate family amino acid biosynthetic process	20	0.0031	2	0.0074	0.1529025	E
<input type="radio"/>	GO:0007105	6,4	cytokinesis, site selection	66	0.0102	4	0.0149	0.1552564	E
<input type="radio"/>	GO:0016567	9	protein ubiquitination	66	0.0102	4	0.0149	0.1552564	E
<input type="radio"/>	GO:0000282	7,9,5,6,10	cellular bud site selection	66	0.0102	4	0.0149	0.1552564	E
<input type="radio"/>	GO:0030468	8,5,9	establishment of cell polarity (sensu Fungi)	66	0.0102	4	0.0149	0.1552564	E
<input type="radio"/>	GO:0030467	7,4,8	establishment and/or maintenance of cell polarity (sensu Fungi)	66	0.0102	4	0.0149	0.1552564	E
<input type="radio"/>	GO:0008361	4,6,7	regulation of cell size	129	0.0199	6	0.0223	0.1599107	E
<input type="radio"/>	GO:0045324	8,6,7	late endosome to vacuole transport	21	0.0032	2	0.0074	0.1620083	E
<input type="radio"/>	GO:0006812	5,6	cation transport	97	0.0150	5	0.0186	0.1620112	E
<input type="radio"/>	GO:0055080	7	cation homeostasis	102	0.0158	5	0.0186	0.1694885	E
<input type="radio"/>	GO:0030003	8,6	cellular cation homeostasis	102	0.0158	5	0.0186	0.1694885	E
<input type="radio"/>	GO:0006312	7	mitotic recombination	45	0.0069	3	0.0112	0.1717010	E
<input type="radio"/>	GO:0055071	9	manganese ion homeostasis	5	0.0008	1	0.0037	0.1753743	E
<input type="radio"/>	GO:0000707	11,9,8,5,6,10,7,4	meiotic DNA recombinase assembly	5	0.0008	1	0.0037	0.1753743	E
<input type="radio"/>	GO:0046487	5,7	glyoxylate metabolic process	5	0.0008	1	0.0037	0.1753743	E
<input type="radio"/>	GO:0015680	7,5,9,6,10	intracellular copper ion transport	5	0.0008	1	0.0037	0.1753743	E
<input type="radio"/>	GO:0051083	8	cotranslational protein folding	5	0.0008	1	0.0037	0.1753743	E
<input type="radio"/>	GO:0008655	5	pyrimidine salvage	5	0.0008	1	0.0037	0.1753743	E
<input type="radio"/>	GO:0009264	6,7	deoxyribonucleotide catabolic process	5	0.0008	1	0.0037	0.1753743	E
<input type="radio"/>	GO:0031385	6,8,11,10,9,7,12	regulation of termination of mating projection growth	5	0.0008	1	0.0037	0.1753743	E
<input type="radio"/>	GO:0006213	6	pyrimidine nucleoside metabolic process	5	0.0008	1	0.0037	0.1753743	E
<input type="radio"/>	GO:0044273	5	sulfur compound catabolic process	5	0.0008	1	0.0037	0.1753743	E

<input type="radio"/>	GO:0006816	7,8	calcium ion transport	5	0.0008	1	0.0037	0.1753743	E
<input type="radio"/>	GO:0051247	6,5	positive regulation of protein metabolic process	5	0.0008	1	0.0037	0.1753743	E
<input type="radio"/>	GO:0033261	7,8,6	regulation of progression through S phase	5	0.0008	1	0.0037	0.1753743	E
<input type="radio"/>	GO:0000076	11,9,8,10	DNA replication checkpoint	5	0.0008	1	0.0037	0.1753743	E
<input type="radio"/>	GO:0018410	8	peptide or protein carboxyl-terminal blocking	5	0.0008	1	0.0037	0.1753743	E
<input type="radio"/>	GO:0016233	9	telomere capping	5	0.0008	1	0.0037	0.1753743	E
<input type="radio"/>	GO:0006221	6,7	pyrimidine nucleotide biosynthetic process	5	0.0008	1	0.0037	0.1753743	E
<input type="radio"/>	GO:0030026	10,8	cellular manganese ion homeostasis	5	0.0008	1	0.0037	0.1753743	E
<input type="radio"/>	GO:0000730	7,9,10,8,6	DNA recombinase assembly	5	0.0008	1	0.0037	0.1753743	E
<input type="radio"/>	GO:0006089	7	lactate metabolic process	5	0.0008	1	0.0037	0.1753743	E
<input type="radio"/>	GO:0006479	9,7	protein amino acid methylation	23	0.0036	2	0.0074	0.1793675	E
<input type="radio"/>	GO:0008213	8	protein amino acid alkylation	23	0.0036	2	0.0074	0.1793675	E
<input type="radio"/>	GO:0055082	6,4	cellular chemical homeostasis	115	0.0178	5	0.0186	0.1801062	E
<input type="radio"/>	GO:0006873	7,5	cellular ion homeostasis	115	0.0178	5	0.0186	0.1801062	E
<input type="radio"/>	GO:0006631	5,7,6	fatty acid metabolic process	47	0.0073	3	0.0112	0.1803074	E
<input type="radio"/>	GO:0006461	6,5	protein complex assembly	116	0.0179	5	0.0186	0.1804074	E
<input type="radio"/>	GO:0050801	6	ion homeostasis	119	0.0184	5	0.0186	0.1808934	E
<input type="radio"/>	GO:0046483	4	heterocycle metabolic process	76	0.0117	4	0.0149	0.1811374	E
<input type="radio"/>	GO:0042157	6	lipoprotein metabolic process	48	0.0074	3	0.0112	0.1843703	E
<input type="radio"/>	GO:0042158	7,5	lipoprotein biosynthetic process	48	0.0074	3	0.0112	0.1843703	E
<input type="radio"/>	GO:0006497	8,7,6	protein amino acid lipidation	48	0.0074	3	0.0112	0.1843703	E
<input type="radio"/>	GO:0051188	5	cofactor biosynthetic process	79	0.0122	4	0.0149	0.1868528	E
<input type="radio"/>	GO:0016197	7,5,6	endosome transport	49	0.0076	3	0.0112	0.1882674	E
<input type="radio"/>	GO:0000226	7	microtubule cytoskeleton organization and biogenesis	81	0.0125	4	0.0149	0.1901161	E
<input type="radio"/>	GO:0032446	8	protein modification by small protein conjugation	84	0.0130	4	0.0149	0.1941912	E
<input type="radio"/>	GO:0051453	11,8,9	regulation of cellular pH	25	0.0039	2	0.0074	0.1954511	E
<input type="radio"/>	GO:0000724	8,7	double-strand break repair via homologous recombination	25	0.0039	2	0.0074	0.1954511	E
<input type="radio"/>	GO:0030641	10,8	cellular hydrogen ion homeostasis	25	0.0039	2	0.0074	0.1954511	E
<input type="radio"/>	GO:0032506	5,3	cytokinetic process	88	0.0136	4	0.0149	0.1981159	E
<input type="radio"/>	GO:0048468	3,5	cell development	52	0.0080	3	0.0112	0.1989314	E
<input type="radio"/>	GO:0019236	4	response to pheromone	94	0.0145	4	0.0149	0.2009056	E
<input type="radio"/>	GO:0031383	5,7,10,9,8,6,11	regulation of mating projection biogenesis	6	0.0009	1	0.0037	0.2017333	E
<input type="radio"/>	GO:0019795	7,8	nonprotein amino acid biosynthetic process	6	0.0009	1	0.0037	0.2017333	E
<input type="radio"/>	GO:0006000	7,8	fructose metabolic process	6	0.0009	1	0.0037	0.2017333	E
<input type="radio"/>	GO:0016236	4	macroautophagy	6	0.0009	1	0.0037	0.2017333	E
<input type="radio"/>	GO:0006013	7,8	mannose metabolic process	6	0.0009	1	0.0037	0.2017333	E
<input type="radio"/>	GO:0007089	8,9,7,6	traversing start control point of mitotic cell cycle	6	0.0009	1	0.0037	0.2017333	E
<input type="radio"/>	GO:0032297	10,8,9	negative regulation of DNA replication initiation	6	0.0009	1	0.0037	0.2017333	E
<input type="radio"/>	GO:0046185	5	aldehyde catabolic process	6	0.0009	1	0.0037	0.2017333	E
<input type="radio"/>	GO:0043254	6,7,5	regulation of protein complex assembly	6	0.0009	1	0.0037	0.2017333	E
<input type="radio"/>	GO:0031344	4,6,8,7,5,9	regulation of cell projection organization and biogenesis	6	0.0009	1	0.0037	0.2017333	E
<input type="radio"/>	GO:0000075	7,6	cell cycle checkpoint	53	0.0082	3	0.0112	0.2021359	E
<input type="radio"/>	GO:0015749	5,6	monosaccharide transport	26	0.0040	2	0.0074	0.2029750	E

<input type="radio"/>	GO:0006506	10,9,8,7,11	GPI anchor biosynthetic process	26	0.0040	2	0.0074	0.2029750	E
<input type="radio"/>	GO:0008645	6,7	hexose transport	26	0.0040	2	0.0074	0.2029750	E
<input type="radio"/>	GO:0007088	7,9,8,6	regulation of mitosis	55	0.0085	3	0.0112	0.2080108	E
<input type="radio"/>	GO:0006505	9,10	GPI anchor metabolic process	27	0.0042	2	0.0074	0.2101386	E
<input type="radio"/>	GO:0051318	6,7,5	G1 phase	27	0.0042	2	0.0074	0.2101386	E
<input type="radio"/>	GO:0009142	6,7	nucleoside triphosphate biosynthetic process	27	0.0042	2	0.0074	0.2101386	E
<input type="radio"/>	GO:0000080	7,8,6	G1 phase of mitotic cell cycle	27	0.0042	2	0.0074	0.2101386	E
<input type="radio"/>	GO:0006302	7,6	double-strand break repair	57	0.0088	3	0.0112	0.2131705	E
<input type="radio"/>	GO:0000749	5	response to pheromone during conjugation with cellular fusion	57	0.0088	3	0.0112	0.2131705	E
<input type="radio"/>	GO:0046489	9,8,10	phosphoinositide biosynthetic process	28	0.0043	2	0.0074	0.2169338	E
<input type="radio"/>	GO:0051651	5,4,3	maintenance of cellular localization	29	0.0045	2	0.0074	0.2233547	E
<input type="radio"/>	GO:0006885	7	regulation of pH	29	0.0045	2	0.0074	0.2233547	E
<input type="radio"/>	GO:0006470	8,7	protein amino acid dephosphorylation	29	0.0045	2	0.0074	0.2233547	E
<input type="radio"/>	GO:0032507	6,5,4	maintenance of cellular protein localization	29	0.0045	2	0.0074	0.2233547	E
<input type="radio"/>	GO:0000256	6	allantoin catabolic process	7	0.0011	1	0.0037	0.2256066	E
<input type="radio"/>	GO:0006465	9,5	signal peptide processing	7	0.0011	1	0.0037	0.2256066	E
<input type="radio"/>	GO:0009225	5	nucleotide-sugar metabolic process	7	0.0011	1	0.0037	0.2256066	E
<input type="radio"/>	GO:0009166	5,6	nucleotide catabolic process	7	0.0011	1	0.0037	0.2256066	E
<input type="radio"/>	GO:0009410	4	response to xenobiotic stimulus	7	0.0011	1	0.0037	0.2256066	E
<input type="radio"/>	GO:0015833	4,5	peptide transport	7	0.0011	1	0.0037	0.2256066	E
<input type="radio"/>	GO:0045332	5,7,6,8	phospholipid translocation	7	0.0011	1	0.0037	0.2256066	E
<input type="radio"/>	GO:0009311	5	oligosaccharide metabolic process	7	0.0011	1	0.0037	0.2256066	E
<input type="radio"/>	GO:0006621	7,6,5,4	protein retention in ER	7	0.0011	1	0.0037	0.2256066	E
<input type="radio"/>	GO:0000755	6,5	cytogamy	7	0.0011	1	0.0037	0.2256066	E
<input type="radio"/>	GO:0000255	5	allantoin metabolic process	7	0.0011	1	0.0037	0.2256066	E
<input type="radio"/>	GO:0046700	5	heterocycle catabolic process	7	0.0011	1	0.0037	0.2256066	E
<input type="radio"/>	GO:0009086	8,9,7	methionine biosynthetic process	7	0.0011	1	0.0037	0.2256066	E
<input type="radio"/>	GO:0031382	9,8,10,7	mating projection biogenesis	7	0.0011	1	0.0037	0.2256066	E
<input type="radio"/>	GO:0006220	6	pyrimidine nucleotide metabolic process	7	0.0011	1	0.0037	0.2256066	E
<input type="radio"/>	GO:0000289	11,9,10	poly(A) tail shortening	7	0.0011	1	0.0037	0.2256066	E
<input type="radio"/>	GO:0030005	9,7	cellular di-, tri-valent inorganic cation homeostasis	64	0.0099	3	0.0112	0.2256779	E
<input type="radio"/>	GO:0055066	8	di-, tri-valent inorganic cation homeostasis	64	0.0099	3	0.0112	0.2256779	E
<input type="radio"/>	GO:0009108	6	coenzyme biosynthetic process	66	0.0102	3	0.0112	0.2277242	E
<input type="radio"/>	GO:0007033	5	vacuole organization and biogenesis	67	0.0103	3	0.0112	0.2285058	E
<input type="radio"/>	GO:0051128	5,4	regulation of cellular component organization and biogenesis	30	0.0046	2	0.0074	0.2293978	E
<input type="radio"/>	GO:0045185	5,4,3	maintenance of protein localization	30	0.0046	2	0.0074	0.2293978	E
<input type="radio"/>	GO:0030466	11,7,8,12,10	chromatin silencing at silent mating-type cassette	30	0.0046	2	0.0074	0.2293978	E
<input type="radio"/>	GO:0009141	6	nucleoside triphosphate metabolic process	30	0.0046	2	0.0074	0.2293978	E
<input type="radio"/>	GO:0042546	6	cell wall biogenesis	33	0.0051	2	0.0074	0.2452499	E
<input type="radio"/>	GO:0009272	7	chitin- and beta-glucan-containing cell wall biogenesis	33	0.0051	2	0.0074	0.2452499	E
<input type="radio"/>	GO:0051235	3,2	maintenance of localization	33	0.0051	2	0.0074	0.2452499	E
<input type="radio"/>	GO:0008156	9,8	negative regulation of DNA replication	8	0.0012	1	0.0037	0.2471544	E
<input type="radio"/>	GO:0006808	6,5	regulation of nitrogen utilization	8	0.0012	1	0.0037	0.2471544	E
<input type="radio"/>	GO:0010870	6,10	lysine biosynthetic process via aminoadipic	8	0.0012	1	0.0037	0.2471544	E

<input type="radio"/>	GO:0019878	7,10	acid	8	0.0012	1	0.0037	0.2471544	E
<input type="radio"/>	GO:0006828	8,9	manganese ion transport	8	0.0012	1	0.0037	0.2471544	E
<input type="radio"/>	GO:0032990	5,6	cell part morphogenesis	8	0.0012	1	0.0037	0.2471544	E
<input type="radio"/>	GO:0019660	6	glycolytic fermentation	8	0.0012	1	0.0037	0.2471544	E
<input type="radio"/>	GO:0048858	6,7	cell projection morphogenesis	8	0.0012	1	0.0037	0.2471544	E
<input type="radio"/>	GO:0030030	7,6,8	cell projection organization and biogenesis	8	0.0012	1	0.0037	0.2471544	E
<input type="radio"/>	GO:0051171	5,4	regulation of nitrogen metabolic process	8	0.0012	1	0.0037	0.2471544	E
<input type="radio"/>	GO:0007119	7,6,5	budding cell isotropic bud growth	8	0.0012	1	0.0037	0.2471544	E
<input type="radio"/>	GO:0030011	7,4,8	maintenance of cell polarity	8	0.0012	1	0.0037	0.2471544	E
<input type="radio"/>	GO:0030031	8,7,9	cell projection biogenesis	8	0.0012	1	0.0037	0.2471544	E
<input type="radio"/>	GO:0030004	9,7	cellular monovalent inorganic cation homeostasis	34	0.0053	2	0.0074	0.2497796	E
<input type="radio"/>	GO:0015674	6,7	di-, tri-valent inorganic cation transport	34	0.0053	2	0.0074	0.2497796	E
<input type="radio"/>	GO:0006869	4,5	lipid transport	34	0.0053	2	0.0074	0.2497796	E
<input type="radio"/>	GO:0055067	8	monovalent inorganic cation homeostasis	34	0.0053	2	0.0074	0.2497796	E
<input type="radio"/>	GO:0000086	8,5,6,7,4	G2/M transition of mitotic cell cycle	35	0.0054	2	0.0074	0.2539377	E
<input type="radio"/>	GO:0030433	9,11,10,12	ER-associated protein catabolic process	35	0.0054	2	0.0074	0.2539377	E
<input type="radio"/>	GO:0009605	3	response to external stimulus	37	0.0057	2	0.0074	0.2611610	E
<input type="radio"/>	GO:0031667	5	response to nutrient levels	37	0.0057	2	0.0074	0.2611610	E
<input type="radio"/>	GO:0009991	4	response to extracellular stimulus	37	0.0057	2	0.0074	0.2611610	E
<input type="radio"/>	GO:0008643	4,5	carbohydrate transport	38	0.0059	2	0.0074	0.2642389	E
<input type="radio"/>	GO:0006879	10,8	cellular iron ion homeostasis	38	0.0059	2	0.0074	0.2642389	E
<input type="radio"/>	GO:0006515	8,9	misfolded or incompletely synthesized protein catabolic process	38	0.0059	2	0.0074	0.2642389	E
<input type="radio"/>	GO:0055072	9	iron ion homeostasis	38	0.0059	2	0.0074	0.2642389	E
<input type="radio"/>	GO:0006744	8,7	ubiquinone biosynthetic process	9	0.0014	1	0.0037	0.2665278	E
<input type="radio"/>	GO:0009085	8,9	lysine biosynthetic process	9	0.0014	1	0.0037	0.2665278	E
<input type="radio"/>	GO:0006760	5,7	folic acid and derivative metabolic process	9	0.0014	1	0.0037	0.2665278	E
<input type="radio"/>	GO:0006553	7,8	lysine metabolic process	9	0.0014	1	0.0037	0.2665278	E
<input type="radio"/>	GO:0000501	4	flocculation via cell wall protein-carbohydrate interaction	9	0.0014	1	0.0037	0.2665278	E
<input type="radio"/>	GO:0007155	3	cell adhesion	9	0.0014	1	0.0037	0.2665278	E
<input type="radio"/>	GO:0030968	7,5,6	unfolded protein response	9	0.0014	1	0.0037	0.2665278	E
<input type="radio"/>	GO:0022610	2	biological adhesion	9	0.0014	1	0.0037	0.2665278	E
<input type="radio"/>	GO:0006743	7,6	ubiquinone metabolic process	9	0.0014	1	0.0037	0.2665278	E
<input type="radio"/>	GO:0042375	5	quinone cofactor metabolic process	9	0.0014	1	0.0037	0.2665278	E
<input type="radio"/>	GO:0030950	8,7	establishment and/or maintenance of actin cytoskeleton polarity	9	0.0014	1	0.0037	0.2665278	E
<input type="radio"/>	GO:0000128	3	flocculation	9	0.0014	1	0.0037	0.2665278	E
<input type="radio"/>	GO:0030952	6	establishment and/or maintenance of cytoskeleton polarity	9	0.0014	1	0.0037	0.2665278	E
<input type="radio"/>	GO:0015802	6,7,8	basic amino acid transport	9	0.0014	1	0.0037	0.2665278	E
<input type="radio"/>	GO:0045426	7,6	quinone cofactor biosynthetic process	9	0.0014	1	0.0037	0.2665278	E
<input type="radio"/>	GO:0032185	6	septin cytoskeleton organization and biogenesis	9	0.0014	1	0.0037	0.2665278	E
<input type="radio"/>	GO:0000921	8,7	septin ring assembly	9	0.0014	1	0.0037	0.2665278	E
<input type="radio"/>	GO:0009262	6	deoxyribonucleotide metabolic process	9	0.0014	1	0.0037	0.2665278	E
<input type="radio"/>	GO:0031106	7	septin ring organization	9	0.0014	1	0.0037	0.2665278	E
<input type="radio"/>	GO:0006984	6	ER-nuclear signaling pathway	9	0.0014	1	0.0037	0.2665278	E
<input type="radio"/>	GO:0006112	5	energy reserve metabolic process	39	0.0060	2	0.0074	0.2669711	E

<input type="radio"/>	GO:0006612	9,7,8	protein targeting to membrane	39	0.0060	2	0.0074	0.2669711	E
<input type="radio"/>	GO:0009260	6,7	ribonucleotide biosynthetic process	40	0.0062	2	0.0074	0.2693657	E
<input type="radio"/>	GO:0048308	5	organelle inheritance	40	0.0062	2	0.0074	0.2693657	E
<input type="radio"/>	GO:0006164	6,7	purine nucleotide biosynthetic process	41	0.0063	2	0.0074	0.2714315	E
<input type="radio"/>	GO:0051052	7,6	regulation of DNA metabolic process	41	0.0063	2	0.0074	0.2714315	E
<input type="radio"/>	GO:0016311	6	dephosphorylation	41	0.0063	2	0.0074	0.2714315	E
<input type="radio"/>	GO:0016125	5,6,7	sterol metabolic process	42	0.0065	2	0.0074	0.2731778	E
<input type="radio"/>	GO:0030384	8,9	phosphoinositide metabolic process	43	0.0066	2	0.0074	0.2746142	E
<input type="radio"/>	GO:0008202	5,6	steroid metabolic process	43	0.0066	2	0.0074	0.2746142	E
<input type="radio"/>	GO:0009259	6	ribonucleotide metabolic process	43	0.0066	2	0.0074	0.2746142	E
<input type="radio"/>	GO:0007052	5,4,9	mitotic spindle organization and biogenesis	44	0.0068	2	0.0074	0.2757505	E
<input type="radio"/>	GO:0006887	8,6,5,7	exocytosis	44	0.0068	2	0.0074	0.2757505	E
<input type="radio"/>	GO:0031505	6	chitin- and beta-glucan-containing cell wall organization and biogenesis	44	0.0068	2	0.0074	0.2757505	E
<input type="radio"/>	GO:0009066	6,7	aspartate family amino acid metabolic process	46	0.0071	2	0.0074	0.2771639	E
<input type="radio"/>	GO:0046164	5	alcohol catabolic process	47	0.0073	2	0.0074	0.2774618	E
<input type="radio"/>	GO:0006163	6	purine nucleotide metabolic process	47	0.0073	2	0.0074	0.2774618	E
<input type="radio"/>	GO:0007051	8	spindle organization and biogenesis	47	0.0073	2	0.0074	0.2774618	E
<input type="radio"/>	GO:0006487	9,8,7	protein amino acid N-linked glycosylation	48	0.0074	2	0.0074	0.2775012	E
<input type="radio"/>	GO:0015718	6,7	monocarboxylic acid transport	10	0.0015	1	0.0037	0.2838696	E
<input type="radio"/>	GO:0005991	6,7	trehalose metabolic process	10	0.0015	1	0.0037	0.2838696	E
<input type="radio"/>	GO:0030174	9,7,8	regulation of DNA replication initiation	10	0.0015	1	0.0037	0.2838696	E
<input type="radio"/>	GO:0006616	9,12,11,7,10,8	SRP-dependent cotranslational protein targeting to membrane, translocation	10	0.0015	1	0.0037	0.2838696	E
<input type="radio"/>	GO:0008298	5	intracellular mRNA localization	10	0.0015	1	0.0037	0.2838696	E
<input type="radio"/>	GO:0001558	5,6,4,8,9	regulation of cell growth	11	0.0017	1	0.0037	0.2993143	E
<input type="radio"/>	GO:0006972	5	hyperosmotic response	11	0.0017	1	0.0037	0.2993143	E
<input type="radio"/>	GO:0016237	4,6	microautophagy	11	0.0017	1	0.0037	0.2993143	E
<input type="radio"/>	GO:0006116	10,9	NADH oxidation	11	0.0017	1	0.0037	0.2993143	E
<input type="radio"/>	GO:0051049	5,4	regulation of transport	11	0.0017	1	0.0037	0.2993143	E
<input type="radio"/>	GO:0065002	8,6,7	intracellular protein transport across a membrane	11	0.0017	1	0.0037	0.2993143	E
<input type="radio"/>	GO:0006384	8,9,7	transcription initiation from RNA polymerase III promoter	11	0.0017	1	0.0037	0.2993143	E
<input type="radio"/>	GO:0015846	5,6	polyamine transport	12	0.0019	1	0.0037	0.3129889	E
<input type="radio"/>	GO:0007007	6,7	inner mitochondrial membrane organization and biogenesis	12	0.0019	1	0.0037	0.3129889	E
<input type="radio"/>	GO:0015914	5,6	phospholipid transport	12	0.0019	1	0.0037	0.3129889	E
<input type="radio"/>	GO:0006783	7,6,8	heme biosynthetic process	13	0.0020	1	0.0037	0.3250133	E
<input type="radio"/>	GO:0000097	7,8,6	sulfur amino acid biosynthetic process	13	0.0020	1	0.0037	0.3250133	E
<input type="radio"/>	GO:0006779	6,7	porphyrin biosynthetic process	13	0.0020	1	0.0037	0.3250133	E
<input type="radio"/>	GO:0040008	4,3	regulation of growth	13	0.0020	1	0.0037	0.3250133	E
<input type="radio"/>	GO:0007346	7,5,6	regulation of progression through mitotic cell cycle	13	0.0020	1	0.0037	0.3250133	E
<input type="radio"/>	GO:0033014	6	tetrapyrrole biosynthetic process	13	0.0020	1	0.0037	0.3250133	E
<input type="radio"/>	GO:0006038	9,10,7,8,11	cell wall chitin biosynthetic process	13	0.0020	1	0.0037	0.3250133	E
<input type="radio"/>	GO:0031929	6	TOR signaling pathway	13	0.0020	1	0.0037	0.3250133	E
<input type="radio"/>	GO:0009119	6	ribonucleoside metabolic process	13	0.0020	1	0.0037	0.3250133	E
<input type="radio"/>	GO:0006301	7,6	postreplication repair	13	0.0020	1	0.0037	0.3250133	E

<input type="radio"/>	GO:0006734	9,8	NADH metabolic process	14	0.0022	1	0.0037	0.3355003	E
<input type="radio"/>	GO:0006388	9,8	tRNA splicing	14	0.0022	1	0.0037	0.3355003	E
<input type="radio"/>	GO:0030474	5,6,4,7	spindle pole body duplication	14	0.0022	1	0.0037	0.3355003	E
<input type="radio"/>	GO:0000028	9,7,8,6	ribosomal small subunit assembly and maintenance	14	0.0022	1	0.0037	0.3355003	E
<input type="radio"/>	GO:0006188	9,10	IMP biosynthetic process	14	0.0022	1	0.0037	0.3355003	E
<input type="radio"/>	GO:0006272	9,8	leading strand elongation	14	0.0022	1	0.0037	0.3355003	E
<input type="radio"/>	GO:0042168	6,7,5	heme metabolic process	14	0.0022	1	0.0037	0.3355003	E
<input type="radio"/>	GO:0000077	9,8,6	DNA damage checkpoint	14	0.0022	1	0.0037	0.3355003	E
<input type="radio"/>	GO:0006037	8,9,6,7,10	cell wall chitin metabolic process	14	0.0022	1	0.0037	0.3355003	E
<input type="radio"/>	GO:0000394	8	RNA splicing, via endonucleolytic cleavage and ligation	14	0.0022	1	0.0037	0.3355003	E
<input type="radio"/>	GO:0046040	9	IMP metabolic process	14	0.0022	1	0.0037	0.3355003	E
<input type="radio"/>	GO:0006778	5,6	porphyrin metabolic process	14	0.0022	1	0.0037	0.3355003	E
<input type="radio"/>	GO:0042770	5	DNA damage response, signal transduction	14	0.0022	1	0.0037	0.3355003	E
<input type="radio"/>	GO:0000011	6	vacuole inheritance	14	0.0022	1	0.0037	0.3355003	E
<input type="radio"/>	GO:0033013	5	tetrapyrrole metabolic process	14	0.0022	1	0.0037	0.3355003	E
<input type="radio"/>	GO:0022401	7,6	adaptation of signaling pathway	15	0.0023	1	0.0037	0.3445565	E
<input type="radio"/>	GO:0009168	8,9	purine ribonucleoside monophosphate biosynthetic process	15	0.0023	1	0.0037	0.3445565	E
<input type="radio"/>	GO:0030473	8,9,6,7	nuclear migration, microtubule-mediated	15	0.0023	1	0.0037	0.3445565	E
<input type="radio"/>	GO:0019856	7,6	pyrimidine base biosynthetic process	15	0.0023	1	0.0037	0.3445565	E
<input type="radio"/>	GO:0000754	8,7,5	adaptation to pheromone during conjugation with cellular fusion	15	0.0023	1	0.0037	0.3445565	E
<input type="radio"/>	GO:0007018	8,7,6	microtubule-based movement	15	0.0023	1	0.0037	0.3445565	E
<input type="radio"/>	GO:0015918	5,6	sterol transport	15	0.0023	1	0.0037	0.3445565	E
<input type="radio"/>	GO:0009156	7,8	ribonucleoside monophosphate biosynthetic process	15	0.0023	1	0.0037	0.3445565	E
<input type="radio"/>	GO:0009651	5	response to salt stress	15	0.0023	1	0.0037	0.3445565	E
<input type="radio"/>	GO:0031023	5	microtubule organizing center organization and biogenesis	16	0.0025	1	0.0037	0.3522820	E
<input type="radio"/>	GO:0015698	6,7	inorganic anion transport	16	0.0025	1	0.0037	0.3522820	E
<input type="radio"/>	GO:0006493	9,8,7	protein amino acid O-linked glycosylation	16	0.0025	1	0.0037	0.3522820	E
<input type="radio"/>	GO:0051300	5,4,6	spindle pole body organization and biogenesis	16	0.0025	1	0.0037	0.3522820	E
<input type="radio"/>	GO:0009127	7,8	purine nucleoside monophosphate biosynthetic process	16	0.0025	1	0.0037	0.3522820	E
<input type="radio"/>	GO:0010383	7,5,6	cell wall polysaccharide metabolic process	16	0.0025	1	0.0037	0.3522820	E
<input type="radio"/>	GO:0009124	6,7	nucleoside monophosphate biosynthetic process	17	0.0026	1	0.0037	0.3587714	E
<input type="radio"/>	GO:0007004	9	telomere maintenance via telomerase	17	0.0026	1	0.0037	0.3587714	E
<input type="radio"/>	GO:0006820	5,6	anion transport	17	0.0026	1	0.0037	0.3587714	E
<input type="radio"/>	GO:0009161	7	ribonucleoside monophosphate metabolic process	17	0.0026	1	0.0037	0.3587714	E
<input type="radio"/>	GO:0030705	7,5,6	cytoskeleton-dependent intracellular transport	17	0.0026	1	0.0037	0.3587714	E
<input type="radio"/>	GO:0006206	6	pyrimidine base metabolic process	17	0.0026	1	0.0037	0.3587714	E
<input type="radio"/>	GO:0009968	6,5	negative regulation of signal transduction	17	0.0026	1	0.0037	0.3587714	E
<input type="radio"/>	GO:0009167	8	purine ribonucleoside monophosphate metabolic process	17	0.0026	1	0.0037	0.3587714	E
<input type="radio"/>	GO:0010038	5	response to metal ion	18	0.0028	1	0.0037	0.3641136	E
<input type="radio"/>	GO:0000084	8,7,6	S phase of mitotic cell cycle	18	0.0028	1	0.0037	0.3641136	E
<input type="radio"/>	GO:0009126	7	purine nucleoside monophosphate metabolic process	18	0.0028	1	0.0037	0.3641136	E

<input type="radio"/>	GO:0009116	5	nucleoside metabolic process	18	0.0028	1	0.0037	0.3641136	E
<input type="radio"/>	GO:0006273	9,8	lagging strand elongation	18	0.0028	1	0.0037	0.3641136	E
<input type="radio"/>	GO:0007584	6,4	response to nutrient	18	0.0028	1	0.0037	0.3641136	E
<input type="radio"/>	GO:0016571	11,9,10,8	histone methylation	18	0.0028	1	0.0037	0.3641136	E
<input type="radio"/>	GO:0031669	6,5	cellular response to nutrient levels	19	0.0029	1	0.0037	0.3683924	E
<input type="radio"/>	GO:0031668	5,4	cellular response to extracellular stimulus	19	0.0029	1	0.0037	0.3683924	E
<input type="radio"/>	GO:0043094	4	metabolic compound salvage	19	0.0029	1	0.0037	0.3683924	E
<input type="radio"/>	GO:0042594	6,4	response to starvation	19	0.0029	1	0.0037	0.3683924	E
<input type="radio"/>	GO:0009123	6	nucleoside monophosphate metabolic process	19	0.0029	1	0.0037	0.3683924	E
<input type="radio"/>	GO:0009267	7,6,5	cellular response to starvation	19	0.0029	1	0.0037	0.3683924	E
<input type="radio"/>	GO:0000722	9,8	telomere maintenance via recombination	19	0.0029	1	0.0037	0.3683924	E
<input type="radio"/>	GO:0046148	5	pigment biosynthetic process	19	0.0029	1	0.0037	0.3683924	E
<input type="radio"/>	GO:0030148	7,6,8	sphingolipid biosynthetic process	20	0.0031	1	0.0037	0.3716865	E
<input type="radio"/>	GO:0007094	9,11,10,8	mitotic cell cycle spindle assembly checkpoint	20	0.0031	1	0.0037	0.3716865	E
<input type="radio"/>	GO:0006614	11,10,9,8,7	SRP-dependent cotranslational protein targeting to membrane	20	0.0031	1	0.0037	0.3716865	E
<input type="radio"/>	GO:0042440	4	pigment metabolic process	20	0.0031	1	0.0037	0.3716865	E
<input type="radio"/>	GO:0000022	6,5,10,8	mitotic spindle elongation	20	0.0031	1	0.0037	0.3716865	E
<input type="radio"/>	GO:0045053	7,6,5,4	protein retention in Golgi	20	0.0031	1	0.0037	0.3716865	E
<input type="radio"/>	GO:0051647	6,5	nucleus localization	20	0.0031	1	0.0037	0.3716865	E
<input type="radio"/>	GO:0051231	5,4,9,7	spindle elongation	20	0.0031	1	0.0037	0.3716865	E
<input type="radio"/>	GO:0006826	7,8,9	iron ion transport	20	0.0031	1	0.0037	0.3716865	E
<input type="radio"/>	GO:0051053	8,7	negative regulation of DNA metabolic process	20	0.0031	1	0.0037	0.3716865	E
<input type="radio"/>	GO:0040023	6,7,4,5	establishment of nucleus localization	20	0.0031	1	0.0037	0.3716865	E
<input type="radio"/>	GO:0007097	7,8,5,6	nuclear migration	20	0.0031	1	0.0037	0.3716865	E
<input type="radio"/>	GO:0046112	6,5	nucleobase biosynthetic process	21	0.0032	1	0.0037	0.3740699	E
<input type="radio"/>	GO:0051716	3	cellular response to stimulus	21	0.0032	1	0.0037	0.3740699	E
<input type="radio"/>	GO:0033554	4	cellular response to stress	21	0.0032	1	0.0037	0.3740699	E
<input type="radio"/>	GO:0048284	5	organelle fusion	22	0.0034	1	0.0037	0.3756125	E
<input type="radio"/>	GO:0040020	7,9,8,6	regulation of meiosis	22	0.0034	1	0.0037	0.3756125	E
<input type="radio"/>	GO:0007120	8,6,10,7,11,5	axial cellular bud site selection	22	0.0034	1	0.0037	0.3756125	E
<input type="radio"/>	GO:0007231	6,5	osmosensory signaling pathway	22	0.0034	1	0.0037	0.3756125	E
<input type="radio"/>	GO:0044272	5	sulfur compound biosynthetic process	22	0.0034	1	0.0037	0.3756125	E
<input type="radio"/>	GO:0030150	10,9,8,7	protein import into mitochondrial matrix	22	0.0034	1	0.0037	0.3756125	E
<input type="radio"/>	GO:0006513	10	protein monoubiquitination	22	0.0034	1	0.0037	0.3756125	E
<input type="radio"/>	GO:0006311	10,8,7,5,9,6,4	meiotic gene conversion	22	0.0034	1	0.0037	0.3756125	E
<input type="radio"/>	GO:0030472	6,5,10	mitotic spindle organization and biogenesis in nucleus	22	0.0034	1	0.0037	0.3756125	E
<input type="radio"/>	GO:0006613	10,9,8,7,6	cotranslational protein targeting to membrane	23	0.0036	1	0.0037	0.3763797	E
<input type="radio"/>	GO:0043044	10	ATP-dependent chromatin remodeling	23	0.0036	1	0.0037	0.3763797	E
<input type="radio"/>	GO:0006303	8,7	double-strand break repair via nonhomologous end joining	23	0.0036	1	0.0037	0.3763797	E
<input type="radio"/>	GO:0006610	10,11,8,9,7	ribosomal protein import into nucleus	23	0.0036	1	0.0037	0.3763797	E
<input type="radio"/>	GO:0006607	10,11,8,9,7	NLS-bearing substrate import into nucleus	23	0.0036	1	0.0037	0.3763797	E
<input type="radio"/>	GO:0006608	10,11,8,9,7	snRNP protein import into nucleus	23	0.0036	1	0.0037	0.3763797	E
<input type="radio"/>	GO:0051030	5,7,6,8	snRNA transport	23	0.0036	1	0.0037	0.3763797	E

<input type="radio"/>	GO:0006408	11,9,6,8,10,7	snRNA export from nucleus	23	0.0036	1	0.0037	0.3763797	E
<input type="radio"/>	GO:0019748	3	secondary metabolic process	23	0.0036	1	0.0037	0.3763797	E
<input type="radio"/>	GO:0051278	8,7	chitin- and beta-glucan-containing cell wall polysaccharide biosynthetic process	24	0.0037	1	0.0037	0.3764329	E
<input type="radio"/>	GO:0016575	11,9	histone deacetylation	24	0.0037	1	0.0037	0.3764329	E
<input type="radio"/>	GO:0006555	7,8,6	methionine metabolic process	24	0.0037	1	0.0037	0.3764329	E
<input type="radio"/>	GO:0006096	9,10	glycolysis	24	0.0037	1	0.0037	0.3764329	E
<input type="radio"/>	GO:0009201	7,8	ribonucleoside triphosphate biosynthetic process	24	0.0037	1	0.0037	0.3764329	E
<input type="radio"/>	GO:0045851	8	pH reduction	24	0.0037	1	0.0037	0.3764329	E
<input type="radio"/>	GO:0007096	8,10,9,7	regulation of exit from mitosis	24	0.0037	1	0.0037	0.3764329	E
<input type="radio"/>	GO:0000288	10,8,9	mRNA catabolic process, deadenylation-dependent decay	24	0.0037	1	0.0037	0.3764329	E
<input type="radio"/>	GO:0007035	13,10,6,11	vacuolar acidification	24	0.0037	1	0.0037	0.3764329	E
<input type="radio"/>	GO:0007006	5,6	mitochondrial membrane organization and biogenesis	24	0.0037	1	0.0037	0.3764329	E
<input type="radio"/>	GO:0006576	5,6	biogenic amine metabolic process	24	0.0037	1	0.0037	0.3764329	E
<input type="radio"/>	GO:0051452	12,9,10	cellular pH reduction	24	0.0037	1	0.0037	0.3764329	E
<input type="radio"/>	GO:0010035	4	response to inorganic substance	24	0.0037	1	0.0037	0.3764329	E
<input type="radio"/>	GO:0031577	8,7	spindle checkpoint	24	0.0037	1	0.0037	0.3764329	E
<input type="radio"/>	GO:0046352	7	disaccharide catabolic process	24	0.0037	1	0.0037	0.3764329	E
<input type="radio"/>	GO:0008150	1	biological process	6476	1.0000	269	1.0000	1.0000000	D
<input type="radio"/>	GO:0045005	8,6	maintenance of fidelity during DNA-dependent DNA replication	25	0.0039	1	0.0037	0.3758301	D
<input type="radio"/>	GO:0006609	10,11,8,9,7	mRNA-binding (hnRNP) protein import into nucleus	25	0.0039	1	0.0037	0.3758301	D
<input type="radio"/>	GO:0009199	7	ribonucleoside triphosphate metabolic process	25	0.0039	1	0.0037	0.3758301	D
<input type="radio"/>	GO:0006298	7,9,6	mismatch repair	25	0.0039	1	0.0037	0.3758301	D
<input type="radio"/>	GO:0009966	5,4	regulation of signal transduction	26	0.0040	1	0.0037	0.3746253	D
<input type="radio"/>	GO:0006407	11,9,6,8,10,7	rRNA export from nucleus	26	0.0040	1	0.0037	0.3746253	D
<input type="radio"/>	GO:0006476	8	protein amino acid deacetylation	26	0.0040	1	0.0037	0.3746253	D
<input type="radio"/>	GO:0010382	6,4	cell wall metabolic process	26	0.0040	1	0.0037	0.3746253	D
<input type="radio"/>	GO:0000001	8,7,6	mitochondrion inheritance	26	0.0040	1	0.0037	0.3746253	D
<input type="radio"/>	GO:0051029	5,7,6,8	rRNA transport	26	0.0040	1	0.0037	0.3746253	D
<input type="radio"/>	GO:0048311	7,6	mitochondrion distribution	26	0.0040	1	0.0037	0.3746253	D
<input type="radio"/>	GO:0042274	6,5	ribosomal small subunit biogenesis and assembly	26	0.0040	1	0.0037	0.3746253	D
<input type="radio"/>	GO:0051646	6,5	mitochondrion localization	27	0.0042	1	0.0037	0.3728694	D
<input type="radio"/>	GO:0007093	8,10,9,7	mitotic cell cycle checkpoint	27	0.0042	1	0.0037	0.3728694	D
<input type="radio"/>	GO:0018193	7	peptidyl-amino acid modification	28	0.0043	1	0.0037	0.3706102	D
<input type="radio"/>	GO:0042144	6	vacuole fusion, non-autophagic	28	0.0043	1	0.0037	0.3706102	D
<input type="radio"/>	GO:0006999	6	nuclear pore organization and biogenesis	29	0.0045	1	0.0037	0.3678924	D
<input type="radio"/>	GO:0006109	5,4	regulation of carbohydrate metabolic process	29	0.0045	1	0.0037	0.3678924	D
<input type="radio"/>	GO:0006409	11,9,6,8,10,7	tRNA export from nucleus	29	0.0045	1	0.0037	0.3678924	D
<input type="radio"/>	GO:0006665	6,7	sphingolipid metabolic process	30	0.0046	1	0.0037	0.3647578	D
<input type="radio"/>	GO:0043488	9,8,7	regulation of mRNA stability	30	0.0046	1	0.0037	0.3647578	D
<input type="radio"/>	GO:0043487	8,7	regulation of RNA stability	30	0.0046	1	0.0037	0.3647578	D
<input type="radio"/>	GO:0051031	5,7,6,8	tRNA transport	30	0.0046	1	0.0037	0.3647578	D
<input type="radio"/>	GO:0006575	5	amino acid derivative metabolic process	31	0.0048	1	0.0037	0.3612457	D
<input type="radio"/>	GO:0005984	6	disaccharide metabolic process	31	0.0048	1	0.0037	0.3612457	D

<input type="checkbox"/>	GO:0009112	5	nucleobase metabolic process	31	0.0048	1	0.0037	0.3612457	D
<input type="checkbox"/>	GO:0006271	8,7	DNA strand elongation during DNA replication	32	0.0049	1	0.0037	0.3573926	D
<input type="checkbox"/>	GO:0006418	8,7,9,6	tRNA aminoacylation for protein translation	32	0.0049	1	0.0037	0.3573926	D
<input type="checkbox"/>	GO:0043039	7,8	tRNA aminoacylation	32	0.0049	1	0.0037	0.3573926	D
<input type="checkbox"/>	GO:0043038	6,7	amino acid activation	32	0.0049	1	0.0037	0.3573926	D
<input type="checkbox"/>	GO:0022616	6	DNA strand elongation	32	0.0049	1	0.0037	0.3573926	D
<input type="checkbox"/>	GO:0005977	7,6,8	glycogen metabolic process	32	0.0049	1	0.0037	0.3573926	D
<input type="checkbox"/>	GO:0000096	6,7,5	sulfur amino acid metabolic process	33	0.0051	1	0.0037	0.3532330	D
<input type="checkbox"/>	GO:0006270	8,6	DNA replication initiation	33	0.0051	1	0.0037	0.3532330	D
<input type="checkbox"/>	GO:0045047	9,8,7,6,5	protein targeting to ER	33	0.0051	1	0.0037	0.3532330	D
<input type="checkbox"/>	GO:0006007	8,9	glucose catabolic process	34	0.0053	1	0.0037	0.3487989	D
<input type="checkbox"/>	GO:0051252	7,6	regulation of RNA metabolic process	36	0.0056	1	0.0037	0.3392248	D
<input type="checkbox"/>	GO:0022411	4	cellular component disassembly	36	0.0056	1	0.0037	0.3392248	D
<input type="checkbox"/>	GO:0006383	8,7	transcription from RNA polymerase III promoter	38	0.0059	1	0.0037	0.3288864	D
<input type="checkbox"/>	GO:0009152	7,8	purine ribonucleotide biosynthetic process	38	0.0059	1	0.0037	0.3288864	D
<input type="checkbox"/>	GO:0019320	7,8	hexose catabolic process	39	0.0060	1	0.0037	0.3234901	D
<input type="checkbox"/>	GO:0001522	7	pseudouridine synthesis	39	0.0060	1	0.0037	0.3234901	D
<input type="checkbox"/>	GO:0000027	9,7,8,6	ribosomal large subunit assembly and maintenance	41	0.0063	1	0.0037	0.3123488	D
<input type="checkbox"/>	GO:0009150	7	purine ribonucleotide metabolic process	41	0.0063	1	0.0037	0.3123488	D
<input type="checkbox"/>	GO:0001403	6,4,8,9	invasive growth (sensu Saccharomyces)	42	0.0065	1	0.0037	0.3066414	D
<input type="checkbox"/>	GO:0006752	6	group transfer coenzyme metabolic process	44	0.0068	1	0.0037	0.2950367	D
<input type="checkbox"/>	GO:0046365	6,7	monosaccharide catabolic process	44	0.0068	1	0.0037	0.2950367	D
<input type="checkbox"/>	GO:0031167	8,9	rRNA methylation	44	0.0068	1	0.0037	0.2950367	D
<input type="checkbox"/>	GO:0006367	8,9,7	transcription initiation from RNA polymerase II promoter	44	0.0068	1	0.0037	0.2950367	D
<input type="checkbox"/>	GO:0006289	7,6	nucleotide-excision repair	44	0.0068	1	0.0037	0.2950367	D
<input type="checkbox"/>	GO:0006073	6,7	glucan metabolic process	46	0.0071	1	0.0037	0.2832771	D
<input type="checkbox"/>	GO:0006417	7,6,5	regulation of translation	47	0.0073	1	0.0037	0.2773718	D
<input type="checkbox"/>	GO:0000082	8,5,6,7,4	G1/S transition of mitotic cell cycle	52	0.0080	2	0.0074	0.2752853	D
<input type="checkbox"/>	GO:0006368	9,7,8	RNA elongation from RNA polymerase II promoter	53	0.0082	2	0.0074	0.2741905	D
<input type="checkbox"/>	GO:0006352	7,8,6	transcription initiation	55	0.0085	2	0.0074	0.2714239	D
<input type="checkbox"/>	GO:0042257	8,7	ribosomal subunit assembly	55	0.0085	2	0.0074	0.2714239	D
<input type="checkbox"/>	GO:0007131	10,8,7,5,9,6,4	meiotic recombination	55	0.0085	2	0.0074	0.2714239	D
<input type="checkbox"/>	GO:0006611	9,10,7,8	protein export from nucleus	56	0.0086	2	0.0074	0.2697722	D
<input type="checkbox"/>	GO:0006997	5	nuclear organization and biogenesis	57	0.0088	2	0.0074	0.2679546	D
<input type="checkbox"/>	GO:0006413	7,6	translational initiation	49	0.0076	1	0.0037	0.2655664	D
<input type="checkbox"/>	GO:0006944	5	membrane fusion	59	0.0091	2	0.0074	0.2638599	D
<input type="checkbox"/>	GO:0000070	9,7,5,8,6,4	mitotic sister chromatid segregation	59	0.0091	2	0.0074	0.2638599	D
<input type="checkbox"/>	GO:0006354	8,6,7	RNA elongation	59	0.0091	2	0.0074	0.2638599	D
<input type="checkbox"/>	GO:0006725	4	aromatic compound metabolic process	60	0.0093	2	0.0074	0.2616011	D
<input type="checkbox"/>	GO:0006348	11,7,8,12,10	chromatin silencing at telomere	60	0.0093	2	0.0074	0.2616011	D
<input type="checkbox"/>	GO:0031509	7,11	telomeric heterochromatin formation	60	0.0093	2	0.0074	0.2616011	D
<input type="checkbox"/>	GO:0006606	9,10,7,8,6	protein import into nucleus	50	0.0077	1	0.0037	0.2596862	D
<input type="checkbox"/>	GO:0051170	9,7,8	nuclear import	50	0.0077	1	0.0037	0.2596862	D
<input type="checkbox"/>	GO:0000819	7,4	sister chromatid segregation	62	0.0096	2	0.0074	0.2567055	D

<input type="radio"/>	GO:0043161	10,9,11	proteasomal ubiquitin-dependent protein catabolic process	63	0.0097	2	0.0074	0.2540857	D
<input type="radio"/>	GO:0006400	7,8	tRNA modification	52	0.0080	1	0.0037	0.2480146	D
<input type="radio"/>	GO:0042255	7,6	ribosome assembly	66	0.0102	2	0.0074	0.2456351	D
<input type="radio"/>	GO:0043413	6	biopolymer glycosylation	73	0.0113	3	0.0112	0.2300256	D
<input type="radio"/>	GO:0006486	8,7,6	protein amino acid glycosylation	73	0.0113	3	0.0112	0.2300256	D
<input type="radio"/>	GO:0065004	6,5	protein-DNA complex assembly	74	0.0114	3	0.0112	0.2297853	D
<input type="radio"/>	GO:0009101	7,5	glycoprotein biosynthetic process	78	0.0120	3	0.0112	0.2275596	D
<input type="radio"/>	GO:0051246	5,4	regulation of protein metabolic process	72	0.0111	2	0.0074	0.2267330	D
<input type="radio"/>	GO:0009100	6	glycoprotein metabolic process	79	0.0122	3	0.0112	0.2267078	D
<input type="radio"/>	GO:0006888	8,6,5,7	ER to Golgi vesicle-mediated transport	81	0.0125	3	0.0112	0.2246794	D
<input type="radio"/>	GO:0032259	5	methylation	83	0.0128	3	0.0112	0.2222456	D
<input type="radio"/>	GO:0043414	6	biopolymer methylation	83	0.0128	3	0.0112	0.2222456	D
<input type="radio"/>	GO:0006457	6	protein folding	84	0.0130	3	0.0112	0.2208873	D
<input type="radio"/>	GO:0007127	9,7,6,8,5	meiosis I	75	0.0116	2	0.0074	0.2166319	D
<input type="radio"/>	GO:0001510	7	RNA methylation	60	0.0093	1	0.0037	0.2034639	D
<input type="radio"/>	GO:0006402	7	mRNA catabolic process	60	0.0093	1	0.0037	0.2034639	D
<input type="radio"/>	GO:0006342	10,6,7,11,9	chromatin silencing	95	0.0147	3	0.0112	0.2009620	D
<input type="radio"/>	GO:0031507	6,10	heterochromatin formation	95	0.0147	3	0.0112	0.2009620	D
<input type="radio"/>	GO:0045814	5	negative regulation of gene expression, epigenetic	95	0.0147	3	0.0112	0.2009620	D
<input type="radio"/>	GO:0016458	5	gene silencing	95	0.0147	3	0.0112	0.2009620	D
<input type="radio"/>	GO:0007017	6	microtubule-based process	101	0.0156	4	0.0149	0.1998685	D
<input type="radio"/>	GO:0016052	5	carbohydrate catabolic process	80	0.0124	2	0.0074	0.1993410	D
<input type="radio"/>	GO:0044275	6	cellular carbohydrate catabolic process	80	0.0124	2	0.0074	0.1993410	D
<input type="radio"/>	GO:0006261	7	DNA-dependent DNA replication	97	0.0150	3	0.0112	0.1965887	D
<input type="radio"/>	GO:0000910	4	cytokinesis	109	0.0168	4	0.0149	0.1938684	D
<input type="radio"/>	GO:0017038	5,6,7	protein import	109	0.0168	4	0.0149	0.1938684	D
<input type="radio"/>	GO:0051329	7,5,6	interphase of mitotic cell cycle	112	0.0173	4	0.0149	0.1905156	D
<input type="radio"/>	GO:0051325	6,5	interphase	112	0.0173	4	0.0149	0.1905156	D
<input type="radio"/>	GO:0040029	4	regulation of gene expression, epigenetic	100	0.0154	3	0.0112	0.1897360	D
<input type="radio"/>	GO:0000122	10,9	negative regulation of transcription from RNA polymerase II promoter	63	0.0097	1	0.0037	0.1879647	D
<input type="radio"/>	GO:0006468	8,7	protein amino acid phosphorylation	101	0.0156	3	0.0112	0.1873863	D
<input type="radio"/>	GO:0008033	7	tRNA processing	84	0.0130	2	0.0074	0.1854146	D
<input type="radio"/>	GO:0006260	6	DNA replication	117	0.0181	4	0.0149	0.1838356	D
<input type="radio"/>	GO:0042273	6,5	ribosomal large subunit biogenesis and assembly	64	0.0099	1	0.0037	0.1829685	D
<input type="radio"/>	GO:0000747	4	conjugation with cellular fusion	118	0.0182	4	0.0149	0.1823561	D
<input type="radio"/>	GO:0019953	3	sexual reproduction	118	0.0182	4	0.0149	0.1823561	D
<input type="radio"/>	GO:0000746	3	conjugation	118	0.0182	4	0.0149	0.1823561	D
<input type="radio"/>	GO:0048878	5	chemical homeostasis	121	0.0187	5	0.0186	0.1808791	D
<input type="radio"/>	GO:0031497	5,9	chromatin assembly	104	0.0161	3	0.0112	0.1801827	D
<input type="radio"/>	GO:0007067	8,6,7,5	mitosis	127	0.0196	5	0.0186	0.1793130	D
<input type="radio"/>	GO:0000087	7,5,6	M phase of mitotic cell cycle	129	0.0199	5	0.0186	0.1783168	D
<input type="radio"/>	GO:0042493	4	response to drug	121	0.0187	4	0.0149	0.1776705	D
<input type="radio"/>	GO:0006310	6	DNA recombination	122	0.0188	4	0.0149	0.1760333	D
<input type="radio"/>	GO:0006406	11,9,6,8,10,7	mRNA export from nucleus	66	0.0102	1	0.0037	0.1732418	D

<input type="checkbox"/>	GO:0051028	5,7,6,8	mRNA transport	66	0.0102	1	0.0037	0.1732418	D
<input type="checkbox"/>	GO:0007242	5	intracellular signaling cascade	137	0.0212	5	0.0186	0.1722540	D
<input type="checkbox"/>	GO:0051704	2	multi-organism process	139	0.0215	5	0.0186	0.1702765	D
<input type="checkbox"/>	GO:0031326	6,5	regulation of cellular biosynthetic process	67	0.0103	1	0.0037	0.1685138	D
<input type="checkbox"/>	GO:0006511	9,8,10	ubiquitin-dependent protein catabolic process	148	0.0229	6	0.0223	0.1655224	D
<input type="checkbox"/>	GO:0019941	8,7,9	modification-dependent protein catabolic process	148	0.0229	6	0.0223	0.1655224	D
<input type="checkbox"/>	GO:0006403	4	RNA localization	90	0.0139	2	0.0074	0.1648885	D
<input type="checkbox"/>	GO:0051603	7,8	proteolysis involved in cellular protein catabolic process	151	0.0233	6	0.0223	0.1647134	D
<input type="checkbox"/>	GO:0043632	6	modification-dependent macromolecule catabolic process	155	0.0239	6	0.0223	0.1630053	D
<input type="checkbox"/>	GO:0016569	9	covalent chromatin modification	91	0.0141	2	0.0074	0.1615450	D
<input type="checkbox"/>	GO:0016570	10,8	histone modification	91	0.0141	2	0.0074	0.1615450	D
<input type="checkbox"/>	GO:0043623	7,6	cellular protein complex assembly	69	0.0107	1	0.0037	0.1593325	D
<input type="checkbox"/>	GO:0009889	5,4	regulation of biosynthetic process	69	0.0107	1	0.0037	0.1593325	D
<input type="checkbox"/>	GO:0006892	8,6,5,7	post-Golgi vesicle-mediated transport	69	0.0107	1	0.0037	0.1593325	D
<input type="checkbox"/>	GO:0031325	6,5	positive regulation of cellular metabolic process	116	0.0179	3	0.0112	0.1502724	D
<input type="checkbox"/>	GO:0009893	5,4	positive regulation of metabolic process	116	0.0179	3	0.0112	0.1502724	D
<input type="checkbox"/>	GO:0006333	8	chromatin assembly or disassembly	119	0.0184	3	0.0112	0.1428106	D
<input type="checkbox"/>	GO:0007165	4	signal transduction	209	0.0323	8	0.0297	0.1402976	D
<input type="checkbox"/>	GO:0006401	6	RNA catabolic process	74	0.0114	1	0.0037	0.1379977	D
<input type="checkbox"/>	GO:0006399	6	tRNA metabolic process	121	0.0187	3	0.0112	0.1378888	D
<input type="checkbox"/>	GO:0048193	7,5,6	Golgi vesicle transport	166	0.0256	5	0.0186	0.1323689	D
<input type="checkbox"/>	GO:0048518	4	positive regulation of biological process	124	0.0191	3	0.0112	0.1306123	D
<input type="checkbox"/>	GO:0048522	5,4	positive regulation of cellular process	124	0.0191	3	0.0112	0.1306123	D
<input type="checkbox"/>	GO:0048523	5,4	negative regulation of cellular process	239	0.0369	9	0.0335	0.1301715	D
<input type="checkbox"/>	GO:0045944	10,9	positive regulation of transcription from RNA polymerase II promoter	76	0.0117	1	0.0037	0.1301089	D
<input type="checkbox"/>	GO:0045941	8,7	positive regulation of transcription	101	0.0156	2	0.0074	0.1299220	D
<input type="checkbox"/>	GO:0048519	4	negative regulation of biological process	242	0.0374	9	0.0335	0.1284154	D
<input type="checkbox"/>	GO:0051168	9,7,8	nuclear export	102	0.0158	2	0.0074	0.1269702	D
<input type="checkbox"/>	GO:0007126	8,6,7,5	meiosis	148	0.0229	4	0.0149	0.1267710	D
<input type="checkbox"/>	GO:0051321	4	meiotic cell cycle	148	0.0229	4	0.0149	0.1267710	D
<input type="checkbox"/>	GO:0051327	7,5,6	M phase of meiotic cell cycle	148	0.0229	4	0.0149	0.1267710	D
<input type="checkbox"/>	GO:0000278	4	mitotic cell cycle	266	0.0411	11	0.0409	0.1244801	D
<input type="checkbox"/>	GO:0032200	7	telomere organization and biogenesis	274	0.0423	11	0.0409	0.1235480	D
<input type="checkbox"/>	GO:0000723	8	telomere maintenance	274	0.0423	11	0.0409	0.1235480	D
<input type="checkbox"/>	GO:0043285	5	biopolymer catabolic process	277	0.0428	11	0.0409	0.1228734	D
<input type="checkbox"/>	GO:0006405	10,8,5,7,9,6	RNA export from nucleus	79	0.0122	1	0.0037	0.1189538	D
<input type="checkbox"/>	GO:0000279	6,5	M phase	258	0.0398	9	0.0335	0.1165645	D
<input type="checkbox"/>	GO:0050658	4,6,5,7	RNA transport	80	0.0124	1	0.0037	0.1154129	D
<input type="checkbox"/>	GO:0051236	3,4,5	establishment of RNA localization	80	0.0124	1	0.0037	0.1154129	D
<input type="checkbox"/>	GO:0050657	5,6	nucleic acid transport	80	0.0124	1	0.0037	0.1154129	D
<input type="checkbox"/>	GO:0044265	5	cellular macromolecule catabolic process	314	0.0485	12	0.0446	0.1138533	D
<input type="checkbox"/>	GO:0006338	9	chromatin remodeling	155	0.0239	4	0.0149	0.1132379	D
<input type="checkbox"/>	GO:0016310	6	phosphorylation	155	0.0239	4	0.0149	0.1132379	D
<input type="checkbox"/>	GO:0045045	7,5,4,6	secretory pathway	243	0.0375	8	0.0297	0.1120038	D

<input type="radio"/>	GO:0045892	9,8	negative regulation of transcription, DNA-dependent	156	0.0241	4	0.0149	0.1113456	D
<input type="radio"/>	GO:0045934	7,6	negative regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	179	0.0276	5	0.0186	0.1111512	D
<input type="radio"/>	GO:0045935	7,6	positive regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	108	0.0167	2	0.0074	0.1101636	D
<input type="radio"/>	GO:0009057	4	macromolecule catabolic process	345	0.0533	13	0.0483	0.1071167	D
<input type="radio"/>	GO:0032940	6,4,5	secretion by cell	250	0.0386	8	0.0297	0.1045268	D
<input type="radio"/>	GO:0046903	3,4	secretion	250	0.0386	8	0.0297	0.1045268	D
<input type="radio"/>	GO:0016481	8,7	negative regulation of transcription	162	0.0250	4	0.0149	0.1002767	D
<input type="radio"/>	GO:0000154	7,8	rRNA modification	85	0.0131	1	0.0037	0.0989931	D
<input type="radio"/>	GO:0022402	4,3	cell cycle process	439	0.0678	18	0.0669	0.0987756	D
<input type="radio"/>	GO:0006793	4	phosphorus metabolic process	212	0.0327	6	0.0223	0.0961507	D
<input type="radio"/>	GO:0006796	5	phosphate metabolic process	212	0.0327	6	0.0223	0.0961507	D
<input type="radio"/>	GO:0007049	3	cell cycle	458	0.0707	18	0.0669	0.0958004	D
<input type="radio"/>	GO:0022403	5,4	cell cycle phase	353	0.0545	12	0.0446	0.0897342	D
<input type="radio"/>	GO:0022618	6,5	protein-RNA complex assembly	144	0.0222	3	0.0112	0.0871254	D
<input type="radio"/>	GO:0015931	4,5	nucleobase, nucleoside, nucleotide and nucleic acid transport	90	0.0139	1	0.0037	0.0846011	D
<input type="radio"/>	GO:0007059	3	chromosome segregation	119	0.0184	2	0.0074	0.0835359	D
<input type="radio"/>	GO:0031324	6,5	negative regulation of cellular metabolic process	198	0.0306	5	0.0186	0.0819250	D
<input type="radio"/>	GO:0006259	5	DNA metabolic process	523	0.0808	19	0.0706	0.0787363	D
<input type="radio"/>	GO:0065003	5,4	macromolecular complex assembly	328	0.0506	10	0.0372	0.0725831	D
<input type="radio"/>	GO:0045893	9,8	positive regulation of transcription, DNA-dependent	95	0.0147	1	0.0037	0.0720660	D
<input type="radio"/>	GO:0065007	2	biological regulation	948	0.1464	39	0.1450	0.0702441	D
<input type="radio"/>	GO:0009892	5,4	negative regulation of metabolic process	208	0.0321	5	0.0186	0.0683537	D
<input type="radio"/>	GO:0051169	7,5,6	nuclear transport	129	0.0199	2	0.0074	0.0639381	D
<input type="radio"/>	GO:0006913	8,6,7	nucleocytoplasmic transport	129	0.0199	2	0.0074	0.0639381	D
<input type="radio"/>	GO:0016568	8	chromatin modification	223	0.0344	5	0.0186	0.0509037	D
<input type="radio"/>	GO:0016043	3	cellular component organization and biogenesis	2264	0.3496	91	0.3383	0.0484413	D
<input type="radio"/>	GO:0009451	6	RNA modification	139	0.0215	2	0.0074	0.0483136	D
<input type="radio"/>	GO:0045449	7,6	regulation of transcription	386	0.0596	11	0.0409	0.0466704	D
<input type="radio"/>	GO:0007001	6	chromosome organization and biogenesis (sensu Eukaryota)	567	0.0876	17	0.0632	0.0323255	D
<input type="radio"/>	GO:0006355	8,7	regulation of transcription, DNA-dependent	359	0.0554	9	0.0335	0.0306253	D
<input type="radio"/>	GO:0019219	6,5	regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	440	0.0679	12	0.0446	0.0305915	D
<input type="radio"/>	GO:0051276	5	chromosome organization and biogenesis	572	0.0883	17	0.0632	0.0302428	D
<input type="radio"/>	GO:0019538	4	protein metabolic process	1547	0.2389	56	0.2082	0.0288152	D
<input type="radio"/>	GO:0006357	9,8	regulation of transcription from RNA polymerase II promoter	221	0.0341	4	0.0149	0.0276204	D
<input type="radio"/>	GO:0006323	6	DNA packaging	253	0.0391	5	0.0186	0.0262910	D
<input type="radio"/>	GO:0006325	7	establishment and/or maintenance of chromatin architecture	253	0.0391	5	0.0186	0.0262910	D
<input type="radio"/>	GO:0006996	4	organelle organization and biogenesis	1388	0.2143	49	0.1822	0.0261838	D
<input type="radio"/>	GO:0009059	4	macromolecule biosynthetic process	886	0.1368	28	0.1041	0.0206069	D
<input type="radio"/>	GO:0008380	7	RNA splicing	132	0.0204	1	0.0037	0.0203758	D
<input type="radio"/>	GO:0044267	5	cellular protein metabolic process	1498	0.2313	52	0.1933	0.0191357	D

<input type="checkbox"/>	GO:0044260	4	cellular macromolecule metabolic process	1552	0.2397	54	0.2007	0.0183933	D
<input type="checkbox"/>	GO:0031323	5,4	regulation of cellular metabolic process	507	0.0783	13	0.0483	0.0156153	D
<input type="checkbox"/>	GO:0019222	4,3	regulation of metabolic process	538	0.0831	14	0.0520	0.0147415	D
<input type="checkbox"/>	GO:0006366	8,7	transcription from RNA polymerase II promoter	343	0.0530	7	0.0260	0.0130572	D
<input type="checkbox"/>	GO:0006350	5	transcription	567	0.0876	14	0.0520	0.0086581	D
<input type="checkbox"/>	GO:0006397	7	mRNA processing	157	0.0242	1	0.0037	0.0082205	D
<input type="checkbox"/>	GO:0006351	7,6	transcription, DNA-dependent	522	0.0806	12	0.0446	0.0067046	D
<input type="checkbox"/>	GO:0032774	6	RNA biosynthetic process	524	0.0809	12	0.0446	0.0064297	D
<input type="checkbox"/>	GO:0043170	3	macromolecule metabolic process	2841	0.4387	101	0.3755	0.0050946	D
<input type="checkbox"/>	GO:0016071	6	mRNA metabolic process	210	0.0324	1	0.0037	0.0010952	D
<input type="checkbox"/>	GO:0043284	5	biopolymer biosynthetic process	354	0.0547	4	0.0149	0.0005449	D
<input type="checkbox"/>	GO:0006139	4	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	1532	0.2366	42	0.1561	0.0002793	D
<input type="checkbox"/>	GO:0006412	6,5	translation	688	0.1062	13	0.0483	0.0002722	D
<input type="checkbox"/>	GO:0006364	6,7	rRNA processing	249	0.0384	1	0.0037	0.0002348	D
<input type="checkbox"/>	GO:0016072	6	rRNA metabolic process	256	0.0395	1	0.0037	0.0001774	D
<input type="checkbox"/>	GO:0042254	5	ribosome biogenesis and assembly	410	0.0633	4	0.0149	8.152014E-05	D
<input type="checkbox"/>	GO:0043283	4	biopolymer metabolic process	2230	0.3443	64	0.2379	3.322746E-05	D
<input type="checkbox"/>	GO:0022613	4	ribonucleoprotein complex biogenesis and assembly	483	0.0746	5	0.0186	2.621706E-05	D
<input type="checkbox"/>	GO:0006414	7,6	translational elongation	313	0.0483	1	0.0037	1.741819E-05	D
<input type="checkbox"/>	GO:0006396	6	RNA processing	491	0.0758	4	0.0149	4.400004E-06	D
<input type="checkbox"/>	GO:0016070	5	RNA metabolic process	1058	0.1634	17	0.0632	2.836324E-07	D