

GO-Stats Results

Your dataset contains **196** annotated gene products.

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

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

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

GO ID	Level	GO Term	RO	RF	DO	DF	P-value	E/D
<input type="radio"/> GO:0009987	2	cellular process	4654	0.7187	174	0.8878	2.780559E-06	E
<input type="radio"/> GO:0065007	2	biological regulation	948	0.1464	57	0.2908	4.413952E-05	E
<input type="radio"/> GO:0007049	3	cell cycle	458	0.0707	34	0.1735	0.0003405	E
<input type="radio"/> GO:0006139	4	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	1532	0.2366	76	0.3878	0.0004581	E
<input type="radio"/> GO:0050794	4,3	regulation of cellular process	738	0.1140	45	0.2296	0.0010205	E
<input type="radio"/> GO:0022402	4,3	cell cycle process	439	0.0678	32	0.1633	0.0011217	E
<input type="radio"/> GO:0050789	3	regulation of biological process	761	0.1175	45	0.2296	0.0022909	E
<input type="radio"/> GO:0022403	5,4	cell cycle phase	353	0.0545	26	0.1327	0.0092880	E
<input type="radio"/> GO:0006350	5	transcription	567	0.0876	35	0.1786	0.0131994	E
<input type="radio"/> GO:0016070	5	RNA metabolic process	1058	0.1634	54	0.2755	0.0148882	E
<input type="radio"/> GO:0032774	6	RNA biosynthetic process	524	0.0809	32	0.1633	0.0370625	E
<input type="radio"/> GO:0016575	11,9	histone deacetylation	24	0.0037	6	0.0306	0.0408318	E
<input type="radio"/> GO:0000279	6,5	M phase	258	0.0398	20	0.1020	0.0462148	E
<input type="radio"/> GO:0019219	6,5	regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	440	0.0679	28	0.1429	0.0552789	E
<input type="radio"/> GO:0030952	6	establishment and/or maintenance of cytoskeleton polarity	9	0.0014	4	0.0204	0.0642557	E
<input type="radio"/> GO:0030950	8,7	establishment and/or maintenance of actin cytoskeleton polarity	9	0.0014	4	0.0204	0.0642557	E
<input type="radio"/> GO:0006476	8	protein amino acid deacetylation	26	0.0040	6	0.0306	0.0657905	E
<input type="radio"/> GO:0006351	7,6	transcription, DNA-dependent	522	0.0806	31	0.1582	0.0790085	E
<input type="radio"/> GO:0016071	6	mRNA metabolic process	210	0.0324	17	0.0867	0.0961658	E
<input type="radio"/> GO:0045449	7,6	regulation of transcription	386	0.0596	25	0.1276	0.1011766	E
<input type="radio"/> GO:0031323	5,4	regulation of cellular metabolic process	507	0.0783	30	0.1531	0.1077726	E
<input type="radio"/> GO:0019222	4,3	regulation of metabolic process	538	0.0831	31	0.1582	0.1319992	E
<input type="radio"/> GO:0016043	3	cellular component organization and biogenesis	2264	0.3496	91	0.4643	0.1522962	E
<input type="radio"/> GO:0001558	5,6,4,8,9	regulation of cell growth	11	0.0017	4	0.0204	0.1584437	E
<input type="radio"/> GO:0006259	5	DNA metabolic process	523	0.0808	30	0.1531	0.1790360	E

<input type="checkbox"/>	GO:0043283	4	biopolymer metabolic process	2230	0.3443	89	0.4541	0.2372700	E
<input type="checkbox"/>	GO:0040008	4,3	regulation of growth	13	0.0020	4	0.0204	0.3232053	E
<input type="checkbox"/>	GO:0031929	6	TOR signaling pathway	13	0.0020	4	0.0204	0.3232053	E
<input type="checkbox"/>	GO:0006355	8,7	regulation of transcription, DNA-dependent	359	0.0554	22	0.1122	0.4938358	E
<input type="checkbox"/>	GO:0007001	6	chromosome organization and biogenesis (sensu Eukaryota)	567	0.0876	30	0.1531	0.6195178	E
<input type="checkbox"/>	GO:0006366	8,7	transcription from RNA polymerase II promoter	343	0.0530	21	0.1071	0.6476277	E
<input type="checkbox"/>	GO:0051276	5	chromosome organization and biogenesis	572	0.0883	30	0.1531	0.7039842	E
<input type="checkbox"/>	GO:0051327	7,5,6	M phase of meiotic cell cycle	148	0.0229	12	0.0612	0.8485356	E
<input type="checkbox"/>	GO:0051321	4	meiotic cell cycle	148	0.0229	12	0.0612	0.8485356	E
<input type="checkbox"/>	GO:0007126	8,6,7,5	meiosis	148	0.0229	12	0.0612	0.8485356	E
<input type="checkbox"/>	GO:0000375	8	RNA splicing, via transesterification reactions	110	0.0170	10	0.0510	0.9265651	E
<input type="checkbox"/>	GO:0065008	3	regulation of biological quality	260	0.0401	17	0.0867	0.9655369	E
<input type="checkbox"/>	GO:0043148	10,9,6,5,4,13,11,8	mitotic spindle stabilization	2	0.0003	1	0.0051	1.0000000	E
<input type="checkbox"/>	GO:0006417	7,6,5	regulation of translation	47	0.0073	2	0.0102	1.0000000	E
<input type="checkbox"/>	GO:0007004	9	telomere maintenance via telomerase	17	0.0026	1	0.0051	1.0000000	E
<input type="checkbox"/>	GO:0009636	4	response to toxin	28	0.0043	1	0.0051	1.0000000	E
<input type="checkbox"/>	GO:0051017	9	actin filament bundle formation	5	0.0008	2	0.0102	1.0000000	E
<input type="checkbox"/>	GO:0000082	8,5,6,7,4	G1/S transition of mitotic cell cycle	52	0.0080	3	0.0153	1.0000000	E
<input type="checkbox"/>	GO:0006369	9,8	transcription termination from RNA polymerase II promoter	18	0.0028	1	0.0051	1.0000000	E
<input type="checkbox"/>	GO:0006887	8,6,5,7	exocytosis	44	0.0068	2	0.0102	1.0000000	E
<input type="checkbox"/>	GO:0007020	8	microtubule nucleation	23	0.0036	2	0.0102	1.0000000	E
<input type="checkbox"/>	GO:0016567	9	protein ubiquitination	66	0.0102	2	0.0102	1.0000000	E
<input type="checkbox"/>	GO:0007242	5	intracellular signaling cascade	137	0.0212	8	0.0408	1.0000000	E
<input type="checkbox"/>	GO:0031109	8	microtubule polymerization or depolymerization	16	0.0025	3	0.0153	1.0000000	E
<input type="checkbox"/>	GO:0032505	4,3	reproduction of a single-celled organism	194	0.0300	10	0.0510	1.0000000	E
<input type="checkbox"/>	GO:0019236	4	response to pheromone	94	0.0145	4	0.0204	1.0000000	E
<input type="checkbox"/>	GO:0000002	6	mitochondrial genome maintenance	31	0.0048	1	0.0051	1.0000000	E
<input type="checkbox"/>	GO:0006109	5,4	regulation of carbohydrate metabolic process	29	0.0045	2	0.0102	1.0000000	E
<input type="checkbox"/>	GO:0048610	3,4	reproductive cellular process	149	0.0230	6	0.0306	1.0000000	E
<input type="checkbox"/>	GO:0009991	4	response to extracellular stimulus	37	0.0057	3	0.0153	1.0000000	E
<input type="checkbox"/>	GO:0032989	4,5	cellular structure morphogenesis	248	0.0383	11	0.0561	1.0000000	E
<input type="checkbox"/>	GO:0000079	8,7,6	regulation of cyclin-dependent protein kinase activity	15	0.0023	1	0.0051	1.0000000	E
<input type="checkbox"/>	GO:0030468	8,5,9	establishment of cell polarity (sensu Fungi)	66	0.0102	4	0.0204	1.0000000	E
<input type="checkbox"/>	GO:0044265	5	cellular macromolecule catabolic process	314	0.0485	10	0.0510	1.0000000	E
<input type="checkbox"/>	GO:0000245	7,6,9,11	spliceosome assembly	19	0.0029	1	0.0051	1.0000000	E
<input type="checkbox"/>	GO:0007006	5,6	mitochondrial membrane organization and biogenesis	24	0.0037	1	0.0051	1.0000000	E
<input type="checkbox"/>	GO:0006974	4	response to DNA damage stimulus	234	0.0361	9	0.0459	1.0000000	E
<input type="checkbox"/>	GO:0045103	6	intermediate filament-based process	1	0.0002	1	0.0051	1.0000000	E
<input type="checkbox"/>	GO:0032185	6	septin cytoskeleton organization and biogenesis	9	0.0014	1	0.0051	1.0000000	E
<input type="checkbox"/>	GO:0051452	12,9,10	cellular pH reduction	24	0.0037	1	0.0051	1.0000000	E
<input type="checkbox"/>	GO:0046999	5,4	regulation of conjugation	30	0.0046	1	0.0051	1.0000000	E
<input type="checkbox"/>	GO:0031497	5,9	chromatin assembly	104	0.0161	6	0.0306	1.0000000	E

<input type="radio"/>	GO:0000749	5	response to pheromone during conjugation with cellular fusion	57	0.0088	2	0.0102	1.0000000	E
<input type="radio"/>	GO:0016584	6,10	nucleosome positioning	3	0.0005	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0051236	3,4,5	establishment of RNA localization	80	0.0124	3	0.0153	1.0000000	E
<input type="radio"/>	GO:0030641	10,8	cellular hydrogen ion homeostasis	25	0.0039	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0019751	5	polyol metabolic process	9	0.0014	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0006893	9,7,6,8	Golgi to plasma membrane transport	30	0.0046	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0000350	8,7,10,12	generation of catalytic spliceosome for second transesterification step	4	0.0006	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0040029	4	regulation of gene expression, epigenetic	100	0.0154	6	0.0306	1.0000000	E
<input type="radio"/>	GO:0045732	7,8,6	positive regulation of protein catabolic process	1	0.0002	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0030150	10,9,8,7	protein import into mitochondrial matrix	22	0.0034	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0006512	8	ubiquitin cycle	88	0.0136	3	0.0153	1.0000000	E
<input type="radio"/>	GO:0045739	9,8,7	positive regulation of DNA repair	1	0.0002	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0000128	3	flocculation	9	0.0014	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0006367	8,9,7	transcription initiation from RNA polymerase II promoter	44	0.0068	3	0.0153	1.0000000	E
<input type="radio"/>	GO:0051318	6,7,5	G1 phase	27	0.0042	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0051028	5,7,6,8	mRNA transport	66	0.0102	3	0.0153	1.0000000	E
<input type="radio"/>	GO:0015682	8,9,10	ferric iron transport	1	0.0002	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0006811	4,5	ion transport	115	0.0178	5	0.0255	1.0000000	E
<input type="radio"/>	GO:0006434	9,8,10,7	seryl-tRNA aminoacylation	2	0.0003	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0007114	5,4	cell budding	85	0.0131	4	0.0204	1.0000000	E
<input type="radio"/>	GO:0051641	4,3	cellular localization	642	0.0991	24	0.1224	1.0000000	E
<input type="radio"/>	GO:0045132	9,7,8,6,4	meiotic chromosome segregation	17	0.0026	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0016570	10,8	histone modification	91	0.0141	8	0.0408	1.0000000	E
<input type="radio"/>	GO:0006882	10,8	cellular zinc ion homeostasis	10	0.0015	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0007034	7,5,6	vacuolar transport	114	0.0176	4	0.0204	1.0000000	E
<input type="radio"/>	GO:0048308	5	organelle inheritance	40	0.0062	2	0.0102	1.0000000	E
<input type="radio"/>	GO:0030036	7	actin cytoskeleton organization and biogenesis	107	0.0165	7	0.0357	1.0000000	E
<input type="radio"/>	GO:0030466	11,7,8,12,10	chromatin silencing at silent mating-type cassette	30	0.0046	2	0.0102	1.0000000	E
<input type="radio"/>	GO:0019932	6	second-messenger-mediated signaling	32	0.0049	2	0.0102	1.0000000	E
<input type="radio"/>	GO:0007121	8,6,10,7,11,5	bipolar cellular bud site selection	32	0.0049	2	0.0102	1.0000000	E
<input type="radio"/>	GO:0009141	6	nucleoside triphosphate metabolic process	30	0.0046	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0051646	6,5	mitochondrion localization	27	0.0042	2	0.0102	1.0000000	E
<input type="radio"/>	GO:0007076	10,8,5,6,9,7,4	mitotic chromosome condensation	9	0.0014	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0016311	6	dephosphorylation	41	0.0063	2	0.0102	1.0000000	E
<input type="radio"/>	GO:0006334	6,7,10	nucleosome assembly	13	0.0020	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0006613	10,9,8,7,6	cotranslational protein targeting to membrane	23	0.0036	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0051704	2	multi-organism process	139	0.0215	7	0.0357	1.0000000	E
<input type="radio"/>	GO:0009057	4	macromolecule catabolic process	345	0.0533	12	0.0612	1.0000000	E
<input type="radio"/>	GO:0046034	5,9	ATP metabolic process	21	0.0032	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0006913	8,6,7	nucleocytoplasmic transport	129	0.0199	4	0.0204	1.0000000	E
<input type="radio"/>	GO:0000398	8,10	nuclear mRNA splicing, via spliceosome	102	0.0158	9	0.0459	1.0000000	E
<input type="radio"/>	GO:0009607	3	response to biotic stimulus	25	0.0039	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0050657	5,6	nucleic acid transport	80	0.0124	3	0.0153	1.0000000	E

<input type="checkbox"/>	GO:0016568	8	chromatin modification	223	0.0344	15	0.0765	1.0000000	E
<input type="checkbox"/>	GO:0042364	6	water-soluble vitamin biosynthetic process	46	0.0071	2	0.0102	1.0000000	E
<input type="checkbox"/>	GO:0000501	4	flocculation via cell wall protein-carbohydrate interaction	9	0.0014	1	0.0051	1.0000000	E
<input type="checkbox"/>	GO:0030154	4	cell differentiation	173	0.0267	9	0.0459	1.0000000	E
<input type="checkbox"/>	GO:0051292	8,7	nuclear pore complex assembly	2	0.0003	1	0.0051	1.0000000	E
<input type="checkbox"/>	GO:0042592	4	homeostatic process	134	0.0207	10	0.0510	1.0000000	E
<input type="checkbox"/>	GO:0043549	6	regulation of kinase activity	25	0.0039	1	0.0051	1.0000000	E
<input type="checkbox"/>	GO:0045935	7,6	positive regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	108	0.0167	7	0.0357	1.0000000	E
<input type="checkbox"/>	GO:0051865	10	protein autoubiquitination	2	0.0003	1	0.0051	1.0000000	E
<input type="checkbox"/>	GO:0000750	8,7,6	pheromone-dependent signal transduction during conjugation with cellular fusion	28	0.0043	1	0.0051	1.0000000	E
<input type="checkbox"/>	GO:0006891	8,6,5,7	intra-Golgi vesicle-mediated transport	21	0.0032	3	0.0153	1.0000000	E
<input type="checkbox"/>	GO:0048193	7,5,6	Golgi vesicle transport	166	0.0256	9	0.0459	1.0000000	E
<input type="checkbox"/>	GO:0000409	10,8,9,6	regulation of transcription by galactose	5	0.0008	1	0.0051	1.0000000	E
<input type="checkbox"/>	GO:0009228	7,8	thiamin biosynthetic process	19	0.0029	1	0.0051	1.0000000	E
<input type="checkbox"/>	GO:0006111	8,7,9,10,6	regulation of gluconeogenesis	13	0.0020	1	0.0051	1.0000000	E
<input type="checkbox"/>	GO:0048284	5	organelle fusion	22	0.0034	1	0.0051	1.0000000	E
<input type="checkbox"/>	GO:0015672	6,7	monovalent inorganic cation transport	32	0.0049	1	0.0051	1.0000000	E
<input type="checkbox"/>	GO:0000083	10,9,6,5,7,8,4	G1/S-specific transcription in mitotic cell cycle	12	0.0019	2	0.0102	1.0000000	E
<input type="checkbox"/>	GO:0042274	6,5	ribosomal small subunit biogenesis and assembly	26	0.0040	1	0.0051	1.0000000	E
<input type="checkbox"/>	GO:0045005	8,6	maintenance of fidelity during DNA-dependent DNA replication	25	0.0039	1	0.0051	1.0000000	E
<input type="checkbox"/>	GO:0051300	5,4,6	spindle pole body organization and biogenesis	16	0.0025	2	0.0102	1.0000000	E
<input type="checkbox"/>	GO:0006114	7,6	glycerol biosynthetic process	3	0.0005	1	0.0051	1.0000000	E
<input type="checkbox"/>	GO:0009653	4,3	anatomical structure morphogenesis	248	0.0383	11	0.0561	1.0000000	E
<input type="checkbox"/>	GO:0006457	6	protein folding	84	0.0130	6	0.0306	1.0000000	E
<input type="checkbox"/>	GO:0000819	7,4	sister chromatid segregation	62	0.0096	6	0.0306	1.0000000	E
<input type="checkbox"/>	GO:0006896	9,8,7,6	Golgi to vacuole transport	24	0.0037	2	0.0102	1.0000000	E
<input type="checkbox"/>	GO:0042158	7,5	lipoprotein biosynthetic process	48	0.0074	3	0.0153	1.0000000	E
<input type="checkbox"/>	GO:0006269	8,6,7	DNA replication, synthesis of RNA primer	2	0.0003	1	0.0051	1.0000000	E
<input type="checkbox"/>	GO:0030029	6	actin filament-based process	112	0.0173	8	0.0408	1.0000000	E
<input type="checkbox"/>	GO:0009205	8	purine ribonucleoside triphosphate metabolic process	23	0.0036	1	0.0051	1.0000000	E
<input type="checkbox"/>	GO:0006470	8,7	protein amino acid dephosphorylation	29	0.0045	2	0.0102	1.0000000	E
<input type="checkbox"/>	GO:0022607	4	cellular component assembly	471	0.0727	18	0.0918	1.0000000	E
<input type="checkbox"/>	GO:0048278	4,5,6	vesicle docking	14	0.0022	1	0.0051	1.0000000	E
<input type="checkbox"/>	GO:0031086	10,8,9	mRNA catabolic process, deadenylation-independent decay	2	0.0003	1	0.0051	1.0000000	E
<input type="checkbox"/>	GO:0006812	5,6	cation transport	97	0.0150	5	0.0255	1.0000000	E
<input type="checkbox"/>	GO:0031577	8,7	spindle checkpoint	24	0.0037	2	0.0102	1.0000000	E
<input type="checkbox"/>	GO:0048522	5,4	positive regulation of cellular process	124	0.0191	8	0.0408	1.0000000	E
<input type="checkbox"/>	GO:0042594	6,4	response to starvation	19	0.0029	1	0.0051	1.0000000	E
<input type="checkbox"/>	GO:0000393	7,6,9,11	spliceosomal conformational changes to generate catalytic conformation	9	0.0014	2	0.0102	1.0000000	E
<input type="checkbox"/>	GO:0009896	6,5	positive regulation of catabolic process	1	0.0002	1	0.0051	1.0000000	E
<input type="checkbox"/>	GO:0006271	8,7	DNA strand elongation during DNA replication	32	0.0049	3	0.0153	1.0000000	E

<input type="checkbox"/>	GO:0019722	7	calcium-mediated signaling	7	0.0011	1	0.0051	1.0000000	E
<input type="checkbox"/>	GO:0009266	4	response to temperature stimulus	28	0.0043	1	0.0051	1.0000000	E
<input type="checkbox"/>	GO:0043146	9,8,12,10,7	spindle stabilization	2	0.0003	1	0.0051	1.0000000	E
<input type="checkbox"/>	GO:0051083	8	cotranslational protein folding	5	0.0008	1	0.0051	1.0000000	E
<input type="checkbox"/>	GO:0051325	6,5	interphase	112	0.0173	6	0.0306	1.0000000	E
<input type="checkbox"/>	GO:0045722	7,9,8,10,6,11	positive regulation of gluconeogenesis	4	0.0006	1	0.0051	1.0000000	E
<input type="checkbox"/>	GO:0007584	6,4	response to nutrient	18	0.0028	2	0.0102	1.0000000	E
<input type="checkbox"/>	GO:0065004	6,5	protein-DNA complex assembly	74	0.0114	5	0.0255	1.0000000	E
<input type="checkbox"/>	GO:0032940	6,4,5	secretion by cell	250	0.0386	11	0.0561	1.0000000	E
<input type="checkbox"/>	GO:0000746	3	conjugation	118	0.0182	5	0.0255	1.0000000	E
<input type="checkbox"/>	GO:0000372	10	Group I intron splicing	7	0.0011	1	0.0051	1.0000000	E
<input type="checkbox"/>	GO:0000041	7,8	transition metal ion transport	46	0.0071	4	0.0204	1.0000000	E
<input type="checkbox"/>	GO:0000226	7	microtubule cytoskeleton organization and biogenesis	81	0.0125	4	0.0204	1.0000000	E
<input type="checkbox"/>	GO:0030705	7,5,6	cytoskeleton-dependent intracellular transport	17	0.0026	1	0.0051	1.0000000	E
<input type="checkbox"/>	GO:0000011	6	vacuole inheritance	14	0.0022	1	0.0051	1.0000000	E
<input type="checkbox"/>	GO:0032502	2	developmental process	436	0.0673	21	0.1071	1.0000000	E
<input type="checkbox"/>	GO:0033212	11,9	iron assimilation	8	0.0012	2	0.0102	1.0000000	E
<input type="checkbox"/>	GO:0000075	7,6	cell cycle checkpoint	53	0.0082	2	0.0102	1.0000000	E
<input type="checkbox"/>	GO:0009373	9,8,5	regulation of transcription by pheromones	10	0.0015	1	0.0051	1.0000000	E
<input type="checkbox"/>	GO:0019954	3	asexual reproduction	85	0.0131	4	0.0204	1.0000000	E
<input type="checkbox"/>	GO:0006888	8,6,5,7	ER to Golgi vesicle-mediated transport	81	0.0125	3	0.0153	1.0000000	E
<input type="checkbox"/>	GO:0048869	3	cellular developmental process	173	0.0267	9	0.0459	1.0000000	E
<input type="checkbox"/>	GO:0006506	10,9,8,7,11	GPI anchor biosynthetic process	26	0.0040	2	0.0102	1.0000000	E
<input type="checkbox"/>	GO:0051320	7,6,5	S phase	20	0.0031	1	0.0051	1.0000000	E
<input type="checkbox"/>	GO:0006904	9,5,7,6,8	vesicle docking during exocytosis	12	0.0019	1	0.0051	1.0000000	E
<input type="checkbox"/>	GO:0030472	6,5,10	mitotic spindle organization and biogenesis in nucleus	22	0.0034	2	0.0102	1.0000000	E
<input type="checkbox"/>	GO:0007323	9	peptide pheromone maturation	8	0.0012	2	0.0102	1.0000000	E
<input type="checkbox"/>	GO:0000080	7,8,6	G1 phase of mitotic cell cycle	27	0.0042	1	0.0051	1.0000000	E
<input type="checkbox"/>	GO:0015757	7,8	galactose transport	2	0.0003	1	0.0051	1.0000000	E
<input type="checkbox"/>	GO:0032506	5,3	cytokinetic process	88	0.0136	6	0.0306	1.0000000	E
<input type="checkbox"/>	GO:0000087	7,5,6	M phase of mitotic cell cycle	129	0.0199	9	0.0459	1.0000000	E
<input type="checkbox"/>	GO:0051246	5,4	regulation of protein metabolic process	72	0.0111	4	0.0204	1.0000000	E
<input type="checkbox"/>	GO:0000735	7,9,8	removal of nonhomologous ends	4	0.0006	1	0.0051	1.0000000	E
<input type="checkbox"/>	GO:0051338	5	regulation of transferase activity	26	0.0040	1	0.0051	1.0000000	E
<input type="checkbox"/>	GO:0008654	7,6,8	phospholipid biosynthetic process	58	0.0090	2	0.0102	1.0000000	E
<input type="checkbox"/>	GO:0046020	11,10,7	negative regulation of transcription from RNA polymerase II promoter by pheromones	6	0.0009	1	0.0051	1.0000000	E
<input type="checkbox"/>	GO:0000074	6,5	regulation of progression through cell cycle	167	0.0258	8	0.0408	1.0000000	E
<input type="checkbox"/>	GO:0048622	6,5	reproductive sporulation	108	0.0167	6	0.0306	1.0000000	E
<input type="checkbox"/>	GO:0007097	7,8,5,6	nuclear migration	20	0.0031	2	0.0102	1.0000000	E
<input type="checkbox"/>	GO:0045013	10,8,9,6	negative regulation of transcription by carbon catabolites	8	0.0012	1	0.0051	1.0000000	E
<input type="checkbox"/>	GO:0031087	11,9,10	deadenylation-independent decapping	2	0.0003	1	0.0051	1.0000000	E
<input type="checkbox"/>	GO:0051329	7,5,6	interphase of mitotic cell cycle	112	0.0173	6	0.0306	1.0000000	E
<input type="checkbox"/>	GO:0009110	5	vitamin biosynthetic process	46	0.0071	2	0.0102	1.0000000	E

<input type="checkbox"/>	GO:0009892	5,4	negative regulation of metabolic process	208	0.0321	9	0.0459	1.0000000	E
<input type="checkbox"/>	GO:0030473	8,9,6,7	nuclear migration, microtubule-mediated	15	0.0023	1	0.0051	1.0000000	E
<input type="checkbox"/>	GO:0007064	10,8,5,6,9,7,4	mitotic sister chromatid cohesion	22	0.0034	2	0.0102	1.0000000	E
<input type="checkbox"/>	GO:0030001	6,7	metal ion transport	62	0.0096	4	0.0204	1.0000000	E
<input type="checkbox"/>	GO:0006260	6	DNA replication	117	0.0181	6	0.0306	1.0000000	E
<input type="checkbox"/>	GO:0051054	8,7	positive regulation of DNA metabolic process	3	0.0005	1	0.0051	1.0000000	E
<input type="checkbox"/>	GO:0000741	6	karyogamy	17	0.0026	1	0.0051	1.0000000	E
<input type="checkbox"/>	GO:0006270	8,6	DNA replication initiation	33	0.0051	1	0.0051	1.0000000	E
<input type="checkbox"/>	GO:0000278	4	mitotic cell cycle	266	0.0411	17	0.0867	1.0000000	E
<input type="checkbox"/>	GO:0007096	8,10,9,7	regulation of exit from mitosis	24	0.0037	1	0.0051	1.0000000	E
<input type="checkbox"/>	GO:0009145	7,8	purine nucleoside triphosphate biosynthetic process	22	0.0034	1	0.0051	1.0000000	E
<input type="checkbox"/>	GO:0055069	9	zinc ion homeostasis	10	0.0015	1	0.0051	1.0000000	E
<input type="checkbox"/>	GO:0042724	7	thiamin and derivative biosynthetic process	20	0.0031	1	0.0051	1.0000000	E
<input type="checkbox"/>	GO:0006644	6,7	phospholipid metabolic process	97	0.0150	4	0.0204	1.0000000	E
<input type="checkbox"/>	GO:0031505	6	chitin- and beta-glucan-containing cell wall organization and biogenesis	44	0.0068	3	0.0153	1.0000000	E
<input type="checkbox"/>	GO:0045011	10	actin cable formation	5	0.0008	2	0.0102	1.0000000	E
<input type="checkbox"/>	GO:0030435	5	sporulation	123	0.0190	7	0.0357	1.0000000	E
<input type="checkbox"/>	GO:0031326	6,5	regulation of cellular biosynthetic process	67	0.0103	3	0.0153	1.0000000	E
<input type="checkbox"/>	GO:0015985	6,8,7,9	energy coupled proton transport, down electrochemical gradient	20	0.0031	1	0.0051	1.0000000	E
<input type="checkbox"/>	GO:0006323	6	DNA packaging	253	0.0391	16	0.0816	1.0000000	E
<input type="checkbox"/>	GO:0006403	4	RNA localization	90	0.0139	3	0.0153	1.0000000	E
<input type="checkbox"/>	GO:0000376	9	RNA splicing, via transesterification reactions with guanosine as nucleophile	7	0.0011	1	0.0051	1.0000000	E
<input type="checkbox"/>	GO:0051235	3,2	maintenance of localization	33	0.0051	1	0.0051	1.0000000	E
<input type="checkbox"/>	GO:0000282	7,9,5,6,10	cellular bud site selection	66	0.0102	4	0.0204	1.0000000	E
<input type="checkbox"/>	GO:0006282	8,7,6	regulation of DNA repair	2	0.0003	1	0.0051	1.0000000	E
<input type="checkbox"/>	GO:0022413	5,4	reproductive process in single-celled organism	149	0.0230	6	0.0306	1.0000000	E
<input type="checkbox"/>	GO:0032780	7	negative regulation of ATPase activity	1	0.0002	1	0.0051	1.0000000	E
<input type="checkbox"/>	GO:0006997	5	nuclear organization and biogenesis	57	0.0088	2	0.0102	1.0000000	E
<input type="checkbox"/>	GO:0005977	7,6,8	glycogen metabolic process	32	0.0049	1	0.0051	1.0000000	E
<input type="checkbox"/>	GO:0045835	8,10,9,7	negative regulation of meiosis	7	0.0011	2	0.0102	1.0000000	E
<input type="checkbox"/>	GO:0006357	9,8	regulation of transcription from RNA polymerase II promoter	221	0.0341	14	0.0714	1.0000000	E
<input type="checkbox"/>	GO:0045229	4	external encapsulating structure organization and biogenesis	200	0.0309	9	0.0459	1.0000000	E
<input type="checkbox"/>	GO:0045014	11,9,10,7	negative regulation of transcription by glucose	7	0.0011	1	0.0051	1.0000000	E
<input type="checkbox"/>	GO:0030846	10,9	transcription termination from Pol II promoter, RNA polymerase(A) coupled	10	0.0015	1	0.0051	1.0000000	E
<input type="checkbox"/>	GO:0007033	5	vacuole organization and biogenesis	67	0.0103	5	0.0255	1.0000000	E
<input type="checkbox"/>	GO:0043624	7,6	cellular protein complex disassembly	28	0.0043	1	0.0051	1.0000000	E
<input type="checkbox"/>	GO:0006406	11,9,6,8,10,7	mRNA export from nucleus	66	0.0102	3	0.0153	1.0000000	E
<input type="checkbox"/>	GO:0016044	4	membrane organization and biogenesis	188	0.0290	8	0.0408	1.0000000	E
<input type="checkbox"/>	GO:0051716	3	cellular response to stimulus	21	0.0032	1	0.0051	1.0000000	E
<input type="checkbox"/>	GO:0006379	8	mRNA cleavage	26	0.0040	1	0.0051	1.0000000	E
<input type="checkbox"/>	GO:0009893	5,4	positive regulation of metabolic process	116	0.0179	8	0.0408	1.0000000	E
<input type="checkbox"/>	GO:0046907	6,4,5	intracellular transport	545	0.0842	20	0.1020	1.0000000	E

<input type="radio"/>	GO:0006505	9,10	GPI anchor metabolic process	27	0.0042	2	0.0102	1.0000000	E
<input type="radio"/>	GO:0016126	6,7,8	sterol biosynthetic process	32	0.0049	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0016050	5	vesicle organization and biogenesis	16	0.0025	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0015890	5,6	nicotinamide mononucleotide transport	1	0.0002	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0007127	9,7,6,8,5	meiosis I	75	0.0116	5	0.0255	1.0000000	E
<input type="radio"/>	GO:0030005	9,7	cellular di-, tri-valent inorganic cation homeostasis	64	0.0099	6	0.0306	1.0000000	E
<input type="radio"/>	GO:0006826	7,8,9	iron ion transport	20	0.0031	3	0.0153	1.0000000	E
<input type="radio"/>	GO:0030543	5	2-micrometer plasmid partitioning	3	0.0005	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0031106	7	septin ring organization	9	0.0014	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0016458	5	gene silencing	95	0.0147	6	0.0306	1.0000000	E
<input type="radio"/>	GO:0043330	5,6	response to exogenous dsRNA	7	0.0011	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0051726	5,4	regulation of cell cycle	167	0.0258	8	0.0408	1.0000000	E
<input type="radio"/>	GO:0051252	7,6	regulation of RNA metabolic process	36	0.0056	3	0.0153	1.0000000	E
<input type="radio"/>	GO:0007052	5,4,9	mitotic spindle organization and biogenesis	44	0.0068	3	0.0153	1.0000000	E
<input type="radio"/>	GO:0051248	6,5	negative regulation of protein metabolic process	18	0.0028	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0051181	4,5	cofactor transport	10	0.0015	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0006353	8,7	transcription termination	20	0.0031	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0006308	5,6	DNA catabolic process	20	0.0031	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0006265	6	DNA topological change	7	0.0011	2	0.0102	1.0000000	E
<input type="radio"/>	GO:0006333	8	chromatin assembly or disassembly	119	0.0184	6	0.0306	1.0000000	E
<input type="radio"/>	GO:0007091	9,7,5,8,6,4	mitotic metaphase/anaphase transition	15	0.0023	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0018318	10,9,8	protein amino acid palmitoylation	8	0.0012	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0000723	8	telomere maintenance	274	0.0423	10	0.0510	1.0000000	E
<input type="radio"/>	GO:0033554	4	cellular response to stress	21	0.0032	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0015677	9,10	copper ion import	8	0.0012	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0000730	7,9,10,8,6	DNA recombinase assembly	5	0.0008	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0051656	6,3,5,4	establishment of organelle localization	29	0.0045	2	0.0102	1.0000000	E
<input type="radio"/>	GO:0009605	3	response to external stimulus	37	0.0057	3	0.0153	1.0000000	E
<input type="radio"/>	GO:0000288	10,8,9	mRNA catabolic process, deadenylation-dependent decay	24	0.0037	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0015986	8,10,7,9,11,5	ATP synthesis coupled proton transport	20	0.0031	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0022414	3,2	reproductive process	183	0.0283	8	0.0408	1.0000000	E
<input type="radio"/>	GO:0015791	4,5	polyol transport	6	0.0009	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0006261	7	DNA-dependent DNA replication	97	0.0150	5	0.0255	1.0000000	E
<input type="radio"/>	GO:0006418	8,7,9,6	tRNA aminoacylation for protein translation	32	0.0049	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0006338	9	chromatin remodeling	155	0.0239	8	0.0408	1.0000000	E
<input type="radio"/>	GO:0006825	8,9	copper ion transport	14	0.0022	2	0.0102	1.0000000	E
<input type="radio"/>	GO:0006113	5	fermentation	17	0.0026	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0009303	8,7	rRNA transcription	3	0.0005	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0030437	7,6	sporulation (sensu Fungi)	108	0.0167	6	0.0306	1.0000000	E
<input type="radio"/>	GO:0006325	7	establishment and/or maintenance of chromatin architecture	253	0.0391	16	0.0816	1.0000000	E
<input type="radio"/>	GO:0006497	8,7,6	protein amino acid lipidation	48	0.0074	3	0.0153	1.0000000	E
<input type="radio"/>	GO:0007534	6,8,7	gene conversion at mating-type locus	23	0.0036	2	0.0102	1.0000000	E
<input type="radio"/>	GO:0030003	8,6	cellular cation homeostasis	102	0.0158	8	0.0408	1.0000000	E
<input type="radio"/>	GO:0045324	8,6,7	late endosome to vacuole transport	21	0.0032	2	0.0102	1.0000000	E

<input type="radio"/>	GO:0031669	6,5	cellular response to nutrient levels	19	0.0029	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0045859	7	regulation of protein kinase activity	25	0.0039	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0006754	7,9,6,8,10	ATP biosynthetic process	20	0.0031	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0006312	7	mitotic recombination	45	0.0069	3	0.0153	1.0000000	E
<input type="radio"/>	GO:0000737	6,7	DNA catabolic process, endonucleolytic	15	0.0023	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0045185	5,4,3	maintenance of protein localization	30	0.0046	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0031325	6,5	positive regulation of cellular metabolic process	116	0.0179	8	0.0408	1.0000000	E
<input type="radio"/>	GO:0046173	6	polyol biosynthetic process	3	0.0005	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0048856	3	anatomical structure development	248	0.0383	11	0.0561	1.0000000	E
<input type="radio"/>	GO:0006006	7,8	glucose metabolic process	65	0.0100	2	0.0102	1.0000000	E
<input type="radio"/>	GO:0051707	3,4	response to other organism	7	0.0011	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0015793	5,6	glycerol transport	4	0.0006	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0000742	7,5	karyogamy during conjugation with cellular fusion	17	0.0026	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0022406	3	membrane docking	14	0.0022	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0007264	6	small GTPase mediated signal transduction	61	0.0094	2	0.0102	1.0000000	E
<input type="radio"/>	GO:0019935	7	cyclic-nucleotide-mediated signaling	9	0.0014	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0016578	11,9,10	histone deubiquitination	1	0.0002	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0045913	6,5	positive regulation of carbohydrate metabolic process	7	0.0011	2	0.0102	1.0000000	E
<input type="radio"/>	GO:0000910	4	cytokinesis	109	0.0168	6	0.0306	1.0000000	E
<input type="radio"/>	GO:0000724	8,7	double-strand break repair via homologous recombination	25	0.0039	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0050790	4	regulation of catalytic activity	45	0.0069	2	0.0102	1.0000000	E
<input type="radio"/>	GO:0000429	10,8,9,6	regulation of transcription from RNA polymerase II promoter by carbon catabolites	7	0.0011	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0015892	13,11,8,9,5,10,6	siderophore-iron transport	6	0.0009	2	0.0102	1.0000000	E
<input type="radio"/>	GO:0006094	8,9	gluconeogenesis	28	0.0043	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0006031	9,7,8,10	chitin biosynthetic process	15	0.0023	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0043039	7,8	tRNA aminoacylation	32	0.0049	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0006772	7	thiamin metabolic process	20	0.0031	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0031114	7,10,6,8	regulation of microtubule depolymerization	5	0.0008	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0006397	7	mRNA processing	157	0.0242	11	0.0561	1.0000000	E
<input type="radio"/>	GO:0045045	7,5,4,6	secretory pathway	243	0.0375	11	0.0561	1.0000000	E
<input type="radio"/>	GO:0007047	5	cell wall organization and biogenesis	200	0.0309	9	0.0459	1.0000000	E
<input type="radio"/>	GO:0045892	9,8	negative regulation of transcription, DNA-dependent	156	0.0241	8	0.0408	1.0000000	E
<input type="radio"/>	GO:0009302	8,7	snoRNA transcription	1	0.0002	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0016049	5,3,7,8	cell growth	102	0.0158	7	0.0357	1.0000000	E
<input type="radio"/>	GO:0055082	6,4	cellular chemical homeostasis	115	0.0178	9	0.0459	1.0000000	E
<input type="radio"/>	GO:0045039	10,9,7,8	protein import into mitochondrial inner membrane	8	0.0012	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0043687	7	post-translational protein modification	388	0.0599	17	0.0867	1.0000000	E
<input type="radio"/>	GO:0044272	5	sulfur compound biosynthetic process	22	0.0034	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0031110	6,9,5	regulation of microtubule polymerization or depolymerization	15	0.0023	3	0.0153	1.0000000	E
<input type="radio"/>	GO:0000433	12,10,11,8	negative regulation of transcription from RNA polymerase II promoter by glucose	7	0.0011	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0000377	9	RNA splicing, via transesterification reactions with bulged adenosine as nucleophile	103	0.0159	9	0.0459	1.0000000	E

<input type="radio"/>	GO:0030467	7,4,8	establishment and/or maintenance of cell polarity (sensu Fungi)	66	0.0102	4	0.0204	1.0000000	E
<input type="radio"/>	GO:0042144	6	vacuole fusion, non-autophagic	28	0.0043	2	0.0102	1.0000000	E
<input type="radio"/>	GO:0045786	6,7,5	negative regulation of progression through cell cycle	13	0.0020	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0019933	8	cAMP-mediated signaling	9	0.0014	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0042710	3	biofilm formation	5	0.0008	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0051234	2,3	establishment of localization	1004	0.1550	37	0.1888	1.0000000	E
<input type="radio"/>	GO:0048518	4	positive regulation of biological process	124	0.0191	8	0.0408	1.0000000	E
<input type="radio"/>	GO:0046474	8,7,9	glycerophospholipid biosynthetic process	39	0.0060	2	0.0102	1.0000000	E
<input type="radio"/>	GO:0006767	5	water-soluble vitamin metabolic process	89	0.0137	3	0.0153	1.0000000	E
<input type="radio"/>	GO:0019953	3	sexual reproduction	118	0.0182	5	0.0255	1.0000000	E
<input type="radio"/>	GO:0042816	6	vitamin B6 metabolic process	8	0.0012	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0000747	4	conjugation with cellular fusion	118	0.0182	5	0.0255	1.0000000	E
<input type="radio"/>	GO:0000086	8,5,6,7,4	G2/M transition of mitotic cell cycle	35	0.0054	3	0.0153	1.0000000	E
<input type="radio"/>	GO:0006273	9,8	lagging strand elongation	18	0.0028	2	0.0102	1.0000000	E
<input type="radio"/>	GO:0000054	10,11,6,8,9	ribosome export from nucleus	28	0.0043	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0000731	7,6	DNA synthesis during DNA repair	4	0.0006	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0031111	7,10,6	negative regulation of microtubule polymerization or depolymerization	5	0.0008	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0019319	7,8	hexose biosynthetic process	30	0.0046	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0008645	6,7	hexose transport	26	0.0040	3	0.0153	1.0000000	E
<input type="radio"/>	GO:0043488	9,8,7	regulation of mRNA stability	30	0.0046	3	0.0153	1.0000000	E
<input type="radio"/>	GO:0043331	4	response to dsRNA	7	0.0011	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0000018	8,7	regulation of DNA recombination	18	0.0028	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0007154	3	cell communication	240	0.0371	12	0.0612	1.0000000	E
<input type="radio"/>	GO:0055080	7	cation homeostasis	102	0.0158	8	0.0408	1.0000000	E
<input type="radio"/>	GO:0000920	6,4	cell separation during cytokinesis	13	0.0020	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0006766	4	vitamin metabolic process	89	0.0137	3	0.0153	1.0000000	E
<input type="radio"/>	GO:0048311	7,6	mitochondrion distribution	26	0.0040	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0007088	7,9,8,6	regulation of mitosis	55	0.0085	3	0.0153	1.0000000	E
<input type="radio"/>	GO:0006979	4	response to oxidative stress	71	0.0110	3	0.0153	1.0000000	E
<input type="radio"/>	GO:0007530	4,5	sex determination	35	0.0054	2	0.0102	1.0000000	E
<input type="radio"/>	GO:0045944	10,9	positive regulation of transcription from RNA polymerase II promoter	76	0.0117	4	0.0204	1.0000000	E
<input type="radio"/>	GO:0000710	11,9,8,6,5,10,7,4	meiotic mismatch repair	7	0.0011	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0045821	7,11,12,6	positive regulation of glycolysis	3	0.0005	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0040007	2	growth	141	0.0218	7	0.0357	1.0000000	E
<input type="radio"/>	GO:0001403	6,4,8,9	invasive growth (sensu Saccharomyces)	42	0.0065	2	0.0102	1.0000000	E
<input type="radio"/>	GO:0000070	9,7,5,8,6,4	mitotic sister chromatid segregation	59	0.0091	6	0.0306	1.0000000	E
<input type="radio"/>	GO:0043161	10,9,11	proteasomal ubiquitin-dependent protein catabolic process	63	0.0097	3	0.0153	1.0000000	E
<input type="radio"/>	GO:0051651	5,4,3	maintenance of cellular localization	29	0.0045	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0009267	7,6,5	cellular response to starvation	19	0.0029	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0003006	3,4	reproductive developmental process	35	0.0054	2	0.0102	1.0000000	E
<input type="radio"/>	GO:0007533	5,7,6	mating type switching	29	0.0045	2	0.0102	1.0000000	E
<input type="radio"/>	GO:0050658	4,6,5,7	RNA transport	80	0.0124	3	0.0153	1.0000000	E
<input type="radio"/>	GO:0015674	6,7	di-, tri-valent inorganic cation transport	34	0.0053	3	0.0153	1.0000000	E
<input type="radio"/>	GO:0009408	5,4	response to heat	23	0.0036	1	0.0051	1.0000000	E

<input type="checkbox"/>	GO:0040020	7,9,8,6	regulation of meiosis	22	0.0034	2	0.0102	1.0000000	E
<input type="checkbox"/>	GO:0006996	4	organelle organization and biogenesis	1388	0.2143	58	0.2959	1.0000000	E
<input type="checkbox"/>	GO:0006042	7,8	glucosamine biosynthetic process	17	0.0026	1	0.0051	1.0000000	E
<input type="checkbox"/>	GO:0051336	5	regulation of hydrolase activity	10	0.0015	1	0.0051	1.0000000	E
<input type="checkbox"/>	GO:0007039	7,8	vacuolar protein catabolic process	11	0.0017	1	0.0051	1.0000000	E
<input type="checkbox"/>	GO:0030010	7,4,8	establishment of cell polarity	103	0.0159	4	0.0204	1.0000000	E
<input type="checkbox"/>	GO:0031145	11,10,12	anaphase-promoting complex-dependent proteasomal ubiquitin-dependent protein catabolic process	15	0.0023	1	0.0051	1.0000000	E
<input type="checkbox"/>	GO:0043241	6,5	protein complex disassembly	28	0.0043	1	0.0051	1.0000000	E
<input type="checkbox"/>	GO:0007105	6,4	cytokinesis, site selection	66	0.0102	4	0.0204	1.0000000	E
<input type="checkbox"/>	GO:0000437	11,9,10,7	negative regulation of transcription from RNA polymerase II promoter by carbon catabolites	7	0.0011	1	0.0051	1.0000000	E
<input type="checkbox"/>	GO:0006342	10,6,7,11,9	chromatin silencing	95	0.0147	6	0.0306	1.0000000	E
<input type="checkbox"/>	GO:0007531	4,6,5	mating type determination	35	0.0054	2	0.0102	1.0000000	E
<input type="checkbox"/>	GO:0065009	3	regulation of a molecular function	46	0.0071	2	0.0102	1.0000000	E
<input type="checkbox"/>	GO:0006950	3	response to stress	488	0.0754	19	0.0969	1.0000000	E
<input type="checkbox"/>	GO:0065002	8,6,7	intracellular protein transport across a membrane	11	0.0017	1	0.0051	1.0000000	E
<input type="checkbox"/>	GO:0000114	10,8,9,5,7,4	G1-specific transcription in mitotic cell cycle	15	0.0023	1	0.0051	1.0000000	E
<input type="checkbox"/>	GO:0000184	8	mRNA catabolic process, nonsense-mediated decay	9	0.0014	2	0.0102	1.0000000	E
<input type="checkbox"/>	GO:0032984	5	macromolecular complex disassembly	32	0.0049	1	0.0051	1.0000000	E
<input type="checkbox"/>	GO:0043412	5	biopolymer modification	664	0.1025	23	0.1173	1.0000000	E
<input type="checkbox"/>	GO:0044238	3	primary metabolic process	3247	0.5014	109	0.5561	1.0000000	E
<input type="checkbox"/>	GO:0006354	8,6,7	RNA elongation	59	0.0091	2	0.0102	1.0000000	E
<input type="checkbox"/>	GO:0032005	7,6	signal transduction during conjugation with cellular fusion	28	0.0043	1	0.0051	1.0000000	E
<input type="checkbox"/>	GO:0007120	8,6,10,7,11,5	axial cellular bud site selection	22	0.0034	1	0.0051	1.0000000	E
<input type="checkbox"/>	GO:0030474	5,6,4,7	spindle pole body duplication	14	0.0022	2	0.0102	1.0000000	E
<input type="checkbox"/>	GO:0045990	9,7,8,5	regulation of transcription by carbon catabolites	14	0.0022	2	0.0102	1.0000000	E
<input type="checkbox"/>	GO:0006110	6,10,11,5	regulation of glycolysis	6	0.0009	1	0.0051	1.0000000	E
<input type="checkbox"/>	GO:0045941	8,7	positive regulation of transcription	101	0.0156	7	0.0357	1.0000000	E
<input type="checkbox"/>	GO:0042147	8,6,7	retrograde transport, endosome to Golgi	17	0.0026	1	0.0051	1.0000000	E
<input type="checkbox"/>	GO:0006402	7	mRNA catabolic process	60	0.0093	5	0.0255	1.0000000	E
<input type="checkbox"/>	GO:0006885	7	regulation of pH	29	0.0045	2	0.0102	1.0000000	E
<input type="checkbox"/>	GO:0010035	4	response to inorganic substance	24	0.0037	1	0.0051	1.0000000	E
<input type="checkbox"/>	GO:0007026	8,7,11,9,6	negative regulation of microtubule depolymerization	5	0.0008	1	0.0051	1.0000000	E
<input type="checkbox"/>	GO:0048468	3,5	cell development	52	0.0080	2	0.0102	1.0000000	E
<input type="checkbox"/>	GO:0007035	13,10,6,11	vacuolar acidification	24	0.0037	1	0.0051	1.0000000	E
<input type="checkbox"/>	GO:0050896	2	response to stimulus	763	0.1178	27	0.1378	1.0000000	E
<input type="checkbox"/>	GO:0000917	6,4	barrier septum formation	3	0.0005	1	0.0051	1.0000000	E
<input type="checkbox"/>	GO:0016051	5	carbohydrate biosynthetic process	77	0.0119	3	0.0153	1.0000000	E
<input type="checkbox"/>	GO:0006096	9,10	glycolysis	24	0.0037	1	0.0051	1.0000000	E
<input type="checkbox"/>	GO:0045851	8	pH reduction	24	0.0037	1	0.0051	1.0000000	E
<input type="checkbox"/>	GO:0000084	8,7,6	S phase of mitotic cell cycle	18	0.0028	1	0.0051	1.0000000	E
<input type="checkbox"/>	GO:0031137	6,5	regulation of conjugation with cellular fusion	30	0.0046	1	0.0051	1.0000000	E

<input type="radio"/>	GO:0007103	6,7,5,8	spindle pole body duplication in nuclear envelope	13	0.0020	2	0.0102	1.0000000	E
<input type="radio"/>	GO:0009250	7,8	glucan biosynthetic process	25	0.0039	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0006999	6	nuclear pore organization and biogenesis	29	0.0045	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0007062	7,4	sister chromatid cohesion	31	0.0048	3	0.0153	1.0000000	E
<input type="radio"/>	GO:0031146	11,10,12	SCF-dependent proteasomal ubiquitin-dependent protein catabolic process	8	0.0012	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0006890	8,6,5,7	retrograde vesicle-mediated transport, Golgi to ER	24	0.0037	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0000902	5,6	cell morphogenesis	248	0.0383	11	0.0561	1.0000000	E
<input type="radio"/>	GO:0031578	9,11,10,8	mitotic cell cycle spindle orientation checkpoint	4	0.0006	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0006892	8,6,5,7	post-Golgi vesicle-mediated transport	69	0.0107	3	0.0153	1.0000000	E
<input type="radio"/>	GO:0006650	7,8	glycerophospholipid metabolic process	60	0.0093	2	0.0102	1.0000000	E
<input type="radio"/>	GO:0009272	7	chitin- and beta-glucan-containing cell wall biogenesis	33	0.0051	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0046685	5	response to arsenic	9	0.0014	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0031163	5	metallo-sulfur cluster assembly	11	0.0017	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0000301	9,7,6,8	retrograde transport, vesicle recycling within Golgi	4	0.0006	2	0.0102	1.0000000	E
<input type="radio"/>	GO:0043543	7	protein amino acid acylation	62	0.0096	2	0.0102	1.0000000	E
<input type="radio"/>	GO:0043462	6	regulation of ATPase activity	1	0.0002	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0043487	8,7	regulation of RNA stability	30	0.0046	3	0.0153	1.0000000	E
<input type="radio"/>	GO:0045047	9,8,7,6,5	protein targeting to ER	33	0.0051	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0016485	8	protein processing	38	0.0059	2	0.0102	1.0000000	E
<input type="radio"/>	GO:0009894	5,4	regulation of catabolic process	15	0.0023	2	0.0102	1.0000000	E
<input type="radio"/>	GO:0051169	7,5,6	nuclear transport	129	0.0199	4	0.0204	1.0000000	E
<input type="radio"/>	GO:0016192	4,5	vesicle-mediated transport	328	0.0506	16	0.0816	1.0000000	E
<input type="radio"/>	GO:0007059	3	chromosome segregation	119	0.0184	8	0.0408	1.0000000	E
<input type="radio"/>	GO:0044237	3	cellular metabolic process	3403	0.5255	113	0.5765	1.0000000	E
<input type="radio"/>	GO:0006467	7,8	protein thiol-disulfide exchange	2	0.0003	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0009452	7	RNA capping	4	0.0006	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0006944	5	membrane fusion	59	0.0091	3	0.0153	1.0000000	E
<input type="radio"/>	GO:0009206	8,9	purine ribonucleoside triphosphate biosynthetic process	22	0.0034	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0006283	8,7	transcription-coupled nucleotide-excision repair	9	0.0014	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0000183	11,7,8,12,10	chromatin silencing at rDNA	18	0.0028	2	0.0102	1.0000000	E
<input type="radio"/>	GO:0000921	8,7	septin ring assembly	9	0.0014	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0000019	9,8	regulation of mitotic recombination	8	0.0012	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0050801	6	ion homeostasis	119	0.0184	10	0.0510	1.0000000	E
<input type="radio"/>	GO:0043285	5	biopolymer catabolic process	277	0.0428	11	0.0561	1.0000000	E
<input type="radio"/>	GO:0051052	7,6	regulation of DNA metabolic process	41	0.0063	2	0.0102	1.0000000	E
<input type="radio"/>	GO:0009615	4,5	response to virus	7	0.0011	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0007109	7,6,5,4	cytokinesis, completion of separation	11	0.0017	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0015992	5,7,6,8	proton transport	24	0.0037	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0008152	2	metabolic process	3516	0.5429	114	0.5816	1.0000000	E
<input type="radio"/>	GO:0006368	9,7,8	RNA elongation from RNA polymerase II promoter	53	0.0082	2	0.0102	1.0000000	E
<input type="radio"/>	GO:0046015	10,8,9,6	regulation of transcription by glucose	8	0.0012	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0015891	4,5	siderophore transport	9	0.0014	2	0.0102	1.0000000	E
<input type="radio"/>	GO:0046010	10,8,6	regulation of transcription from RNA	10	0.0015	1	0.0051	1.0000000	E

<input type="radio"/>	GO:0048019	10,9,0	polymerase II promoter by pheromones	10	0.0015	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0008105	5	asymmetric protein localization	1	0.0002	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0006810	3,4	transport	981	0.1515	36	0.1837	1.0000000	E
<input type="radio"/>	GO:0051128	5,4	regulation of cellular component organization and biogenesis	30	0.0046	3	0.0153	1.0000000	E
<input type="radio"/>	GO:0006066	4	alcohol metabolic process	163	0.0252	6	0.0306	1.0000000	E
<input type="radio"/>	GO:0006643	5,6	membrane lipid metabolic process	125	0.0193	4	0.0204	1.0000000	E
<input type="radio"/>	GO:0042244	5,6	spore wall assembly	42	0.0065	3	0.0153	1.0000000	E
<input type="radio"/>	GO:0016226	6	iron-sulfur cluster assembly	11	0.0017	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0048523	5,4	negative regulation of cellular process	239	0.0369	10	0.0510	1.0000000	E
<input type="radio"/>	GO:0006310	6	DNA recombination	122	0.0188	7	0.0357	1.0000000	E
<input type="radio"/>	GO:0006012	7,8	galactose metabolic process	10	0.0015	2	0.0102	1.0000000	E
<input type="radio"/>	GO:0045934	7,6	negative regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	179	0.0276	8	0.0408	1.0000000	E
<input type="radio"/>	GO:0031668	5,4	cellular response to extracellular stimulus	19	0.0029	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0007067	8,6,7,5	mitosis	127	0.0196	9	0.0459	1.0000000	E
<input type="radio"/>	GO:0016197	7,5,6	endosome transport	49	0.0076	3	0.0153	1.0000000	E
<input type="radio"/>	GO:0019674	9,8	NAD metabolic process	21	0.0032	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0016569	9	covalent chromatin modification	91	0.0141	8	0.0408	1.0000000	E
<input type="radio"/>	GO:0007015	8	actin filament organization	61	0.0094	3	0.0153	1.0000000	E
<input type="radio"/>	GO:0008380	7	RNA splicing	132	0.0204	10	0.0510	1.0000000	E
<input type="radio"/>	GO:0000725	7,6	recombinational repair	29	0.0045	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0051649	5,3,4	establishment of cellular localization	606	0.0936	22	0.1122	1.0000000	E
<input type="radio"/>	GO:0022616	6	DNA strand elongation	32	0.0049	3	0.0153	1.0000000	E
<input type="radio"/>	GO:0031023	5	microtubule organizing center organization and biogenesis	16	0.0025	2	0.0102	1.0000000	E
<input type="radio"/>	GO:0046903	3,4	secretion	250	0.0386	11	0.0561	1.0000000	E
<input type="radio"/>	GO:0042546	6	cell wall biogenesis	33	0.0051	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0006311	10,8,7,5,9,6,4	meiotic gene conversion	22	0.0034	2	0.0102	1.0000000	E
<input type="radio"/>	GO:0006352	7,8,6	transcription initiation	55	0.0085	3	0.0153	1.0000000	E
<input type="radio"/>	GO:0051453	11,8,9	regulation of cellular pH	25	0.0039	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0031507	6,10	heterochromatin formation	95	0.0147	6	0.0306	1.0000000	E
<input type="radio"/>	GO:0007093	8,10,9,7	mitotic cell cycle checkpoint	27	0.0042	2	0.0102	1.0000000	E
<input type="radio"/>	GO:0009142	6,7	nucleoside triphosphate biosynthetic process	27	0.0042	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0042930	5,6	enterobactin transport	1	0.0002	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0000411	11,9,10,7	positive regulation of transcription by galactose	5	0.0008	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0015931	4,5	nucleobase, nucleoside, nucleotide and nucleic acid transport	90	0.0139	3	0.0153	1.0000000	E
<input type="radio"/>	GO:0000349	8,7,10,12	generation of catalytic spliceosome for first transesterification step	4	0.0006	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0031930	6	mitochondrial signaling pathway	6	0.0009	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0045991	10,8,9,6	positive regulation of transcription by carbon catabolites	5	0.0008	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0005976	5	polysaccharide metabolic process	65	0.0100	2	0.0102	1.0000000	E
<input type="radio"/>	GO:0030261	6	chromosome condensation	11	0.0017	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0007017	6	microtubule-based process	101	0.0156	6	0.0306	1.0000000	E
<input type="radio"/>	GO:0055066	8	di-, tri-valent inorganic cation homeostasis	64	0.0099	6	0.0306	1.0000000	E
<input type="radio"/>	GO:0048878	5	chemical homeostasis	121	0.0187	10	0.0510	1.0000000	E
<input type="radio"/>	GO:0046349	6,7	amino sugar biosynthetic process	17	0.0026	1	0.0051	1.0000000	E

<input type="radio"/>	GO:0007163	6,3,7	establishment and/or maintenance of cell polarity	115	0.0178	4	0.0204	1.0000000	E
<input type="radio"/>	GO:0030242	4,6	peroxisome degradation	3	0.0005	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0000096	6,7,5	sulfur amino acid metabolic process	33	0.0051	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0030541	4	plasmid partitioning	3	0.0005	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0045893	9,8	positive regulation of transcription, DNA-dependent	95	0.0147	5	0.0255	1.0000000	E
<input type="radio"/>	GO:0030447	3	filamentous growth	94	0.0145	3	0.0153	1.0000000	E
<input type="radio"/>	GO:0006030	8,6,7,9	chitin metabolic process	17	0.0026	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0051177	10,8,7,5,9,6,4	meiotic sister chromatid cohesion	2	0.0003	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0006071	6	glycerol metabolic process	9	0.0014	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0046364	6,7	monosaccharide biosynthetic process	30	0.0046	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0007051	8	spindle organization and biogenesis	47	0.0073	3	0.0153	1.0000000	E
<input type="radio"/>	GO:0042723	6	thiamin and derivative metabolic process	22	0.0034	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0006040	5,6	amino sugar metabolic process	19	0.0029	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0005996	5,6	monosaccharide metabolic process	92	0.0142	4	0.0204	1.0000000	E
<input type="radio"/>	GO:0006401	6	RNA catabolic process	74	0.0114	5	0.0255	1.0000000	E
<input type="radio"/>	GO:0042221	3	response to chemical stimulus	382	0.0590	12	0.0612	1.0000000	E
<input type="radio"/>	GO:0051301	3	cell division	246	0.0380	12	0.0612	1.0000000	E
<input type="radio"/>	GO:0051129	6,5	negative regulation of cell organization and biogenesis	7	0.0011	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0042157	6	lipoprotein metabolic process	48	0.0074	3	0.0153	1.0000000	E
<input type="radio"/>	GO:0010324	5	membrane invagination	96	0.0148	4	0.0204	1.0000000	E
<input type="radio"/>	GO:0008643	4,5	carbohydrate transport	38	0.0059	3	0.0153	1.0000000	E
<input type="radio"/>	GO:0006768	5,7,6	biotin metabolic process	7	0.0011	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0007124	6,4,8,9	pseudohyphal growth	61	0.0094	2	0.0102	1.0000000	E
<input type="radio"/>	GO:0006298	7,9,6	mismatch repair	25	0.0039	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0006041	6,7	glucosamine metabolic process	19	0.0029	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0040023	6,7,4,5	establishment of nucleus localization	20	0.0031	2	0.0102	1.0000000	E
<input type="radio"/>	GO:0006281	6,5	DNA repair	193	0.0298	7	0.0357	1.0000000	E
<input type="radio"/>	GO:0030476	8,6,7	spore wall assembly (sensu Fungi)	42	0.0065	3	0.0153	1.0000000	E
<input type="radio"/>	GO:0000271	6,7	polysaccharide biosynthetic process	41	0.0063	2	0.0102	1.0000000	E
<input type="radio"/>	GO:0015749	5,6	monosaccharide transport	26	0.0040	3	0.0153	1.0000000	E
<input type="radio"/>	GO:0043170	3	macromolecule metabolic process	2841	0.4387	101	0.5153	1.0000000	E
<input type="radio"/>	GO:0019725	5,3	cellular homeostasis	128	0.0198	9	0.0459	1.0000000	E
<input type="radio"/>	GO:0007010	5	cytoskeleton organization and biogenesis	227	0.0351	14	0.0714	1.0000000	E
<input type="radio"/>	GO:0008614	7	pyridoxine metabolic process	8	0.0012	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0006818	4,5	hydrogen transport	24	0.0037	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0031324	6,5	negative regulation of cellular metabolic process	198	0.0306	8	0.0408	1.0000000	E
<input type="radio"/>	GO:0009889	5,4	regulation of biosynthetic process	69	0.0107	3	0.0153	1.0000000	E
<input type="radio"/>	GO:0000707	11,9,8,5,6,10,7,4	meiotic DNA recombinase assembly	5	0.0008	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0000430	11,9,10,7	regulation of transcription from RNA polymerase II promoter by glucose	7	0.0011	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0051168	9,7,8	nuclear export	102	0.0158	4	0.0204	1.0000000	E
<input type="radio"/>	GO:0031667	5	response to nutrient levels	37	0.0057	3	0.0153	1.0000000	E
<input type="radio"/>	GO:0045053	7,6,5,4	protein retention in Golgi	20	0.0031	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0051647	6,5	nucleus localization	20	0.0031	2	0.0102	1.0000000	E
<input type="radio"/>	GO:0018345	9,8,7	protein palmitoylation	8	0.0012	1	0.0051	1.0000000	E

<input type="radio"/>	GO:0000209	10	protein polyubiquitination	20	0.0031	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0030847	10,9	transcription termination from Pol II promoter, RNA polymerase(A)-independent	9	0.0014	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0007131	10,8,7,5,9,6,4	meiotic recombination	55	0.0085	4	0.0204	1.0000000	E
<input type="radio"/>	GO:0033214	12,10	iron assimilation by chelation and transport	6	0.0009	2	0.0102	1.0000000	E
<input type="radio"/>	GO:0048519	4	negative regulation of biological process	242	0.0374	10	0.0510	1.0000000	E
<input type="radio"/>	GO:0051247	6,5	positive regulation of protein metabolic process	5	0.0008	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0007165	4	signal transduction	209	0.0323	9	0.0459	1.0000000	E
<input type="radio"/>	GO:0000751	8,9,7,6	cell cycle arrest in response to pheromone	8	0.0012	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0005978	8,7,9	glycogen biosynthetic process	15	0.0023	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0051640	5,4	organelle localization	56	0.0086	4	0.0204	1.0000000	E
<input type="radio"/>	GO:0009237	5	siderophore metabolic process	1	0.0002	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0051754	11,9,8,6,5,10,7,4	meiotic sister chromatid cohesion, centromeric	1	0.0002	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0030384	8,9	phosphoinositide metabolic process	43	0.0066	2	0.0102	1.0000000	E
<input type="radio"/>	GO:0006897	6,5	endocytosis	86	0.0133	4	0.0204	1.0000000	E
<input type="radio"/>	GO:0006616	9,12,11,7,10,8	SRP-dependent cotranslational protein targeting to membrane, translocation	10	0.0015	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0009102	6,7,8	biotin biosynthetic process	7	0.0011	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0006396	6	RNA processing	491	0.0758	18	0.0918	1.0000000	E
<input type="radio"/>	GO:0045814	5	negative regulation of gene expression, epigenetic	95	0.0147	6	0.0306	1.0000000	E
<input type="radio"/>	GO:0006873	7,5	cellular ion homeostasis	115	0.0178	9	0.0459	1.0000000	E
<input type="radio"/>	GO:0009199	7	ribonucleoside triphosphate metabolic process	25	0.0039	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0007094	9,11,10,8	mitotic cell cycle spindle assembly checkpoint	20	0.0031	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0051261	6	protein depolymerization	10	0.0015	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0043255	7,6,5	regulation of carbohydrate biosynthetic process	19	0.0029	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0006464	6	protein modification process	520	0.0803	21	0.1071	1.0000000	E
<input type="radio"/>	GO:0000122	10,9	negative regulation of transcription from RNA polymerase II promoter	63	0.0097	3	0.0153	1.0000000	E
<input type="radio"/>	GO:0042787	10,9,11	protein ubiquitination during ubiquitin-dependent protein catabolic process	14	0.0022	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0006302	7,6	double-strand break repair	57	0.0088	2	0.0102	1.0000000	E
<input type="radio"/>	GO:0007019	9,7	microtubule depolymerization	6	0.0009	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0009144	7	purine nucleoside triphosphate metabolic process	23	0.0036	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0045996	10,9,6	negative regulation of transcription by pheromones	6	0.0009	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0051179	2	localization	1051	0.1623	40	0.2041	1.0000000	E
<input type="radio"/>	GO:0015685	14,12,9,10,6,11,7	ferric-enterobactin transport	1	0.0002	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0006044	7,8	N-acetylglucosamine metabolic process	19	0.0029	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0006614	11,10,9,8,7	SRP-dependent cotranslational protein targeting to membrane	20	0.0031	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0007018	8,7,6	microtubule-based movement	15	0.0023	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0000003	2	reproduction	323	0.0499	16	0.0816	1.0000000	E
<input type="radio"/>	GO:0016481	8,7	negative regulation of transcription	162	0.0250	8	0.0408	1.0000000	E
<input type="radio"/>	GO:0042176	6,7,5	regulation of protein catabolic process	5	0.0008	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0006276	3	plasmid maintenance	11	0.0017	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0030071	8,10,6,9,7,5	regulation of mitotic metaphase/anaphase transition	4	0.0006	1	0.0051	1.0000000	E

<input type="radio"/>	GO:0009201	7,8	ribonucleoside triphosphate biosynthetic process	24	0.0037	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0046165	5	alcohol biosynthetic process	35	0.0054	2	0.0102	1.0000000	E
<input type="radio"/>	GO:0006405	10,8,5,7,9,6	RNA export from nucleus	79	0.0122	3	0.0153	1.0000000	E
<input type="radio"/>	GO:0007050	7,8,6	cell cycle arrest	11	0.0017	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0043038	6,7	amino acid activation	32	0.0049	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0007005	5	mitochondrion organization and biogenesis	110	0.0170	5	0.0255	1.0000000	E
<input type="radio"/>	GO:0009719	3	response to endogenous stimulus	243	0.0375	9	0.0459	1.0000000	E
<input type="radio"/>	GO:0045003	9,8	double-strand break repair via synthesis-dependent strand annealing	17	0.0026	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0006370	8	mRNA capping	3	0.0005	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0007007	6,7	inner mitochondrial membrane organization and biogenesis	12	0.0019	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0006906	6,5	vesicle fusion	28	0.0043	2	0.0102	1.0000000	E
<input type="radio"/>	GO:0006753	7	nucleoside phosphate metabolic process	20	0.0031	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0019318	6,7	hexose metabolic process	85	0.0131	4	0.0204	1.0000000	E
<input type="radio"/>	GO:0055072	9	iron ion homeostasis	38	0.0059	5	0.0255	1.0000000	E
<input type="radio"/>	GO:0006045	8,9	N-acetylglucosamine biosynthetic process	17	0.0026	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0006400	7,8	tRNA modification	52	0.0080	2	0.0102	1.0000000	E
<input type="radio"/>	GO:0016579	9	protein deubiquitination	20	0.0031	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0006879	10,8	cellular iron ion homeostasis	38	0.0059	5	0.0255	1.0000000	E
<input type="radio"/>	GO:0032200	7	telomere organization and biogenesis	274	0.0423	10	0.0510	1.0000000	E
<input type="radio"/>	GO:0006694	6,5,7	steroid biosynthetic process	32	0.0049	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0044264	5,6	cellular polysaccharide metabolic process	65	0.0100	2	0.0102	1.0000000	E
<input type="radio"/>	GO:0000001	8,7,6	mitochondrion inheritance	26	0.0040	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0046489	9,8,10	phosphoinositide biosynthetic process	28	0.0043	2	0.0102	1.0000000	E
<input type="radio"/>	GO:0032507	6,5,4	maintenance of cellular protein localization	29	0.0045	1	0.0051	1.0000000	E
<input type="radio"/>	GO:0065003	5,4	macromolecular complex assembly	328	0.0506	10	0.0510	1.0000000	E
<input type="radio"/>	GO:0008361	4,6,7	regulation of cell size	129	0.0199	7	0.0357	1.0000000	E
<input type="radio"/>	GO:0045184	3,4,5	establishment of protein localization	296	0.0457	7	0.0357	1.0000000	D
<input type="radio"/>	GO:0006520	5,6	amino acid metabolic process	187	0.0289	2	0.0102	1.0000000	D
<input type="radio"/>	GO:0007568	3	aging	49	0.0076	1	0.0051	1.0000000	D
<input type="radio"/>	GO:0006606	9,10,7,8,6	protein import into nucleus	50	0.0077	1	0.0051	1.0000000	D
<input type="radio"/>	GO:0009260	6,7	ribonucleotide biosynthetic process	40	0.0062	1	0.0051	1.0000000	D
<input type="radio"/>	GO:0022618	6,5	protein-RNA complex assembly	144	0.0222	3	0.0153	1.0000000	D
<input type="radio"/>	GO:0009108	6	coenzyme biosynthetic process	66	0.0102	1	0.0051	1.0000000	D
<input type="radio"/>	GO:0008104	4	protein localization	330	0.0510	9	0.0459	1.0000000	D
<input type="radio"/>	GO:0043413	6	biopolymer glycosylation	73	0.0113	1	0.0051	1.0000000	D
<input type="radio"/>	GO:0016072	6	rRNA metabolic process	256	0.0395	4	0.0204	1.0000000	D
<input type="radio"/>	GO:0007031	5	peroxisome organization and biogenesis	40	0.0062	1	0.0051	1.0000000	D
<input type="radio"/>	GO:0022411	4	cellular component disassembly	36	0.0056	1	0.0051	1.0000000	D
<input type="radio"/>	GO:0015837	4,5	amine transport	50	0.0077	1	0.0051	1.0000000	D
<input type="radio"/>	GO:0009259	6	ribonucleotide metabolic process	43	0.0066	1	0.0051	1.0000000	D
<input type="radio"/>	GO:0006473	8	protein amino acid acetylation	48	0.0074	1	0.0051	1.0000000	D
<input type="radio"/>	GO:0051188	5	cofactor biosynthetic process	79	0.0122	1	0.0051	1.0000000	D
<input type="radio"/>	GO:0044260	4	cellular macromolecule metabolic process	1552	0.2397	43	0.2194	1.0000000	D
<input type="radio"/>	GO:0006886	7,5,6	intracellular protein transport	274	0.0423	7	0.0357	1.0000000	D
<input type="radio"/>	GO:0006360	8,7	transcription from RNA polymerase I	24	0.0052	1	0.0051	1.0000000	D

<input type="radio"/>	GO:0006300	9,7	promoter	34	0.0053	1	0.0051	1.0000000	<input type="checkbox"/>
<input type="radio"/>	GO:0030163	6,5	protein catabolic process	173	0.0267	5	0.0255	1.0000000	<input type="checkbox"/>
<input type="radio"/>	GO:0017038	5,6,7	protein import	109	0.0168	2	0.0102	1.0000000	<input type="checkbox"/>
<input type="radio"/>	GO:0006611	9,10,7,8	protein export from nucleus	56	0.0086	1	0.0051	1.0000000	<input type="checkbox"/>
<input type="radio"/>	GO:0006289	7,6	nucleotide-excision repair	44	0.0068	1	0.0051	1.0000000	<input type="checkbox"/>
<input type="radio"/>	GO:0051170	9,7,8	nuclear import	50	0.0077	1	0.0051	1.0000000	<input type="checkbox"/>
<input type="radio"/>	GO:0043284	5	biopolymer biosynthetic process	354	0.0547	4	0.0204	1.0000000	<input type="checkbox"/>
<input type="radio"/>	GO:0046467	6,5,7	membrane lipid biosynthetic process	78	0.0120	2	0.0102	1.0000000	<input type="checkbox"/>
<input type="radio"/>	GO:0006007	8,9	glucose catabolic process	34	0.0053	1	0.0051	1.0000000	<input type="checkbox"/>
<input type="radio"/>	GO:0006605	8,6,7	protein targeting	258	0.0398	5	0.0255	1.0000000	<input type="checkbox"/>
<input type="radio"/>	GO:0006865	5,6,7	amino acid transport	39	0.0060	1	0.0051	1.0000000	<input type="checkbox"/>
<input type="radio"/>	GO:0043632	6	modification-dependent macromolecule catabolic process	155	0.0239	3	0.0153	1.0000000	<input type="checkbox"/>
<input type="radio"/>	GO:0006793	4	phosphorus metabolic process	212	0.0327	5	0.0255	1.0000000	<input type="checkbox"/>
<input type="radio"/>	GO:0019538	4	protein metabolic process	1547	0.2389	43	0.2194	1.0000000	<input type="checkbox"/>
<input type="radio"/>	GO:0019320	7,8	hexose catabolic process	39	0.0060	1	0.0051	1.0000000	<input type="checkbox"/>
<input type="radio"/>	GO:0009059	4	macromolecule biosynthetic process	886	0.1368	18	0.0918	1.0000000	<input type="checkbox"/>
<input type="radio"/>	GO:0043681	6,7,8	protein import into mitochondrion	40	0.0062	1	0.0051	1.0000000	<input type="checkbox"/>
<input type="radio"/>	GO:0006082	4	organic acid metabolic process	314	0.0485	4	0.0204	1.0000000	<input type="checkbox"/>
<input type="radio"/>	GO:0006752	6	group transfer coenzyme metabolic process	44	0.0068	1	0.0051	1.0000000	<input type="checkbox"/>
<input type="radio"/>	GO:0006508	6	proteolysis	178	0.0275	4	0.0204	1.0000000	<input type="checkbox"/>
<input type="radio"/>	GO:0045333	5	cellular respiration	89	0.0137	2	0.0102	1.0000000	<input type="checkbox"/>
<input type="radio"/>	GO:0009056	3	catabolic process	438	0.0676	12	0.0612	1.0000000	<input type="checkbox"/>
<input type="radio"/>	GO:0009628	3	response to abiotic stimulus	117	0.0181	3	0.0153	1.0000000	<input type="checkbox"/>
<input type="radio"/>	GO:0006769	8,7	nicotinamide metabolic process	42	0.0065	1	0.0051	1.0000000	<input type="checkbox"/>
<input type="radio"/>	GO:0031509	7,11	telomeric heterochromatin formation	60	0.0093	1	0.0051	1.0000000	<input type="checkbox"/>
<input type="radio"/>	GO:0016125	5,6,7	sterol metabolic process	42	0.0065	1	0.0051	1.0000000	<input type="checkbox"/>
<input type="radio"/>	GO:0006629	4	lipid metabolic process	242	0.0374	5	0.0255	1.0000000	<input type="checkbox"/>
<input type="radio"/>	GO:0006414	7,6	translational elongation	313	0.0483	2	0.0102	1.0000000	<input type="checkbox"/>
<input type="radio"/>	GO:0042254	5	ribosome biogenesis and assembly	410	0.0633	5	0.0255	1.0000000	<input type="checkbox"/>
<input type="radio"/>	GO:0006412	6,5	translation	688	0.1062	11	0.0561	1.0000000	<input type="checkbox"/>
<input type="radio"/>	GO:0006091	3	generation of precursor metabolites and energy	183	0.0283	5	0.0255	1.0000000	<input type="checkbox"/>
<input type="radio"/>	GO:0006612	9,7,8	protein targeting to membrane	39	0.0060	1	0.0051	1.0000000	<input type="checkbox"/>
<input type="radio"/>	GO:0030004	9,7	cellular monovalent inorganic cation homeostasis	34	0.0053	1	0.0051	1.0000000	<input type="checkbox"/>
<input type="radio"/>	GO:0016573	11,9	histone acetylation	40	0.0062	1	0.0051	1.0000000	<input type="checkbox"/>
<input type="radio"/>	GO:0006515	8,9	misfolded or incompletely synthesized protein catabolic process	38	0.0059	1	0.0051	1.0000000	<input type="checkbox"/>
<input type="radio"/>	GO:0009152	7,8	purine ribonucleotide biosynthetic process	38	0.0059	1	0.0051	1.0000000	<input type="checkbox"/>
<input type="radio"/>	GO:0007265	7	Ras protein signal transduction	39	0.0060	1	0.0051	1.0000000	<input type="checkbox"/>
<input type="radio"/>	GO:0006733	6	oxidoreduction coenzyme metabolic process	56	0.0086	1	0.0051	1.0000000	<input type="checkbox"/>
<input type="radio"/>	GO:0006839	7,5,6	mitochondrial transport	65	0.0100	1	0.0051	1.0000000	<input type="checkbox"/>
<input type="radio"/>	GO:0019752	5	carboxylic acid metabolic process	314	0.0485	4	0.0204	1.0000000	<input type="checkbox"/>
<input type="radio"/>	GO:0006790	4	sulfur metabolic process	67	0.0103	2	0.0102	1.0000000	<input type="checkbox"/>
<input type="radio"/>	GO:0006732	5	coenzyme metabolic process	136	0.0210	2	0.0102	1.0000000	<input type="checkbox"/>
<input type="radio"/>	GO:0055067	8	monovalent inorganic cation homeostasis	34	0.0053	1	0.0051	1.0000000	<input type="checkbox"/>
<input type="radio"/>	GO:0009165	5,6	nucleotide biosynthetic process	59	0.0091	1	0.0051	1.0000000	<input type="checkbox"/>

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<input type="checkbox"/>	GO:0009451	6	RNA modification	139	0.0215	2	0.0102	1.0000000	D
<input type="checkbox"/>	GO:0015849	4,5	organic acid transport	55	0.0085	1	0.0051	1.0000000	D
<input type="checkbox"/>	GO:0006486	8,7,6	protein amino acid glycosylation	73	0.0113	1	0.0051	1.0000000	D
<input type="checkbox"/>	GO:0006461	6,5	protein complex assembly	116	0.0179	3	0.0153	1.0000000	D
<input type="checkbox"/>	GO:0006626	9,8,7,6	protein targeting to mitochondrion	52	0.0080	1	0.0051	1.0000000	D
<input type="checkbox"/>	GO:0006164	6,7	purine nucleotide biosynthetic process	41	0.0063	1	0.0051	1.0000000	D
<input type="checkbox"/>	GO:0044257	6,7	cellular protein catabolic process	160	0.0247	4	0.0204	1.0000000	D
<input type="checkbox"/>	GO:0009100	6	glycoprotein metabolic process	79	0.0122	1	0.0051	1.0000000	D
<input type="checkbox"/>	GO:0006119	7,4	oxidative phosphorylation	46	0.0071	1	0.0051	1.0000000	D
<input type="checkbox"/>	GO:0044262	5	cellular carbohydrate metabolic process	213	0.0329	6	0.0306	1.0000000	D
<input type="checkbox"/>	GO:0051186	4	cofactor metabolic process	170	0.0263	5	0.0255	1.0000000	D
<input type="checkbox"/>	GO:0006914	3	autophagy	45	0.0069	1	0.0051	1.0000000	D
<input type="checkbox"/>	GO:0006364	6,7	rRNA processing	249	0.0384	4	0.0204	1.0000000	D
<input type="checkbox"/>	GO:0006970	4	response to osmotic stress	89	0.0137	2	0.0102	1.0000000	D
<input type="checkbox"/>	GO:0006112	5	energy reserve metabolic process	39	0.0060	1	0.0051	1.0000000	D
<input type="checkbox"/>	GO:0009058	3	biosynthetic process	1249	0.1929	23	0.1173	1.0000000	D
<input type="checkbox"/>	GO:0044275	6	cellular carbohydrate catabolic process	80	0.0124	1	0.0051	1.0000000	D
<input type="checkbox"/>	GO:0022613	4	ribonucleoprotein complex biogenesis and assembly	483	0.0746	8	0.0408	1.0000000	D
<input type="checkbox"/>	GO:0008033	7	tRNA processing	84	0.0130	2	0.0102	1.0000000	D
<input type="checkbox"/>	GO:0042273	6,5	ribosomal large subunit biogenesis and assembly	64	0.0099	1	0.0051	1.0000000	D
<input type="checkbox"/>	GO:0044267	5	cellular protein metabolic process	1498	0.2313	41	0.2092	1.0000000	D
<input type="checkbox"/>	GO:0015980	4	energy derivation by oxidation of organic compounds	145	0.0224	4	0.0204	1.0000000	D
<input type="checkbox"/>	GO:0009308	4	amine metabolic process	228	0.0352	3	0.0153	1.0000000	D
<input type="checkbox"/>	GO:0051603	7,8	proteolysis involved in cellular protein catabolic process	151	0.0233	3	0.0153	1.0000000	D
<input type="checkbox"/>	GO:0009117	5	nucleotide metabolic process	111	0.0171	3	0.0153	1.0000000	D
<input type="checkbox"/>	GO:0008610	5,4,6	lipid biosynthetic process	129	0.0199	3	0.0153	1.0000000	D
<input type="checkbox"/>	GO:0006073	6,7	glucan metabolic process	46	0.0071	1	0.0051	1.0000000	D
<input type="checkbox"/>	GO:0006399	6	tRNA metabolic process	121	0.0187	3	0.0153	1.0000000	D
<input type="checkbox"/>	GO:0009060	6	aerobic respiration	84	0.0130	1	0.0051	1.0000000	D
<input type="checkbox"/>	GO:0046365	6,7	monosaccharide catabolic process	44	0.0068	1	0.0051	1.0000000	D
<input type="checkbox"/>	GO:0015031	4,5,6	protein transport	280	0.0432	7	0.0357	1.0000000	D
<input type="checkbox"/>	GO:0016310	6	phosphorylation	155	0.0239	3	0.0153	1.0000000	D
<input type="checkbox"/>	GO:0044255	4,5	cellular lipid metabolic process	229	0.0354	5	0.0255	1.0000000	D
<input type="checkbox"/>	GO:0006807	3	nitrogen compound metabolic process	251	0.0388	3	0.0153	1.0000000	D
<input type="checkbox"/>	GO:0046942	5,6	carboxylic acid transport	54	0.0083	1	0.0051	1.0000000	D
<input type="checkbox"/>	GO:0042493	4	response to drug	121	0.0187	1	0.0051	1.0000000	D
<input type="checkbox"/>	GO:0001302	5	replicative cell aging	39	0.0060	1	0.0051	1.0000000	D
<input type="checkbox"/>	GO:0006796	5	phosphate metabolic process	212	0.0327	5	0.0255	1.0000000	D
<input type="checkbox"/>	GO:0007569	4	cell aging	49	0.0076	1	0.0051	1.0000000	D
<input type="checkbox"/>	GO:0032446	8	protein modification by small protein conjugation	84	0.0130	2	0.0102	1.0000000	D
<input type="checkbox"/>	GO:0008150	1	biological process	6476	1.0000	196	1.0000	1.0000000	D
<input type="checkbox"/>	GO:0009101	7,5	glycoprotein biosynthetic process	78	0.0120	1	0.0051	1.0000000	D
<input type="checkbox"/>	GO:0010041	8,7,6	modification-dependent protein catabolic	148	0.0230	3	0.0153	1.0000000	D

<input type="checkbox"/>	GO:0019941	0,1,2	process	148	0.0229	3	0.0153	1.0000000	<input type="checkbox"/>
<input type="checkbox"/>	GO:0044248	4	cellular catabolic process	425	0.0656	11	0.0561	1.0000000	<input type="checkbox"/>
<input type="checkbox"/>	GO:0006090	7	pyruvate metabolic process	38	0.0059	1	0.0051	1.0000000	<input type="checkbox"/>
<input type="checkbox"/>	GO:0009150	7	purine ribonucleotide metabolic process	41	0.0063	1	0.0051	1.0000000	<input type="checkbox"/>
<input type="checkbox"/>	GO:0006348	11,7,8,12,10	chromatin silencing at telomere	60	0.0093	1	0.0051	1.0000000	<input type="checkbox"/>
<input type="checkbox"/>	GO:0046483	4	heterocycle metabolic process	76	0.0117	1	0.0051	1.0000000	<input type="checkbox"/>
<input type="checkbox"/>	GO:0008202	5,6	steroid metabolic process	43	0.0066	1	0.0051	1.0000000	<input type="checkbox"/>
<input type="checkbox"/>	GO:0006519	4	amino acid and derivative metabolic process	202	0.0312	2	0.0102	1.0000000	<input type="checkbox"/>
<input type="checkbox"/>	GO:0006623	9,8,7,6	protein targeting to vacuole	67	0.0103	1	0.0051	1.0000000	<input type="checkbox"/>
<input type="checkbox"/>	GO:0016052	5	carbohydrate catabolic process	80	0.0124	1	0.0051	1.0000000	<input type="checkbox"/>
<input type="checkbox"/>	GO:0005975	4	carbohydrate metabolic process	233	0.0360	6	0.0306	1.0000000	<input type="checkbox"/>
<input type="checkbox"/>	GO:0007186	6	G-protein coupled receptor protein signaling pathway	34	0.0053	1	0.0051	1.0000000	<input type="checkbox"/>
<input type="checkbox"/>	GO:0006163	6	purine nucleotide metabolic process	47	0.0073	1	0.0051	1.0000000	<input type="checkbox"/>
<input type="checkbox"/>	GO:0033036	3	macromolecule localization	382	0.0590	11	0.0561	1.0000000	<input type="checkbox"/>
<input type="checkbox"/>	GO:0006468	8,7	protein amino acid phosphorylation	101	0.0156	2	0.0102	1.0000000	<input type="checkbox"/>
<input type="checkbox"/>	GO:0043623	7,6	cellular protein complex assembly	69	0.0107	2	0.0102	1.0000000	<input type="checkbox"/>
<input type="checkbox"/>	GO:0007166	5	cell surface receptor linked signal transduction	52	0.0080	1	0.0051	1.0000000	<input type="checkbox"/>
<input type="checkbox"/>	GO:0030433	9,11,10,12	ER-associated protein catabolic process	35	0.0054	1	0.0051	1.0000000	<input type="checkbox"/>
<input type="checkbox"/>	GO:0032787	6	monocarboxylic acid metabolic process	126	0.0195	2	0.0102	1.0000000	<input type="checkbox"/>
<input type="checkbox"/>	GO:0006511	9,8,10	ubiquitin-dependent protein catabolic process	148	0.0229	3	0.0153	1.0000000	<input type="checkbox"/>
<input type="checkbox"/>	GO:0044249	4	cellular biosynthetic process	366	0.0565	7	0.0357	1.0000000	<input type="checkbox"/>
<input type="checkbox"/>	GO:0046164	5	alcohol catabolic process	47	0.0073	1	0.0051	1.0000000	<input type="checkbox"/>