

GO-Stats Results

Your dataset contains **318** 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:0050896	2	response to stimulus	763	0.1178	77	0.2421	9.762198E-08	E
<input type="radio"/> GO:0019222	4,3	regulation of metabolic process	538	0.0831	53	0.1667	0.0002647	E
<input type="radio"/> GO:0007154	3	cell communication	240	0.0371	31	0.0975	0.0003694	E
<input type="radio"/> GO:0050789	3	regulation of biological process	761	0.1175	66	0.2075	0.0008530	E
<input type="radio"/> GO:0006950	3	response to stress	488	0.0754	48	0.1509	0.0010437	E
<input type="radio"/> GO:0065007	2	biological regulation	948	0.1464	77	0.2421	0.0011867	E
<input type="radio"/> GO:0005975	4	carbohydrate metabolic process	233	0.0360	29	0.0912	0.0018423	E
<input type="radio"/> GO:0042221	3	response to chemical stimulus	382	0.0590	40	0.1258	0.0018818	E
<input type="radio"/> GO:0043687	7	post-translational protein modification	388	0.0599	40	0.1258	0.0027436	E
<input type="radio"/> GO:0031323	5,4	regulation of cellular metabolic process	507	0.0783	47	0.1478	0.0065317	E
<input type="radio"/> GO:0050794	4,3	regulation of cellular process	738	0.1140	61	0.1918	0.0101611	E
<input type="radio"/> GO:0000751	8,9,7,6	cell cycle arrest in response to pheromone	8	0.0012	5	0.0157	0.0127818	E
<input type="radio"/> GO:0009056	3	catabolic process	438	0.0676	40	0.1258	0.0427989	E
<input type="radio"/> GO:0009987	2	cellular process	4654	0.7187	257	0.8082	0.0441972	E
<input type="radio"/> GO:0006109	5,4	regulation of carbohydrate metabolic process	29	0.0045	8	0.0252	0.0453713	E
<input type="radio"/> GO:0007165	4	signal transduction	209	0.0323	24	0.0755	0.0490784	E
<input type="radio"/> GO:0048523	5,4	negative regulation of cellular process	239	0.0369	26	0.0818	0.0596806	E
<input type="radio"/> GO:0006112	5	energy reserve metabolic process	39	0.0060	9	0.0283	0.0692058	E
<input type="radio"/> GO:0048519	4	negative regulation of biological process	242	0.0374	26	0.0818	0.0727929	E
<input type="radio"/> GO:0007050	7,8,6	cell cycle arrest	11	0.0017	5	0.0157	0.0908675	E
<input type="radio"/> GO:0044248	4	cellular catabolic process	425	0.0656	38	0.1195	0.0994059	E
<input type="radio"/> GO:0043285	5	biopolymer catabolic process	277	0.0428	28	0.0881	0.1097672	E
<input type="radio"/> GO:0015980	4	energy derivation by oxidation of organic compounds	145	0.0224	18	0.0566	0.1542448	E
<input type="radio"/> GO:0044262	5	cellular carbohydrate metabolic process	213	0.0329	23	0.0723	0.1675643	E
<input type="radio"/> GO:0009057	4	macromolecule catabolic process	345	0.0533	32	0.1006	0.1759070	E
<input type="radio"/> GO:0006350	5	transcription	567	0.0876	46	0.1447	0.1807244	E
<input type="radio"/> GO:0019219	6,5	regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic	440	0.0679	38	0.1195	0.1935674	E

			process						
<input type="radio"/>	GO:0006464	6	protein modification process	520	0.0803	43	0.1352	0.1938350	E
<input type="radio"/>	GO:0045786	6,7,5	negative regulation of progression through cell cycle	13	0.0020	5	0.0157	0.2292120	E
<input type="radio"/>	GO:0009605	3	response to external stimulus	37	0.0057	8	0.0252	0.2750909	E
<input type="radio"/>	GO:0031667	5	response to nutrient levels	37	0.0057	8	0.0252	0.2750909	E
<input type="radio"/>	GO:0009991	4	response to extracellular stimulus	37	0.0057	8	0.0252	0.2750909	E
<input type="radio"/>	GO:0007034	7,5,6	vacuolar transport	114	0.0176	15	0.0472	0.2794210	E
<input type="radio"/>	GO:0006091	3	generation of precursor metabolites and energy	183	0.0283	20	0.0629	0.3602512	E
<input type="radio"/>	GO:0030163	6,5	protein catabolic process	173	0.0267	19	0.0597	0.4647431	E
<input type="radio"/>	GO:0045721	7,9,8,10,6,11	negative regulation of gluconeogenesis	9	0.0014	4	0.0126	0.5363635	E
<input type="radio"/>	GO:0045912	6,5	negative regulation of carbohydrate metabolic process	9	0.0014	4	0.0126	0.5363635	E
<input type="radio"/>	GO:0045449	7,6	regulation of transcription	386	0.0596	33	0.1038	0.5569984	E
<input type="radio"/>	GO:0044238	3	primary metabolic process	3247	0.5014	185	0.5818	0.5794305	E
<input type="radio"/>	GO:0008152	2	metabolic process	3516	0.5429	198	0.6226	0.5903822	E
<input type="radio"/>	GO:0005977	7,6,8	glycogen metabolic process	32	0.0049	7	0.0220	0.6052997	E
<input type="radio"/>	GO:0006357	9,8	regulation of transcription from RNA polymerase II promoter	221	0.0341	22	0.0692	0.6481141	E
<input type="radio"/>	GO:0006366	8,7	transcription from RNA polymerase II promoter	343	0.0530	30	0.0943	0.6689875	E
<input type="radio"/>	GO:0043162	10,9,11	ubiquitin-dependent protein catabolic process via the multivesicular body pathway	16	0.0025	5	0.0157	0.6702766	E
<input type="radio"/>	GO:0044265	5	cellular macromolecule catabolic process	314	0.0485	28	0.0881	0.7368868	E
<input type="radio"/>	GO:0010033	4	response to organic substance	10	0.0015	4	0.0126	0.8505346	E
<input type="radio"/>	GO:0016051	5	carbohydrate biosynthetic process	77	0.0119	11	0.0346	0.8583524	E
<input type="radio"/>	GO:0044237	3	cellular metabolic process	3403	0.5255	191	0.6006	0.9810996	E
<input type="radio"/>	GO:0007094	9,11,10,8	mitotic cell cycle spindle assembly checkpoint	20	0.0031	2	0.0063	1.0000000	E
<input type="radio"/>	GO:0005981	6,10,9,5,8	regulation of glycogen catabolic process	4	0.0006	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0000737	6,7	DNA catabolic process, endonucleolytic	15	0.0023	2	0.0063	1.0000000	E
<input type="radio"/>	GO:0016579	9	protein deubiquitination	20	0.0031	3	0.0094	1.0000000	E
<input type="radio"/>	GO:0006031	9,7,8,10	chitin biosynthetic process	15	0.0023	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0042149	8,7,6	cellular response to glucose starvation	5	0.0008	3	0.0094	1.0000000	E
<input type="radio"/>	GO:0051789	4	response to protein stimulus	18	0.0028	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0000196	8,6	MAPKKK cascade during cell wall biogenesis	4	0.0006	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0006481	9,10,8	C-terminal protein amino acid methylation	1	0.0002	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0048017	8	inositol lipid-mediated signaling	16	0.0025	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0003006	3,4	reproductive developmental process	35	0.0054	2	0.0063	1.0000000	E
<input type="radio"/>	GO:0006626	9,8,7,6	protein targeting to mitochondrion	52	0.0080	3	0.0094	1.0000000	E
<input type="radio"/>	GO:0006607	10,11,8,9,7	NLS-bearing substrate import into nucleus	23	0.0036	2	0.0063	1.0000000	E
<input type="radio"/>	GO:0006400	7,8	tRNA modification	52	0.0080	3	0.0094	1.0000000	E
<input type="radio"/>	GO:0051261	6	protein depolymerization	10	0.0015	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0031324	6,5	negative regulation of cellular metabolic process	198	0.0306	18	0.0566	1.0000000	E
<input type="radio"/>	GO:0030803	10,8,9,7	negative regulation of cyclic nucleotide biosynthetic process	2	0.0003	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0019547	9,8,10,7,6,5	arginine catabolic process to ornithine	1	0.0002	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0006171	7,8	cAMP biosynthetic process	2	0.0003	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0031365	8	N-terminal protein amino acid modification	15	0.0023	1	0.0031	1.0000000	E

<input type="radio"/>	GO:0008295	8,9	spermidine biosynthetic process	2	0.0003	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0015892	13,11,8,9,5,10,6	siderophore-iron transport	6	0.0009	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0006408	11,9,6,8,10,7	snRNA export from nucleus	23	0.0036	2	0.0063	1.0000000	E
<input type="radio"/>	GO:0007264	6	small GTPase mediated signal transduction	61	0.0094	6	0.0189	1.0000000	E
<input type="radio"/>	GO:0045892	9,8	negative regulation of transcription, DNA-dependent	156	0.0241	10	0.0314	1.0000000	E
<input type="radio"/>	GO:0000279	6,5	M phase	258	0.0398	17	0.0535	1.0000000	E
<input type="radio"/>	GO:0043170	3	macromolecule metabolic process	2841	0.4387	160	0.5031	1.0000000	E
<input type="radio"/>	GO:0006812	5,6	cation transport	97	0.0150	5	0.0157	1.0000000	E
<input type="radio"/>	GO:0044260	4	cellular macromolecule metabolic process	1552	0.2397	90	0.2830	1.0000000	E
<input type="radio"/>	GO:0000003	2	reproduction	323	0.0499	23	0.0723	1.0000000	E
<input type="radio"/>	GO:0007093	8,10,9,7	mitotic cell cycle checkpoint	27	0.0042	3	0.0094	1.0000000	E
<input type="radio"/>	GO:0045045	7,5,4,6	secretory pathway	243	0.0375	18	0.0566	1.0000000	E
<input type="radio"/>	GO:0009075	6,7	histidine family amino acid metabolic process	14	0.0022	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0001558	5,6,4,8,9	regulation of cell growth	11	0.0017	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0000209	10	protein polyubiquitination	20	0.0031	2	0.0063	1.0000000	E
<input type="radio"/>	GO:0022402	4,3	cell cycle process	439	0.0678	29	0.0912	1.0000000	E
<input type="radio"/>	GO:0006631	5,7,6	fatty acid metabolic process	47	0.0073	4	0.0126	1.0000000	E
<input type="radio"/>	GO:0046580	8,9,7	negative regulation of Ras protein signal transduction	6	0.0009	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0044269	5	glycerol ether catabolic process	2	0.0003	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0031114	7,10,6,8	regulation of microtubule depolymerization	5	0.0008	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0016036	8,7,6	cellular response to phosphate starvation	4	0.0006	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0043065	7,8,10,6	positive regulation of apoptosis	3	0.0005	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0031145	11,10,12	anaphase-promoting complex-dependent proteasomal ubiquitin-dependent protein catabolic process	15	0.0023	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0015940	7,8	pantothenate biosynthetic process	8	0.0012	2	0.0063	1.0000000	E
<input type="radio"/>	GO:0006694	6,5,7	steroid biosynthetic process	32	0.0049	2	0.0063	1.0000000	E
<input type="radio"/>	GO:0046349	6,7	amino sugar biosynthetic process	17	0.0026	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0051225	5,9	spindle assembly	3	0.0005	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0050801	6	ion homeostasis	119	0.0184	8	0.0252	1.0000000	E
<input type="radio"/>	GO:0006338	9	chromatin remodeling	155	0.0239	8	0.0252	1.0000000	E
<input type="radio"/>	GO:0044242	5,6	cellular lipid catabolic process	8	0.0012	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0000288	10,8,9	mRNA catabolic process, deadenylation-dependent decay	24	0.0037	2	0.0063	1.0000000	E
<input type="radio"/>	GO:0016485	8	protein processing	38	0.0059	4	0.0126	1.0000000	E
<input type="radio"/>	GO:0006560	7,8	proline metabolic process	7	0.0011	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0000754	8,7,5	adaptation to pheromone during conjugation with cellular fusion	15	0.0023	2	0.0063	1.0000000	E
<input type="radio"/>	GO:0046165	5	alcohol biosynthetic process	35	0.0054	5	0.0157	1.0000000	E
<input type="radio"/>	GO:0000002	6	mitochondrial genome maintenance	31	0.0048	2	0.0063	1.0000000	E
<input type="radio"/>	GO:0022401	7,6	adaptation of signaling pathway	15	0.0023	2	0.0063	1.0000000	E
<input type="radio"/>	GO:0006267	8,7	pre-replicative complex assembly	15	0.0023	2	0.0063	1.0000000	E
<input type="radio"/>	GO:0006896	9,8,7,6	Golgi to vacuole transport	24	0.0037	5	0.0157	1.0000000	E
<input type="radio"/>	GO:0009890	6,5	negative regulation of biosynthetic process	8	0.0012	2	0.0063	1.0000000	E
<input type="radio"/>	GO:0006641	7,6,8	triacylglycerol metabolic process	5	0.0008	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0019933	8	cAMP-mediated signaling	9	0.0014	2	0.0063	1.0000000	E
<input type="radio"/>	GO:0000271	6,7	polysaccharide biosynthetic process	41	0.0063	5	0.0157	1.0000000	E

<input type="checkbox"/>	GO:0046185	5	aldehyde catabolic process	6	0.0009	1	0.0031	1.0000000	E
<input type="checkbox"/>	GO:0006259	5	DNA metabolic process	523	0.0808	26	0.0818	1.0000000	E
<input type="checkbox"/>	GO:0016265	3	death	13	0.0020	1	0.0031	1.0000000	E
<input type="checkbox"/>	GO:0046364	6,7	monosaccharide biosynthetic process	30	0.0046	4	0.0126	1.0000000	E
<input type="checkbox"/>	GO:0033013	5	tetrapyrrole metabolic process	14	0.0022	1	0.0031	1.0000000	E
<input type="checkbox"/>	GO:0055065	8	metal ion homeostasis	19	0.0029	1	0.0031	1.0000000	E
<input type="checkbox"/>	GO:0016044	4	membrane organization and biogenesis	188	0.0290	10	0.0314	1.0000000	E
<input type="checkbox"/>	GO:0015914	5,6	phospholipid transport	12	0.0019	1	0.0031	1.0000000	E
<input type="checkbox"/>	GO:0030800	9,8	negative regulation of cyclic nucleotide metabolic process	2	0.0003	1	0.0031	1.0000000	E
<input type="checkbox"/>	GO:0030814	9,8	regulation of cAMP metabolic process	2	0.0003	1	0.0031	1.0000000	E
<input type="checkbox"/>	GO:0006407	11,9,6,8,10,7	rRNA export from nucleus	26	0.0040	2	0.0063	1.0000000	E
<input type="checkbox"/>	GO:0015908	5,6	fatty acid transport	4	0.0006	1	0.0031	1.0000000	E
<input type="checkbox"/>	GO:0000320	7,6	re-entry into mitotic cell cycle	3	0.0005	1	0.0031	1.0000000	E
<input type="checkbox"/>	GO:0000749	5	response to pheromone during conjugation with cellular fusion	57	0.0088	6	0.0189	1.0000000	E
<input type="checkbox"/>	GO:0019935	7	cyclic-nucleotide-mediated signaling	9	0.0014	2	0.0063	1.0000000	E
<input type="checkbox"/>	GO:0006591	7,8,5,4	ornithine metabolic process	6	0.0009	1	0.0031	1.0000000	E
<input type="checkbox"/>	GO:0030808	8,6,7,5	regulation of nucleotide biosynthetic process	2	0.0003	1	0.0031	1.0000000	E
<input type="checkbox"/>	GO:0032506	5,3	cytokinetic process	88	0.0136	5	0.0157	1.0000000	E
<input type="checkbox"/>	GO:0031111	7,10,6	negative regulation of microtubule polymerization or depolymerization	5	0.0008	1	0.0031	1.0000000	E
<input type="checkbox"/>	GO:0043173	5	nucleotide salvage	4	0.0006	1	0.0031	1.0000000	E
<input type="checkbox"/>	GO:0030818	11,9,10,8	negative regulation of cAMP biosynthetic process	2	0.0003	1	0.0031	1.0000000	E
<input type="checkbox"/>	GO:0005978	8,7,9	glycogen biosynthetic process	15	0.0023	4	0.0126	1.0000000	E
<input type="checkbox"/>	GO:0006562	8,9	proline catabolic process	4	0.0006	1	0.0031	1.0000000	E
<input type="checkbox"/>	GO:0044247	7,6	cellular polysaccharide catabolic process	12	0.0019	3	0.0094	1.0000000	E
<input type="checkbox"/>	GO:0006810	3,4	transport	981	0.1515	66	0.2075	1.0000000	E
<input type="checkbox"/>	GO:0042724	7	thiamin and derivative biosynthetic process	20	0.0031	2	0.0063	1.0000000	E
<input type="checkbox"/>	GO:0006073	6,7	glucan metabolic process	46	0.0071	7	0.0220	1.0000000	E
<input type="checkbox"/>	GO:0001323	4,5,6	age-dependent general metabolic decline during chronological cell aging	6	0.0009	2	0.0063	1.0000000	E
<input type="checkbox"/>	GO:0006898	7,6	receptor-mediated endocytosis	4	0.0006	1	0.0031	1.0000000	E
<input type="checkbox"/>	GO:0019362	7,6	pyridine nucleotide metabolic process	45	0.0069	4	0.0126	1.0000000	E
<input type="checkbox"/>	GO:0046348	6,7	amino sugar catabolic process	2	0.0003	1	0.0031	1.0000000	E
<input type="checkbox"/>	GO:0042787	10,9,11	protein ubiquitination during ubiquitin-dependent protein catabolic process	14	0.0022	2	0.0063	1.0000000	E
<input type="checkbox"/>	GO:0006032	9,10,8,7	chitin catabolic process	2	0.0003	1	0.0031	1.0000000	E
<input type="checkbox"/>	GO:0032984	5	macromolecular complex disassembly	32	0.0049	2	0.0063	1.0000000	E
<input type="checkbox"/>	GO:0045332	5,7,6,8	phospholipid translocation	7	0.0011	1	0.0031	1.0000000	E
<input type="checkbox"/>	GO:0006826	7,8,9	iron ion transport	20	0.0031	2	0.0063	1.0000000	E
<input type="checkbox"/>	GO:0000092	8,9,10,7	mitotic anaphase B	5	0.0008	1	0.0031	1.0000000	E
<input type="checkbox"/>	GO:0046503	6,7	glycerolipid catabolic process	2	0.0003	1	0.0031	1.0000000	E
<input type="checkbox"/>	GO:0030026	10,8	cellular manganese ion homeostasis	5	0.0008	1	0.0031	1.0000000	E
<input type="checkbox"/>	GO:0045047	9,8,7,6,5	protein targeting to ER	33	0.0051	3	0.0094	1.0000000	E
<input type="checkbox"/>	GO:0000736	7,8,9	double-strand break repair via single-strand annealing, removal of nonhomologous ends	2	0.0003	1	0.0031	1.0000000	E
<input type="checkbox"/>	GO:0006461	6,5	protein complex assembly	116	0.0179	11	0.0346	1.0000000	E

<input type="checkbox"/>	GO:0000289	11,9,10	poly(A) tail shortening	7	0.0011	1	0.0031	1.0000000	E
<input type="checkbox"/>	GO:0065008	3	regulation of biological quality	260	0.0401	15	0.0472	1.0000000	E
<input type="checkbox"/>	GO:0007188	8,9	G-protein signaling, coupled to cAMP nucleotide second messenger	5	0.0008	2	0.0063	1.0000000	E
<input type="checkbox"/>	GO:0008104	4	protein localization	330	0.0510	24	0.0755	1.0000000	E
<input type="checkbox"/>	GO:0006515	8,9	misfolded or incompletely synthesized protein catabolic process	38	0.0059	3	0.0094	1.0000000	E
<input type="checkbox"/>	GO:0007187	7,8	G-protein signaling, coupled to cyclic nucleotide second messenger	5	0.0008	2	0.0063	1.0000000	E
<input type="checkbox"/>	GO:0043067	5,6,8,4	regulation of programmed cell death	4	0.0006	1	0.0031	1.0000000	E
<input type="checkbox"/>	GO:0042493	4	response to drug	121	0.0187	6	0.0189	1.0000000	E
<input type="checkbox"/>	GO:0045471	5	response to ethanol	1	0.0002	1	0.0031	1.0000000	E
<input type="checkbox"/>	GO:0051179	2	localization	1051	0.1623	69	0.2170	1.0000000	E
<input type="checkbox"/>	GO:0009889	5,4	regulation of biosynthetic process	69	0.0107	10	0.0314	1.0000000	E
<input type="checkbox"/>	GO:0009746	6,5	response to hexose stimulus	5	0.0008	2	0.0063	1.0000000	E
<input type="checkbox"/>	GO:0006417	7,6,5	regulation of translation	47	0.0073	3	0.0094	1.0000000	E
<input type="checkbox"/>	GO:0006082	4	organic acid metabolic process	314	0.0485	20	0.0629	1.0000000	E
<input type="checkbox"/>	GO:0042402	6,7	biogenic amine catabolic process	3	0.0005	1	0.0031	1.0000000	E
<input type="checkbox"/>	GO:0055072	9	iron ion homeostasis	38	0.0059	5	0.0157	1.0000000	E
<input type="checkbox"/>	GO:0042026	7	protein refolding	9	0.0014	3	0.0094	1.0000000	E
<input type="checkbox"/>	GO:0006616	9,12,11,7,10,8	SRP-dependent cotranslational protein targeting to membrane, translocation	10	0.0015	1	0.0031	1.0000000	E
<input type="checkbox"/>	GO:0000715	7,8	nucleotide-excision repair, DNA damage recognition	7	0.0011	1	0.0031	1.0000000	E
<input type="checkbox"/>	GO:0019751	5	polyol metabolic process	9	0.0014	1	0.0031	1.0000000	E
<input type="checkbox"/>	GO:0006508	6	proteolysis	178	0.0275	17	0.0535	1.0000000	E
<input type="checkbox"/>	GO:0043148	10,9,6,5,4,13,11,8	mitotic spindle stabilization	2	0.0003	1	0.0031	1.0000000	E
<input type="checkbox"/>	GO:0030005	9,7	cellular di-, tri-valent inorganic cation homeostasis	64	0.0099	6	0.0189	1.0000000	E
<input type="checkbox"/>	GO:0016192	4,5	vesicle-mediated transport	328	0.0506	24	0.0755	1.0000000	E
<input type="checkbox"/>	GO:0031684	7	heterotrimeric G-protein complex cycle	3	0.0005	1	0.0031	1.0000000	E
<input type="checkbox"/>	GO:0043068	6,7,9,5	positive regulation of programmed cell death	3	0.0005	1	0.0031	1.0000000	E
<input type="checkbox"/>	GO:0006986	4,5	response to unfolded protein	18	0.0028	1	0.0031	1.0000000	E
<input type="checkbox"/>	GO:0016568	8	chromatin modification	223	0.0344	13	0.0409	1.0000000	E
<input type="checkbox"/>	GO:0015674	6,7	di-, tri-valent inorganic cation transport	34	0.0053	4	0.0126	1.0000000	E
<input type="checkbox"/>	GO:0005984	6	disaccharide metabolic process	31	0.0048	3	0.0094	1.0000000	E
<input type="checkbox"/>	GO:0051651	5,4,3	maintenance of cellular localization	29	0.0045	2	0.0063	1.0000000	E
<input type="checkbox"/>	GO:0045944	10,9	positive regulation of transcription from RNA polymerase II promoter	76	0.0117	7	0.0220	1.0000000	E
<input type="checkbox"/>	GO:0045184	3,4,5	establishment of protein localization	296	0.0457	22	0.0692	1.0000000	E
<input type="checkbox"/>	GO:0006743	7,6	ubiquinone metabolic process	9	0.0014	1	0.0031	1.0000000	E
<input type="checkbox"/>	GO:0006733	6	oxidoreduction coenzyme metabolic process	56	0.0086	5	0.0157	1.0000000	E
<input type="checkbox"/>	GO:0048522	5,4	positive regulation of cellular process	124	0.0191	11	0.0346	1.0000000	E
<input type="checkbox"/>	GO:0044255	4,5	cellular lipid metabolic process	229	0.0354	12	0.0377	1.0000000	E
<input type="checkbox"/>	GO:0045935	7,6	positive regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	108	0.0167	10	0.0314	1.0000000	E
<input type="checkbox"/>	GO:0019216	5,4	regulation of lipid metabolic process	2	0.0003	1	0.0031	1.0000000	E
<input type="checkbox"/>	GO:0009651	5	response to salt stress	15	0.0023	3	0.0094	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	1	0.0031	1.0000000	E

<input type="radio"/>	GO:0006401	6	RNA catabolic process	74	0.0114	4	0.0126	1.0000000	E
<input type="radio"/>	GO:0007001	6	chromosome organization and biogenesis (sensu Eukaryota)	567	0.0876	30	0.0943	1.0000000	E
<input type="radio"/>	GO:0009308	4	amine metabolic process	228	0.0352	12	0.0377	1.0000000	E
<input type="radio"/>	GO:0030802	9,7,8,6	regulation of cyclic nucleotide biosynthetic process	2	0.0003	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0009607	3	response to biotic stimulus	25	0.0039	2	0.0063	1.0000000	E
<input type="radio"/>	GO:0007047	5	cell wall organization and biogenesis	200	0.0309	13	0.0409	1.0000000	E
<input type="radio"/>	GO:0015893	4,5	drug transport	13	0.0020	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0051235	3,2	maintenance of localization	33	0.0051	3	0.0094	1.0000000	E
<input type="radio"/>	GO:0044264	5,6	cellular polysaccharide metabolic process	65	0.0100	9	0.0283	1.0000000	E
<input type="radio"/>	GO:0032200	7	telomere organization and biogenesis	274	0.0423	17	0.0535	1.0000000	E
<input type="radio"/>	GO:0031325	6,5	positive regulation of cellular metabolic process	116	0.0179	10	0.0314	1.0000000	E
<input type="radio"/>	GO:0042773	8,5	ATP synthesis coupled electron transport	25	0.0039	2	0.0063	1.0000000	E
<input type="radio"/>	GO:0009636	4	response to toxin	28	0.0043	3	0.0094	1.0000000	E
<input type="radio"/>	GO:0006290	7,6	pyrimidine dimer repair	1	0.0002	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0018409	9	peptide or protein amino-terminal blocking	15	0.0023	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0000910	4	cytokinesis	109	0.0168	6	0.0189	1.0000000	E
<input type="radio"/>	GO:0031110	6,9,5	regulation of microtubule polymerization or depolymerization	15	0.0023	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0022411	4	cellular component disassembly	36	0.0056	2	0.0063	1.0000000	E
<input type="radio"/>	GO:0009109	6	coenzyme catabolic process	20	0.0031	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0046688	6	response to copper ion	5	0.0008	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0006525	7,8,5,4	arginine metabolic process	15	0.0023	2	0.0063	1.0000000	E
<input type="radio"/>	GO:0043094	4	metabolic compound salvage	19	0.0029	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0016052	5	carbohydrate catabolic process	80	0.0124	7	0.0220	1.0000000	E
<input type="radio"/>	GO:0015749	5,6	monosaccharide transport	26	0.0040	5	0.0157	1.0000000	E
<input type="radio"/>	GO:0031669	6,5	cellular response to nutrient levels	19	0.0029	5	0.0157	1.0000000	E
<input type="radio"/>	GO:0009065	7,8	glutamine family amino acid catabolic process	13	0.0020	2	0.0063	1.0000000	E
<input type="radio"/>	GO:0007127	9,7,6,8,5	meiosis I	75	0.0116	8	0.0252	1.0000000	E
<input type="radio"/>	GO:0001578	8	microtubule bundle formation	1	0.0002	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0008608	7,4	attachment of spindle microtubules to kinetochore	4	0.0006	2	0.0063	1.0000000	E
<input type="radio"/>	GO:0006100	6	tricarboxylic acid cycle intermediate metabolic process	20	0.0031	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0032297	10,8,9	negative regulation of DNA replication initiation	6	0.0009	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0007051	8	spindle organization and biogenesis	47	0.0073	5	0.0157	1.0000000	E
<input type="radio"/>	GO:0030435	5	sporulation	123	0.0190	12	0.0377	1.0000000	E
<input type="radio"/>	GO:0006769	8,7	nicotinamide metabolic process	42	0.0065	3	0.0094	1.0000000	E
<input type="radio"/>	GO:0007019	9,7	microtubule depolymerization	6	0.0009	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0018318	10,9,8	protein amino acid palmitoylation	8	0.0012	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0016311	6	dephosphorylation	41	0.0063	3	0.0094	1.0000000	E
<input type="radio"/>	GO:0007026	8,7,11,9,6	negative regulation of microtubule depolymerization	5	0.0008	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0016310	6	phosphorylation	155	0.0239	14	0.0440	1.0000000	E
<input type="radio"/>	GO:0042732	7,8	D-xylose metabolic process	4	0.0006	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0006517	8	protein deglycosylation	1	0.0002	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0046578	7,8,6	regulation of Ras protein signal transduction	6	0.0009	1	0.0031	1.0000000	E

<input type="checkbox"/>	GO:0015880	6,7	coenzyme A transport	1	0.0002	1	0.0031	1.0000000	E
<input type="checkbox"/>	GO:0000921	8,7	septin ring assembly	9	0.0014	1	0.0031	1.0000000	E
<input type="checkbox"/>	GO:0000256	6	allantoin catabolic process	7	0.0011	1	0.0031	1.0000000	E
<input type="checkbox"/>	GO:0043488	9,8,7	regulation of mRNA stability	30	0.0046	2	0.0063	1.0000000	E
<input type="checkbox"/>	GO:0007531	4,6,5	mating type determination	35	0.0054	2	0.0063	1.0000000	E
<input type="checkbox"/>	GO:0046483	4	heterocycle metabolic process	76	0.0117	4	0.0126	1.0000000	E
<input type="checkbox"/>	GO:0006512	8	ubiquitin cycle	88	0.0136	10	0.0314	1.0000000	E
<input type="checkbox"/>	GO:0007015	8	actin filament organization	61	0.0094	3	0.0094	1.0000000	E
<input type="checkbox"/>	GO:0009893	5,4	positive regulation of metabolic process	116	0.0179	10	0.0314	1.0000000	E
<input type="checkbox"/>	GO:0044249	4	cellular biosynthetic process	366	0.0565	22	0.0692	1.0000000	E
<input type="checkbox"/>	GO:0006369	9,8	transcription termination from RNA polymerase II promoter	18	0.0028	1	0.0031	1.0000000	E
<input type="checkbox"/>	GO:0000920	6,4	cell separation during cytokinesis	13	0.0020	1	0.0031	1.0000000	E
<input type="checkbox"/>	GO:0042138	11,9,8,5,6,10,7,4	meiotic DNA double-strand break formation	9	0.0014	1	0.0031	1.0000000	E
<input type="checkbox"/>	GO:0016925	9	protein sumoylation	10	0.0015	1	0.0031	1.0000000	E
<input type="checkbox"/>	GO:0006642	8,7,9	triacylglycerol mobilization	2	0.0003	1	0.0031	1.0000000	E
<input type="checkbox"/>	GO:0051322	6,7,5	anaphase	6	0.0009	1	0.0031	1.0000000	E
<input type="checkbox"/>	GO:0009310	5,6	amine catabolic process	32	0.0049	3	0.0094	1.0000000	E
<input type="checkbox"/>	GO:0006081	4	aldehyde metabolic process	21	0.0032	2	0.0063	1.0000000	E
<input type="checkbox"/>	GO:0000074	6,5	regulation of progression through cell cycle	167	0.0258	14	0.0440	1.0000000	E
<input type="checkbox"/>	GO:0051238	4,3	sequestering of metal ion	3	0.0005	1	0.0031	1.0000000	E
<input type="checkbox"/>	GO:0006037	8,9,6,7,10	cell wall chitin metabolic process	14	0.0022	2	0.0063	1.0000000	E
<input type="checkbox"/>	GO:0006352	7,8,6	transcription initiation	55	0.0085	3	0.0094	1.0000000	E
<input type="checkbox"/>	GO:0006625	9,8,6,7	protein targeting to peroxisome	20	0.0031	4	0.0126	1.0000000	E
<input type="checkbox"/>	GO:0045014	11,9,10,7	negative regulation of transcription by glucose	7	0.0011	3	0.0094	1.0000000	E
<input type="checkbox"/>	GO:0045426	7,6	quinone cofactor biosynthetic process	9	0.0014	1	0.0031	1.0000000	E
<input type="checkbox"/>	GO:0006113	5	fermentation	17	0.0026	2	0.0063	1.0000000	E
<input type="checkbox"/>	GO:0019358	9,7,8	nicotinate nucleotide salvage	2	0.0003	1	0.0031	1.0000000	E
<input type="checkbox"/>	GO:0009749	7,6	response to glucose stimulus	5	0.0008	2	0.0063	1.0000000	E
<input type="checkbox"/>	GO:0000272	6	polysaccharide catabolic process	12	0.0019	3	0.0094	1.0000000	E
<input type="checkbox"/>	GO:0051596	6	methylglyoxal catabolic process	3	0.0005	1	0.0031	1.0000000	E
<input type="checkbox"/>	GO:0046351	6,7	disaccharide biosynthetic process	7	0.0011	2	0.0063	1.0000000	E
<input type="checkbox"/>	GO:0016043	3	cellular component organization and biogenesis	2264	0.3496	113	0.3553	1.0000000	E
<input type="checkbox"/>	GO:0007265	7	Ras protein signal transduction	39	0.0060	5	0.0157	1.0000000	E
<input type="checkbox"/>	GO:0006617	8,12,11,7,10,9	SRP-dependent cotranslational protein targeting to membrane, signal sequence recognition	7	0.0011	1	0.0031	1.0000000	E
<input type="checkbox"/>	GO:0051726	5,4	regulation of cell cycle	167	0.0258	14	0.0440	1.0000000	E
<input type="checkbox"/>	GO:0006085	7	acetyl-CoA biosynthetic process	4	0.0006	2	0.0063	1.0000000	E
<input type="checkbox"/>	GO:0048869	3	cellular developmental process	173	0.0267	15	0.0472	1.0000000	E
<input type="checkbox"/>	GO:0019318	6,7	hexose metabolic process	85	0.0131	8	0.0252	1.0000000	E
<input type="checkbox"/>	GO:0045185	5,4,3	maintenance of protein localization	30	0.0046	2	0.0063	1.0000000	E
<input type="checkbox"/>	GO:0030865	6	cortical cytoskeleton organization and biogenesis	16	0.0025	1	0.0031	1.0000000	E
<input type="checkbox"/>	GO:0042592	4	homeostatic process	134	0.0207	8	0.0252	1.0000000	E
<input type="checkbox"/>	GO:0030437	7,6	sporulation (sensu Fungi)	108	0.0167	10	0.0314	1.0000000	E
<input type="checkbox"/>	GO:0000430	11,9,10,7	regulation of transcription from RNA	7	0.0011	3	0.0094	1.0000000	E

<input type="radio"/>	GO:0000430	11,9,10,7	polymerase II promoter by glucose	7	0.0011	5	0.0094	1.0000000	E
<input type="radio"/>	GO:0050810	8,7,6	regulation of steroid biosynthetic process	1	0.0002	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0007534	6,8,7	gene conversion at mating-type locus	23	0.0036	2	0.0063	1.0000000	E
<input type="radio"/>	GO:0006325	7	establishment and/or maintenance of chromatin architecture	253	0.0391	13	0.0409	1.0000000	E
<input type="radio"/>	GO:0009968	6,5	negative regulation of signal transduction	17	0.0026	2	0.0063	1.0000000	E
<input type="radio"/>	GO:0043330	5,6	response to exogenous dsRNA	7	0.0011	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0019740	4	nitrogen utilization	17	0.0026	3	0.0094	1.0000000	E
<input type="radio"/>	GO:0055066	8	di-, tri-valent inorganic cation homeostasis	64	0.0099	6	0.0189	1.0000000	E
<input type="radio"/>	GO:0006537	8,9	glutamate biosynthetic process	13	0.0020	2	0.0063	1.0000000	E
<input type="radio"/>	GO:0019725	5,3	cellular homeostasis	128	0.0198	8	0.0252	1.0000000	E
<input type="radio"/>	GO:0019748	3	secondary metabolic process	23	0.0036	2	0.0063	1.0000000	E
<input type="radio"/>	GO:0051336	5	regulation of hydrolase activity	10	0.0015	2	0.0063	1.0000000	E
<input type="radio"/>	GO:0006038	9,10,7,8,11	cell wall chitin biosynthetic process	13	0.0020	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0051246	5,4	regulation of protein metabolic process	72	0.0111	6	0.0189	1.0000000	E
<input type="radio"/>	GO:0009409	5,4	response to cold	7	0.0011	3	0.0094	1.0000000	E
<input type="radio"/>	GO:0044270	5,4	nitrogen compound catabolic process	32	0.0049	3	0.0094	1.0000000	E
<input type="radio"/>	GO:0015698	6,7	inorganic anion transport	16	0.0025	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0017038	5,6,7	protein import	109	0.0168	7	0.0220	1.0000000	E
<input type="radio"/>	GO:0006066	4	alcohol metabolic process	163	0.0252	13	0.0409	1.0000000	E
<input type="radio"/>	GO:0005985	7	sucrose metabolic process	6	0.0009	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0006627	10,9,8,7	mitochondrial protein processing	6	0.0009	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0008219	4,6	cell death	13	0.0020	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0006067	5	ethanol metabolic process	12	0.0019	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0051056	6,7,5	regulation of small GTPase mediated signal transduction	6	0.0009	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0006519	4	amino acid and derivative metabolic process	202	0.0312	10	0.0314	1.0000000	E
<input type="radio"/>	GO:0019323	7,8	pentose catabolic process	5	0.0008	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0016926	8	protein desumoylation	2	0.0003	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0051300	5,4,6	spindle pole body organization and biogenesis	16	0.0025	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0033212	11,9	iron assimilation	8	0.0012	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0051704	2	multi-organism process	139	0.0215	15	0.0472	1.0000000	E
<input type="radio"/>	GO:0016560	8,11,10,7,9	protein import into peroxisome matrix, docking	5	0.0008	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0006638	5,6	neutral lipid metabolic process	5	0.0008	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0019320	7,8	hexose catabolic process	39	0.0060	2	0.0063	1.0000000	E
<input type="radio"/>	GO:0019752	5	carboxylic acid metabolic process	314	0.0485	20	0.0629	1.0000000	E
<input type="radio"/>	GO:0006351	7,6	transcription, DNA-dependent	522	0.0806	37	0.1164	1.0000000	E
<input type="radio"/>	GO:0006121	10,7,5	mitochondrial electron transport, succinate to ubiquinone	4	0.0006	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0042723	6	thiamin and derivative metabolic process	22	0.0034	2	0.0063	1.0000000	E
<input type="radio"/>	GO:0043412	5	biopolymer modification	664	0.1025	46	0.1447	1.0000000	E
<input type="radio"/>	GO:0043283	4	biopolymer metabolic process	2230	0.3443	124	0.3899	1.0000000	E
<input type="radio"/>	GO:0006099	8,7,6	tricarboxylic acid cycle	15	0.0023	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0008535	8,7	cytochrome c oxidase complex assembly	9	0.0014	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0007052	5,4,9	mitotic spindle organization and biogenesis	44	0.0068	4	0.0126	1.0000000	E
<input type="radio"/>	GO:0006353	8,7	transcription termination	20	0.0031	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0048193	7,5,6	Golgi vesicle transport	166	0.0256	13	0.0409	1.0000000	E

<input type="radio"/>	GO:0016049	5,3,7,8	cell growth	102	0.0158	7	0.0220	1.0000000	E
<input type="radio"/>	GO:0031578	9,11,10,8	mitotic cell cycle spindle orientation checkpoint	4	0.0006	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0048250	8,6,9,7,10	mitochondrial iron ion transport	2	0.0003	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0045002	8,7	double-strand break repair via single-strand annealing	14	0.0022	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0015891	4,5	siderophore transport	9	0.0014	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0010038	5	response to metal ion	18	0.0028	2	0.0063	1.0000000	E
<input type="radio"/>	GO:0042398	6,5	amino acid derivative biosynthetic process	20	0.0031	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0016226	6	iron-sulfur cluster assembly	11	0.0017	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0006783	7,6,8	heme biosynthetic process	13	0.0020	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0006120	10,7,5	mitochondrial electron transport, NADH to ubiquinone	1	0.0002	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0016573	11,9	histone acetylation	40	0.0062	4	0.0126	1.0000000	E
<input type="radio"/>	GO:0031327	7,6	negative regulation of cellular biosynthetic process	6	0.0009	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0051716	3	cellular response to stimulus	21	0.0032	5	0.0157	1.0000000	E
<input type="radio"/>	GO:0065002	8,6,7	intracellular protein transport across a membrane	11	0.0017	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0042440	4	pigment metabolic process	20	0.0031	2	0.0063	1.0000000	E
<input type="radio"/>	GO:0006979	4	response to oxidative stress	71	0.0110	7	0.0220	1.0000000	E
<input type="radio"/>	GO:0019538	4	protein metabolic process	1547	0.2389	84	0.2642	1.0000000	E
<input type="radio"/>	GO:0046148	5	pigment biosynthetic process	19	0.0029	2	0.0063	1.0000000	E
<input type="radio"/>	GO:0006086	8	acetyl-CoA biosynthetic process from pyruvate	2	0.0003	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0006390	8,7	transcription from mitochondrial promoter	3	0.0005	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0009060	6	aerobic respiration	84	0.0130	7	0.0220	1.0000000	E
<input type="radio"/>	GO:0016569	9	covalent chromatin modification	91	0.0141	6	0.0189	1.0000000	E
<input type="radio"/>	GO:0006467	7,8	protein thiol-disulfide exchange	2	0.0003	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0006039	9,10,7,6,11,8	cell wall chitin catabolic process	1	0.0002	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0051252	7,6	regulation of RNA metabolic process	36	0.0056	2	0.0063	1.0000000	E
<input type="radio"/>	GO:0006474	10,9	N-terminal protein amino acid acetylation	9	0.0014	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0046834	6,7	lipid phosphorylation	5	0.0008	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0006772	7	thiamin metabolic process	20	0.0031	2	0.0063	1.0000000	E
<input type="radio"/>	GO:0043574	7,5,6	peroxisomal transport	20	0.0031	4	0.0126	1.0000000	E
<input type="radio"/>	GO:0050821	7	protein stabilization	3	0.0005	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0030799	8,7	regulation of cyclic nucleotide metabolic process	2	0.0003	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0006609	10,11,8,9,7	mRNA-binding (hnRNP) protein import into nucleus	25	0.0039	2	0.0063	1.0000000	E
<input type="radio"/>	GO:0006097	6,8	glyoxylate cycle	4	0.0006	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0010035	4	response to inorganic substance	24	0.0037	3	0.0094	1.0000000	E
<input type="radio"/>	GO:0031109	8	microtubule polymerization or depolymerization	16	0.0025	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0019243	7,8,6	methylglyoxal catabolic process to D-lactate	3	0.0005	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0016567	9	protein ubiquitination	66	0.0102	7	0.0220	1.0000000	E
<input type="radio"/>	GO:0006820	5,6	anion transport	17	0.0026	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0006739	9,8	NADP metabolic process	17	0.0026	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0030817	10,8,9,7	regulation of cAMP biosynthetic process	2	0.0003	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0031106	7	septin ring organization	9	0.0014	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0046356	7	acetyl-CoA catabolic process	15	0.0023	1	0.0031	1.0000000	E

<input type="checkbox"/>	GO:0051327	7,5,6	M phase of meiotic cell cycle	148	0.0229	13	0.0409	1.0000000	E
<input type="checkbox"/>	GO:0006732	5	coenzyme metabolic process	136	0.0210	11	0.0346	1.0000000	E
<input type="checkbox"/>	GO:0051248	6,5	negative regulation of protein metabolic process	18	0.0028	2	0.0063	1.0000000	E
<input type="checkbox"/>	GO:0048015	7	phosphoinositide-mediated signaling	16	0.0025	1	0.0031	1.0000000	E
<input type="checkbox"/>	GO:0006516	7	glycoprotein catabolic process	1	0.0002	1	0.0031	1.0000000	E
<input type="checkbox"/>	GO:0008298	5	intracellular mRNA localization	10	0.0015	1	0.0031	1.0000000	E
<input type="checkbox"/>	GO:0015939	7	pantothenate metabolic process	8	0.0012	2	0.0063	1.0000000	E
<input type="checkbox"/>	GO:0000726	7,6	non-recombinational repair	35	0.0054	2	0.0063	1.0000000	E
<input type="checkbox"/>	GO:0015693	7,8	magnesium ion transport	5	0.0008	2	0.0063	1.0000000	E
<input type="checkbox"/>	GO:0045941	8,7	positive regulation of transcription	101	0.0156	10	0.0314	1.0000000	E
<input type="checkbox"/>	GO:0009410	4	response to xenobiotic stimulus	7	0.0011	2	0.0063	1.0000000	E
<input type="checkbox"/>	GO:0006090	7	pyruvate metabolic process	38	0.0059	5	0.0157	1.0000000	E
<input type="checkbox"/>	GO:0043161	10,9,11	proteasomal ubiquitin-dependent protein catabolic process	63	0.0097	4	0.0126	1.0000000	E
<input type="checkbox"/>	GO:0000727	9,8	double-strand break repair via break-induced replication	7	0.0011	1	0.0031	1.0000000	E
<input type="checkbox"/>	GO:0006880	11,9,5,4	intracellular sequestering of iron ion	3	0.0005	1	0.0031	1.0000000	E
<input type="checkbox"/>	GO:0000719	8,7	photoreactive repair	1	0.0002	1	0.0031	1.0000000	E
<input type="checkbox"/>	GO:0032787	6	monocarboxylic acid metabolic process	126	0.0195	14	0.0440	1.0000000	E
<input type="checkbox"/>	GO:0008643	4,5	carbohydrate transport	38	0.0059	5	0.0157	1.0000000	E
<input type="checkbox"/>	GO:0000226	7	microtubule cytoskeleton organization and biogenesis	81	0.0125	7	0.0220	1.0000000	E
<input type="checkbox"/>	GO:0051791	6,8,7	medium-chain fatty acid metabolic process	3	0.0005	1	0.0031	1.0000000	E
<input type="checkbox"/>	GO:0006451	8,7,6	translational readthrough	2	0.0003	1	0.0031	1.0000000	E
<input type="checkbox"/>	GO:0006610	10,11,8,9,7	ribosomal protein import into nucleus	23	0.0036	2	0.0063	1.0000000	E
<input type="checkbox"/>	GO:0006629	4	lipid metabolic process	242	0.0374	12	0.0377	1.0000000	E
<input type="checkbox"/>	GO:0044275	6	cellular carbohydrate catabolic process	80	0.0124	7	0.0220	1.0000000	E
<input type="checkbox"/>	GO:0007049	3	cell cycle	458	0.0707	29	0.0912	1.0000000	E
<input type="checkbox"/>	GO:0043632	6	modification-dependent macromolecule catabolic process	155	0.0239	13	0.0409	1.0000000	E
<input type="checkbox"/>	GO:0051641	4,3	cellular localization	642	0.0991	44	0.1384	1.0000000	E
<input type="checkbox"/>	GO:0006310	6	DNA recombination	122	0.0188	8	0.0252	1.0000000	E
<input type="checkbox"/>	GO:0005991	6,7	trehalose metabolic process	10	0.0015	2	0.0063	1.0000000	E
<input type="checkbox"/>	GO:0001300	5	chronological cell aging	13	0.0020	4	0.0126	1.0000000	E
<input type="checkbox"/>	GO:0042364	6	water-soluble vitamin biosynthetic process	46	0.0071	3	0.0094	1.0000000	E
<input type="checkbox"/>	GO:0032940	6,4,5	secretion by cell	250	0.0386	18	0.0566	1.0000000	E
<input type="checkbox"/>	GO:0007109	7,6,5,4	cytokinesis, completion of separation	11	0.0017	1	0.0031	1.0000000	E
<input type="checkbox"/>	GO:0043620	8,7,5	regulation of transcription in response to stress	4	0.0006	2	0.0063	1.0000000	E
<input type="checkbox"/>	GO:0032502	2	developmental process	436	0.0673	27	0.0849	1.0000000	E
<input type="checkbox"/>	GO:0006547	7,8	histidine metabolic process	14	0.0022	1	0.0031	1.0000000	E
<input type="checkbox"/>	GO:0006308	5,6	DNA catabolic process	20	0.0031	2	0.0063	1.0000000	E
<input type="checkbox"/>	GO:0006839	7,5,6	mitochondrial transport	65	0.0100	5	0.0157	1.0000000	E
<input type="checkbox"/>	GO:0006043	7,8	glucosamine catabolic process	2	0.0003	1	0.0031	1.0000000	E
<input type="checkbox"/>	GO:0006045	8,9	N-acetylglucosamine biosynthetic process	17	0.0026	1	0.0031	1.0000000	E
<input type="checkbox"/>	GO:0000059	8,10,11,7,9	protein import into nucleus, docking	4	0.0006	1	0.0031	1.0000000	E
<input type="checkbox"/>	GO:0031668	5,4	cellular response to extracellular stimulus	19	0.0029	5	0.0157	1.0000000	E
<input type="checkbox"/>	GO:0000290	11,8,9,10	deadenylation-dependent decapping	9	0.0014	1	0.0031	1.0000000	E
<input type="checkbox"/>	GO:0000221	9,8,7,6	re-entry into mitotic cell cycle after	2	0.0005	1	0.0031	1.0000000	E

<input type="radio"/>	GO:0000521	9,0,1,0	pheromone arrest	5	0.0003	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0009110	5	vitamin biosynthetic process	46	0.0071	3	0.0094	1.0000000	E
<input type="radio"/>	GO:0006576	5,6	biogenic amine metabolic process	24	0.0037	2	0.0063	1.0000000	E
<input type="radio"/>	GO:0019568	8,9	arabinose catabolic process	4	0.0006	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0010133	9,8,10	proline catabolic process to glutamate	2	0.0003	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0030474	5,6,4,7	spindle pole body duplication	14	0.0022	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0022414	3,2	reproductive process	183	0.0283	13	0.0409	1.0000000	E
<input type="radio"/>	GO:0046058	7	cAMP metabolic process	2	0.0003	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0006139	4	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	1532	0.2366	81	0.2547	1.0000000	E
<input type="radio"/>	GO:0043623	7,6	cellular protein complex assembly	69	0.0107	8	0.0252	1.0000000	E
<input type="radio"/>	GO:0006083	7	acetate metabolic process	6	0.0009	2	0.0063	1.0000000	E
<input type="radio"/>	GO:0009228	7,8	thiamin biosynthetic process	19	0.0029	2	0.0063	1.0000000	E
<input type="radio"/>	GO:0006041	6,7	glucosamine metabolic process	19	0.0029	2	0.0063	1.0000000	E
<input type="radio"/>	GO:0006323	6	DNA packaging	253	0.0391	13	0.0409	1.0000000	E
<input type="radio"/>	GO:0043087	6	regulation of GTPase activity	5	0.0008	2	0.0063	1.0000000	E
<input type="radio"/>	GO:0006623	9,8,7,6	protein targeting to vacuole	67	0.0103	10	0.0314	1.0000000	E
<input type="radio"/>	GO:0006598	7,8	polyamine catabolic process	3	0.0005	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0006970	4	response to osmotic stress	89	0.0137	7	0.0220	1.0000000	E
<input type="radio"/>	GO:0006040	5,6	amino sugar metabolic process	19	0.0029	2	0.0063	1.0000000	E
<input type="radio"/>	GO:0006042	7,8	glucosamine biosynthetic process	17	0.0026	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0006998	5,6	nuclear membrane organization and biogenesis	7	0.0011	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0007584	6,4	response to nutrient	18	0.0028	3	0.0094	1.0000000	E
<input type="radio"/>	GO:0015846	5,6	polyamine transport	12	0.0019	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0006614	11,10,9,8,7	SRP-dependent cotranslational protein targeting to membrane	20	0.0031	2	0.0063	1.0000000	E
<input type="radio"/>	GO:0051321	4	meiotic cell cycle	148	0.0229	13	0.0409	1.0000000	E
<input type="radio"/>	GO:0006415	8,7,6	translational termination	7	0.0011	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0009266	4	response to temperature stimulus	28	0.0043	6	0.0189	1.0000000	E
<input type="radio"/>	GO:0000066	8,6,7,9	mitochondrial ornithine transport	1	0.0002	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0009628	3	response to abiotic stimulus	117	0.0181	12	0.0377	1.0000000	E
<input type="radio"/>	GO:0048878	5	chemical homeostasis	121	0.0187	8	0.0252	1.0000000	E
<input type="radio"/>	GO:0048610	3,4	reproductive cellular process	149	0.0230	11	0.0346	1.0000000	E
<input type="radio"/>	GO:0043624	7,6	cellular protein complex disassembly	28	0.0043	2	0.0063	1.0000000	E
<input type="radio"/>	GO:0015031	4,5,6	protein transport	280	0.0432	22	0.0692	1.0000000	E
<input type="radio"/>	GO:0006814	7,8	sodium ion transport	4	0.0006	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0006914	3	autophagy	45	0.0069	6	0.0189	1.0000000	E
<input type="radio"/>	GO:0045980	8,7	negative regulation of nucleotide metabolic process	2	0.0003	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0016572	11,9,8	histone phosphorylation	2	0.0003	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0000183	11,7,8,12,10	chromatin silencing at rDNA	18	0.0028	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0032320	8,9,10	positive regulation of Ras GTPase activity	2	0.0003	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0009267	7,6,5	cellular response to starvation	19	0.0029	5	0.0157	1.0000000	E
<input type="radio"/>	GO:0010324	5	membrane invagination	96	0.0148	7	0.0220	1.0000000	E
<input type="radio"/>	GO:0046890	7,6,5	regulation of lipid biosynthetic process	1	0.0002	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0043248	8,7	proteasome assembly	7	0.0011	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0043487	8,7	regulation of RNA stability	30	0.0046	2	0.0063	1.0000000	E
<input type="radio"/>	GO:0043458	7,8	ethanol biosynthetic process during	2	0.0003	1	0.0031	1.0000000	E

<input type="radio"/>	GO:0043430	1,0	fermentation	2	0.0003	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0009084	7,8	glutamine family amino acid biosynthetic process	27	0.0042	3	0.0094	1.0000000	E
<input type="radio"/>	GO:0030003	8,6	cellular cation homeostasis	102	0.0158	8	0.0252	1.0000000	E
<input type="radio"/>	GO:0032318	7,8,9	regulation of Ras GTPase activity	2	0.0003	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0000746	3	conjugation	118	0.0182	12	0.0377	1.0000000	E
<input type="radio"/>	GO:0001101	4	response to acid	11	0.0017	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0007091	9,7,5,8,6,4	mitotic metaphase/anaphase transition	15	0.0023	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0008054	7,6,11,10,12	cyclin catabolic process	12	0.0019	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0046685	5	response to arsenic	9	0.0014	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0006140	7,6	regulation of nucleotide metabolic process	2	0.0003	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0032258	10,9,8,7	CVT pathway	4	0.0006	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0042981	6,7,9,5	regulation of apoptosis	4	0.0006	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0045116	9	protein neddylation	6	0.0009	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0031326	6,5	regulation of cellular biosynthetic process	67	0.0103	9	0.0283	1.0000000	E
<input type="radio"/>	GO:0006089	7	lactate metabolic process	5	0.0008	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0031570	8,7	DNA integrity checkpoint	18	0.0028	2	0.0063	1.0000000	E
<input type="radio"/>	GO:0046907	6,4,5	intracellular transport	545	0.0842	40	0.1258	1.0000000	E
<input type="radio"/>	GO:0030476	8,6,7	spore wall assembly (sensu Fungi)	42	0.0065	5	0.0157	1.0000000	E
<input type="radio"/>	GO:0000077	9,8,6	DNA damage checkpoint	14	0.0022	2	0.0063	1.0000000	E
<input type="radio"/>	GO:0040007	2	growth	141	0.0218	8	0.0252	1.0000000	E
<input type="radio"/>	GO:0031930	6	mitochondrial signaling pathway	6	0.0009	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0006402	7	mRNA catabolic process	60	0.0093	4	0.0126	1.0000000	E
<input type="radio"/>	GO:0022607	4	cellular component assembly	471	0.0727	27	0.0849	1.0000000	E
<input type="radio"/>	GO:0019236	4	response to pheromone	94	0.0145	10	0.0314	1.0000000	E
<input type="radio"/>	GO:0019319	7,8	hexose biosynthetic process	30	0.0046	4	0.0126	1.0000000	E
<input type="radio"/>	GO:0001324	5,6,7	age-dependent response to oxidative stress during chronological cell aging	6	0.0009	2	0.0063	1.0000000	E
<input type="radio"/>	GO:0006888	8,6,5,7	ER to Golgi vesicle-mediated transport	81	0.0125	4	0.0126	1.0000000	E
<input type="radio"/>	GO:0031577	8,7	spindle checkpoint	24	0.0037	3	0.0094	1.0000000	E
<input type="radio"/>	GO:0042775	9,6	organelle ATP synthesis coupled electron transport	25	0.0039	2	0.0063	1.0000000	E
<input type="radio"/>	GO:0006536	7,8	glutamate metabolic process	16	0.0025	2	0.0063	1.0000000	E
<input type="radio"/>	GO:0000075	7,6	cell cycle checkpoint	53	0.0082	5	0.0157	1.0000000	E
<input type="radio"/>	GO:0007571	3,4	age-dependent general metabolic decline	7	0.0011	2	0.0063	1.0000000	E
<input type="radio"/>	GO:0007088	7,9,8,6	regulation of mitosis	55	0.0085	3	0.0094	1.0000000	E
<input type="radio"/>	GO:0043200	5,4	response to amino acid stimulus	3	0.0005	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0019321	6,7	pentose metabolic process	11	0.0017	2	0.0063	1.0000000	E
<input type="radio"/>	GO:0009250	7,8	glucan biosynthetic process	25	0.0039	4	0.0126	1.0000000	E
<input type="radio"/>	GO:0030004	9,7	cellular monovalent inorganic cation homeostasis	34	0.0053	2	0.0063	1.0000000	E
<input type="radio"/>	GO:0006020	7,8	inositol metabolic process	6	0.0009	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0007131	10,8,7,5,9,6,4	meiotic recombination	55	0.0085	6	0.0189	1.0000000	E
<input type="radio"/>	GO:0051599	5,4	response to hydrostatic pressure	2	0.0003	2	0.0063	1.0000000	E
<input type="radio"/>	GO:0046464	7,6,8	acylglycerol catabolic process	2	0.0003	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0006662	4	glycerol ether metabolic process	5	0.0008	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0006883	10,8	cellular sodium ion homeostasis	3	0.0005	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0043618	9,10,8,6	regulation of transcription from RNA polymerase II promoter in response to	4	0.0006	2	0.0063	1.0000000	E

			stress						
<input type="radio"/>	GO:0006893	9,7,6,8	Golgi to plasma membrane transport	30	0.0046	3	0.0094	1.0000000	E
<input type="radio"/>	GO:0006312	7	mitotic recombination	45	0.0069	3	0.0094	1.0000000	E
<input type="radio"/>	GO:0006879	10,8	cellular iron ion homeostasis	38	0.0059	5	0.0157	1.0000000	E
<input type="radio"/>	GO:0006869	4,5	lipid transport	34	0.0053	2	0.0063	1.0000000	E
<input type="radio"/>	GO:0046015	10,8,9,6	regulation of transcription by glucose	8	0.0012	3	0.0094	1.0000000	E
<input type="radio"/>	GO:0018410	8	peptide or protein carboxyl-terminal blocking	5	0.0008	2	0.0063	1.0000000	E
<input type="radio"/>	GO:0006744	8,7	ubiquinone biosynthetic process	9	0.0014	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0009719	3	response to endogenous stimulus	243	0.0375	17	0.0535	1.0000000	E
<input type="radio"/>	GO:0046486	5,6	glycerolipid metabolic process	5	0.0008	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0007569	4	cell aging	49	0.0076	6	0.0189	1.0000000	E
<input type="radio"/>	GO:0016237	4,6	microautophagy	11	0.0017	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0050826	6,5	response to freezing	2	0.0003	2	0.0063	1.0000000	E
<input type="radio"/>	GO:0042219	6,5	amino acid derivative catabolic process	5	0.0008	2	0.0063	1.0000000	E
<input type="radio"/>	GO:0009268	4	response to pH	5	0.0008	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0009117	5	nucleotide metabolic process	111	0.0171	6	0.0189	1.0000000	E
<input type="radio"/>	GO:0051649	5,3,4	establishment of cellular localization	606	0.0936	43	0.1352	1.0000000	E
<input type="radio"/>	GO:0000245	7,6,9,11	spliceosome assembly	19	0.0029	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0009615	4,5	response to virus	7	0.0011	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0055067	8	monovalent inorganic cation homeostasis	34	0.0053	2	0.0063	1.0000000	E
<input type="radio"/>	GO:0006897	6,5	endocytosis	86	0.0133	6	0.0189	1.0000000	E
<input type="radio"/>	GO:0019388	8,9	galactose catabolic process	5	0.0008	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0016126	6,7,8	sterol biosynthetic process	32	0.0049	2	0.0063	1.0000000	E
<input type="radio"/>	GO:0007129	10,8,7,5,9,6,4	synapsis	10	0.0015	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0007124	6,4,8,9	pseudohyphal growth	61	0.0094	4	0.0126	1.0000000	E
<input type="radio"/>	GO:0051188	5	cofactor biosynthetic process	79	0.0122	4	0.0126	1.0000000	E
<input type="radio"/>	GO:0006116	10,9	NADH oxidation	11	0.0017	2	0.0063	1.0000000	E
<input type="radio"/>	GO:0006811	4,5	ion transport	115	0.0178	6	0.0189	1.0000000	E
<input type="radio"/>	GO:0008156	9,8	negative regulation of DNA replication	8	0.0012	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0031146	11,10,12	SCF-dependent proteasomal ubiquitin-dependent protein catabolic process	8	0.0012	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0042168	6,7,5	heme metabolic process	14	0.0022	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0006766	4	vitamin metabolic process	89	0.0137	7	0.0220	1.0000000	E
<input type="radio"/>	GO:0030866	8,7	cortical actin cytoskeleton organization and biogenesis	16	0.0025	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0051171	5,4	regulation of nitrogen metabolic process	8	0.0012	2	0.0063	1.0000000	E
<input type="radio"/>	GO:0007103	6,7,5,8	spindle pole body duplication in nuclear envelope	13	0.0020	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0000710	11,9,8,6,5,10,7,4	meiotic mismatch repair	7	0.0011	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0006118	4	electron transport	33	0.0051	3	0.0094	1.0000000	E
<input type="radio"/>	GO:0032774	6	RNA biosynthetic process	524	0.0809	37	0.1164	1.0000000	E
<input type="radio"/>	GO:0006778	5,6	porphyrin metabolic process	14	0.0022	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0000147	5,9,8	actin cortical patch assembly	14	0.0022	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0009190	6,7	cyclic nucleotide biosynthetic process	2	0.0003	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0006144	6	purine base metabolic process	14	0.0022	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0050000	6,5	chromosome localization	4	0.0006	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0016540	9	protein autoprocessing	2	0.0003	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0030174	9,7,8	regulation of DNA replication initiation	10	0.0015	2	0.0063	1.0000000	E

<input type="radio"/>	GO:0055080	7	cation homeostasis	102	0.0158	8	0.0252	1.0000000	E
<input type="radio"/>	GO:0009251	8,7	glucan catabolic process	9	0.0014	2	0.0063	1.0000000	E
<input type="radio"/>	GO:0006265	6	DNA topological change	7	0.0011	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0008204	6,7,8	ergosterol metabolic process	26	0.0040	2	0.0063	1.0000000	E
<input type="radio"/>	GO:0051030	5,7,6,8	snRNA transport	23	0.0036	2	0.0063	1.0000000	E
<input type="radio"/>	GO:0000105	8,9	histidine biosynthetic process	14	0.0022	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0043328	10,9,11,8,7,12	protein targeting to vacuole during ubiquitin-dependent protein catabolic process via the MVB pathway	3	0.0005	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0007031	5	peroxisome organization and biogenesis	40	0.0062	7	0.0220	1.0000000	E
<input type="radio"/>	GO:0043331	4	response to dsRNA	7	0.0011	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0042770	5	DNA damage response, signal transduction	14	0.0022	2	0.0063	1.0000000	E
<input type="radio"/>	GO:0006270	8,6	DNA replication initiation	33	0.0051	3	0.0094	1.0000000	E
<input type="radio"/>	GO:0042401	6,7	biogenic amine biosynthetic process	18	0.0028	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0007130	11,9,8,6,5,10,7,4	synaptonemal complex assembly	6	0.0009	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0006575	5	amino acid derivative metabolic process	31	0.0048	3	0.0094	1.0000000	E
<input type="radio"/>	GO:0031023	5	microtubule organizing center organization and biogenesis	16	0.0025	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0019433	8,7,9	triacylglycerol catabolic process	2	0.0003	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0019674	9,8	NAD metabolic process	21	0.0032	2	0.0063	1.0000000	E
<input type="radio"/>	GO:0007242	5	intracellular signaling cascade	137	0.0212	13	0.0409	1.0000000	E
<input type="radio"/>	GO:0051084	7	posttranslational protein folding	1	0.0002	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0000022	6,5,10,8	mitotic spindle elongation	20	0.0031	3	0.0094	1.0000000	E
<input type="radio"/>	GO:0006457	6	protein folding	84	0.0130	9	0.0283	1.0000000	E
<input type="radio"/>	GO:0012501	5,7	programmed cell death	13	0.0020	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0006012	7,8	galactose metabolic process	10	0.0015	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0048622	6,5	reproductive sporulation	108	0.0167	10	0.0314	1.0000000	E
<input type="radio"/>	GO:0055082	6,4	cellular chemical homeostasis	115	0.0178	8	0.0252	1.0000000	E
<input type="radio"/>	GO:0019932	6	second-messenger-mediated signaling	32	0.0049	5	0.0157	1.0000000	E
<input type="radio"/>	GO:0009415	4	response to water	2	0.0003	2	0.0063	1.0000000	E
<input type="radio"/>	GO:0010383	7,5,6	cell wall polysaccharide metabolic process	16	0.0025	2	0.0063	1.0000000	E
<input type="radio"/>	GO:0000338	8	protein deneddylation	5	0.0008	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0000735	7,9,8	removal of nonhomologous ends	4	0.0006	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0019941	8,7,9	modification-dependent protein catabolic process	148	0.0229	13	0.0409	1.0000000	E
<input type="radio"/>	GO:0043631	8	RNA polyadenylation	24	0.0037	3	0.0094	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	3	0.0094	1.0000000	E
<input type="radio"/>	GO:0005980	9,8,7	glycogen catabolic process	7	0.0011	2	0.0063	1.0000000	E
<input type="radio"/>	GO:0006046	8,9	N-acetylglucosamine catabolic process	2	0.0003	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0017148	8,7,6	negative regulation of protein biosynthetic process	6	0.0009	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0033014	6	tetrapyrrole biosynthetic process	13	0.0020	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0031647	6	regulation of protein stability	3	0.0005	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0022403	5,4	cell cycle phase	353	0.0545	21	0.0660	1.0000000	E
<input type="radio"/>	GO:0019722	7	calcium-mediated signaling	7	0.0011	2	0.0063	1.0000000	E
<input type="radio"/>	GO:0009063	6,7	amino acid catabolic process	29	0.0045	2	0.0063	1.0000000	E
<input type="radio"/>	GO:0006975	9,8,5	DNA damage induced protein phosphorylation	2	0.0003	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0006275	8,7	regulation of DNA replication	19	0.0029	3	0.0094	1.0000000	E

<input type="radio"/>	GO:0051052	7,6	regulation of DNA metabolic process	41	0.0063	3	0.0094	1.0000000	E
<input type="radio"/>	GO:0000255	5	allantoin metabolic process	7	0.0011	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0006793	4	phosphorus metabolic process	212	0.0327	17	0.0535	1.0000000	E
<input type="radio"/>	GO:0010286	6,5	heat acclimation	2	0.0003	2	0.0063	1.0000000	E
<input type="radio"/>	GO:0046365	6,7	monosaccharide catabolic process	44	0.0068	3	0.0094	1.0000000	E
<input type="radio"/>	GO:0016998	5	cell wall catabolic process	1	0.0002	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0006892	8,6,5,7	post-Golgi vesicle-mediated transport	69	0.0107	8	0.0252	1.0000000	E
<input type="radio"/>	GO:0016197	7,5,6	endosome transport	49	0.0076	4	0.0126	1.0000000	E
<input type="radio"/>	GO:0048308	5	organelle inheritance	40	0.0062	2	0.0063	1.0000000	E
<input type="radio"/>	GO:0042594	6,4	response to starvation	19	0.0029	5	0.0157	1.0000000	E
<input type="radio"/>	GO:0010382	6,4	cell wall metabolic process	26	0.0040	2	0.0063	1.0000000	E
<input type="radio"/>	GO:0007126	8,6,7,5	meiosis	148	0.0229	13	0.0409	1.0000000	E
<input type="radio"/>	GO:0046497	8,7	nicotinate nucleotide metabolic process	2	0.0003	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0006101	6,7	citrate metabolic process	4	0.0006	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0051301	3	cell division	246	0.0380	15	0.0472	1.0000000	E
<input type="radio"/>	GO:0055078	9	sodium ion homeostasis	3	0.0005	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0030447	3	filamentous growth	94	0.0145	6	0.0189	1.0000000	E
<input type="radio"/>	GO:0006006	7,8	glucose metabolic process	65	0.0100	6	0.0189	1.0000000	E
<input type="radio"/>	GO:0043254	6,7,5	regulation of protein complex assembly	6	0.0009	2	0.0063	1.0000000	E
<input type="radio"/>	GO:0016584	6,10	nucleosome positioning	3	0.0005	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0008216	7,8	spermidine metabolic process	2	0.0003	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0006071	6	glycerol metabolic process	9	0.0014	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0015822	6,7,8	ornithine transport	1	0.0002	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0006030	8,6,7,9	chitin metabolic process	17	0.0026	2	0.0063	1.0000000	E
<input type="radio"/>	GO:0006605	8,6,7	protein targeting	258	0.0398	21	0.0660	1.0000000	E
<input type="radio"/>	GO:0043112	6	receptor metabolic process	5	0.0008	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0033554	4	cellular response to stress	21	0.0032	5	0.0157	1.0000000	E
<input type="radio"/>	GO:0009966	5,4	regulation of signal transduction	26	0.0040	3	0.0094	1.0000000	E
<input type="radio"/>	GO:0051276	5	chromosome organization and biogenesis	572	0.0883	30	0.0943	1.0000000	E
<input type="radio"/>	GO:0030815	10,9	negative regulation of cAMP metabolic process	2	0.0003	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0007020	8	microtubule nucleation	23	0.0036	2	0.0063	1.0000000	E
<input type="radio"/>	GO:0001306	4,5	age-dependent response to oxidative stress	6	0.0009	2	0.0063	1.0000000	E
<input type="radio"/>	GO:0007089	8,9,7,6	traversing start control point of mitotic cell cycle	6	0.0009	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0007039	7,8	vacuolar protein catabolic process	11	0.0017	3	0.0094	1.0000000	E
<input type="radio"/>	GO:0006111	8,7,9,10,6	regulation of gluconeogenesis	13	0.0020	4	0.0126	1.0000000	E
<input type="radio"/>	GO:0030001	6,7	metal ion transport	62	0.0096	5	0.0157	1.0000000	E
<input type="radio"/>	GO:0051182	5,6	coenzyme transport	1	0.0002	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0046686	6	response to cadmium ion	4	0.0006	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0007530	4,5	sex determination	35	0.0054	2	0.0063	1.0000000	E
<input type="radio"/>	GO:0009064	6,7	glutamine family amino acid metabolic process	43	0.0066	4	0.0126	1.0000000	E
<input type="radio"/>	GO:0019218	6,5,7	regulation of steroid metabolic process	1	0.0002	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0006513	10	protein monoubiquitination	22	0.0034	2	0.0063	1.0000000	E
<input type="radio"/>	GO:0006470	8,7	protein amino acid dephosphorylation	29	0.0045	3	0.0094	1.0000000	E
<input type="radio"/>	GO:0046903	3,4	secretion	250	0.0386	18	0.0566	1.0000000	E

<input type="checkbox"/>	GO:0051186	4	cofactor metabolic process	170	0.0263	14	0.0440	1.0000000	E
<input type="checkbox"/>	GO:0040008	4,3	regulation of growth	13	0.0020	1	0.0031	1.0000000	E
<input type="checkbox"/>	GO:0000011	6	vacuole inheritance	14	0.0022	1	0.0031	1.0000000	E
<input type="checkbox"/>	GO:0045021	7,6	error-free DNA repair	4	0.0006	1	0.0031	1.0000000	E
<input type="checkbox"/>	GO:0009187	6	cyclic nucleotide metabolic process	2	0.0003	1	0.0031	1.0000000	E
<input type="checkbox"/>	GO:0048468	3,5	cell development	52	0.0080	4	0.0126	1.0000000	E
<input type="checkbox"/>	GO:0032185	6	septin cytoskeleton organization and biogenesis	9	0.0014	1	0.0031	1.0000000	E
<input type="checkbox"/>	GO:0042147	8,6,7	retrograde transport, endosome to Golgi	17	0.0026	3	0.0094	1.0000000	E
<input type="checkbox"/>	GO:0006808	6,5	regulation of nitrogen utilization	8	0.0012	2	0.0063	1.0000000	E
<input type="checkbox"/>	GO:0032446	8	protein modification by small protein conjugation	84	0.0130	9	0.0283	1.0000000	E
<input type="checkbox"/>	GO:0000076	11,9,8,10	DNA replication checkpoint	5	0.0008	1	0.0031	1.0000000	E
<input type="checkbox"/>	GO:0006612	9,7,8	protein targeting to membrane	39	0.0060	3	0.0094	1.0000000	E
<input type="checkbox"/>	GO:0042244	5,6	spore wall assembly	42	0.0065	5	0.0157	1.0000000	E
<input type="checkbox"/>	GO:0019365	8,6,7	pyridine nucleotide salvage	2	0.0003	1	0.0031	1.0000000	E
<input type="checkbox"/>	GO:0006813	7,8	potassium ion transport	5	0.0008	1	0.0031	1.0000000	E
<input type="checkbox"/>	GO:0005987	8	sucrose catabolic process	6	0.0009	1	0.0031	1.0000000	E
<input type="checkbox"/>	GO:0006098	9,10,11	pentose-phosphate shunt	11	0.0017	1	0.0031	1.0000000	E
<input type="checkbox"/>	GO:0000165	7	MAPKKK cascade	20	0.0031	1	0.0031	1.0000000	E
<input type="checkbox"/>	GO:0006367	8,9,7	transcription initiation from RNA polymerase II promoter	44	0.0068	3	0.0094	1.0000000	E
<input type="checkbox"/>	GO:0000302	5	response to reactive oxygen species	12	0.0019	1	0.0031	1.0000000	E
<input type="checkbox"/>	GO:0006749	6,5	glutathione metabolic process	14	0.0022	1	0.0031	1.0000000	E
<input type="checkbox"/>	GO:0016558	10,9,7,8,6	protein import into peroxisome matrix	17	0.0026	4	0.0126	1.0000000	E
<input type="checkbox"/>	GO:0000747	4	conjugation with cellular fusion	118	0.0182	12	0.0377	1.0000000	E
<input type="checkbox"/>	GO:0005992	7,8	trehalose biosynthetic process	7	0.0011	2	0.0063	1.0000000	E
<input type="checkbox"/>	GO:0006311	10,8,7,5,9,6,4	meiotic gene conversion	22	0.0034	2	0.0063	1.0000000	E
<input type="checkbox"/>	GO:0030809	9,7,8,6	negative regulation of nucleotide biosynthetic process	2	0.0003	1	0.0031	1.0000000	E
<input type="checkbox"/>	GO:0001403	6,4,8,9	invasive growth (sensu Saccharomyces)	42	0.0065	5	0.0157	1.0000000	E
<input type="checkbox"/>	GO:0030488	8,9	tRNA methylation	15	0.0023	1	0.0031	1.0000000	E
<input type="checkbox"/>	GO:0046700	5	heterocycle catabolic process	7	0.0011	1	0.0031	1.0000000	E
<input type="checkbox"/>	GO:0006895	8,9,6,7	Golgi to endosome transport	13	0.0020	1	0.0031	1.0000000	E
<input type="checkbox"/>	GO:0006974	4	response to DNA damage stimulus	234	0.0361	14	0.0440	1.0000000	E
<input type="checkbox"/>	GO:0051231	5,4,9,7	spindle elongation	20	0.0031	3	0.0094	1.0000000	E
<input type="checkbox"/>	GO:0045990	9,7,8,5	regulation of transcription by carbon catabolites	14	0.0022	3	0.0094	1.0000000	E
<input type="checkbox"/>	GO:0006595	6,7	polyamine metabolic process	7	0.0011	2	0.0063	1.0000000	E
<input type="checkbox"/>	GO:0051181	4,5	cofactor transport	10	0.0015	1	0.0031	1.0000000	E
<input type="checkbox"/>	GO:0006608	10,11,8,9,7	snRNP protein import into nucleus	23	0.0036	2	0.0063	1.0000000	E
<input type="checkbox"/>	GO:0006915	6,8	apoptosis	13	0.0020	1	0.0031	1.0000000	E
<input type="checkbox"/>	GO:0008361	4,6,7	regulation of cell size	129	0.0199	7	0.0220	1.0000000	E
<input type="checkbox"/>	GO:0042843	8,9	D-xylose catabolic process	4	0.0006	1	0.0031	1.0000000	E
<input type="checkbox"/>	GO:0019660	6	glycolytic fermentation	8	0.0012	1	0.0031	1.0000000	E
<input type="checkbox"/>	GO:0032505	4,3	reproduction of a single-celled organism	194	0.0300	11	0.0346	1.0000000	E
<input type="checkbox"/>	GO:0043543	7	protein amino acid acylation	62	0.0096	6	0.0189	1.0000000	E
<input type="checkbox"/>	GO:0019654	8,6	acetate fermentation	1	0.0002	1	0.0031	1.0000000	E
<input type="checkbox"/>	GO:0045934	7,6	negative regulation of nucleobase, nucleoside, nucleotide and nucleic acid	179	0.0276	13	0.0409	1.0000000	E

			metabolic process							
<input type="radio"/>	GO:0006468	8,7	protein amino acid phosphorylation	101	0.0156	12	0.0377	1.0000000	E	
<input type="radio"/>	GO:0006526	8,9,6,5	arginine biosynthetic process	10	0.0015	1	0.0031	1.0000000	E	
<input type="radio"/>	GO:0009076	7,8	histidine family amino acid biosynthetic process	14	0.0022	1	0.0031	1.0000000	E	
<input type="radio"/>	GO:0009894	5,4	regulation of catabolic process	15	0.0023	1	0.0031	1.0000000	E	
<input type="radio"/>	GO:0019566	7,8	arabinose metabolic process	4	0.0006	1	0.0031	1.0000000	E	
<input type="radio"/>	GO:0016562	6,11,10,8,9,7	protein import into peroxisome matrix, receptor recycling	5	0.0008	1	0.0031	1.0000000	E	
<input type="radio"/>	GO:0006449	8,7,9,6	regulation of translational termination	3	0.0005	1	0.0031	1.0000000	E	
<input type="radio"/>	GO:0007533	5,7,6	mating type switching	29	0.0045	2	0.0063	1.0000000	E	
<input type="radio"/>	GO:0042710	3	biofilm formation	5	0.0008	2	0.0063	1.0000000	E	
<input type="radio"/>	GO:0006473	8	protein amino acid acetylation	48	0.0074	5	0.0157	1.0000000	E	
<input type="radio"/>	GO:0006527	8,9,6,5	arginine catabolic process	2	0.0003	1	0.0031	1.0000000	E	
<input type="radio"/>	GO:0006501	9,8,7	C-terminal protein lipidation	4	0.0006	1	0.0031	1.0000000	E	
<input type="radio"/>	GO:0000722	9,8	telomere maintenance via recombination	19	0.0029	1	0.0031	1.0000000	E	
<input type="radio"/>	GO:0051707	3,4	response to other organism	7	0.0011	1	0.0031	1.0000000	E	
<input type="radio"/>	GO:0000090	7,8,9,6	mitotic anaphase	6	0.0009	1	0.0031	1.0000000	E	
<input type="radio"/>	GO:0032443	9,8,7,10	regulation of ergosterol biosynthetic process	1	0.0002	1	0.0031	1.0000000	E	
<input type="radio"/>	GO:0006044	7,8	N-acetylglucosamine metabolic process	19	0.0029	2	0.0063	1.0000000	E	
<input type="radio"/>	GO:0046487	5,7	glyoxylate metabolic process	5	0.0008	1	0.0031	1.0000000	E	
<input type="radio"/>	GO:0006639	6,5,7	acylglycerol metabolic process	5	0.0008	1	0.0031	1.0000000	E	
<input type="radio"/>	GO:0005979	8,7,9,10,6	regulation of glycogen biosynthetic process	6	0.0009	1	0.0031	1.0000000	E	
<input type="radio"/>	GO:0007017	6	microtubule-based process	101	0.0156	9	0.0283	1.0000000	E	
<input type="radio"/>	GO:0016570	10,8	histone modification	91	0.0141	6	0.0189	1.0000000	E	
<input type="radio"/>	GO:0006596	7,8	polyamine biosynthetic process	4	0.0006	1	0.0031	1.0000000	E	
<input type="radio"/>	GO:0005996	5,6	monosaccharide metabolic process	92	0.0142	9	0.0283	1.0000000	E	
<input type="radio"/>	GO:0006873	7,5	cellular ion homeostasis	115	0.0178	8	0.0252	1.0000000	E	
<input type="radio"/>	GO:0045333	5	cellular respiration	89	0.0137	7	0.0220	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	3	0.0094	1.0000000	E	
<input type="radio"/>	GO:0006511	9,8,10	ubiquitin-dependent protein catabolic process	148	0.0229	13	0.0409	1.0000000	E	
<input type="radio"/>	GO:0009102	6,7,8	biotin biosynthetic process	7	0.0011	1	0.0031	1.0000000	E	
<input type="radio"/>	GO:0007186	6	G-protein coupled receptor protein signaling pathway	34	0.0053	3	0.0094	1.0000000	E	
<input type="radio"/>	GO:0030258	5,6	lipid modification	13	0.0020	1	0.0031	1.0000000	E	
<input type="radio"/>	GO:0006779	6,7	porphyrin biosynthetic process	13	0.0020	1	0.0031	1.0000000	E	
<input type="radio"/>	GO:0044267	5	cellular protein metabolic process	1498	0.2313	82	0.2579	1.0000000	E	
<input type="radio"/>	GO:0043255	7,6,5	regulation of carbohydrate biosynthetic process	19	0.0029	5	0.0157	1.0000000	E	
<input type="radio"/>	GO:0045013	10,8,9,6	negative regulation of transcription by carbon catabolites	8	0.0012	3	0.0094	1.0000000	E	
<input type="radio"/>	GO:0032507	6,5,4	maintenance of cellular protein localization	29	0.0045	2	0.0063	1.0000000	E	
<input type="radio"/>	GO:0019655	6,7	glucose catabolic process to ethanol	7	0.0011	1	0.0031	1.0000000	E	
<input type="radio"/>	GO:0009408	5,4	response to heat	23	0.0036	5	0.0157	1.0000000	E	
<input type="radio"/>	GO:0006817	7,8	phosphate transport	10	0.0015	1	0.0031	1.0000000	E	
<input type="radio"/>	GO:0055071	9	manganese ion homeostasis	5	0.0008	1	0.0031	1.0000000	E	
<input type="radio"/>	GO:0006875	9,7	cellular metal ion homeostasis	19	0.0029	1	0.0031	1.0000000	E	
<input type="radio"/>	GO:0006734	9,8	NADH metabolic process	14	0.0022	2	0.0063	1.0000000	E	

<input type="radio"/>	GO:0007166	5	cell surface receptor linked signal transduction	52	0.0080	5	0.0157	1.0000000	E
<input type="radio"/>	GO:0031929	6	TOR signaling pathway	13	0.0020	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0042375	5	quinone cofactor metabolic process	9	0.0014	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0009892	5,4	negative regulation of metabolic process	208	0.0321	19	0.0597	1.0000000	E
<input type="radio"/>	GO:0006613	10,9,8,7,6	cotranslational protein targeting to membrane	23	0.0036	2	0.0063	1.0000000	E
<input type="radio"/>	GO:0007568	3	aging	49	0.0076	6	0.0189	1.0000000	E
<input type="radio"/>	GO:0006740	10,9	NADPH regeneration	14	0.0022	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0000916	6,5,4	cytokinesis, contractile ring contraction	4	0.0006	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0019794	6,7	nonprotein amino acid metabolic process	9	0.0014	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0051058	7,8,6	negative regulation of small GTPase mediated signal transduction	6	0.0009	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0051129	6,5	negative regulation of cell organization and biogenesis	7	0.0011	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0006807	3	nitrogen compound metabolic process	251	0.0388	15	0.0472	1.0000000	E
<input type="radio"/>	GO:0045229	4	external encapsulating structure organization and biogenesis	200	0.0309	13	0.0409	1.0000000	E
<input type="radio"/>	GO:0000051	4,3	urea cycle intermediate metabolic process	15	0.0023	2	0.0063	1.0000000	E
<input type="radio"/>	GO:0001881	5,7	receptor recycling	5	0.0008	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0048518	4	positive regulation of biological process	124	0.0191	11	0.0346	1.0000000	E
<input type="radio"/>	GO:0046164	5	alcohol catabolic process	47	0.0073	3	0.0094	1.0000000	E
<input type="radio"/>	GO:0007231	6,5	osmosensory signaling pathway	22	0.0034	2	0.0063	1.0000000	E
<input type="radio"/>	GO:0016042	4,5	lipid catabolic process	8	0.0012	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0019953	3	sexual reproduction	118	0.0182	12	0.0377	1.0000000	E
<input type="radio"/>	GO:0006999	6	nuclear pore organization and biogenesis	29	0.0045	2	0.0063	1.0000000	E
<input type="radio"/>	GO:0051234	2,3	establishment of localization	1004	0.1550	66	0.2075	1.0000000	E
<input type="radio"/>	GO:0006094	8,9	gluconeogenesis	28	0.0043	4	0.0126	1.0000000	E
<input type="radio"/>	GO:0006261	7	DNA-dependent DNA replication	97	0.0150	5	0.0157	1.0000000	E
<input type="radio"/>	GO:0006355	8,7	regulation of transcription, DNA-dependent	359	0.0554	29	0.0912	1.0000000	E
<input type="radio"/>	GO:0051085	8	chaperone cofactor-dependent protein folding	1	0.0002	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0006084	6	acetyl-CoA metabolic process	20	0.0031	3	0.0094	1.0000000	E
<input type="radio"/>	GO:0006768	5,7,6	biotin metabolic process	7	0.0011	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0045053	7,6,5,4	protein retention in Golgi	20	0.0031	2	0.0063	1.0000000	E
<input type="radio"/>	GO:0006886	7,5,6	intracellular protein transport	274	0.0423	22	0.0692	1.0000000	E
<input type="radio"/>	GO:0007010	5	cytoskeleton organization and biogenesis	227	0.0351	13	0.0409	1.0000000	E
<input type="radio"/>	GO:0006767	5	water-soluble vitamin metabolic process	89	0.0137	7	0.0220	1.0000000	E
<input type="radio"/>	GO:0051603	7,8	proteolysis involved in cellular protein catabolic process	151	0.0233	15	0.0472	1.0000000	E
<input type="radio"/>	GO:0046461	6,7	neutral lipid catabolic process	2	0.0003	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0043241	6,5	protein complex disassembly	28	0.0043	2	0.0063	1.0000000	E
<input type="radio"/>	GO:0051053	8,7	negative regulation of DNA metabolic process	20	0.0031	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0000437	11,9,10,7	negative regulation of transcription from RNA polymerase II promoter by carbon catabolites	7	0.0011	3	0.0094	1.0000000	E
<input type="radio"/>	GO:0006115	6	ethanol biosynthetic process	2	0.0003	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0051595	5	response to methylglyoxal	3	0.0005	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0046854	7,9,8,10	phosphoinositide phosphorylation	5	0.0008	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0022413	5,4	reproductive process in single-celled organism	149	0.0230	11	0.0346	1.0000000	E

<input type="radio"/>	GO:0009113	7,6	purine base biosynthetic process	6	0.0009	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0006855	5,6	multidrug transport	8	0.0012	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0016481	8,7	negative regulation of transcription	162	0.0250	11	0.0346	1.0000000	E
<input type="radio"/>	GO:0031321	4,8,6,7	prospore formation	4	0.0006	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0001302	5	replicative cell aging	39	0.0060	4	0.0126	1.0000000	E
<input type="radio"/>	GO:0045893	9,8	positive regulation of transcription, DNA-dependent	95	0.0147	8	0.0252	1.0000000	E
<input type="radio"/>	GO:0033036	3	macromolecule localization	382	0.0590	26	0.0818	1.0000000	E
<input type="radio"/>	GO:0000122	10,9	negative regulation of transcription from RNA polymerase II promoter	63	0.0097	6	0.0189	1.0000000	E
<input type="radio"/>	GO:0043486	11	histone exchange	9	0.0014	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0006379	8	mRNA cleavage	26	0.0040	3	0.0094	1.0000000	E
<input type="radio"/>	GO:0030154	4	cell differentiation	173	0.0267	15	0.0472	1.0000000	E
<input type="radio"/>	GO:0006378	9	mRNA polyadenylation	18	0.0028	3	0.0094	1.0000000	E
<input type="radio"/>	GO:0018345	9,8,7	protein palmitoylation	8	0.0012	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0000723	8	telomere maintenance	274	0.0423	17	0.0535	1.0000000	E
<input type="radio"/>	GO:0007346	7,5,6	regulation of progression through mitotic cell cycle	13	0.0020	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0006696	7,8,9	ergosterol biosynthetic process	26	0.0040	2	0.0063	1.0000000	E
<input type="radio"/>	GO:0009051	10,7,11,12,8	pentose-phosphate shunt, oxidative branch	5	0.0008	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0033214	12,10	iron assimilation by chelation and transport	6	0.0009	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0043146	9,8,12,10,7	spindle stabilization	2	0.0003	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0031163	5	metallo-sulfur cluster assembly	11	0.0017	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0006796	5	phosphate metabolic process	212	0.0327	17	0.0535	1.0000000	E
<input type="radio"/>	GO:0009743	5,4	response to carbohydrate stimulus	6	0.0009	2	0.0063	1.0000000	E
<input type="radio"/>	GO:0009438	5	methylglyoxal metabolic process	3	0.0005	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0051029	5,7,6,8	rRNA transport	26	0.0040	2	0.0063	1.0000000	E
<input type="radio"/>	GO:0008645	6,7	hexose transport	26	0.0040	5	0.0157	1.0000000	E
<input type="radio"/>	GO:0033205	5,4	cytokinesis during cell cycle	7	0.0011	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0044257	6,7	cellular protein catabolic process	160	0.0247	17	0.0535	1.0000000	E
<input type="radio"/>	GO:0005976	5	polysaccharide metabolic process	65	0.0100	9	0.0283	1.0000000	E
<input type="radio"/>	GO:0046777	9,10,8	protein amino acid autophosphorylation	2	0.0003	1	0.0031	1.0000000	E
<input type="radio"/>	GO:0007163	6,3,7	establishment and/or maintenance of cell polarity	115	0.0178	4	0.0126	1.0000000	D
<input type="radio"/>	GO:0009165	5,6	nucleotide biosynthetic process	59	0.0091	1	0.0031	1.0000000	D
<input type="radio"/>	GO:0051453	11,8,9	regulation of cellular pH	25	0.0039	1	0.0031	1.0000000	D
<input type="radio"/>	GO:0006405	10,8,5,7,9,6	RNA export from nucleus	79	0.0122	3	0.0094	1.0000000	D
<input type="radio"/>	GO:0006996	4	organelle organization and biogenesis	1388	0.2143	56	0.1761	1.0000000	D
<input type="radio"/>	GO:0000819	7,4	sister chromatid segregation	62	0.0096	1	0.0031	1.0000000	D
<input type="radio"/>	GO:0048590	3	non-developmental growth	35	0.0054	1	0.0031	1.0000000	D
<input type="radio"/>	GO:0051640	5,4	organelle localization	56	0.0086	2	0.0063	1.0000000	D
<input type="radio"/>	GO:0008202	5,6	steroid metabolic process	43	0.0066	2	0.0063	1.0000000	D
<input type="radio"/>	GO:0046999	5,4	regulation of conjugation	30	0.0046	1	0.0031	1.0000000	D
<input type="radio"/>	GO:0007243	6	protein kinase cascade	23	0.0036	1	0.0031	1.0000000	D
<input type="radio"/>	GO:0000087	7,5,6	M phase of mitotic cell cycle	129	0.0199	5	0.0157	1.0000000	D
<input type="radio"/>	GO:0009451	6	RNA modification	139	0.0215	3	0.0094	1.0000000	D
<input type="radio"/>	GO:0000750	8,7,6	pheromone-dependent signal transduction during conjugation with cellular fusion	28	0.0043	1	0.0031	1.0000000	D

<input type="radio"/>	GO:0016070	5	RNA metabolic process	1058	0.1634	49	0.1541	1.0000000	D
<input type="radio"/>	GO:0006497	8,7,6	protein amino acid lipidation	48	0.0074	2	0.0063	1.0000000	D
<input type="radio"/>	GO:0048311	7,6	mitochondrion distribution	26	0.0040	1	0.0031	1.0000000	D
<input type="radio"/>	GO:0009653	4,3	anatomical structure morphogenesis	248	0.0383	11	0.0346	1.0000000	D
<input type="radio"/>	GO:0007121	8,6,10,7,11,5	bipolar cellular bud site selection	32	0.0049	1	0.0031	1.0000000	D
<input type="radio"/>	GO:0031497	5,9	chromatin assembly	104	0.0161	5	0.0157	1.0000000	D
<input type="radio"/>	GO:0009272	7	chitin- and beta-glucan-containing cell wall biogenesis	33	0.0051	1	0.0031	1.0000000	D
<input type="radio"/>	GO:0032989	4,5	cellular structure morphogenesis	248	0.0383	11	0.0346	1.0000000	D
<input type="radio"/>	GO:0031137	6,5	regulation of conjugation with cellular fusion	30	0.0046	1	0.0031	1.0000000	D
<input type="radio"/>	GO:0006413	7,6	translational initiation	49	0.0076	1	0.0031	1.0000000	D
<input type="radio"/>	GO:0000096	6,7,5	sulfur amino acid metabolic process	33	0.0051	1	0.0031	1.0000000	D
<input type="radio"/>	GO:0044271	5,4	nitrogen compound biosynthetic process	115	0.0178	5	0.0157	1.0000000	D
<input type="radio"/>	GO:0048856	3	anatomical structure development	248	0.0383	11	0.0346	1.0000000	D
<input type="radio"/>	GO:0000001	8,7,6	mitochondrion inheritance	26	0.0040	1	0.0031	1.0000000	D
<input type="radio"/>	GO:0040029	4	regulation of gene expression, epigenetic	100	0.0154	4	0.0126	1.0000000	D
<input type="radio"/>	GO:0006368	9,7,8	RNA elongation from RNA polymerase II promoter	53	0.0082	1	0.0031	1.0000000	D
<input type="radio"/>	GO:0045814	5	negative regulation of gene expression, epigenetic	95	0.0147	4	0.0126	1.0000000	D
<input type="radio"/>	GO:0007117	6,5,4	budding cell bud growth	35	0.0054	1	0.0031	1.0000000	D
<input type="radio"/>	GO:0009100	6	glycoprotein metabolic process	79	0.0122	1	0.0031	1.0000000	D
<input type="radio"/>	GO:0006890	8,6,5,7	retrograde vesicle-mediated transport, Golgi to ER	24	0.0037	1	0.0031	1.0000000	D
<input type="radio"/>	GO:0006752	6	group transfer coenzyme metabolic process	44	0.0068	2	0.0063	1.0000000	D
<input type="radio"/>	GO:0006730	4	one-carbon compound metabolic process	97	0.0150	2	0.0063	1.0000000	D
<input type="radio"/>	GO:0051170	9,7,8	nuclear import	50	0.0077	2	0.0063	1.0000000	D
<input type="radio"/>	GO:0016575	11,9	histone deacetylation	24	0.0037	1	0.0031	1.0000000	D
<input type="radio"/>	GO:0006399	6	tRNA metabolic process	121	0.0187	3	0.0094	1.0000000	D
<input type="radio"/>	GO:0006409	11,9,6,8,10,7	tRNA export from nucleus	29	0.0045	1	0.0031	1.0000000	D
<input type="radio"/>	GO:0006520	5,6	amino acid metabolic process	187	0.0289	7	0.0220	1.0000000	D
<input type="radio"/>	GO:0015837	4,5	amine transport	50	0.0077	2	0.0063	1.0000000	D
<input type="radio"/>	GO:0006997	5	nuclear organization and biogenesis	57	0.0088	2	0.0063	1.0000000	D
<input type="radio"/>	GO:0009112	5	nucleobase metabolic process	31	0.0048	1	0.0031	1.0000000	D
<input type="radio"/>	GO:0006665	6,7	sphingolipid metabolic process	30	0.0046	1	0.0031	1.0000000	D
<input type="radio"/>	GO:0006476	8	protein amino acid deacetylation	26	0.0040	1	0.0031	1.0000000	D
<input type="radio"/>	GO:0009108	6	coenzyme biosynthetic process	66	0.0102	3	0.0094	1.0000000	D
<input type="radio"/>	GO:0008150	1	biological process	6476	1.0000	318	1.0000	1.0000000	D
<input type="radio"/>	GO:0000282	7,9,5,6,10	cellular bud site selection	66	0.0102	3	0.0094	1.0000000	D
<input type="radio"/>	GO:0016071	6	mRNA metabolic process	210	0.0324	10	0.0314	1.0000000	D
<input type="radio"/>	GO:0000070	9,7,5,8,6,4	mitotic sister chromatid segregation	59	0.0091	1	0.0031	1.0000000	D
<input type="radio"/>	GO:0043284	5	biopolymer biosynthetic process	354	0.0547	7	0.0220	1.0000000	D
<input type="radio"/>	GO:0032259	5	methylation	83	0.0128	2	0.0063	1.0000000	D
<input type="radio"/>	GO:0046352	7	disaccharide catabolic process	24	0.0037	1	0.0031	1.0000000	D
<input type="radio"/>	GO:0030468	8,5,9	establishment of cell polarity (sensu Fungi)	66	0.0102	3	0.0094	1.0000000	D
<input type="radio"/>	GO:0043681	6,7,8	protein import into mitochondrion	40	0.0062	1	0.0031	1.0000000	D
<input type="radio"/>	GO:0018193	7	peptidyl-amino acid modification	28	0.0043	1	0.0031	1.0000000	D

<input type="radio"/>	GO:0007114	5,4	cell budding	85	0.0131	2	0.0063	1.0000000	D
<input type="radio"/>	GO:0007067	8,6,7,5	mitosis	127	0.0196	5	0.0157	1.0000000	D
<input type="radio"/>	GO:0019954	3	asexual reproduction	85	0.0131	2	0.0063	1.0000000	D
<input type="radio"/>	GO:0008380	7	RNA splicing	132	0.0204	3	0.0094	1.0000000	D
<input type="radio"/>	GO:0009069	6,7	serine family amino acid metabolic process	24	0.0037	1	0.0031	1.0000000	D
<input type="radio"/>	GO:0006007	8,9	glucose catabolic process	34	0.0053	1	0.0031	1.0000000	D
<input type="radio"/>	GO:0006260	6	DNA replication	117	0.0181	5	0.0157	1.0000000	D
<input type="radio"/>	GO:0030384	8,9	phosphoinositide metabolic process	43	0.0066	1	0.0031	1.0000000	D
<input type="radio"/>	GO:0007035	13,10,6,11	vacuolar acidification	24	0.0037	1	0.0031	1.0000000	D
<input type="radio"/>	GO:0006397	7	mRNA processing	157	0.0242	6	0.0189	1.0000000	D
<input type="radio"/>	GO:0000377	9	RNA splicing, via transesterification reactions with bulged adenosine as nucleophile	103	0.0159	2	0.0063	1.0000000	D
<input type="radio"/>	GO:0022618	6,5	protein-RNA complex assembly	144	0.0222	2	0.0063	1.0000000	D
<input type="radio"/>	GO:0042157	6	lipoprotein metabolic process	48	0.0074	2	0.0063	1.0000000	D
<input type="radio"/>	GO:0006725	4	aromatic compound metabolic process	60	0.0093	1	0.0031	1.0000000	D
<input type="radio"/>	GO:0006606	9,10,7,8,6	protein import into nucleus	50	0.0077	2	0.0063	1.0000000	D
<input type="radio"/>	GO:0006406	11,9,6,8,10,7	mRNA export from nucleus	66	0.0102	3	0.0094	1.0000000	D
<input type="radio"/>	GO:0006333	8	chromatin assembly or disassembly	119	0.0184	5	0.0157	1.0000000	D
<input type="radio"/>	GO:0050658	4,6,5,7	RNA transport	80	0.0124	3	0.0094	1.0000000	D
<input type="radio"/>	GO:0000086	8,5,6,7,4	G2/M transition of mitotic cell cycle	35	0.0054	1	0.0031	1.0000000	D
<input type="radio"/>	GO:0045005	8,6	maintenance of fidelity during DNA-dependent DNA replication	25	0.0039	1	0.0031	1.0000000	D
<input type="radio"/>	GO:0000082	8,5,6,7,4	G1/S transition of mitotic cell cycle	52	0.0080	2	0.0063	1.0000000	D
<input type="radio"/>	GO:0046942	5,6	carboxylic acid transport	54	0.0083	1	0.0031	1.0000000	D
<input type="radio"/>	GO:0009309	5,6	amine biosynthetic process	114	0.0176	5	0.0157	1.0000000	D
<input type="radio"/>	GO:0007059	3	chromosome segregation	119	0.0184	4	0.0126	1.0000000	D
<input type="radio"/>	GO:0043414	6	biopolymer methylation	83	0.0128	2	0.0063	1.0000000	D
<input type="radio"/>	GO:0030467	7,4,8	establishment and/or maintenance of cell polarity (sensu Fungi)	66	0.0102	3	0.0094	1.0000000	D
<input type="radio"/>	GO:0006944	5	membrane fusion	59	0.0091	1	0.0031	1.0000000	D
<input type="radio"/>	GO:0051329	7,5,6	interphase of mitotic cell cycle	112	0.0173	4	0.0126	1.0000000	D
<input type="radio"/>	GO:0051031	5,7,6,8	tRNA transport	30	0.0046	1	0.0031	1.0000000	D
<input type="radio"/>	GO:0051278	8,7	chitin- and beta-glucan-containing cell wall polysaccharide biosynthetic process	24	0.0037	1	0.0031	1.0000000	D
<input type="radio"/>	GO:0032005	7,6	signal transduction during conjugation with cellular fusion	28	0.0043	1	0.0031	1.0000000	D
<input type="radio"/>	GO:0051318	6,7,5	G1 phase	27	0.0042	1	0.0031	1.0000000	D
<input type="radio"/>	GO:0051236	3,4,5	establishment of RNA localization	80	0.0124	3	0.0094	1.0000000	D
<input type="radio"/>	GO:0006865	5,6,7	amino acid transport	39	0.0060	1	0.0031	1.0000000	D
<input type="radio"/>	GO:0051128	5,4	regulation of cellular component organization and biogenesis	30	0.0046	1	0.0031	1.0000000	D
<input type="radio"/>	GO:0051452	12,9,10	cellular pH reduction	24	0.0037	1	0.0031	1.0000000	D
<input type="radio"/>	GO:0000724	8,7	double-strand break repair via homologous recombination	25	0.0039	1	0.0031	1.0000000	D
<input type="radio"/>	GO:0016458	5	gene silencing	95	0.0147	4	0.0126	1.0000000	D
<input type="radio"/>	GO:0007105	6,4	cytokinesis, site selection	66	0.0102	3	0.0094	1.0000000	D
<input type="radio"/>	GO:0008033	7	tRNA processing	84	0.0130	3	0.0094	1.0000000	D
<input type="radio"/>	GO:0006790	4	sulfur metabolic process	67	0.0103	3	0.0094	1.0000000	D
<input type="radio"/>	GO:0006643	5,6	membrane lipid metabolic process	125	0.0193	4	0.0126	1.0000000	D
<input type="radio"/>	GO:0006354	8,6,7	RNA elongation	59	0.0091	1	0.0031	1.0000000	D

<input type="checkbox"/>	GO:0000398	8,10	nuclear mRNA splicing, via spliceosome	102	0.0158	2	0.0063	1.0000000	D
<input type="checkbox"/>	GO:0006650	7,8	glycerophospholipid metabolic process	60	0.0093	1	0.0031	1.0000000	D
<input type="checkbox"/>	GO:0030641	10,8	cellular hydrogen ion homeostasis	25	0.0039	1	0.0031	1.0000000	D
<input type="checkbox"/>	GO:0030010	7,4,8	establishment of cell polarity	103	0.0159	4	0.0126	1.0000000	D
<input type="checkbox"/>	GO:0007006	5,6	mitochondrial membrane organization and biogenesis	24	0.0037	1	0.0031	1.0000000	D
<input type="checkbox"/>	GO:0007005	5	mitochondrion organization and biogenesis	110	0.0170	5	0.0157	1.0000000	D
<input type="checkbox"/>	GO:0008610	5,4,6	lipid biosynthetic process	129	0.0199	4	0.0126	1.0000000	D
<input type="checkbox"/>	GO:0006289	7,6	nucleotide-excision repair	44	0.0068	2	0.0063	1.0000000	D
<input type="checkbox"/>	GO:0040020	7,9,8,6	regulation of meiosis	22	0.0034	1	0.0031	1.0000000	D
<input type="checkbox"/>	GO:0043044	10	ATP-dependent chromatin remodeling	23	0.0036	1	0.0031	1.0000000	D
<input type="checkbox"/>	GO:0044272	5	sulfur compound biosynthetic process	22	0.0034	1	0.0031	1.0000000	D
<input type="checkbox"/>	GO:0031509	7,11	telomeric heterochromatin formation	60	0.0093	1	0.0031	1.0000000	D
<input type="checkbox"/>	GO:0007096	8,10,9,7	regulation of exit from mitosis	24	0.0037	1	0.0031	1.0000000	D
<input type="checkbox"/>	GO:0065009	3	regulation of a molecular function	46	0.0071	2	0.0063	1.0000000	D
<input type="checkbox"/>	GO:0030150	10,9,8,7	protein import into mitochondrial matrix	22	0.0034	1	0.0031	1.0000000	D
<input type="checkbox"/>	GO:0000902	5,6	cell morphogenesis	248	0.0383	11	0.0346	1.0000000	D
<input type="checkbox"/>	GO:0006119	7,4	oxidative phosphorylation	46	0.0071	2	0.0063	1.0000000	D
<input type="checkbox"/>	GO:0015672	6,7	monovalent inorganic cation transport	32	0.0049	1	0.0031	1.0000000	D
<input type="checkbox"/>	GO:0006403	4	RNA localization	90	0.0139	4	0.0126	1.0000000	D
<input type="checkbox"/>	GO:0050657	5,6	nucleic acid transport	80	0.0124	3	0.0094	1.0000000	D
<input type="checkbox"/>	GO:0001510	7	RNA methylation	60	0.0093	1	0.0031	1.0000000	D
<input type="checkbox"/>	GO:0006555	7,8,6	methionine metabolic process	24	0.0037	1	0.0031	1.0000000	D
<input type="checkbox"/>	GO:0008652	6,7	amino acid biosynthetic process	106	0.0164	4	0.0126	1.0000000	D
<input type="checkbox"/>	GO:0000041	7,8	transition metal ion transport	46	0.0071	2	0.0063	1.0000000	D
<input type="checkbox"/>	GO:0065004	6,5	protein-DNA complex assembly	74	0.0114	3	0.0094	1.0000000	D
<input type="checkbox"/>	GO:0030466	11,7,8,12,10	chromatin silencing at silent mating-type cassette	30	0.0046	1	0.0031	1.0000000	D
<input type="checkbox"/>	GO:0006298	7,9,6	mismatch repair	25	0.0039	1	0.0031	1.0000000	D
<input type="checkbox"/>	GO:0065003	5,4	macromolecular complex assembly	328	0.0506	16	0.0503	1.0000000	D
<input type="checkbox"/>	GO:0008213	8	protein amino acid alkylation	23	0.0036	1	0.0031	1.0000000	D
<input type="checkbox"/>	GO:0006644	6,7	phospholipid metabolic process	97	0.0150	3	0.0094	1.0000000	D
<input type="checkbox"/>	GO:0000725	7,6	recombinational repair	29	0.0045	1	0.0031	1.0000000	D
<input type="checkbox"/>	GO:0046467	6,5,7	membrane lipid biosynthetic process	78	0.0120	1	0.0031	1.0000000	D
<input type="checkbox"/>	GO:0006303	8,7	double-strand break repair via nonhomologous end joining	23	0.0036	1	0.0031	1.0000000	D
<input type="checkbox"/>	GO:0000080	7,8,6	G1 phase of mitotic cell cycle	27	0.0042	1	0.0031	1.0000000	D
<input type="checkbox"/>	GO:0006479	9,7	protein amino acid methylation	23	0.0036	1	0.0031	1.0000000	D
<input type="checkbox"/>	GO:0007033	5	vacuole organization and biogenesis	67	0.0103	2	0.0063	1.0000000	D
<input type="checkbox"/>	GO:0006348	11,7,8,12,10	chromatin silencing at telomere	60	0.0093	1	0.0031	1.0000000	D
<input type="checkbox"/>	GO:0006885	7	regulation of pH	29	0.0045	1	0.0031	1.0000000	D
<input type="checkbox"/>	GO:0008654	7,6,8	phospholipid biosynthetic process	58	0.0090	1	0.0031	1.0000000	D
<input type="checkbox"/>	GO:0006611	9,10,7,8	protein export from nucleus	56	0.0086	2	0.0063	1.0000000	D
<input type="checkbox"/>	GO:0046112	6,5	nucleobase biosynthetic process	21	0.0032	1	0.0031	1.0000000	D
<input type="checkbox"/>	GO:0030433	9,11,10,12	ER-associated protein catabolic process	35	0.0054	1	0.0031	1.0000000	D
<input type="checkbox"/>	GO:0031505	6	chitin- and beta-glucan-containing cell wall organization and biogenesis	44	0.0068	2	0.0063	1.0000000	D
<input type="checkbox"/>	GO:0051028	5,7,6,8	mRNA transport	66	0.0102	3	0.0094	1.0000000	D

<input type="radio"/>	GO:0006281	6,5	DNA repair	193	0.0298	9	0.0283	1.0000000	D
<input type="radio"/>	GO:0031507	6,10	heterochromatin formation	95	0.0147	4	0.0126	1.0000000	D
<input type="radio"/>	GO:0006906	6,5	vesicle fusion	28	0.0043	1	0.0031	1.0000000	D
<input type="radio"/>	GO:0042158	7,5	lipoprotein biosynthetic process	48	0.0074	2	0.0063	1.0000000	D
<input type="radio"/>	GO:0030036	7	actin cytoskeleton organization and biogenesis	107	0.0165	5	0.0157	1.0000000	D
<input type="radio"/>	GO:0000375	8	RNA splicing, via transesterification reactions	110	0.0170	2	0.0063	1.0000000	D
<input type="radio"/>	GO:0030029	6	actin filament-based process	112	0.0173	5	0.0157	1.0000000	D
<input type="radio"/>	GO:0015849	4,5	organic acid transport	55	0.0085	1	0.0031	1.0000000	D
<input type="radio"/>	GO:0006887	8,6,5,7	exocytosis	44	0.0068	1	0.0031	1.0000000	D
<input type="radio"/>	GO:0051325	6,5	interphase	112	0.0173	4	0.0126	1.0000000	D
<input type="radio"/>	GO:0045851	8	pH reduction	24	0.0037	1	0.0031	1.0000000	D
<input type="radio"/>	GO:0006913	8,6,7	nucleocytoplasmic transport	129	0.0199	3	0.0094	1.0000000	D
<input type="radio"/>	GO:0051168	9,7,8	nuclear export	102	0.0158	3	0.0094	1.0000000	D
<input type="radio"/>	GO:0042546	6	cell wall biogenesis	33	0.0051	1	0.0031	1.0000000	D
<input type="radio"/>	GO:0051187	5	cofactor catabolic process	21	0.0032	1	0.0031	1.0000000	D
<input type="radio"/>	GO:0051646	6,5	mitochondrion localization	27	0.0042	1	0.0031	1.0000000	D
<input type="radio"/>	GO:0016125	5,6,7	sterol metabolic process	42	0.0065	2	0.0063	1.0000000	D
<input type="radio"/>	GO:0015931	4,5	nucleobase, nucleoside, nucleotide and nucleic acid transport	90	0.0139	3	0.0094	1.0000000	D
<input type="radio"/>	GO:0009066	6,7	aspartate family amino acid metabolic process	46	0.0071	1	0.0031	1.0000000	D
<input type="radio"/>	GO:0000278	4	mitotic cell cycle	266	0.0411	11	0.0346	1.0000000	D
<input type="radio"/>	GO:0051169	7,5,6	nuclear transport	129	0.0199	3	0.0094	1.0000000	D
<input type="radio"/>	GO:0050790	4	regulation of catalytic activity	45	0.0069	2	0.0063	1.0000000	D
<input type="radio"/>	GO:0006302	7,6	double-strand break repair	57	0.0088	2	0.0063	1.0000000	D
<input type="radio"/>	GO:0006342	10,6,7,11,9	chromatin silencing	95	0.0147	4	0.0126	1.0000000	D
<input type="radio"/>	GO:0006396	6	RNA processing	491	0.0758	10	0.0314	0.3464252	D
<input type="radio"/>	GO:0009058	3	biosynthetic process	1249	0.1929	39	0.1226	0.1854711	D
<input type="radio"/>	GO:0009059	4	macromolecule biosynthetic process	886	0.1368	22	0.0692	0.0408618	D
<input type="radio"/>	GO:0006414	7,6	translational elongation	313	0.0483	2	0.0063	0.0131677	D
<input type="radio"/>	GO:0006412	6,5	translation	688	0.1062	9	0.0283	6.841967E-05	D
<input type="radio"/>	GO:0022613	4	ribonucleoprotein complex biogenesis and assembly	483	0.0746	2	0.0063	3.589231E-06	D