

GO-Stats Results

Your dataset contains **510** 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:0022613	4	ribonucleoprotein complex biogenesis and assembly	483	0.0746	164	0.3216	1.038014E-68	E
<input type="radio"/> GO:0042254	5	ribosome biogenesis and assembly	410	0.0633	147	0.2882	1.684421E-64	E
<input type="radio"/> GO:0006996	4	organelle organization and biogenesis	1388	0.2143	231	0.4529	1.258821E-36	E
<input type="radio"/> GO:0016072	6	rRNA metabolic process	256	0.0395	86	0.1686	3.722833E-34	E
<input type="radio"/> GO:0016070	5	RNA metabolic process	1058	0.1634	189	0.3706	9.558379E-33	E
<input type="radio"/> GO:0006396	6	RNA processing	491	0.0758	119	0.2333	5.740126E-32	E
<input type="radio"/> GO:0016043	3	cellular component organization and biogenesis	2264	0.3496	302	0.5922	1.405735E-31	E
<input type="radio"/> GO:0006364	6,7	rRNA processing	249	0.0384	81	0.1588	5.110072E-31	E
<input type="radio"/> GO:0006139	4	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	1532	0.2366	231	0.4529	1.989852E-29	E
<input type="radio"/> GO:0009987	2	cellular process	4654	0.7187	463	0.9078	8.506596E-28	E
<input type="radio"/> GO:0008152	2	metabolic process	3516	0.5429	370	0.7255	5.825835E-19	E
<input type="radio"/> GO:0042273	6,5	ribosomal large subunit biogenesis and assembly	64	0.0099	31	0.0608	3.558912E-18	E
<input type="radio"/> GO:0044238	3	primary metabolic process	3247	0.5014	345	0.6765	3.575562E-17	E
<input type="radio"/> GO:0022618	6,5	protein-RNA complex assembly	144	0.0222	45	0.0882	9.407307E-17	E
<input type="radio"/> GO:0044237	3	cellular metabolic process	3403	0.5255	354	0.6941	3.023395E-16	E
<input type="radio"/> GO:0000466	8,9	maturation of 5.8S rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	34	0.0053	21	0.0412	1.502091E-15	E
<input type="radio"/> GO:0000460	7,8	maturation of 5.8S rRNA	36	0.0056	21	0.0412	7.696127E-15	E
<input type="radio"/> GO:0043170	3	macromolecule metabolic process	2841	0.4387	299	0.5863	1.081423E-12	E
<input type="radio"/> GO:0043283	4	biopolymer metabolic process	2230	0.3443	248	0.4863	2.022841E-12	E
<input type="radio"/> GO:0022607	4	cellular component assembly	471	0.0727	81	0.1588	2.128381E-12	E
<input type="radio"/> GO:0065002	5,4	macromolecular complex assembly	228	0.0506	62	0.1216	1.890902E-	E

<input type="radio"/>	GO:0003003	3,4	macromolecular complex assembly	320	0.0000	02	0.1210	11		E
<input type="radio"/>	GO:0042255	7,6	ribosome assembly	66	0.0102	24	0.0471	4.491668E-11		E
<input type="radio"/>	GO:0000463	8,9	maturation of LSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	14	0.0022	11	0.0216	1.870059E-10		E
<input type="radio"/>	GO:0000470	7,8	maturation of LSU-rRNA	14	0.0022	11	0.0216	1.870059E-10		E
<input type="radio"/>	GO:0030490	7,8	maturation of SSU-rRNA	45	0.0069	19	0.0373	2.428457E-10		E
<input type="radio"/>	GO:0000462	8,9	maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	45	0.0069	19	0.0373	2.428457E-10		E
<input type="radio"/>	GO:0000027	9,7,8,6	ribosomal large subunit assembly and maintenance	41	0.0063	18	0.0353	3.340811E-10		E
<input type="radio"/>	GO:0006360	8,7	transcription from RNA polymerase I promoter	34	0.0053	16	0.0314	9.236192E-10		E
<input type="radio"/>	GO:0006399	6	tRNA metabolic process	121	0.0187	31	0.0608	1.556166E-09		E
<input type="radio"/>	GO:0000054	10,11,6,8,9	ribosome export from nucleus	28	0.0043	14	0.0275	3.916084E-09		E
<input type="radio"/>	GO:0042257	8,7	ribosomal subunit assembly	55	0.0085	19	0.0373	1.262150E-08		E
<input type="radio"/>	GO:0006413	7,6	translational initiation	49	0.0076	17	0.0333	6.842231E-08		E
<input type="radio"/>	GO:0006611	9,10,7,8	protein export from nucleus	56	0.0086	18	0.0353	1.063006E-07		E
<input type="radio"/>	GO:0051169	7,5,6	nuclear transport	129	0.0199	29	0.0569	1.127548E-07		E
<input type="radio"/>	GO:0006913	8,6,7	nucleocytoplasmic transport	129	0.0199	29	0.0569	1.127548E-07		E
<input type="radio"/>	GO:0051168	9,7,8	nuclear export	102	0.0158	25	0.0490	1.471001E-07		E
<input type="radio"/>	GO:0000478	7,8	endonucleolytic cleavages during rRNA processing	20	0.0031	10	0.0196	6.980923E-07		E
<input type="radio"/>	GO:0000479	8,9	endonucleolytic cleavage of tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	20	0.0031	10	0.0196	6.980923E-07		E
<input type="radio"/>	GO:0000447	9,10	endonucleolytic cleavage between SSU-rRNA and 5.8S rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	20	0.0031	10	0.0196	6.980923E-07		E
<input type="radio"/>	GO:0006401	6	RNA catabolic process	74	0.0114	19	0.0373	2.120627E-06		E
<input type="radio"/>	GO:0016073	6	snRNA metabolic process	15	0.0023	8	0.0157	5.138617E-06		E
<input type="radio"/>	GO:0006725	4	aromatic compound metabolic process	60	0.0093	16	0.0314	7.843797E-06		E
<input type="radio"/>	GO:0016074	6	snoRNA metabolic process	17	0.0026	8	0.0157	1.651294E-05		E
<input type="radio"/>	GO:0044249	4	cellular biosynthetic process	366	0.0565	51	0.1000	1.678004E-05		E
<input type="radio"/>	GO:0016071	6	mRNA metabolic process	210	0.0324	34	0.0667	2.129300E-05		E
<input type="radio"/>	GO:0006519	4	amino acid and derivative metabolic process	202	0.0312	33	0.0647	2.321338E-05		E
<input type="radio"/>	GO:0006400	7,8	tRNA modification	52	0.0080	14	0.0275	2.520019E-05		E
<input type="radio"/>	GO:0006520	5,6	amino acid metabolic process	187	0.0289	31	0.0608	3.024700E-05		E
<input type="radio"/>	GO:0008033	7	tRNA processing	84	0.0130	18	0.0353	5.081798E-05		E
<input type="radio"/>	GO:0019856	7,6	pyrimidine base biosynthetic process	15	0.0023	7	0.0137	6.087678E-05		E
<input type="radio"/>	GO:0006383	8,7	transcription from RNA polymerase III promoter	38	0.0059	11	0.0216	8.952169E-05		E
<input type="radio"/>	GO:0043038	6,7	amino acid activation	32	0.0049	10	0.0196	9.257149E-05		E

<input type="radio"/>	GO:0006418	8,7,9,6	tRNA aminoacylation for protein translation	32	0.0049	10	0.0196	9.257149E-05	E
<input type="radio"/>	GO:0043039	7,8	tRNA aminoacylation	32	0.0049	10	0.0196	9.257149E-05	E
<input type="radio"/>	GO:0006206	6	pyrimidine base metabolic process	17	0.0026	7	0.0137	0.0001564	E
<input type="radio"/>	GO:0016075	7	rRNA catabolic process	5	0.0008	4	0.0078	0.0001754	E
<input type="radio"/>	GO:0043630	9,10	ncRNA polyadenylation during polyadenylation-dependent ncRNA catabolic process	5	0.0008	4	0.0078	0.0001754	E
<input type="radio"/>	GO:0043629	9	ncRNA polyadenylation	5	0.0008	4	0.0078	0.0001754	E
<input type="radio"/>	GO:0000398	8,10	nuclear mRNA splicing, via spliceosome	102	0.0158	19	0.0373	0.0002113	E
<input type="radio"/>	GO:0000377	9	RNA splicing, via transesterification reactions with bulged adenosine as nucleophile	103	0.0159	19	0.0373	0.0002392	E
<input type="radio"/>	GO:0033036	3	macromolecule localization	382	0.0590	48	0.0941	0.0003088	E
<input type="radio"/>	GO:0009112	5	nucleobase metabolic process	31	0.0048	9	0.0176	0.0003721	E
<input type="radio"/>	GO:0006886	7,5,6	intracellular protein transport	274	0.0423	37	0.0725	0.0003724	E
<input type="radio"/>	GO:0009308	4	amine metabolic process	228	0.0352	32	0.0627	0.0004556	E
<input type="radio"/>	GO:0006402	7	mRNA catabolic process	60	0.0093	13	0.0255	0.0004608	E
<input type="radio"/>	GO:0006605	8,6,7	protein targeting	258	0.0398	35	0.0686	0.0004768	E
<input type="radio"/>	GO:0031327	7,6	negative regulation of cellular biosynthetic process	6	0.0009	4	0.0078	0.0004850	E
<input type="radio"/>	GO:0017148	8,7,6	negative regulation of protein biosynthetic process	6	0.0009	4	0.0078	0.0004850	E
<input type="radio"/>	GO:0000375	8	RNA splicing, via transesterification reactions	110	0.0170	19	0.0373	0.0005363	E
<input type="radio"/>	GO:0015031	4,5,6	protein transport	280	0.0432	37	0.0725	0.0005458	E
<input type="radio"/>	GO:0030488	8,9	tRNA methylation	15	0.0023	6	0.0118	0.0005597	E
<input type="radio"/>	GO:0006397	7	mRNA processing	157	0.0242	24	0.0471	0.0006638	E
<input type="radio"/>	GO:0046112	6,5	nucleobase biosynthetic process	21	0.0032	7	0.0137	0.0006763	E
<input type="radio"/>	GO:0009451	6	RNA modification	139	0.0215	22	0.0431	0.0006829	E
<input type="radio"/>	GO:0000055	11,12,7,9,10	ribosomal large subunit export from nucleus	11	0.0017	5	0.0098	0.0008439	E
<input type="radio"/>	GO:0006351	7,6	transcription, DNA-dependent	522	0.0806	59	0.1157	0.0009324	E
<input type="radio"/>	GO:0046907	6,4,5	intracellular transport	545	0.0842	61	0.1196	0.0009760	E
<input type="radio"/>	GO:0032774	6	RNA biosynthetic process	524	0.0809	59	0.1157	0.0010117	E
<input type="radio"/>	GO:0043634	8	polyadenylation-dependent ncRNA catabolic process	7	0.0011	4	0.0078	0.0010431	E
<input type="radio"/>	GO:0043633	7	modification-dependent RNA catabolic process	7	0.0011	4	0.0078	0.0010431	E
<input type="radio"/>	GO:0006807	3	nitrogen compound metabolic process	251	0.0388	33	0.0647	0.0010830	E
<input type="radio"/>	GO:0006082	4	organic acid metabolic process	314	0.0485	39	0.0765	0.0011907	E
<input type="radio"/>	GO:0019752	5	carboxylic acid metabolic process	314	0.0485	39	0.0765	0.0011907	E
<input type="radio"/>	GO:0045184	3,4,5	establishment of protein localization	296	0.0457	37	0.0725	0.0013758	E
<input type="radio"/>	GO:0046483	4	heterocycle metabolic process	76	0.0117	14	0.0275	0.0014181	E
<input type="radio"/>	GO:0009117	5	nucleotide metabolic process	111	0.0171	18	0.0353	0.0014565	E
<input type="radio"/>	GO:0007001	6	chromosome organization and biogenesis (sensu Eukaryota)	567	0.0876	62	0.1216	0.0014863	E
<input type="radio"/>	GO:0031507	6,10	heterochromatin formation	95	0.0147	16	0.0314	0.0017385	E
<input type="radio"/>	GO:0045814	5	negative regulation of gene expression, epigenetic	95	0.0147	16	0.0314	0.0017385	E
<input type="radio"/>	GO:0016458	5	gene silencing	95	0.0147	16	0.0314	0.0017385	E
<input type="radio"/>	GO:0006342	10,6,7,11,9	chromatin silencing	95	0.0147	16	0.0314	0.0017385	E
<input type="radio"/>	GO:0031497	5,9	chromatin assembly	104	0.0161	17	0.0333	0.0017600	E

<input type="checkbox"/>	GO:0051276	5	chromosome organization and biogenesis	572	0.0883	62	0.1216	0.0017819	E
<input type="checkbox"/>	GO:0016077	7	snoRNA catabolic process	4	0.0006	3	0.0059	0.0017909	E
<input type="checkbox"/>	GO:0045943	10,9	positive regulation of transcription from RNA polymerase I promoter	4	0.0006	3	0.0059	0.0017909	E
<input type="checkbox"/>	GO:0016076	7	snRNA catabolic process	4	0.0006	3	0.0059	0.0017909	E
<input type="checkbox"/>	GO:0008380	7	RNA splicing	132	0.0204	20	0.0392	0.0018490	E
<input type="checkbox"/>	GO:0009890	6,5	negative regulation of biosynthetic process	8	0.0012	4	0.0078	0.0019230	E
<input type="checkbox"/>	GO:0009123	6	nucleoside monophosphate metabolic process	19	0.0029	6	0.0118	0.0021925	E
<input type="checkbox"/>	GO:0006417	7,6,5	regulation of translation	47	0.0073	10	0.0196	0.0022093	E
<input type="checkbox"/>	GO:0006403	4	RNA localization	90	0.0139	15	0.0294	0.0025687	E
<input type="checkbox"/>	GO:0008104	4	protein localization	330	0.0510	39	0.0765	0.0026206	E
<input type="checkbox"/>	GO:0040029	4	regulation of gene expression, epigenetic	100	0.0154	16	0.0314	0.0028334	E
<input type="checkbox"/>	GO:0006997	5	nuclear organization and biogenesis	57	0.0088	11	0.0216	0.0029572	E
<input type="checkbox"/>	GO:0051028	5,7,6,8	mRNA transport	66	0.0102	12	0.0235	0.0032131	E
<input type="checkbox"/>	GO:0006406	11,9,6,8,10,7	mRNA export from nucleus	66	0.0102	12	0.0235	0.0032131	E
<input type="checkbox"/>	GO:0051649	5,3,4	establishment of cellular localization	606	0.0936	63	0.1235	0.0037751	E
<input type="checkbox"/>	GO:0018193	7	peptidyl-amino acid modification	28	0.0043	7	0.0137	0.0039015	E
<input type="checkbox"/>	GO:0006221	6,7	pyrimidine nucleotide biosynthetic process	5	0.0008	3	0.0059	0.0041265	E
<input type="checkbox"/>	GO:0018202	8	peptidyl-histidine modification	5	0.0008	3	0.0059	0.0041265	E
<input type="checkbox"/>	GO:0017182	9	peptidyl-diphthamide metabolic process	5	0.0008	3	0.0059	0.0041265	E
<input type="checkbox"/>	GO:0016078	7	tRNA catabolic process	5	0.0008	3	0.0059	0.0041265	E
<input type="checkbox"/>	GO:0017183	10,4	peptidyl-diphthamide biosynthetic process from peptidyl-histidine	5	0.0008	3	0.0059	0.0041265	E
<input type="checkbox"/>	GO:0006350	5	transcription	567	0.0876	59	0.1157	0.0046226	E
<input type="checkbox"/>	GO:0006405	10,8,5,7,9,6	RNA export from nucleus	79	0.0122	13	0.0255	0.0050760	E
<input type="checkbox"/>	GO:0009081	6,7	branched chain family amino acid metabolic process	16	0.0025	5	0.0098	0.0053119	E
<input type="checkbox"/>	GO:0051641	4,3	cellular localization	642	0.0991	65	0.1275	0.0054958	E
<input type="checkbox"/>	GO:0051236	3,4,5	establishment of RNA localization	80	0.0124	13	0.0255	0.0055900	E
<input type="checkbox"/>	GO:0050657	5,6	nucleic acid transport	80	0.0124	13	0.0255	0.0055900	E
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<input type="checkbox"/>	GO:0046039	9	GTP metabolic process	2	0.0003	2	0.0039	0.0061907	E
<input type="checkbox"/>	GO:0006183	9,10	GTP biosynthetic process	2	0.0003	2	0.0039	0.0061907	E
<input type="checkbox"/>	GO:0046515	7,6	hypusine biosynthetic process	2	0.0003	2	0.0039	0.0061907	E
<input type="checkbox"/>	GO:0007000	6	nucleolus organization and biogenesis	2	0.0003	2	0.0039	0.0061907	E
<input type="checkbox"/>	GO:0046516	6	hypusine metabolic process	2	0.0003	2	0.0039	0.0061907	E
<input type="checkbox"/>	GO:0015723	7,8	bilirubin transport	2	0.0003	2	0.0039	0.0061907	E
<input type="checkbox"/>	GO:0015691	7,8,9	cadmium ion transport	2	0.0003	2	0.0039	0.0061907	E
<input type="checkbox"/>	GO:0006333	8	chromatin assembly or disassembly	119	0.0184	17	0.0333	0.0062322	E
<input type="checkbox"/>	GO:0016568	8	chromatin modification	223	0.0344	27	0.0529	0.0069233	E
<input type="checkbox"/>	GO:0016053	5	organic acid biosynthetic process	17	0.0026	5	0.0098	0.0069369	E
<input type="checkbox"/>	GO:0009167	8	purine ribonucleoside monophosphate metabolic process	17	0.0026	5	0.0098	0.0069369	E
<input type="checkbox"/>	GO:0009124	6,7	nucleoside monophosphate biosynthetic process	17	0.0026	5	0.0098	0.0069369	E
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<input type="checkbox"/>	GO:0009161	7	ribonucleoside monophosphate metabolic process	17	0.0026	5	0.0098	0.0069369	E
<input type="checkbox"/>	GO:0007021	7	tubulin folding	11	0.0017	4	0.0078	0.0070997	E

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<input type="radio"/>	GO:0009126	7	purine nucleoside monophosphate metabolic process	18	0.0028	5	0.0098	0.0088539	E
<input type="radio"/>	GO:0019438	5	aromatic compound biosynthetic process	18	0.0028	5	0.0098	0.0088539	E
<input type="radio"/>	GO:0000183	11,7,8,12,10	chromatin silencing at rDNA	18	0.0028	5	0.0098	0.0088539	E
<input type="radio"/>	GO:0006270	8,6	DNA replication initiation	33	0.0051	7	0.0137	0.0093774	E
<input type="radio"/>	GO:0031324	6,5	negative regulation of cellular metabolic process	198	0.0306	24	0.0471	0.0096491	E
<input type="radio"/>	GO:0008652	6,7	amino acid biosynthetic process	106	0.0164	15	0.0294	0.0099856	E
<input type="radio"/>	GO:0006325	7	establishment and/or maintenance of chromatin architecture	253	0.0391	29	0.0569	0.0100867	E
<input type="radio"/>	GO:0006323	6	DNA packaging	253	0.0391	29	0.0569	0.0100867	E
<input type="radio"/>	GO:0006407	11,9,6,8,10,7	rRNA export from nucleus	26	0.0040	6	0.0118	0.0105300	E
<input type="radio"/>	GO:0051029	5,7,6,8	rRNA transport	26	0.0040	6	0.0118	0.0105300	E
<input type="radio"/>	GO:0006730	4	one-carbon compound metabolic process	97	0.0150	14	0.0275	0.0105756	E
<input type="radio"/>	GO:0006261	7	DNA-dependent DNA replication	97	0.0150	14	0.0275	0.0105756	E
<input type="radio"/>	GO:0006348	11,7,8,12,10	chromatin silencing at telomere	60	0.0093	10	0.0196	0.0112169	E
<input type="radio"/>	GO:0031509	7,11	telomeric heterochromatin formation	60	0.0093	10	0.0196	0.0112169	E
<input type="radio"/>	GO:0009259	6	ribonucleotide metabolic process	43	0.0066	8	0.0157	0.0119676	E
<input type="radio"/>	GO:0051707	3,4	response to other organism	7	0.0011	3	0.0059	0.0122681	E
<input type="radio"/>	GO:0043331	4	response to dsRNA	7	0.0011	3	0.0059	0.0122681	E
<input type="radio"/>	GO:0043330	5,6	response to exogenous dsRNA	7	0.0011	3	0.0059	0.0122681	E
<input type="radio"/>	GO:0031120	8	snRNA pseudouridine synthesis	7	0.0011	3	0.0059	0.0122681	E
<input type="radio"/>	GO:0006220	6	pyrimidine nucleotide metabolic process	7	0.0011	3	0.0059	0.0122681	E
<input type="radio"/>	GO:0009615	4,5	response to virus	7	0.0011	3	0.0059	0.0122681	E
<input type="radio"/>	GO:0000056	11,12,7,9,10	ribosomal small subunit export from nucleus	7	0.0011	3	0.0059	0.0122681	E
<input type="radio"/>	GO:0040031	7	snRNA modification	7	0.0011	3	0.0059	0.0122681	E
<input type="radio"/>	GO:0015931	4,5	nucleobase, nucleoside, nucleotide and nucleic acid transport	90	0.0139	13	0.0255	0.0129745	E
<input type="radio"/>	GO:0009082	7,8	branched chain family amino acid biosynthetic process	13	0.0020	4	0.0078	0.0130689	E
<input type="radio"/>	GO:0006633	7,6,8,5	fatty acid biosynthetic process	13	0.0020	4	0.0078	0.0130689	E
<input type="radio"/>	GO:0051647	6,5	nucleus localization	20	0.0031	5	0.0098	0.0136135	E
<input type="radio"/>	GO:0040023	6,7,4,5	establishment of nucleus localization	20	0.0031	5	0.0098	0.0136135	E
<input type="radio"/>	GO:0007097	7,8,5,6	nuclear migration	20	0.0031	5	0.0098	0.0136135	E
<input type="radio"/>	GO:0051246	5,4	regulation of protein metabolic process	72	0.0111	11	0.0216	0.0143685	E
<input type="radio"/>	GO:0009892	5,4	negative regulation of metabolic process	208	0.0321	24	0.0471	0.0151155	E
<input type="radio"/>	GO:0009058	3	biosynthetic process	1249	0.1929	111	0.2176	0.0154822	E
<input type="radio"/>	GO:0032259	5	methylation	83	0.0128	12	0.0235	0.0159564	E
<input type="radio"/>	GO:0043414	6	biopolymer methylation	83	0.0128	12	0.0235	0.0159564	E
<input type="radio"/>	GO:0045892	9,8	negative regulation of transcription, DNA-dependent	156	0.0241	19	0.0373	0.0167233	E
<input type="radio"/>	GO:0009309	5,6	amine biosynthetic process	114	0.0176	15	0.0294	0.0167991	E
<input type="radio"/>	GO:0006259	5	DNA metabolic process	523	0.0808	51	0.1000	0.0168742	E
<input type="radio"/>	GO:0009066	6,7	aspartate family amino acid metabolic process	46	0.0071	8	0.0157	0.0168759	E
<input type="radio"/>	GO:0006432	9,8,10,7	phenylalanyl-tRNA aminoacylation	3	0.0005	2	0.0039	0.0171149	E
<input type="radio"/>	GO:0046500	6,5	S-adenosylmethionine metabolic process	3	0.0005	2	0.0039	0.0171149	E
<input type="radio"/>	GO:0046083	7	adenine metabolic process	3	0.0005	2	0.0039	0.0171149	E
<input type="radio"/>	GO:0045934	7,6	negative regulation of nucleobase, nucleoside, nucleotide and nucleic acid	179	0.0276	21	0.0412	0.0178049	E

			metabolic process						
<input type="radio"/>	GO:0044271	5,4	nitrogen compound biosynthetic process	115	0.0178	15	0.0294	0.0178158	E
<input type="radio"/>	GO:0042816	6	vitamin B6 metabolic process	8	0.0012	3	0.0059	0.0180905	E
<input type="radio"/>	GO:0043144	7	snoRNA processing	8	0.0012	3	0.0059	0.0180905	E
<input type="radio"/>	GO:0006620	10,9,8,7,6	posttranslational protein targeting to membrane	8	0.0012	3	0.0059	0.0180905	E
<input type="radio"/>	GO:0006356	9,8	regulation of transcription from RNA polymerase I promoter	8	0.0012	3	0.0059	0.0180905	E
<input type="radio"/>	GO:0008614	7	pyridoxine metabolic process	8	0.0012	3	0.0059	0.0180905	E
<input type="radio"/>	GO:0006163	6	purine nucleotide metabolic process	47	0.0073	8	0.0157	0.0187499	E
<input type="radio"/>	GO:0009653	4,3	anatomical structure morphogenesis	248	0.0383	27	0.0529	0.0193324	E
<input type="radio"/>	GO:0000902	5,6	cell morphogenesis	248	0.0383	27	0.0529	0.0193324	E
<input type="radio"/>	GO:0032989	4,5	cellular structure morphogenesis	248	0.0383	27	0.0529	0.0193324	E
<input type="radio"/>	GO:0048856	3	anatomical structure development	248	0.0383	27	0.0529	0.0193324	E
<input type="radio"/>	GO:0048284	5	organelle fusion	22	0.0034	5	0.0098	0.0196468	E
<input type="radio"/>	GO:0006260	6	DNA replication	117	0.0181	15	0.0294	0.0199598	E
<input type="radio"/>	GO:0043412	5	biopolymer modification	664	0.1025	62	0.1216	0.0200196	E
<input type="radio"/>	GO:0031323	5,4	regulation of cellular metabolic process	507	0.0783	49	0.0961	0.0200228	E
<input type="radio"/>	GO:0065007	2	biological regulation	948	0.1464	85	0.1667	0.0205383	E
<input type="radio"/>	GO:0051704	2	multi-organism process	139	0.0215	17	0.0333	0.0207747	E
<input type="radio"/>	GO:0031326	6,5	regulation of cellular biosynthetic process	67	0.0103	10	0.0196	0.0209029	E
<input type="radio"/>	GO:0000747	4	conjugation with cellular fusion	118	0.0182	15	0.0294	0.0210865	E
<input type="radio"/>	GO:0000746	3	conjugation	118	0.0182	15	0.0294	0.0210865	E
<input type="radio"/>	GO:0019953	3	sexual reproduction	118	0.0182	15	0.0294	0.0210865	E
<input type="radio"/>	GO:0009156	7,8	ribonucleoside monophosphate biosynthetic process	15	0.0023	4	0.0078	0.0211956	E
<input type="radio"/>	GO:0030473	8,9,6,7	nuclear migration, microtubule-mediated	15	0.0023	4	0.0078	0.0211956	E
<input type="radio"/>	GO:0007018	8,7,6	microtubule-based movement	15	0.0023	4	0.0078	0.0211956	E
<input type="radio"/>	GO:0009168	8,9	purine ribonucleoside monophosphate biosynthetic process	15	0.0023	4	0.0078	0.0211956	E
<input type="radio"/>	GO:0008610	5,4,6	lipid biosynthetic process	129	0.0199	16	0.0314	0.0215227	E
<input type="radio"/>	GO:0016481	8,7	negative regulation of transcription	162	0.0250	19	0.0373	0.0220316	E
<input type="radio"/>	GO:0009260	6,7	ribonucleotide biosynthetic process	40	0.0062	7	0.0137	0.0231603	E
<input type="radio"/>	GO:0009165	5,6	nucleotide biosynthetic process	59	0.0091	9	0.0176	0.0239451	E
<input type="radio"/>	GO:0009889	5,4	regulation of biosynthetic process	69	0.0107	10	0.0196	0.0243627	E
<input type="radio"/>	GO:0043101	5	purine salvage	9	0.0014	3	0.0059	0.0250087	E
<input type="radio"/>	GO:0009262	6	deoxyribonucleotide metabolic process	9	0.0014	3	0.0059	0.0250087	E
<input type="radio"/>	GO:0006606	9,10,7,8,6	protein import into nucleus	50	0.0077	8	0.0157	0.0250824	E
<input type="radio"/>	GO:0051170	9,7,8	nuclear import	50	0.0077	8	0.0157	0.0250824	E
<input type="radio"/>	GO:0006694	6,5,7	steroid biosynthetic process	32	0.0049	6	0.0118	0.0254327	E
<input type="radio"/>	GO:0016126	6,7,8	sterol biosynthetic process	32	0.0049	6	0.0118	0.0254327	E
<input type="radio"/>	GO:0009150	7	purine ribonucleotide metabolic process	41	0.0063	7	0.0137	0.0257458	E
<input type="radio"/>	GO:0009127	7,8	purine nucleoside monophosphate biosynthetic process	16	0.0025	4	0.0078	0.0260476	E
<input type="radio"/>	GO:0009073	7,6,8	aromatic amino acid family biosynthetic process	16	0.0025	4	0.0078	0.0260476	E
<input type="radio"/>	GO:0006338	9	chromatin remodeling	155	0.0239	18	0.0353	0.0261681	E
<input type="radio"/>	GO:0043631	8	RNA polyadenylation	24	0.0037	5	0.0098	0.0269419	E
<input type="radio"/>	GO:0051452	12,9,10	cellular pH reduction	24	0.0037	5	0.0098	0.0269419	E
<input type="radio"/>	GO:0007035	13,10,6,11	vacuolar acidification	24	0.0037	5	0.0098	0.0269419	E

<input type="radio"/>	GO:0045851	8	pH reduction	24	0.0037	5	0.0098	0.0269419	E
<input type="radio"/>	GO:0016570	10,8	histone modification	91	0.0141	12	0.0235	0.0271585	E
<input type="radio"/>	GO:0016569	9	covalent chromatin modification	91	0.0141	12	0.0235	0.0271585	E
<input type="radio"/>	GO:0000096	6,7,5	sulfur amino acid metabolic process	33	0.0051	6	0.0118	0.0286532	E
<input type="radio"/>	GO:0030010	7,4,8	establishment of cell polarity	103	0.0159	13	0.0255	0.0294452	E
<input type="radio"/>	GO:0000723	8	telomere maintenance	274	0.0423	28	0.0549	0.0299657	E
<input type="radio"/>	GO:0032200	7	telomere organization and biogenesis	274	0.0423	28	0.0549	0.0299657	E
<input type="radio"/>	GO:0051453	11,8,9	regulation of cellular pH	25	0.0039	5	0.0098	0.0310414	E
<input type="radio"/>	GO:0009607	3	response to biotic stimulus	25	0.0039	5	0.0098	0.0310414	E
<input type="radio"/>	GO:0030641	10,8	cellular hydrogen ion homeostasis	25	0.0039	5	0.0098	0.0310414	E
<input type="radio"/>	GO:0000741	6	karyogamy	17	0.0026	4	0.0078	0.0313942	E
<input type="radio"/>	GO:0000742	7,5	karyogamy during conjugation with cellular fusion	17	0.0026	4	0.0078	0.0313942	E
<input type="radio"/>	GO:0030705	7,5,6	cytoskeleton-dependent intracellular transport	17	0.0026	4	0.0078	0.0313942	E
<input type="radio"/>	GO:0000743	9,10,8,7,6	nuclear migration during conjugation with cellular fusion	4	0.0006	2	0.0039	0.0315434	E
<input type="radio"/>	GO:0000059	8,10,11,7,9	protein import into nucleus, docking	4	0.0006	2	0.0039	0.0315434	E
<input type="radio"/>	GO:0016180	7	snRNA processing	4	0.0006	2	0.0039	0.0315434	E
<input type="radio"/>	GO:0019222	4,3	regulation of metabolic process	538	0.0831	49	0.0961	0.0347855	E
<input type="radio"/>	GO:0006696	7,8,9	ergosterol biosynthetic process	26	0.0040	5	0.0098	0.0354237	E
<input type="radio"/>	GO:0008204	6,7,8	ergosterol metabolic process	26	0.0040	5	0.0098	0.0354237	E
<input type="radio"/>	GO:0042274	6,5	ribosomal small subunit biogenesis and assembly	26	0.0040	5	0.0098	0.0354237	E
<input type="radio"/>	GO:0051248	6,5	negative regulation of protein metabolic process	18	0.0028	4	0.0078	0.0372018	E
<input type="radio"/>	GO:0065008	3	regulation of biological quality	260	0.0401	26	0.0510	0.0385015	E
<input type="radio"/>	GO:0006355	8,7	regulation of transcription, DNA-dependent	359	0.0554	34	0.0667	0.0394605	E
<input type="radio"/>	GO:0017038	5,6,7	protein import	109	0.0168	13	0.0255	0.0395078	E
<input type="radio"/>	GO:0051318	6,7,5	G1 phase	27	0.0042	5	0.0098	0.0400707	E
<input type="radio"/>	GO:0000080	7,8,6	G1 phase of mitotic cell cycle	27	0.0042	5	0.0098	0.0400707	E
<input type="radio"/>	GO:0048523	5,4	negative regulation of cellular process	239	0.0369	24	0.0471	0.0415552	E
<input type="radio"/>	GO:0006098	9,10,11	pentose-phosphate shunt	11	0.0017	3	0.0059	0.0417232	E
<input type="radio"/>	GO:0043094	4	metabolic compound salvage	19	0.0029	4	0.0078	0.0434301	E
<input type="radio"/>	GO:0000245	7,6,9,11	spliceosome assembly	19	0.0029	4	0.0078	0.0434301	E
<input type="radio"/>	GO:0048519	4	negative regulation of biological process	242	0.0374	24	0.0471	0.0446257	E
<input type="radio"/>	GO:0006810	3,4	transport	981	0.1515	81	0.1588	0.0449270	E
<input type="radio"/>	GO:0051179	2	localization	1051	0.1623	86	0.1686	0.0453482	E
<input type="radio"/>	GO:0007017	6	microtubule-based process	101	0.0156	12	0.0235	0.0455271	E
<input type="radio"/>	GO:0051234	2,3	establishment of localization	1004	0.1550	82	0.1608	0.0467643	E
<input type="radio"/>	GO:0009152	7,8	purine ribonucleotide biosynthetic process	38	0.0059	6	0.0118	0.0475212	E
<input type="radio"/>	GO:0030003	8,6	cellular cation homeostasis	102	0.0158	12	0.0235	0.0475667	E
<input type="radio"/>	GO:0055080	7	cation homeostasis	102	0.0158	12	0.0235	0.0475667	E
<input type="radio"/>	GO:0050794	4,3	regulation of cellular process	738	0.1140	62	0.1216	0.0482397	E
<input type="radio"/>	GO:0031385	6,8,11,10,9,7,12	regulation of termination of mating projection growth	5	0.0008	2	0.0039	0.0484458	E
<input type="radio"/>	GO:0007023	8	post-chaperonin tubulin folding pathway	5	0.0008	2	0.0039	0.0484458	E
<input type="radio"/>	GO:0043137	7,10,6,9	DNA replication, removal of RNA primer	5	0.0008	2	0.0039	0.0484458	E
<input type="radio"/>	GO:0016233	9	telomere capping	5	0.0008	2	0.0039	0.0484458	E

<input type="checkbox"/>	GO:0006885	7	regulation of pH	29	0.0045	5	0.0098	0.0500739	E
<input type="checkbox"/>	GO:0006999	6	nuclear pore organization and biogenesis	29	0.0045	5	0.0098	0.0500739	E
<input type="checkbox"/>	GO:0051656	6,3,5,4	establishment of organelle localization	29	0.0045	5	0.0098	0.0500739	E
<input type="checkbox"/>	GO:0006873	7,5	cellular ion homeostasis	115	0.0178	13	0.0255	0.0506845	E
<input type="checkbox"/>	GO:0055082	6,4	cellular chemical homeostasis	115	0.0178	13	0.0255	0.0506845	E
<input type="checkbox"/>	GO:0007163	6,3,7	establishment and/or maintenance of cell polarity	115	0.0178	13	0.0255	0.0506845	E
<input type="checkbox"/>	GO:0019219	6,5	regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	440	0.0679	39	0.0765	0.0510816	E
<input type="checkbox"/>	GO:0006284	7,6	base-excision repair	12	0.0019	3	0.0059	0.0512682	E
<input type="checkbox"/>	GO:0006612	9,7,8	protein targeting to membrane	39	0.0060	6	0.0118	0.0517649	E
<input type="checkbox"/>	GO:0001510	7	RNA methylation	60	0.0093	8	0.0157	0.0529645	E
<input type="checkbox"/>	GO:0022403	5,4	cell cycle phase	353	0.0545	32	0.0627	0.0536903	E
<input type="checkbox"/>	GO:0050789	3	regulation of biological process	761	0.1175	62	0.1216	0.0539156	E
<input type="checkbox"/>	GO:0007010	5	cytoskeleton organization and biogenesis	227	0.0351	22	0.0431	0.0551330	E
<input type="checkbox"/>	GO:0030466	11,7,8,12,10	chromatin silencing at silent mating-type cassette	30	0.0046	5	0.0098	0.0553818	E
<input type="checkbox"/>	GO:0016573	11,9	histone acetylation	40	0.0062	6	0.0118	0.0561315	E
<input type="checkbox"/>	GO:0032502	2	developmental process	436	0.0673	38	0.0745	0.0563047	E
<input type="checkbox"/>	GO:0009072	6,5,7	aromatic amino acid family metabolic process	21	0.0032	4	0.0078	0.0569618	E
<input type="checkbox"/>	GO:0006629	4	lipid metabolic process	242	0.0374	23	0.0451	0.0577218	E
<input type="checkbox"/>	GO:0045449	7,6	regulation of transcription	386	0.0596	34	0.0667	0.0582660	E
<input type="checkbox"/>	GO:0050801	6	ion homeostasis	119	0.0184	13	0.0255	0.0585089	E
<input type="checkbox"/>	GO:0000003	2	reproduction	323	0.0499	29	0.0569	0.0605788	E
<input type="checkbox"/>	GO:0006164	6,7	purine nucleotide biosynthetic process	41	0.0063	6	0.0118	0.0606049	E
<input type="checkbox"/>	GO:0006575	5	amino acid derivative metabolic process	31	0.0048	5	0.0098	0.0608590	E
<input type="checkbox"/>	GO:0007062	7,4	sister chromatid cohesion	31	0.0048	5	0.0098	0.0608590	E
<input type="checkbox"/>	GO:0000097	7,8,6	sulfur amino acid biosynthetic process	13	0.0020	3	0.0059	0.0614212	E
<input type="checkbox"/>	GO:0006450	8,7,6	regulation of translational fidelity	13	0.0020	3	0.0059	0.0614212	E
<input type="checkbox"/>	GO:0048878	5	chemical homeostasis	121	0.0187	13	0.0255	0.0624692	E
<input type="checkbox"/>	GO:0042221	3	response to chemical stimulus	382	0.0590	33	0.0647	0.0639170	E
<input type="checkbox"/>	GO:0007064	10,8,5,6,9,7,4	mitotic sister chromatid cohesion	22	0.0034	4	0.0078	0.0641626	E
<input type="checkbox"/>	GO:0040020	7,9,8,6	regulation of meiosis	22	0.0034	4	0.0078	0.0641626	E
<input type="checkbox"/>	GO:0022402	4,3	cell cycle process	439	0.0678	37	0.0725	0.0644047	E
<input type="checkbox"/>	GO:0006310	6	DNA recombination	122	0.0188	13	0.0255	0.0644515	E
<input type="checkbox"/>	GO:0016125	5,6,7	sterol metabolic process	42	0.0065	6	0.0118	0.0651679	E
<input type="checkbox"/>	GO:0007049	3	cell cycle	458	0.0707	38	0.0745	0.0660314	E
<input type="checkbox"/>	GO:0051321	4	meiotic cell cycle	148	0.0229	15	0.0294	0.0669565	E
<input type="checkbox"/>	GO:0007126	8,6,7,5	meiosis	148	0.0229	15	0.0294	0.0669565	E
<input type="checkbox"/>	GO:0051327	7,5,6	M phase of meiotic cell cycle	148	0.0229	15	0.0294	0.0669565	E
<input type="checkbox"/>	GO:0031383	5,7,10,9,8,6,11	regulation of mating projection biogenesis	6	0.0009	2	0.0039	0.0669639	E
<input type="checkbox"/>	GO:0007130	11,9,8,6,5,10,7,4	synaptonemal complex assembly	6	0.0009	2	0.0039	0.0669639	E
<input type="checkbox"/>	GO:0007089	8,9,7,6	traversing start control point of mitotic cell cycle	6	0.0009	2	0.0039	0.0669639	E
<input type="checkbox"/>	GO:0045041	10,9,8,7	protein import into mitochondrial intermembrane space	6	0.0009	2	0.0039	0.0669639	E
<input type="checkbox"/>	GO:0031344	4,6,8,7,5,9	regulation of cell projection organization and biogenesis	6	0.0009	2	0.0039	0.0669639	E
<input type="checkbox"/>	GO:0008299	6,5,7	isoprenoid biosynthetic process	6	0.0009	2	0.0039	0.0669639	E

<input type="checkbox"/>	GO:0006720	5,6	isoprenoid metabolic process	6	0.0009	2	0.0039	0.0669639	E
<input type="checkbox"/>	GO:0006464	6	protein modification process	520	0.0803	41	0.0804	0.0675521	E
<input type="checkbox"/>	GO:0008202	5,6	steroid metabolic process	43	0.0066	6	0.0118	0.0698030	E
<input type="checkbox"/>	GO:0044255	4,5	cellular lipid metabolic process	229	0.0354	21	0.0412	0.0714679	E
<input type="checkbox"/>	GO:0006767	5	water-soluble vitamin metabolic process	89	0.0137	10	0.0196	0.0715567	E
<input type="checkbox"/>	GO:0006766	4	vitamin metabolic process	89	0.0137	10	0.0196	0.0715567	E
<input type="checkbox"/>	GO:0008213	8	protein amino acid alkylation	23	0.0036	4	0.0078	0.0715811	E
<input type="checkbox"/>	GO:0051030	5,7,6,8	snRNA transport	23	0.0036	4	0.0078	0.0715811	E
<input type="checkbox"/>	GO:0006607	10,11,8,9,7	NLS-bearing substrate import into nucleus	23	0.0036	4	0.0078	0.0715811	E
<input type="checkbox"/>	GO:0006408	11,9,6,8,10,7	snRNA export from nucleus	23	0.0036	4	0.0078	0.0715811	E
<input type="checkbox"/>	GO:0006608	10,11,8,9,7	snRNP protein import into nucleus	23	0.0036	4	0.0078	0.0715811	E
<input type="checkbox"/>	GO:0006479	9,7	protein amino acid methylation	23	0.0036	4	0.0078	0.0715811	E
<input type="checkbox"/>	GO:0006610	10,11,8,9,7	ribosomal protein import into nucleus	23	0.0036	4	0.0078	0.0715811	E
<input type="checkbox"/>	GO:0046040	9	IMP metabolic process	14	0.0022	3	0.0059	0.0720400	E
<input type="checkbox"/>	GO:0006188	9,10	IMP biosynthetic process	14	0.0022	3	0.0059	0.0720400	E
<input type="checkbox"/>	GO:0006740	10,9	NADPH regeneration	14	0.0022	3	0.0059	0.0720400	E
<input type="checkbox"/>	GO:0045047	9,8,7,6,5	protein targeting to ER	33	0.0051	5	0.0098	0.0722085	E
<input type="checkbox"/>	GO:0019725	5,3	cellular homeostasis	128	0.0198	13	0.0255	0.0761940	E
<input type="checkbox"/>	GO:0043285	5	biopolymer catabolic process	277	0.0428	24	0.0471	0.0770762	E
<input type="checkbox"/>	GO:0055067	8	monovalent inorganic cation homeostasis	34	0.0053	5	0.0098	0.0780228	E
<input type="checkbox"/>	GO:0030004	9,7	cellular monovalent inorganic cation homeostasis	34	0.0053	5	0.0098	0.0780228	E
<input type="checkbox"/>	GO:0008361	4,6,7	regulation of cell size	129	0.0199	13	0.0255	0.0780990	E
<input type="checkbox"/>	GO:0051640	5,4	organelle localization	56	0.0086	7	0.0137	0.0782337	E
<input type="checkbox"/>	GO:0033353	7,6	S-adenosylmethionine cycle	1	0.0002	1	0.0020	0.0787523	E
<input type="checkbox"/>	GO:0009130	7,8	pyrimidine nucleoside monophosphate biosynthetic process	1	0.0002	1	0.0020	0.0787523	E
<input type="checkbox"/>	GO:0032092	6	positive regulation of protein binding	1	0.0002	1	0.0020	0.0787523	E
<input type="checkbox"/>	GO:0018216	9,10,8	peptidyl-arginine methylation	1	0.0002	1	0.0020	0.0787523	E
<input type="checkbox"/>	GO:0006168	8,7	adenine salvage	1	0.0002	1	0.0020	0.0787523	E
<input type="checkbox"/>	GO:0009398	7,8	FMN biosynthetic process	1	0.0002	1	0.0020	0.0787523	E
<input type="checkbox"/>	GO:0006146	8,7	adenine catabolic process	1	0.0002	1	0.0020	0.0787523	E
<input type="checkbox"/>	GO:0009176	8	pyrimidine deoxyribonucleoside monophosphate metabolic process	1	0.0002	1	0.0020	0.0787523	E
<input type="checkbox"/>	GO:0009229	7,8	thiamin diphosphate biosynthetic process	1	0.0002	1	0.0020	0.0787523	E
<input type="checkbox"/>	GO:0006286	8,7	base-excision repair, base-free sugar-phosphate removal	1	0.0002	1	0.0020	0.0787523	E
<input type="checkbox"/>	GO:0045836	8,10,9,7	positive regulation of meiosis	1	0.0002	1	0.0020	0.0787523	E
<input type="checkbox"/>	GO:0009157	7,8	deoxyribonucleoside monophosphate biosynthetic process	1	0.0002	1	0.0020	0.0787523	E
<input type="checkbox"/>	GO:0000413	8	protein peptidyl-prolyl isomerization	1	0.0002	1	0.0020	0.0787523	E
<input type="checkbox"/>	GO:0000412	11,9	histone peptidyl-prolyl isomerization	1	0.0002	1	0.0020	0.0787523	E
<input type="checkbox"/>	GO:0032264	7,8	IMP salvage	1	0.0002	1	0.0020	0.0787523	E
<input type="checkbox"/>	GO:0046444	6,7	FMN metabolic process	1	0.0002	1	0.0020	0.0787523	E
<input type="checkbox"/>	GO:0032263	7,8	GMP salvage	1	0.0002	1	0.0020	0.0787523	E
<input type="checkbox"/>	GO:0051568	12,10,11,9	histone H3-K4 methylation	1	0.0002	1	0.0020	0.0787523	E
<input type="checkbox"/>	GO:0006387	8	snRNA capping	1	0.0002	1	0.0020	0.0787523	E
<input type="checkbox"/>	GO:0015887	5,6	pantothenate transport	1	0.0002	1	0.0020	0.0787523	E
<input type="checkbox"/>	GO:0001718	8,7,11,10,9	conversion of met-tRNAf to fmet-tRNA	1	0.0002	1	0.0020	0.0787523	E

<input type="radio"/>	GO:0051253	8,7	negative regulation of RNA metabolic process	1	0.0002	1	0.0020	0.0787523	E
<input type="radio"/>	GO:0030259	6,7	lipid glycosylation	1	0.0002	1	0.0020	0.0787523	E
<input type="radio"/>	GO:0000459	7,8	exonucleolytic trimming during rRNA processing	1	0.0002	1	0.0020	0.0787523	E
<input type="radio"/>	GO:0006427	9,8,10,7	histidyl-tRNA aminoacylation	1	0.0002	1	0.0020	0.0787523	E
<input type="radio"/>	GO:0031060	7,9,12,6,10,11,8	regulation of histone methylation	1	0.0002	1	0.0020	0.0787523	E
<input type="radio"/>	GO:0019284	9,7,8,6,10	methionine biosynthetic process from S-adenosylmethionine	1	0.0002	1	0.0020	0.0787523	E
<input type="radio"/>	GO:0000040	8,9,10	low affinity iron ion transport	1	0.0002	1	0.0020	0.0787523	E
<input type="radio"/>	GO:0018256	8	protein amino acid formylation	1	0.0002	1	0.0020	0.0787523	E
<input type="radio"/>	GO:0006438	9,8,10,7	valyl-tRNA aminoacylation	1	0.0002	1	0.0020	0.0787523	E
<input type="radio"/>	GO:0000734	7,9,8	gene conversion at mating-type locus, DNA repair synthesis	1	0.0002	1	0.0020	0.0787523	E
<input type="radio"/>	GO:0048025	10,9,12	negative regulation of nuclear mRNA splicing, via spliceosome	1	0.0002	1	0.0020	0.0787523	E
<input type="radio"/>	GO:0009129	7	pyrimidine nucleoside monophosphate metabolic process	1	0.0002	1	0.0020	0.0787523	E
<input type="radio"/>	GO:0008612	8,7,9	hypusine biosynthetic process from peptidyl-lysine	1	0.0002	1	0.0020	0.0787523	E
<input type="radio"/>	GO:0046113	6,5	nucleobase catabolic process	1	0.0002	1	0.0020	0.0787523	E
<input type="radio"/>	GO:0018004	10,9	N-terminal protein formylation	1	0.0002	1	0.0020	0.0787523	E
<input type="radio"/>	GO:0033559	6,8,7	unsaturated fatty acid metabolic process	1	0.0002	1	0.0020	0.0787523	E
<input type="radio"/>	GO:0006831	9,10	low-affinity zinc ion transport	1	0.0002	1	0.0020	0.0787523	E
<input type="radio"/>	GO:0051098	4	regulation of binding	1	0.0002	1	0.0020	0.0787523	E
<input type="radio"/>	GO:0046498	6	S-adenosylhomocysteine metabolic process	1	0.0002	1	0.0020	0.0787523	E
<input type="radio"/>	GO:0043096	7,6	purine base salvage	1	0.0002	1	0.0020	0.0787523	E
<input type="radio"/>	GO:0032218	5,6	riboflavin transport	1	0.0002	1	0.0020	0.0787523	E
<input type="radio"/>	GO:0046073	9	dTMP metabolic process	1	0.0002	1	0.0020	0.0787523	E
<input type="radio"/>	GO:0006421	9,8,10,7	asparaginyl-tRNA aminoacylation	1	0.0002	1	0.0020	0.0787523	E
<input type="radio"/>	GO:0042819	7	vitamin B6 biosynthetic process	1	0.0002	1	0.0020	0.0787523	E
<input type="radio"/>	GO:0046033	9	AMP metabolic process	1	0.0002	1	0.0020	0.0787523	E
<input type="radio"/>	GO:0006425	9,8,10,7	glutaminyl-tRNA aminoacylation	1	0.0002	1	0.0020	0.0787523	E
<input type="radio"/>	GO:0006636	8,7,9,6	unsaturated fatty acid biosynthetic process	1	0.0002	1	0.0020	0.0787523	E
<input type="radio"/>	GO:0006167	9,10	AMP biosynthetic process	1	0.0002	1	0.0020	0.0787523	E
<input type="radio"/>	GO:0043393	5	regulation of protein binding	1	0.0002	1	0.0020	0.0787523	E
<input type="radio"/>	GO:0009177	8,9	pyrimidine deoxyribonucleoside monophosphate biosynthetic process	1	0.0002	1	0.0020	0.0787523	E
<input type="radio"/>	GO:0050686	9,8	negative regulation of mRNA processing	1	0.0002	1	0.0020	0.0787523	E
<input type="radio"/>	GO:0016259	7,8,6	selenocysteine metabolic process	1	0.0002	1	0.0020	0.0787523	E
<input type="radio"/>	GO:0008615	8	pyridoxine biosynthetic process	1	0.0002	1	0.0020	0.0787523	E
<input type="radio"/>	GO:0051099	5	positive regulation of binding	1	0.0002	1	0.0020	0.0787523	E
<input type="radio"/>	GO:0006231	9,10	dTMP biosynthetic process	1	0.0002	1	0.0020	0.0787523	E
<input type="radio"/>	GO:0042357	6,7	thiamin diphosphate metabolic process	1	0.0002	1	0.0020	0.0787523	E
<input type="radio"/>	GO:0006145	7,6	purine base catabolic process	1	0.0002	1	0.0020	0.0787523	E
<input type="radio"/>	GO:0000415	9,11,14,8,12,13,10	negative regulation of histone H3-K36 methylation	1	0.0002	1	0.0020	0.0787523	E
<input type="radio"/>	GO:0000414	8,10,13,7,11,12,9	regulation of histone H3-K36 methylation	1	0.0002	1	0.0020	0.0787523	E
<input type="radio"/>	GO:0009162	7	deoxyribonucleoside monophosphate metabolic process	1	0.0002	1	0.0020	0.0787523	E
<input type="radio"/>	GO:0000278	4	mitotic cell cycle	266	0.0411	23	0.0451	0.0794291	E
<input type="radio"/>	GO:0000740	5	response to pheromone during	57	0.0088	7	0.0127	0.0821087	E

<input type="radio"/>	GO:0000749	5	conjugation with cellular fusion	57	0.0068	7	0.0137	0.0821987	E
<input type="radio"/>	GO:0006267	8,7	pre-replicative complex assembly	15	0.0023	3	0.0059	0.0829848	E
<input type="radio"/>	GO:0000114	10,8,9,5,7,4	G1-specific transcription in mitotic cell cycle	15	0.0023	3	0.0059	0.0829848	E
<input type="radio"/>	GO:0000279	6,5	M phase	258	0.0398	22	0.0431	0.0838529	E
<input type="radio"/>	GO:0044265	5	cellular macromolecule catabolic process	314	0.0485	25	0.0490	0.0848518	E
<input type="radio"/>	GO:0000710	11,9,8,6,5,10,7,4	meiotic mismatch repair	7	0.0011	2	0.0039	0.0863886	E
<input type="radio"/>	GO:0031382	9,8,10,7	mating projection biogenesis	7	0.0011	2	0.0039	0.0863886	E
<input type="radio"/>	GO:0045896	9,7,5,8,6,4	regulation of transcription, mitotic	7	0.0011	2	0.0039	0.0863886	E
<input type="radio"/>	GO:0007068	10,8,6,9,7,5	negative regulation of transcription, mitotic	7	0.0011	2	0.0039	0.0863886	E
<input type="radio"/>	GO:0006829	8,9	zinc ion transport	7	0.0011	2	0.0039	0.0863886	E
<input type="radio"/>	GO:0006609	10,11,8,9,7	mRNA-binding (hnRNP) protein import into nucleus	25	0.0039	4	0.0078	0.0868494	E
<input type="radio"/>	GO:0042592	4	homeostatic process	134	0.0207	13	0.0255	0.0872344	E
<input type="radio"/>	GO:0006473	8	protein amino acid acetylation	48	0.0074	6	0.0118	0.0934280	E
<input type="radio"/>	GO:0051301	3	cell division	246	0.0380	20	0.0392	0.0934807	E
<input type="radio"/>	GO:0043543	7	protein amino acid acylation	62	0.0096	7	0.0137	0.1016620	E
<input type="radio"/>	GO:0006461	6,5	protein complex assembly	116	0.0179	11	0.0216	0.1039687	E
<input type="radio"/>	GO:0045132	9,7,8,6,4	meiotic chromosome segregation	17	0.0026	3	0.0059	0.1053195	E
<input type="radio"/>	GO:0006739	9,8	NADP metabolic process	17	0.0026	3	0.0059	0.1053195	E
<input type="radio"/>	GO:0007004	9	telomere maintenance via telomerase	17	0.0026	3	0.0059	0.1053195	E
<input type="radio"/>	GO:0032990	5,6	cell part morphogenesis	8	0.0012	2	0.0039	0.1061395	E
<input type="radio"/>	GO:0006566	7,8	threonine metabolic process	8	0.0012	2	0.0039	0.1061395	E
<input type="radio"/>	GO:0030031	8,7,9	cell projection biogenesis	8	0.0012	2	0.0039	0.1061395	E
<input type="radio"/>	GO:0007532	9,5,7,8,6	regulation of transcription, mating-type specific	8	0.0012	2	0.0039	0.1061395	E
<input type="radio"/>	GO:0048858	6,7	cell projection morphogenesis	8	0.0012	2	0.0039	0.1061395	E
<input type="radio"/>	GO:0030030	7,6,8	cell projection organization and biogenesis	8	0.0012	2	0.0039	0.1061395	E
<input type="radio"/>	GO:0045039	10,9,7,8	protein import into mitochondrial inner membrane	8	0.0012	2	0.0039	0.1061395	E
<input type="radio"/>	GO:0000335	10,9,6	negative regulation of DNA transposition	8	0.0012	2	0.0039	0.1061395	E
<input type="radio"/>	GO:0030005	9,7	cellular di-, tri-valent inorganic cation homeostasis	64	0.0099	7	0.0137	0.1090622	E
<input type="radio"/>	GO:0055066	8	di-, tri-valent inorganic cation homeostasis	64	0.0099	7	0.0137	0.1090622	E
<input type="radio"/>	GO:0007059	3	chromosome segregation	119	0.0184	11	0.0216	0.1091265	E
<input type="radio"/>	GO:0040007	2	growth	141	0.0218	12	0.0235	0.1163362	E
<input type="radio"/>	GO:0016571	11,9,10,8	histone methylation	18	0.0028	3	0.0059	0.1164629	E
<input type="radio"/>	GO:0000018	8,7	regulation of DNA recombination	18	0.0028	3	0.0059	0.1164629	E
<input type="radio"/>	GO:0006273	9,8	lagging strand elongation	18	0.0028	3	0.0059	0.1164629	E
<input type="radio"/>	GO:0000753	7,8,6	cellular morphogenesis during conjugation with cellular fusion	18	0.0028	3	0.0059	0.1164629	E
<input type="radio"/>	GO:0030447	3	filamentous growth	94	0.0145	9	0.0176	0.1168915	E
<input type="radio"/>	GO:0019236	4	response to pheromone	94	0.0145	9	0.0176	0.1168915	E
<input type="radio"/>	GO:0000910	4	cytokinesis	109	0.0168	10	0.0196	0.1172085	E
<input type="radio"/>	GO:0000725	7,6	recombinational repair	29	0.0045	4	0.0078	0.1176043	E
<input type="radio"/>	GO:0006409	11,9,6,8,10,7	tRNA export from nucleus	29	0.0045	4	0.0078	0.1176043	E
<input type="radio"/>	GO:0051052	7,6	regulation of DNA metabolic process	41	0.0063	5	0.0098	0.1186296	E
<input type="radio"/>	GO:0007033	5	vacuole organization and biogenesis	67	0.0103	7	0.0137	0.1194867	E
<input type="radio"/>	GO:0006790	4	sulfur metabolic process	67	0.0103	7	0.0137	0.1194867	E

<input type="checkbox"/>	GO:0051325	6,5	interphase	112	0.0173	10	0.0196	0.1217299	E
<input type="checkbox"/>	GO:0051329	7,5,6	interphase of mitotic cell cycle	112	0.0173	10	0.0196	0.1217299	E
<input type="checkbox"/>	GO:0006769	8,7	nicotinamide metabolic process	42	0.0065	5	0.0098	0.1240929	E
<input type="checkbox"/>	GO:0006665	6,7	sphingolipid metabolic process	30	0.0046	4	0.0078	0.1250469	E
<input type="checkbox"/>	GO:0051031	5,7,6,8	tRNA transport	30	0.0046	4	0.0078	0.1250469	E
<input type="checkbox"/>	GO:0051128	5,4	regulation of cellular component organization and biogenesis	30	0.0046	4	0.0078	0.1250469	E
<input type="checkbox"/>	GO:0007242	5	intracellular signaling cascade	137	0.0212	11	0.0216	0.1255494	E
<input type="checkbox"/>	GO:0000184	8	mRNA catabolic process, nonsense-mediated decay	9	0.0014	2	0.0039	0.1257470	E
<input type="checkbox"/>	GO:0006760	5,7	folic acid and derivative metabolic process	9	0.0014	2	0.0039	0.1257470	E
<input type="checkbox"/>	GO:0006984	6	ER-nuclear signaling pathway	9	0.0014	2	0.0039	0.1257470	E
<input type="checkbox"/>	GO:0006283	8,7	transcription-coupled nucleotide-excision repair	9	0.0014	2	0.0039	0.1257470	E
<input type="checkbox"/>	GO:0030968	7,5,6	unfolded protein response	9	0.0014	2	0.0039	0.1257470	E
<input type="checkbox"/>	GO:0051180	4,5	vitamin transport	9	0.0014	2	0.0039	0.1257470	E
<input type="checkbox"/>	GO:0006733	6	oxidoreduction coenzyme metabolic process	56	0.0086	6	0.0118	0.1285858	E
<input type="checkbox"/>	GO:0006289	7,6	nucleotide-excision repair	44	0.0068	5	0.0098	0.1345287	E
<input type="checkbox"/>	GO:0030036	7	actin cytoskeleton organization and biogenesis	107	0.0165	9	0.0176	0.1359848	E
<input type="checkbox"/>	GO:0000767	6,7	cellular morphogenesis during conjugation	20	0.0031	3	0.0059	0.1381594	E
<input type="checkbox"/>	GO:0042724	7	thiamin and derivative biosynthetic process	20	0.0031	3	0.0059	0.1381594	E
<input type="checkbox"/>	GO:0051053	8,7	negative regulation of DNA metabolic process	20	0.0031	3	0.0059	0.1381594	E
<input type="checkbox"/>	GO:0030148	7,6,8	sphingolipid biosynthetic process	20	0.0031	3	0.0059	0.1381594	E
<input type="checkbox"/>	GO:0042398	6,5	amino acid derivative biosynthetic process	20	0.0031	3	0.0059	0.1381594	E
<input type="checkbox"/>	GO:0030029	6	actin filament-based process	112	0.0173	9	0.0176	0.1383300	E
<input type="checkbox"/>	GO:0006271	8,7	DNA strand elongation during DNA replication	32	0.0049	4	0.0078	0.1393315	E
<input type="checkbox"/>	GO:0022616	6	DNA strand elongation	32	0.0049	4	0.0078	0.1393315	E
<input type="checkbox"/>	GO:0019362	7,6	pyridine nucleotide metabolic process	45	0.0069	5	0.0098	0.1394621	E
<input type="checkbox"/>	GO:0065004	6,5	protein-DNA complex assembly	74	0.0114	7	0.0137	0.1394915	E
<input type="checkbox"/>	GO:0007127	9,7,6,8,5	meiosis I	75	0.0116	7	0.0137	0.1417629	E
<input type="checkbox"/>	GO:0000041	7,8	transition metal ion transport	46	0.0071	5	0.0098	0.1441828	E
<input type="checkbox"/>	GO:0006446	8,7,6	regulation of translational initiation	10	0.0015	2	0.0039	0.1448366	E
<input type="checkbox"/>	GO:0009068	7,8	aspartate family amino acid catabolic process	10	0.0015	2	0.0039	0.1448366	E
<input type="checkbox"/>	GO:0008298	5	intracellular mRNA localization	10	0.0015	2	0.0039	0.1448366	E
<input type="checkbox"/>	GO:0006313	7,4	transposition, DNA-mediated	10	0.0015	2	0.0039	0.1448366	E
<input type="checkbox"/>	GO:0007129	10,8,7,5,9,6,4	synapsis	10	0.0015	2	0.0039	0.1448366	E
<input type="checkbox"/>	GO:0055069	9	zinc ion homeostasis	10	0.0015	2	0.0039	0.1448366	E
<input type="checkbox"/>	GO:0006817	7,8	phosphate transport	10	0.0015	2	0.0039	0.1448366	E
<input type="checkbox"/>	GO:0000337	9,8,5	regulation of DNA transposition	10	0.0015	2	0.0039	0.1448366	E
<input type="checkbox"/>	GO:0046019	10,9,6	regulation of transcription from RNA polymerase II promoter by pheromones	10	0.0015	2	0.0039	0.1448366	E
<input type="checkbox"/>	GO:0009373	9,8,5	regulation of transcription by pheromones	10	0.0015	2	0.0039	0.1448366	E
<input type="checkbox"/>	GO:0006882	10,8	cellular zinc ion homeostasis	10	0.0015	2	0.0039	0.1448366	E
<input type="checkbox"/>	GO:0015718	6,7	monocarboxylic acid transport	10	0.0015	2	0.0039	0.1448366	E
<input type="checkbox"/>	GO:0042559	6	pteridine and derivative biosynthetic process	2	0.0003	1	0.0020	0.1451232	E
<input type="checkbox"/>	GO:0006746	7	FADH2 metabolic process	2	0.0003	1	0.0020	0.1451232	E

<input type="radio"/>	GO:0010043	6	response to zinc ion	2	0.0003	1	0.0020	0.1451232	E
<input type="radio"/>	GO:0016572	11,9,8	histone phosphorylation	2	0.0003	1	0.0020	0.1451232	E
<input type="radio"/>	GO:0032261	6,7	purine nucleotide salvage	2	0.0003	1	0.0020	0.1451232	E
<input type="radio"/>	GO:0030969	8,6,7	UFP-specific transcription factor mRNA processing during unfolded protein response	2	0.0003	1	0.0020	0.1451232	E
<input type="radio"/>	GO:0009220	7,8	pyrimidine ribonucleotide biosynthetic process	2	0.0003	1	0.0020	0.1451232	E
<input type="radio"/>	GO:0006975	9,8,5	DNA damage induced protein phosphorylation	2	0.0003	1	0.0020	0.1451232	E
<input type="radio"/>	GO:0046655	6,8	folic acid metabolic process	2	0.0003	1	0.0020	0.1451232	E
<input type="radio"/>	GO:0046037	9	GMP metabolic process	2	0.0003	1	0.0020	0.1451232	E
<input type="radio"/>	GO:0007580	10,6	extrachromosomal circular DNA accumulation during cell aging	2	0.0003	1	0.0020	0.1451232	E
<input type="radio"/>	GO:0031056	6,8,11,5,9,7	regulation of histone modification	2	0.0003	1	0.0020	0.1451232	E
<input type="radio"/>	GO:0019988	7,8,9,6	charged-tRNA modification	2	0.0003	1	0.0020	0.1451232	E
<input type="radio"/>	GO:0045141	9,7,5,8,6,4	telomere clustering	2	0.0003	1	0.0020	0.1451232	E
<input type="radio"/>	GO:0018195	8	peptidyl-arginine modification	2	0.0003	1	0.0020	0.1451232	E
<input type="radio"/>	GO:0000280	3	nuclear division	2	0.0003	1	0.0020	0.1451232	E
<input type="radio"/>	GO:0050667	7,8,6	homocysteine metabolic process	2	0.0003	1	0.0020	0.1451232	E
<input type="radio"/>	GO:0009061	6	anaerobic respiration	2	0.0003	1	0.0020	0.1451232	E
<input type="radio"/>	GO:0009218	7	pyrimidine ribonucleotide metabolic process	2	0.0003	1	0.0020	0.1451232	E
<input type="radio"/>	GO:0006241	9,10	CTP biosynthetic process	2	0.0003	1	0.0020	0.1451232	E
<input type="radio"/>	GO:0009208	8	pyrimidine ribonucleoside triphosphate metabolic process	2	0.0003	1	0.0020	0.1451232	E
<input type="radio"/>	GO:0006556	8,7,6,9,5	S-adenosylmethionine biosynthetic process	2	0.0003	1	0.0020	0.1451232	E
<input type="radio"/>	GO:0046656	7,8,9	folic acid biosynthetic process	2	0.0003	1	0.0020	0.1451232	E
<input type="radio"/>	GO:0042558	5	pteridine and derivative metabolic process	2	0.0003	1	0.0020	0.1451232	E
<input type="radio"/>	GO:0006430	9,8,10,7	lysyl-tRNA aminoacylation	2	0.0003	1	0.0020	0.1451232	E
<input type="radio"/>	GO:0009221	7,8	pyrimidine deoxyribonucleotide biosynthetic process	2	0.0003	1	0.0020	0.1451232	E
<input type="radio"/>	GO:0006429	9,8,10,7	leucyl-tRNA aminoacylation	2	0.0003	1	0.0020	0.1451232	E
<input type="radio"/>	GO:0006541	7,8	glutamine metabolic process	2	0.0003	1	0.0020	0.1451232	E
<input type="radio"/>	GO:0006545	8,9	glycine biosynthetic process	2	0.0003	1	0.0020	0.1451232	E
<input type="radio"/>	GO:0009209	8,9	pyrimidine ribonucleoside triphosphate biosynthetic process	2	0.0003	1	0.0020	0.1451232	E
<input type="radio"/>	GO:0046036	9	CTP metabolic process	2	0.0003	1	0.0020	0.1451232	E
<input type="radio"/>	GO:0006426	9,8,10,7	glycyl-tRNA aminoacylation	2	0.0003	1	0.0020	0.1451232	E
<input type="radio"/>	GO:0016114	7,6,8,5	terpenoid biosynthetic process	2	0.0003	1	0.0020	0.1451232	E
<input type="radio"/>	GO:0006824	7,8,9	cobalt ion transport	2	0.0003	1	0.0020	0.1451232	E
<input type="radio"/>	GO:0006721	6,7,4	terpenoid metabolic process	2	0.0003	1	0.0020	0.1451232	E
<input type="radio"/>	GO:0006631	5,7,6	fatty acid metabolic process	47	0.0073	5	0.0098	0.1486755	E
<input type="radio"/>	GO:0015674	6,7	di-, tri-valent inorganic cation transport	34	0.0053	4	0.0078	0.1525761	E
<input type="radio"/>	GO:0000154	7,8	rRNA modification	85	0.0131	7	0.0137	0.1554211	E
<input type="radio"/>	GO:0032506	5,3	cytokinetic process	88	0.0136	7	0.0137	0.1563103	E
<input type="radio"/>	GO:0006839	7,5,6	mitochondrial transport	65	0.0100	6	0.0118	0.1566521	E
<input type="radio"/>	GO:0044272	5	sulfur compound biosynthetic process	22	0.0034	3	0.0059	0.1584716	E
<input type="radio"/>	GO:0042723	6	thiamin and derivative metabolic process	22	0.0034	3	0.0059	0.1584716	E
<input type="radio"/>	GO:0000282	7,9,5,6,10	cellular bud site selection	66	0.0102	6	0.0118	0.1587706	E
<input type="radio"/>	GO:0007105	6,4	cytokinesis, site selection	66	0.0102	6	0.0118	0.1587706	E

<input type="radio"/>	GO:0030468	8,5,9	establishment of cell polarity (sensu Fungi)	66	0.0102	6	0.0118	0.1587706	E
<input type="radio"/>	GO:0030467	7,4,8	establishment and/or maintenance of cell polarity (sensu Fungi)	66	0.0102	6	0.0118	0.1587706	E
<input type="radio"/>	GO:0043623	7,6	cellular protein complex assembly	69	0.0107	6	0.0118	0.1638437	E
<input type="radio"/>	GO:0006979	4	response to oxidative stress	71	0.0110	6	0.0118	0.1661587	E
<input type="radio"/>	GO:0006879	10,8	cellular iron ion homeostasis	38	0.0059	4	0.0078	0.1750637	E
<input type="radio"/>	GO:0055072	9	iron ion homeostasis	38	0.0059	4	0.0078	0.1750637	E
<input type="radio"/>	GO:0006352	7,8,6	transcription initiation	55	0.0085	5	0.0098	0.1751731	E
<input type="radio"/>	GO:0009201	7,8	ribonucleoside triphosphate biosynthetic process	24	0.0037	3	0.0059	0.1768371	E
<input type="radio"/>	GO:0009069	6,7	serine family amino acid metabolic process	24	0.0037	3	0.0059	0.1768371	E
<input type="radio"/>	GO:0007007	6,7	inner mitochondrial membrane organization and biogenesis	12	0.0019	2	0.0039	0.1803572	E
<input type="radio"/>	GO:0015846	5,6	polyamine transport	12	0.0019	2	0.0039	0.1803572	E
<input type="radio"/>	GO:0045910	9,8	negative regulation of DNA recombination	12	0.0019	2	0.0039	0.1803572	E
<input type="radio"/>	GO:0000083	10,9,6,5,7,8,4	G1/S-specific transcription in mitotic cell cycle	12	0.0019	2	0.0039	0.1803572	E
<input type="radio"/>	GO:0000070	9,7,5,8,6,4	mitotic sister chromatid segregation	59	0.0091	5	0.0098	0.1816496	E
<input type="radio"/>	GO:0007124	6,4,8,9	pseudohyphal growth	61	0.0094	5	0.0098	0.1832162	E
<input type="radio"/>	GO:0000819	7,4	sister chromatid segregation	62	0.0096	5	0.0098	0.1835995	E
<input type="radio"/>	GO:0030001	6,7	metal ion transport	62	0.0096	5	0.0098	0.1835995	E
<input type="radio"/>	GO:0043681	6,7,8	protein import into mitochondrion	40	0.0062	4	0.0078	0.1840114	E
<input type="radio"/>	GO:0006298	7,9,6	mismatch repair	25	0.0039	3	0.0059	0.1851604	E
<input type="radio"/>	GO:0000724	8,7	double-strand break repair via homologous recombination	25	0.0039	3	0.0059	0.1851604	E
<input type="radio"/>	GO:0009199	7	ribonucleoside triphosphate metabolic process	25	0.0039	3	0.0059	0.1851604	E
<input type="radio"/>	GO:0045005	8,6	maintenance of fidelity during DNA-dependent DNA replication	25	0.0039	3	0.0059	0.1851604	E
<input type="radio"/>	GO:0009064	6,7	glutamine family amino acid metabolic process	43	0.0066	4	0.0078	0.1943548	E
<input type="radio"/>	GO:0006334	6,7,10	nucleosome assembly	13	0.0020	2	0.0039	0.1963982	E
<input type="radio"/>	GO:0030258	5,6	lipid modification	13	0.0020	2	0.0039	0.1963982	E
<input type="radio"/>	GO:0006301	7,6	postreplication repair	13	0.0020	2	0.0039	0.1963982	E
<input type="radio"/>	GO:0007346	7,5,6	regulation of progression through mitotic cell cycle	13	0.0020	2	0.0039	0.1963982	E
<input type="radio"/>	GO:0006367	8,9,7	transcription initiation from RNA polymerase II promoter	44	0.0068	4	0.0078	0.1969741	E
<input type="radio"/>	GO:0009142	6,7	nucleoside triphosphate biosynthetic process	27	0.0042	3	0.0059	0.1999144	E
<input type="radio"/>	GO:0006561	8,9	proline biosynthetic process	3	0.0005	1	0.0020	0.2005699	E
<input type="radio"/>	GO:0006431	9,8,10,7	methionyl-tRNA aminoacylation	3	0.0005	1	0.0020	0.2005699	E
<input type="radio"/>	GO:0006285	7,8	base-excision repair, AP site formation	3	0.0005	1	0.0020	0.2005699	E
<input type="radio"/>	GO:0051436	8,6,5	negative regulation of ubiquitin ligase activity during mitotic cell cycle	3	0.0005	1	0.0020	0.2005699	E
<input type="radio"/>	GO:0000387	5,9,11	spliceosomal snRNP biogenesis	3	0.0005	1	0.0020	0.2005699	E
<input type="radio"/>	GO:0042044	4,5	fluid transport	3	0.0005	1	0.0020	0.2005699	E
<input type="radio"/>	GO:0007025	8	beta-tubulin folding	3	0.0005	1	0.0020	0.2005699	E
<input type="radio"/>	GO:0051352	6	negative regulation of ligase activity	3	0.0005	1	0.0020	0.2005699	E
<input type="radio"/>	GO:0009263	6,7	deoxyribonucleotide biosynthetic process	3	0.0005	1	0.0020	0.2005699	E
<input type="radio"/>	GO:0051444	7	negative regulation of ubiquitin ligase activity	3	0.0005	1	0.0020	0.2005699	E
<input type="radio"/>	GO:0006833	5,6	water transport	3	0.0005	1	0.0020	0.2005699	E
<input type="radio"/>	GO:0031027	o	actomyosin structure organization and	3	0.0005	1	0.0020	0.2005699	E

<input type="radio"/>	GO:0051052	0	biogenesis	3	0.0005	1	0.0020	0.2005699	E
<input type="radio"/>	GO:0048024	9,8,11	regulation of nuclear mRNA splicing, via spliceosome	3	0.0005	1	0.0020	0.2005699	E
<input type="radio"/>	GO:0000915	7,6,10,5	cytokinesis, contractile ring formation	3	0.0005	1	0.0020	0.2005699	E
<input type="radio"/>	GO:0006452	8,7,6	translational frameshifting	3	0.0005	1	0.0020	0.2005699	E
<input type="radio"/>	GO:0000912	6,5,9,4	cytokinesis, formation of actomyosin apparatus	3	0.0005	1	0.0020	0.2005699	E
<input type="radio"/>	GO:0045026	6	plasma membrane fusion	3	0.0005	1	0.0020	0.2005699	E
<input type="radio"/>	GO:0009219	7	pyrimidine deoxyribonucleotide metabolic process	3	0.0005	1	0.0020	0.2005699	E
<input type="radio"/>	GO:0000244	7,6,10,12	assembly of spliceosomal tri-snRNP	3	0.0005	1	0.0020	0.2005699	E
<input type="radio"/>	GO:0030100	6,7,5	regulation of endocytosis	3	0.0005	1	0.0020	0.2005699	E
<input type="radio"/>	GO:0006404	10,8,5,7,9,6	RNA import into nucleus	3	0.0005	1	0.0020	0.2005699	E
<input type="radio"/>	GO:0006549	7,8	isoleucine metabolic process	3	0.0005	1	0.0020	0.2005699	E
<input type="radio"/>	GO:0031684	7	heterotrimeric G-protein complex cycle	3	0.0005	1	0.0020	0.2005699	E
<input type="radio"/>	GO:0019413	7,8	acetate biosynthetic process	3	0.0005	1	0.0020	0.2005699	E
<input type="radio"/>	GO:0006567	8,9	threonine catabolic process	3	0.0005	1	0.0020	0.2005699	E
<input type="radio"/>	GO:0050684	8,7	regulation of mRNA processing	3	0.0005	1	0.0020	0.2005699	E
<input type="radio"/>	GO:0042364	6	water-soluble vitamin biosynthetic process	46	0.0071	4	0.0078	0.2009888	E
<input type="radio"/>	GO:0009110	5	vitamin biosynthetic process	46	0.0071	4	0.0078	0.2009888	E
<input type="radio"/>	GO:0015837	4,5	amine transport	50	0.0077	4	0.0078	0.2043465	E
<input type="radio"/>	GO:0032005	7,6	signal transduction during conjugation with cellular fusion	28	0.0043	3	0.0059	0.2063015	E
<input type="radio"/>	GO:0000750	8,7,6	pheromone-dependent signal transduction during conjugation with cellular fusion	28	0.0043	3	0.0059	0.2063015	E
<input type="radio"/>	GO:0006547	7,8	histidine metabolic process	14	0.0022	2	0.0039	0.2111212	E
<input type="radio"/>	GO:0009076	7,8	histidine family amino acid biosynthetic process	14	0.0022	2	0.0039	0.2111212	E
<input type="radio"/>	GO:0000147	5,9,8	actin cortical patch assembly	14	0.0022	2	0.0039	0.2111212	E
<input type="radio"/>	GO:0000105	8,9	histidine biosynthetic process	14	0.0022	2	0.0039	0.2111212	E
<input type="radio"/>	GO:0009075	6,7	histidine family amino acid metabolic process	14	0.0022	2	0.0039	0.2111212	E
<input type="radio"/>	GO:0006144	6	purine base metabolic process	14	0.0022	2	0.0039	0.2111212	E
<input type="radio"/>	GO:0009063	6,7	amino acid catabolic process	29	0.0045	3	0.0059	0.2120125	E
<input type="radio"/>	GO:0031137	6,5	regulation of conjugation with cellular fusion	30	0.0046	3	0.0059	0.2170440	E
<input type="radio"/>	GO:0009141	6	nucleoside triphosphate metabolic process	30	0.0046	3	0.0059	0.2170440	E
<input type="radio"/>	GO:0006893	9,7,6,8	Golgi to plasma membrane transport	30	0.0046	3	0.0059	0.2170440	E
<input type="radio"/>	GO:0046999	5,4	regulation of conjugation	30	0.0046	3	0.0059	0.2170440	E
<input type="radio"/>	GO:0018409	9	peptide or protein amino-terminal blocking	15	0.0023	2	0.0039	0.2244511	E
<input type="radio"/>	GO:0031365	8	N-terminal protein amino acid modification	15	0.0023	2	0.0039	0.2244511	E
<input type="radio"/>	GO:0044270	5,4	nitrogen compound catabolic process	32	0.0049	3	0.0059	0.2250835	E
<input type="radio"/>	GO:0019932	6	second-messenger-mediated signaling	32	0.0049	3	0.0059	0.2250835	E
<input type="radio"/>	GO:0009310	5,6	amine catabolic process	32	0.0049	3	0.0059	0.2250835	E
<input type="radio"/>	GO:0032984	5	macromolecular complex disassembly	32	0.0049	3	0.0059	0.2250835	E
<input type="radio"/>	GO:0006118	4	electron transport	33	0.0051	3	0.0059	0.2281119	E
<input type="radio"/>	GO:0006007	8,9	glucose catabolic process	34	0.0053	3	0.0059	0.2305000	E
<input type="radio"/>	GO:0007186	6	G-protein coupled receptor protein signaling pathway	34	0.0053	3	0.0059	0.2305000	E
<input type="radio"/>	GO:0000726	7,6	non-recombinational repair	35	0.0054	3	0.0059	0.2322678	E
<input type="radio"/>	GO:0007530	4,5	sex determination	35	0.0054	3	0.0059	0.2322678	E

<input type="checkbox"/>	GO:0003006	3,4	reproductive developmental process	35	0.0054	3	0.0059	0.2322678	E
<input type="checkbox"/>	GO:0007531	4,6,5	mating type determination	35	0.0054	3	0.0059	0.2322678	E
<input type="checkbox"/>	GO:0051252	7,6	regulation of RNA metabolic process	36	0.0056	3	0.0059	0.2334381	E
<input type="checkbox"/>	GO:0022411	4	cellular component disassembly	36	0.0056	3	0.0059	0.2334381	E
<input type="checkbox"/>	GO:0031667	5	response to nutrient levels	37	0.0057	3	0.0059	0.2340362	E
<input type="checkbox"/>	GO:0009605	3	response to external stimulus	37	0.0057	3	0.0059	0.2340362	E
<input type="checkbox"/>	GO:0009991	4	response to extracellular stimulus	37	0.0057	3	0.0059	0.2340362	E
<input type="checkbox"/>	GO:0030865	6	cortical cytoskeleton organization and biogenesis	16	0.0025	2	0.0039	0.2363468	E
<input type="checkbox"/>	GO:0030866	8,7	cortical actin cytoskeleton organization and biogenesis	16	0.0025	2	0.0039	0.2363468	E
<input type="checkbox"/>	GO:0032508	7	DNA duplex unwinding	16	0.0025	2	0.0039	0.2363468	E
<input type="checkbox"/>	GO:0015698	6,7	inorganic anion transport	16	0.0025	2	0.0039	0.2363468	E
<input type="checkbox"/>	GO:0048017	8	inositol lipid-mediated signaling	16	0.0025	2	0.0039	0.2363468	E
<input type="checkbox"/>	GO:0032392	6	DNA geometric change	16	0.0025	2	0.0039	0.2363468	E
<input type="checkbox"/>	GO:0048015	7	phosphoinositide-mediated signaling	16	0.0025	2	0.0039	0.2363468	E
<input type="checkbox"/>	GO:0009147	7	pyrimidine nucleoside triphosphate metabolic process	4	0.0006	1	0.0020	0.2463977	E
<input type="checkbox"/>	GO:0018205	8	peptidyl-lysine modification	4	0.0006	1	0.0020	0.2463977	E
<input type="checkbox"/>	GO:0009452	7	RNA capping	4	0.0006	1	0.0020	0.2463977	E
<input type="checkbox"/>	GO:0032988	6	protein-RNA complex disassembly	4	0.0006	1	0.0020	0.2463977	E
<input type="checkbox"/>	GO:0000731	7,6	DNA synthesis during DNA repair	4	0.0006	1	0.0020	0.2463977	E
<input type="checkbox"/>	GO:0043173	5	nucleotide salvage	4	0.0006	1	0.0020	0.2463977	E
<input type="checkbox"/>	GO:0045021	7,6	error-free DNA repair	4	0.0006	1	0.0020	0.2463977	E
<input type="checkbox"/>	GO:0050000	6,5	chromosome localization	4	0.0006	1	0.0020	0.2463977	E
<input type="checkbox"/>	GO:0008053	6	mitochondrial fusion	4	0.0006	1	0.0020	0.2463977	E
<input type="checkbox"/>	GO:0031204	9,11,10,7,8	posttranslational protein targeting to membrane, translocation	4	0.0006	1	0.0020	0.2463977	E
<input type="checkbox"/>	GO:0018348	11,10,9	protein amino acid geranylgeranylation	4	0.0006	1	0.0020	0.2463977	E
<input type="checkbox"/>	GO:0018344	10,9,8	protein geranylgeranylation	4	0.0006	1	0.0020	0.2463977	E
<input type="checkbox"/>	GO:0009083	7,8	branched chain family amino acid catabolic process	4	0.0006	1	0.0020	0.2463977	E
<input type="checkbox"/>	GO:0031578	9,11,10,8	mitotic cell cycle spindle orientation checkpoint	4	0.0006	1	0.0020	0.2463977	E
<input type="checkbox"/>	GO:0000771	6,4	agglutination	4	0.0006	1	0.0020	0.2463977	E
<input type="checkbox"/>	GO:0015780	5,6	nucleotide-sugar transport	4	0.0006	1	0.0020	0.2463977	E
<input type="checkbox"/>	GO:0031565	8,7	cytokinesis checkpoint	4	0.0006	1	0.0020	0.2463977	E
<input type="checkbox"/>	GO:0000390	7,9,11	spliceosome disassembly	4	0.0006	1	0.0020	0.2463977	E
<input type="checkbox"/>	GO:0031384	6,8,11,10,9,7,12	regulation of initiation of mating projection growth	4	0.0006	1	0.0020	0.2463977	E
<input type="checkbox"/>	GO:0000391	8,10,12	U2-dependent spliceosome disassembly	4	0.0006	1	0.0020	0.2463977	E
<input type="checkbox"/>	GO:0000135	9,8	septin checkpoint	4	0.0006	1	0.0020	0.2463977	E
<input type="checkbox"/>	GO:0030497	8,7,9,6	fatty acid elongation	4	0.0006	1	0.0020	0.2463977	E
<input type="checkbox"/>	GO:0007157	5	heterophilic cell adhesion	4	0.0006	1	0.0020	0.2463977	E
<input type="checkbox"/>	GO:0006278	7	RNA-dependent DNA replication	4	0.0006	1	0.0020	0.2463977	E
<input type="checkbox"/>	GO:0016036	8,7,6	cellular response to phosphate starvation	4	0.0006	1	0.0020	0.2463977	E
<input type="checkbox"/>	GO:0000752	7,5,6	agglutination during conjugation with cellular fusion	4	0.0006	1	0.0020	0.2463977	E
<input type="checkbox"/>	GO:0006113	5	fermentation	17	0.0026	2	0.0039	0.2467959	E
<input type="checkbox"/>	GO:0007266	8	Rho protein signal transduction	17	0.0026	2	0.0039	0.2467959	E
<input type="checkbox"/>	GO:0006820	5,6	anion transport	17	0.0026	2	0.0039	0.2467959	E

<input type="radio"/>	GO:0051789	4	response to protein stimulus	18	0.0028	2	0.0039	0.2558085	E
<input type="radio"/>	GO:0010038	5	response to metal ion	18	0.0028	2	0.0039	0.2558085	E
<input type="radio"/>	GO:0006986	4,5	response to unfolded protein	18	0.0028	2	0.0039	0.2558085	E
<input type="radio"/>	GO:0007584	6,4	response to nutrient	18	0.0028	2	0.0039	0.2558085	E
<input type="radio"/>	GO:0000084	8,7,6	S phase of mitotic cell cycle	18	0.0028	2	0.0039	0.2558085	E
<input type="radio"/>	GO:0055065	8	metal ion homeostasis	19	0.0029	2	0.0039	0.2634139	E
<input type="radio"/>	GO:0009228	7,8	thiamin biosynthetic process	19	0.0029	2	0.0039	0.2634139	E
<input type="radio"/>	GO:0006875	9,7	cellular metal ion homeostasis	19	0.0029	2	0.0039	0.2634139	E
<input type="radio"/>	GO:0051320	7,6,5	S phase	20	0.0031	2	0.0039	0.2696555	E
<input type="radio"/>	GO:0006353	8,7	transcription termination	20	0.0031	2	0.0039	0.2696555	E
<input type="radio"/>	GO:0006772	7	thiamin metabolic process	20	0.0031	2	0.0039	0.2696555	E
<input type="radio"/>	GO:0016579	9	protein deubiquitination	20	0.0031	2	0.0039	0.2696555	E
<input type="radio"/>	GO:0006891	8,6,5,7	intra-Golgi vesicle-mediated transport	21	0.0032	2	0.0039	0.2745886	E
<input type="radio"/>	GO:0009145	7,8	purine nucleoside triphosphate biosynthetic process	22	0.0034	2	0.0039	0.2782767	E
<input type="radio"/>	GO:0009206	8,9	purine ribonucleoside triphosphate biosynthetic process	22	0.0034	2	0.0039	0.2782767	E
<input type="radio"/>	GO:0007120	8,6,10,7,11,5	axial cellular bud site selection	22	0.0034	2	0.0039	0.2782767	E
<input type="radio"/>	GO:0030472	6,5,10	mitotic spindle organization and biogenesis in nucleus	22	0.0034	2	0.0039	0.2782767	E
<input type="radio"/>	GO:0006513	10	protein monoubiquitination	22	0.0034	2	0.0039	0.2782767	E
<input type="radio"/>	GO:0006311	10,8,7,5,9,6,4	meiotic gene conversion	22	0.0034	2	0.0039	0.2782767	E
<input type="radio"/>	GO:0006613	10,9,8,7,6	cotranslational protein targeting to membrane	23	0.0036	2	0.0039	0.2807898	E
<input type="radio"/>	GO:0009144	7	purine nucleoside triphosphate metabolic process	23	0.0036	2	0.0039	0.2807898	E
<input type="radio"/>	GO:0006303	8,7	double-strand break repair via nonhomologous end joining	23	0.0036	2	0.0039	0.2807898	E
<input type="radio"/>	GO:0019748	3	secondary metabolic process	23	0.0036	2	0.0039	0.2807898	E
<input type="radio"/>	GO:0009205	8	purine ribonucleoside triphosphate metabolic process	23	0.0036	2	0.0039	0.2807898	E
<input type="radio"/>	GO:0007006	5,6	mitochondrial membrane organization and biogenesis	24	0.0037	2	0.0039	0.2822020	E
<input type="radio"/>	GO:0016575	11,9	histone deacetylation	24	0.0037	2	0.0039	0.2822020	E
<input type="radio"/>	GO:0007096	8,10,9,7	regulation of exit from mitosis	24	0.0037	2	0.0039	0.2822020	E
<input type="radio"/>	GO:0006890	8,6,5,7	retrograde vesicle-mediated transport, Golgi to ER	24	0.0037	2	0.0039	0.2822020	E
<input type="radio"/>	GO:0010035	4	response to inorganic substance	24	0.0037	2	0.0039	0.2822020	E
<input type="radio"/>	GO:0051278	8,7	chitin- and beta-glucan-containing cell wall polysaccharide biosynthetic process	24	0.0037	2	0.0039	0.2822020	E
<input type="radio"/>	GO:0000729	7,8,10,9	DNA double-strand break processing	5	0.0008	1	0.0020	0.2837742	E
<input type="radio"/>	GO:0043001	10,8,7,9	Golgi to plasma membrane protein transport	5	0.0008	1	0.0020	0.2837742	E
<input type="radio"/>	GO:0008283	3	cell proliferation	5	0.0008	1	0.0020	0.2837742	E
<input type="radio"/>	GO:0008655	5	pyrimidine salvage	5	0.0008	1	0.0020	0.2837742	E
<input type="radio"/>	GO:0016337	4	cell-cell adhesion	5	0.0008	1	0.0020	0.2837742	E
<input type="radio"/>	GO:0007329	11,10,7	positive regulation of transcription from RNA polymerase II promoter by pheromones	5	0.0008	1	0.0020	0.2837742	E
<input type="radio"/>	GO:0032447	9	protein urmylation	5	0.0008	1	0.0020	0.2837742	E
<input type="radio"/>	GO:0009098	8,9	leucine biosynthetic process	5	0.0008	1	0.0020	0.2837742	E
<input type="radio"/>	GO:0009264	6,7	deoxyribonucleotide catabolic process	5	0.0008	1	0.0020	0.2837742	E
<input type="radio"/>	GO:0051439	7,5,4	regulation of ubiquitin ligase activity during mitotic cell cycle	5	0.0008	1	0.0020	0.2837742	E
<input type="radio"/>	GO:0000738	6,7	DNA catabolic process, exonucleolytic	5	0.0008	1	0.0020	0.2837742	E

<input type="radio"/>	GO:0051083	8	cotranslational protein folding	5	0.0008	1	0.0020	0.2837742	E
<input type="radio"/>	GO:0006530	8,9	asparagine catabolic process	5	0.0008	1	0.0020	0.2837742	E
<input type="radio"/>	GO:0018346	10,9,8	protein amino acid prenylation	5	0.0008	1	0.0020	0.2837742	E
<input type="radio"/>	GO:0006336	7,8,11	DNA replication-independent nucleosome assembly	5	0.0008	1	0.0020	0.2837742	E
<input type="radio"/>	GO:0009371	10,9,6	positive regulation of transcription by pheromones	5	0.0008	1	0.0020	0.2837742	E
<input type="radio"/>	GO:0043087	6	regulation of GTPase activity	5	0.0008	1	0.0020	0.2837742	E
<input type="radio"/>	GO:0006797	6	polyphosphate metabolic process	5	0.0008	1	0.0020	0.2837742	E
<input type="radio"/>	GO:0000092	8,9,10,7	mitotic anaphase B	5	0.0008	1	0.0020	0.2837742	E
<input type="radio"/>	GO:0018342	9,8,7	protein prenylation	5	0.0008	1	0.0020	0.2837742	E
<input type="radio"/>	GO:0015680	7,5,9,6,10	intracellular copper ion transport	5	0.0008	1	0.0020	0.2837742	E
<input type="radio"/>	GO:0006376	8,7,10,12,3	mRNA splice site selection	6	0.0009	1	0.0020	0.3137435	E
<input type="radio"/>	GO:0031935	11,7,4,8,12,10	regulation of chromatin silencing	6	0.0009	1	0.0020	0.3137435	E
<input type="radio"/>	GO:0007029	5	endoplasmic reticulum organization and biogenesis	6	0.0009	1	0.0020	0.3137435	E
<input type="radio"/>	GO:0006166	6,8	purine ribonucleoside salvage	6	0.0009	1	0.0020	0.3137435	E
<input type="radio"/>	GO:0006544	7,8	glycine metabolic process	6	0.0009	1	0.0020	0.3137435	E
<input type="radio"/>	GO:0009396	6,7,8	folic acid and derivative biosynthetic process	6	0.0009	1	0.0020	0.3137435	E
<input type="radio"/>	GO:0045143	10,8,7,5,9,6,4	homologous chromosome segregation	6	0.0009	1	0.0020	0.3137435	E
<input type="radio"/>	GO:0000717	8,7	nucleotide-excision repair, DNA duplex unwinding	6	0.0009	1	0.0020	0.3137435	E
<input type="radio"/>	GO:0051340	5	regulation of ligase activity	6	0.0009	1	0.0020	0.3137435	E
<input type="radio"/>	GO:0045996	10,9,6	negative regulation of transcription by pheromones	6	0.0009	1	0.0020	0.3137435	E
<input type="radio"/>	GO:0031938	12,8,5,9,13,11	regulation of chromatin silencing at telomere	6	0.0009	1	0.0020	0.3137435	E
<input type="radio"/>	GO:0046021	10,8,5,6,9,7,4	regulation of transcription from RNA polymerase II promoter, mitotic	6	0.0009	1	0.0020	0.3137435	E
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<input type="radio"/>	GO:0006083	7	acetate metabolic process	6	0.0009	1	0.0020	0.3137435	E
<input type="radio"/>	GO:0000090	7,8,9,6	mitotic anaphase	6	0.0009	1	0.0020	0.3137435	E
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<input type="radio"/>	GO:0051438	6	regulation of ubiquitin ligase activity	6	0.0009	1	0.0020	0.3137435	E
<input type="radio"/>	GO:0046020	11,10,7	negative regulation of transcription from RNA polymerase II promoter by pheromones	6	0.0009	1	0.0020	0.3137435	E
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<input type="radio"/>	GO:0019220	7,6	regulation of phosphate metabolic process	7	0.0011	1	0.0020	0.3372379	E
<input type="radio"/>	GO:0000755	6,5	cytogamy	7	0.0011	1	0.0020	0.3372379	E
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<input type="radio"/>	GO:0051174	6,5	regulation of phosphorus metabolic process	7	0.0011	1	0.0020	0.3372379	E
<input type="radio"/>	GO:0000430	11,9,10,7	regulation of transcription from RNA polymerase II promoter by glucose	7	0.0011	1	0.0020	0.3372379	E
<input type="radio"/>	GO:0046839	6,7	phospholipid dephosphorylation	7	0.0011	1	0.0020	0.3372379	E
<input type="radio"/>	GO:0009092	7,8	homoserine metabolic process	7	0.0011	1	0.0020	0.3372379	E
<input type="radio"/>	GO:0000429	10,8,9,6	regulation of transcription from RNA polymerase II promoter by carbon catabolites	7	0.0011	1	0.0020	0.3372379	E
<input type="radio"/>	GO:0006560	7,8	proline metabolic process	7	0.0011	1	0.0020	0.3372379	E
<input type="radio"/>	GO:0045014	11,9,10,7	negative regulation of transcription by glucose	7	0.0011	1	0.0020	0.3372379	E

<input type="checkbox"/>	GO:0033205	5,4	cytokinesis during cell cycle	7	0.0011	1	0.0020	0.3372379	E
<input type="checkbox"/>	GO:0000433	12,10,11,8	negative regulation of transcription from RNA polymerase II promoter by glucose	7	0.0011	1	0.0020	0.3372379	E
<input type="checkbox"/>	GO:0000437	11,9,10,7	negative regulation of transcription from RNA polymerase II promoter by carbon catabolites	7	0.0011	1	0.0020	0.3372379	E
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<input type="checkbox"/>	GO:0009410	4	response to xenobiotic stimulus	7	0.0011	1	0.0020	0.3372379	E
<input type="checkbox"/>	GO:0006078	9,8,10	1,6-beta-glucan biosynthetic process	7	0.0011	1	0.0020	0.3372379	E
<input type="checkbox"/>	GO:0019722	7	calcium-mediated signaling	7	0.0011	1	0.0020	0.3372379	E
<input type="checkbox"/>	GO:0006551	7,8	leucine metabolic process	7	0.0011	1	0.0020	0.3372379	E
<input type="checkbox"/>	GO:0006621	7,6,5,4	protein retention in ER	7	0.0011	1	0.0020	0.3372379	E
<input type="checkbox"/>	GO:0046856	7,9,8,10	phosphoinositide dephosphorylation	7	0.0011	1	0.0020	0.3372379	E
<input type="checkbox"/>	GO:0045013	10,8,9,6	negative regulation of transcription by carbon catabolites	8	0.0012	1	0.0020	0.3550892	E
<input type="checkbox"/>	GO:0042727	7	riboflavin and derivative biosynthetic process	8	0.0012	1	0.0020	0.3550892	E
<input type="checkbox"/>	GO:0007323	9	peptide pheromone maturation	8	0.0012	1	0.0020	0.3550892	E
<input type="checkbox"/>	GO:0046015	10,8,9,6	regulation of transcription by glucose	8	0.0012	1	0.0020	0.3550892	E
<input type="checkbox"/>	GO:0015677	9,10	copper ion import	8	0.0012	1	0.0020	0.3550892	E
<input type="checkbox"/>	GO:0006077	8,9	1,6-beta-glucan metabolic process	8	0.0012	1	0.0020	0.3550892	E
<input type="checkbox"/>	GO:0008156	9,8	negative regulation of DNA replication	8	0.0012	1	0.0020	0.3550892	E
<input type="checkbox"/>	GO:0016973	12,10,7,9,11,8	poly(A)+ mRNA export from nucleus	8	0.0012	1	0.0020	0.3550892	E
<input type="checkbox"/>	GO:0042726	6	riboflavin and derivative metabolic process	8	0.0012	1	0.0020	0.3550892	E
<input type="checkbox"/>	GO:0032185	6	septin cytoskeleton organization and biogenesis	9	0.0014	1	0.0020	0.3680385	E
<input type="checkbox"/>	GO:0043486	11	histone exchange	9	0.0014	1	0.0020	0.3680385	E
<input type="checkbox"/>	GO:0000921	8,7	septin ring assembly	9	0.0014	1	0.0020	0.3680385	E
<input type="checkbox"/>	GO:0022610	2	biological adhesion	9	0.0014	1	0.0020	0.3680385	E
<input type="checkbox"/>	GO:0006528	7,8	asparagine metabolic process	9	0.0014	1	0.0020	0.3680385	E
<input type="checkbox"/>	GO:0015802	6,7,8	basic amino acid transport	9	0.0014	1	0.0020	0.3680385	E
<input type="checkbox"/>	GO:0030950	8,7	establishment and/or maintenance of actin cytoskeleton polarity	9	0.0014	1	0.0020	0.3680385	E
<input type="checkbox"/>	GO:0031106	7	septin ring organization	9	0.0014	1	0.0020	0.3680385	E
<input type="checkbox"/>	GO:0030952	6	establishment and/or maintenance of cytoskeleton polarity	9	0.0014	1	0.0020	0.3680385	E
<input type="checkbox"/>	GO:0006280	6	mutagenesis	9	0.0014	1	0.0020	0.3680385	E
<input type="checkbox"/>	GO:0006474	10,9	N-terminal protein amino acid acetylation	9	0.0014	1	0.0020	0.3680385	E
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<input type="checkbox"/>	GO:0055074	9	calcium ion homeostasis	9	0.0014	1	0.0020	0.3680385	E
<input type="checkbox"/>	GO:0042430	5	indole and derivative metabolic process	10	0.0015	1	0.0020	0.3767458	E
<input type="checkbox"/>	GO:0006568	7,8,6	tryptophan metabolic process	10	0.0015	1	0.0020	0.3767458	E
<input type="checkbox"/>	GO:0042435	7,5	indole derivative biosynthetic process	10	0.0015	1	0.0020	0.3767458	E
<input type="checkbox"/>	GO:0030846	10,9	transcription termination from Pol II promoter, RNA polymerase(A) coupled	10	0.0015	1	0.0020	0.3767458	E
<input type="checkbox"/>	GO:0001301	9,5	progressive alteration of chromatin during cell aging	10	0.0015	1	0.0020	0.3767458	E
<input type="checkbox"/>	GO:0051293	6,7,8,4,5	establishment of spindle localization	10	0.0015	1	0.0020	0.3767458	E
<input type="checkbox"/>	GO:0000162	9,8,7,10	tryptophan biosynthetic process	10	0.0015	1	0.0020	0.3767458	E
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<input type="radio"/>	GO:0000103	6	sulfate assimilation	10	0.0015	1	0.0020	0.3767458	E
<input type="radio"/>	GO:0051294	7,8,9,5,6	establishment of spindle orientation	10	0.0015	1	0.0020	0.3767458	E
<input type="radio"/>	GO:0006586	6,7	indolalkylamine metabolic process	10	0.0015	1	0.0020	0.3767458	E
<input type="radio"/>	GO:0006616	9,12,11,7,10,8	SRP-dependent cotranslational protein targeting to membrane, translocation	10	0.0015	1	0.0020	0.3767458	E
<input type="radio"/>	GO:0040001	5,4,7,8,9,6	establishment of mitotic spindle localization	10	0.0015	1	0.0020	0.3767458	E
<input type="radio"/>	GO:0046219	7,8,6	indolalkylamine biosynthetic process	10	0.0015	1	0.0020	0.3767458	E
<input type="radio"/>	GO:0051336	5	regulation of hydrolase activity	10	0.0015	1	0.0020	0.3767458	E
<input type="radio"/>	GO:0009096	8,7,9	aromatic amino acid family biosynthetic process, anthranilate pathway	10	0.0015	1	0.0020	0.3767458	E
<input type="radio"/>	GO:0006268	8	DNA unwinding during replication	10	0.0015	1	0.0020	0.3767458	E
<input type="radio"/>	GO:0006791	5	sulfur utilization	10	0.0015	1	0.0020	0.3767458	E
<input type="radio"/>	GO:0042434	6	indole derivative metabolic process	10	0.0015	1	0.0020	0.3767458	E
<input type="radio"/>	GO:0051274	8,9	beta-glucan biosynthetic process	11	0.0017	1	0.0020	0.3817974	E
<input type="radio"/>	GO:0016237	4,6	microautophagy	11	0.0017	1	0.0020	0.3817974	E
<input type="radio"/>	GO:0001558	5,6,4,8,9	regulation of cell growth	11	0.0017	1	0.0020	0.3817974	E
<input type="radio"/>	GO:0046128	7	purine ribonucleoside metabolic process	11	0.0017	1	0.0020	0.3817974	E
<input type="radio"/>	GO:0051049	5,4	regulation of transport	11	0.0017	1	0.0020	0.3817974	E
<input type="radio"/>	GO:0006488	10,9,8	dolichol-linked oligosaccharide biosynthetic process	11	0.0017	1	0.0020	0.3817974	E
<input type="radio"/>	GO:0065002	8,6,7	intracellular protein transport across a membrane	11	0.0017	1	0.0020	0.3817974	E
<input type="radio"/>	GO:0006384	8,9,7	transcription initiation from RNA polymerase III promoter	11	0.0017	1	0.0020	0.3817974	E
<input type="radio"/>	GO:0006116	10,9	NADH oxidation	11	0.0017	1	0.0020	0.3817974	E
<input type="radio"/>	GO:0001101	4	response to acid	11	0.0017	1	0.0020	0.3817974	E
<input type="radio"/>	GO:0043086	5	negative regulation of enzyme activity	11	0.0017	1	0.0020	0.3817974	E
<input type="radio"/>	GO:0009070	7,8	serine family amino acid biosynthetic process	12	0.0019	1	0.0020	0.3837141	E
<input type="radio"/>	GO:0051273	7,8	beta-glucan metabolic process	12	0.0019	1	0.0020	0.3837141	E
<input type="radio"/>	GO:0015914	5,6	phospholipid transport	12	0.0019	1	0.0020	0.3837141	E
<input type="radio"/>	GO:0042278	6	purine nucleoside metabolic process	12	0.0019	1	0.0020	0.3837141	E
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<input type="radio"/>	GO:0009119	6	ribonucleoside metabolic process	13	0.0020	1	0.0020	0.3829572	D
<input type="radio"/>	GO:0009065	7,8	glutamine family amino acid catabolic process	13	0.0020	1	0.0020	0.3829572	D
<input type="radio"/>	GO:0040008	4,3	regulation of growth	13	0.0020	1	0.0020	0.3829572	D
<input type="radio"/>	GO:0007103	6,7,5,8	spindle pole body duplication in nuclear envelope	13	0.0020	1	0.0020	0.3829572	D
<input type="radio"/>	GO:0031929	6	TOR signaling pathway	13	0.0020	1	0.0020	0.3829572	D
<input type="radio"/>	GO:0033014	6	tetrapyrrole biosynthetic process	13	0.0020	1	0.0020	0.3829572	D
<input type="radio"/>	GO:0006783	7,6,8	heme biosynthetic process	13	0.0020	1	0.0020	0.3829572	D
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<input type="radio"/>	GO:0006779	6,7	porphyrin biosynthetic process	13	0.0020	1	0.0020	0.3829572	D
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<input type="radio"/>	GO:0006388	9,8	tRNA splicing	14	0.0022	1	0.0020	0.3799353	D
<input type="radio"/>	GO:0042770	5	DNA damage response, signal transduction	14	0.0022	1	0.0020	0.3799353	D

<input type="radio"/>	GO:0042168	6,7,5	heme metabolic process	14	0.0022	1	0.0020	0.3799353	D
<input type="radio"/>	GO:0000028	9,7,8,6	ribosomal small subunit assembly and maintenance	14	0.0022	1	0.0020	0.3799353	D
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<input type="radio"/>	GO:0006825	8,9	copper ion transport	14	0.0022	1	0.0020	0.3799353	D
<input type="radio"/>	GO:0045002	8,7	double-strand break repair via single-strand annealing	14	0.0022	1	0.0020	0.3799353	D
<input type="radio"/>	GO:0006734	9,8	NADH metabolic process	14	0.0022	1	0.0020	0.3799353	D
<input type="radio"/>	GO:0000394	8	RNA splicing, via endonucleolytic cleavage and ligation	14	0.0022	1	0.0020	0.3799353	D
<input type="radio"/>	GO:0030474	5,6,4,7	spindle pole body duplication	14	0.0022	1	0.0020	0.3799353	D
<input type="radio"/>	GO:0006272	9,8	leading strand elongation	14	0.0022	1	0.0020	0.3799353	D
<input type="radio"/>	GO:0006037	8,9,6,7,10	cell wall chitin metabolic process	14	0.0022	1	0.0020	0.3799353	D
<input type="radio"/>	GO:0006749	6,5	glutathione metabolic process	14	0.0022	1	0.0020	0.3799353	D
<input type="radio"/>	GO:0000077	9,8,6	DNA damage checkpoint	14	0.0022	1	0.0020	0.3799353	D
<input type="radio"/>	GO:0006778	5,6	porphyrin metabolic process	14	0.0022	1	0.0020	0.3799353	D
<input type="radio"/>	GO:0006374	9,11	nuclear mRNA splicing via U2-type spliceosome	15	0.0023	1	0.0020	0.3750091	D
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<input type="radio"/>	GO:0006031	9,7,8,10	chitin biosynthetic process	15	0.0023	1	0.0020	0.3750091	D
<input type="radio"/>	GO:0031109	8	microtubule polymerization or depolymerization	16	0.0025	1	0.0020	0.3684968	D
<input type="radio"/>	GO:0031023	5	microtubule organizing center organization and biogenesis	16	0.0025	1	0.0020	0.3684968	D
<input type="radio"/>	GO:0051300	5,4,6	spindle pole body organization and biogenesis	16	0.0025	1	0.0020	0.3684968	D
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<input type="radio"/>	GO:0006536	7,8	glutamate metabolic process	16	0.0025	1	0.0020	0.3684968	D
<input type="radio"/>	GO:0010383	7,5,6	cell wall polysaccharide metabolic process	16	0.0025	1	0.0020	0.3684968	D
<input type="radio"/>	GO:0019740	4	nitrogen utilization	17	0.0026	1	0.0020	0.3606783	D
<input type="radio"/>	GO:0006030	8,6,7,9	chitin metabolic process	17	0.0026	1	0.0020	0.3606783	D
<input type="radio"/>	GO:0016558	10,9,7,8,6	protein import into peroxisome matrix	17	0.0026	1	0.0020	0.3606783	D
<input type="radio"/>	GO:0006042	7,8	glucosamine biosynthetic process	17	0.0026	1	0.0020	0.3606783	D
<input type="radio"/>	GO:0045003	9,8	double-strand break repair via synthesis-dependent strand annealing	17	0.0026	1	0.0020	0.3606783	D
<input type="radio"/>	GO:0006045	8,9	N-acetylglucosamine biosynthetic process	17	0.0026	1	0.0020	0.3606783	D
<input type="radio"/>	GO:0046349	6,7	amino sugar biosynthetic process	17	0.0026	1	0.0020	0.3606783	D
<input type="radio"/>	GO:0006369	9,8	transcription termination from RNA polymerase II promoter	18	0.0028	1	0.0020	0.3517996	D
<input type="radio"/>	GO:0042401	6,7	biogenic amine biosynthetic process	18	0.0028	1	0.0020	0.3517996	D
<input type="radio"/>	GO:0006378	9	mRNA polyadenylation	18	0.0028	1	0.0020	0.3517996	D
<input type="radio"/>	GO:0009116	5	nucleoside metabolic process	18	0.0028	1	0.0020	0.3517996	D
<input type="radio"/>	GO:0031570	8,7	DNA integrity checkpoint	18	0.0028	1	0.0020	0.3517996	D
<input type="radio"/>	GO:0046148	5	pigment biosynthetic process	19	0.0029	1	0.0020	0.3420758	D
<input type="radio"/>	GO:0006041	6,7	glucosamine metabolic process	19	0.0029	1	0.0020	0.3420758	D
<input type="radio"/>	GO:0009267	7,6,5	cellular response to starvation	19	0.0029	1	0.0020	0.3420758	D
<input type="radio"/>	GO:0042594	6,4	response to starvation	19	0.0029	1	0.0020	0.3420758	D
<input type="radio"/>	GO:0006040	5,6	amino sugar metabolic process	19	0.0029	1	0.0020	0.3420758	D
<input type="radio"/>	GO:0031668	5,4	cellular response to extracellular stimulus	19	0.0029	1	0.0020	0.3420758	D
<input type="radio"/>	GO:0031669	6,5	cellular response to nutrient levels	19	0.0029	1	0.0020	0.3420758	D

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<input type="checkbox"/>	GO:0000022	6,5,10,8	mitotic spindle elongation	20	0.0031	1	0.0020	0.3316950	D
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<input type="checkbox"/>	GO:0006308	5,6	DNA catabolic process	20	0.0031	1	0.0020	0.3316950	D
<input type="checkbox"/>	GO:0051231	5,4,9,7	spindle elongation	20	0.0031	1	0.0020	0.3316950	D
<input type="checkbox"/>	GO:0006614	11,10,9,8,7	SRP-dependent cotranslational protein targeting to membrane	20	0.0031	1	0.0020	0.3316950	D
<input type="checkbox"/>	GO:0009067	7,8	aspartate family amino acid biosynthetic process	20	0.0031	1	0.0020	0.3316950	D
<input type="checkbox"/>	GO:0000209	10	protein polyubiquitination	20	0.0031	1	0.0020	0.3316950	D
<input type="checkbox"/>	GO:0043574	7,5,6	peroxisomal transport	20	0.0031	1	0.0020	0.3316950	D
<input type="checkbox"/>	GO:0042440	4	pigment metabolic process	20	0.0031	1	0.0020	0.3316950	D
<input type="checkbox"/>	GO:0006826	7,8,9	iron ion transport	20	0.0031	1	0.0020	0.3316950	D
<input type="checkbox"/>	GO:0051716	3	cellular response to stimulus	21	0.0032	1	0.0020	0.3208209	D
<input type="checkbox"/>	GO:0033554	4	cellular response to stress	21	0.0032	1	0.0020	0.3208209	D
<input type="checkbox"/>	GO:0019674	9,8	NAD metabolic process	21	0.0032	1	0.0020	0.3208209	D
<input type="checkbox"/>	GO:0007243	6	protein kinase cascade	23	0.0036	1	0.0020	0.2981417	D
<input type="checkbox"/>	GO:0007020	8	microtubule nucleation	23	0.0036	1	0.0020	0.2981417	D
<input type="checkbox"/>	GO:0043044	10	ATP-dependent chromatin remodeling	23	0.0036	1	0.0020	0.2981417	D
<input type="checkbox"/>	GO:0007534	6,8,7	gene conversion at mating-type locus	23	0.0036	1	0.0020	0.2981417	D
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<input type="checkbox"/>	GO:0006576	5,6	biogenic amine metabolic process	24	0.0037	1	0.0020	0.2865651	D
<input type="checkbox"/>	GO:0006476	8	protein amino acid deacetylation	26	0.0040	2	0.0039	0.2820314	D
<input type="checkbox"/>	GO:0006506	10,9,8,7,11	GPI anchor biosynthetic process	26	0.0040	2	0.0039	0.2820314	D
<input type="checkbox"/>	GO:0006379	8	mRNA cleavage	26	0.0040	2	0.0039	0.2820314	D
<input type="checkbox"/>	GO:0009084	7,8	glutamine family amino acid biosynthetic process	27	0.0042	2	0.0039	0.2806042	D
<input type="checkbox"/>	GO:0006505	9,10	GPI anchor metabolic process	27	0.0042	2	0.0039	0.2806042	D
<input type="checkbox"/>	GO:0043241	6,5	protein complex disassembly	28	0.0043	2	0.0039	0.2783851	D
<input type="checkbox"/>	GO:0046489	9,8,10	phosphoinositide biosynthetic process	28	0.0043	2	0.0039	0.2783851	D
<input type="checkbox"/>	GO:0043624	7,6	cellular protein complex disassembly	28	0.0043	2	0.0039	0.2783851	D
<input type="checkbox"/>	GO:0009250	7,8	glucan biosynthetic process	25	0.0039	1	0.0020	0.2749561	D
<input type="checkbox"/>	GO:0043487	8,7	regulation of RNA stability	30	0.0046	2	0.0039	0.2718695	D
<input type="checkbox"/>	GO:0043488	9,8,7	regulation of mRNA stability	30	0.0046	2	0.0039	0.2718695	D
<input type="checkbox"/>	GO:0048311	7,6	mitochondrion distribution	26	0.0040	1	0.0020	0.2633919	D
<input type="checkbox"/>	GO:0010382	6,4	cell wall metabolic process	26	0.0040	1	0.0020	0.2633919	D
<input type="checkbox"/>	GO:0015749	5,6	monosaccharide transport	26	0.0040	1	0.0020	0.2633919	D
<input type="checkbox"/>	GO:0000001	8,7,6	mitochondrion inheritance	26	0.0040	1	0.0020	0.2633919	D
<input type="checkbox"/>	GO:0008645	6,7	hexose transport	26	0.0040	1	0.0020	0.2633919	D
<input type="checkbox"/>	GO:0007121	8,6,10,7,11,5	bipolar cellular bud site selection	32	0.0049	2	0.0039	0.2630553	D
<input type="checkbox"/>	GO:0005977	7,6,8	glycogen metabolic process	32	0.0049	2	0.0039	0.2630553	D
<input type="checkbox"/>	GO:0042546	6	cell wall biogenesis	33	0.0051	2	0.0039	0.2579512	D
<input type="checkbox"/>	GO:0009272	7	chitin- and beta-glucan-containing cell wall biogenesis	33	0.0051	2	0.0039	0.2579512	D
<input type="checkbox"/>	GO:0051646	6,5	mitochondrion localization	27	0.0042	1	0.0020	0.2519374	D
<input type="checkbox"/>	GO:0007093	8,10,9,7	mitotic cell cycle checkpoint	27	0.0042	1	0.0020	0.2519374	D
<input type="checkbox"/>	GO:0030433	9,11,10,12	ER-associated protein catabolic process	35	0.0054	2	0.0039	0.2466494	D

<input type="checkbox"/>	GO:0048590	3	non-developmental growth	35	0.0054	2	0.0039	0.2466494	D
<input type="checkbox"/>	GO:0007117	6,5,4	budding cell bud growth	35	0.0054	2	0.0039	0.2466494	D
<input type="checkbox"/>	GO:0009636	4	response to toxin	28	0.0043	1	0.0020	0.2406473	D
<input type="checkbox"/>	GO:0006906	6,5	vesicle fusion	28	0.0043	1	0.0020	0.2406473	D
<input type="checkbox"/>	GO:0042144	6	vacuole fusion, non-autophagic	28	0.0043	1	0.0020	0.2406473	D
<input type="checkbox"/>	GO:0001522	7	pseudouridine synthesis	39	0.0060	3	0.0059	0.2336256	D
<input type="checkbox"/>	GO:0019320	7,8	hexose catabolic process	39	0.0060	3	0.0059	0.2336256	D
<input type="checkbox"/>	GO:0016311	6	dephosphorylation	41	0.0063	3	0.0059	0.2312680	D
<input type="checkbox"/>	GO:0051651	5,4,3	maintenance of cellular localization	29	0.0045	1	0.0020	0.2295669	D
<input type="checkbox"/>	GO:0006470	8,7	protein amino acid dephosphorylation	29	0.0045	1	0.0020	0.2295669	D
<input type="checkbox"/>	GO:0007533	5,7,6	mating type switching	29	0.0045	1	0.0020	0.2295669	D
<input type="checkbox"/>	GO:0032507	6,5,4	maintenance of cellular protein localization	29	0.0045	1	0.0020	0.2295669	D
<input type="checkbox"/>	GO:0001403	6,4,8,9	invasive growth (sensu Saccharomyces)	42	0.0065	3	0.0059	0.2294351	D
<input type="checkbox"/>	GO:0030476	8,6,7	spore wall assembly (sensu Fungi)	42	0.0065	3	0.0059	0.2294351	D
<input type="checkbox"/>	GO:0042244	5,6	spore wall assembly	42	0.0065	3	0.0059	0.2294351	D
<input type="checkbox"/>	GO:0006515	8,9	misfolded or incompletely synthesized protein catabolic process	38	0.0059	2	0.0039	0.2277531	D
<input type="checkbox"/>	GO:0008643	4,5	carbohydrate transport	38	0.0059	2	0.0039	0.2277531	D
<input type="checkbox"/>	GO:0030384	8,9	phosphoinositide metabolic process	43	0.0066	3	0.0059	0.2272072	D
<input type="checkbox"/>	GO:0046365	6,7	monosaccharide catabolic process	44	0.0068	3	0.0059	0.2246151	D
<input type="checkbox"/>	GO:0006914	3	autophagy	45	0.0069	3	0.0059	0.2216892	D
<input type="checkbox"/>	GO:0006865	5,6,7	amino acid transport	39	0.0060	2	0.0039	0.2211214	D
<input type="checkbox"/>	GO:0001302	5	replicative cell aging	39	0.0060	2	0.0039	0.2211214	D
<input type="checkbox"/>	GO:0006112	5	energy reserve metabolic process	39	0.0060	2	0.0039	0.2211214	D
<input type="checkbox"/>	GO:0046474	8,7,9	glycerophospholipid biosynthetic process	39	0.0060	2	0.0039	0.2211214	D
<input type="checkbox"/>	GO:0007265	7	Ras protein signal transduction	39	0.0060	2	0.0039	0.2211214	D
<input type="checkbox"/>	GO:0045185	5,4,3	maintenance of protein localization	30	0.0046	1	0.0020	0.2187333	D
<input type="checkbox"/>	GO:0065009	3	regulation of a molecular function	46	0.0071	3	0.0059	0.2184593	D
<input type="checkbox"/>	GO:0006073	6,7	glucan metabolic process	46	0.0071	3	0.0059	0.2184593	D
<input type="checkbox"/>	GO:0046164	5	alcohol catabolic process	47	0.0073	3	0.0059	0.2149545	D
<input type="checkbox"/>	GO:0006497	8,7,6	protein amino acid lipidation	48	0.0074	3	0.0059	0.2112030	D
<input type="checkbox"/>	GO:0042157	6	lipoprotein metabolic process	48	0.0074	3	0.0059	0.2112030	D
<input type="checkbox"/>	GO:0006487	9,8,7	protein amino acid N-linked glycosylation	48	0.0074	3	0.0059	0.2112030	D
<input type="checkbox"/>	GO:0042158	7,5	lipoprotein biosynthetic process	48	0.0074	3	0.0059	0.2112030	D
<input type="checkbox"/>	GO:0000002	6	mitochondrial genome maintenance	31	0.0048	1	0.0020	0.2081767	D
<input type="checkbox"/>	GO:0031118	8,9	rRNA pseudouridine synthesis	31	0.0048	1	0.0020	0.2081767	D
<input type="checkbox"/>	GO:0000271	6,7	polysaccharide biosynthetic process	41	0.0063	2	0.0039	0.2075949	D
<input type="checkbox"/>	GO:0006626	9,8,7,6	protein targeting to mitochondrion	52	0.0080	4	0.0078	0.2038721	D
<input type="checkbox"/>	GO:0046942	5,6	carboxylic acid transport	54	0.0083	4	0.0078	0.2021131	D
<input type="checkbox"/>	GO:0007131	10,8,7,5,9,6,4	meiotic recombination	55	0.0085	4	0.0078	0.2007913	D
<input type="checkbox"/>	GO:0015849	4,5	organic acid transport	55	0.0085	4	0.0078	0.2007913	D
<input type="checkbox"/>	GO:0006302	7,6	double-strand break repair	57	0.0088	4	0.0078	0.1973454	D
<input type="checkbox"/>	GO:0000082	8,5,6,7,4	G1/S transition of mitotic cell cycle	52	0.0080	3	0.0059	0.1942624	D
<input type="checkbox"/>	GO:0007166	5	cell surface receptor linked signal transduction	52	0.0080	3	0.0059	0.1942624	D
<input type="checkbox"/>	GO:0048468	3,5	cell development	52	0.0080	3	0.0059	0.1942624	D
<input type="checkbox"/>	GO:0006650	7,8	glycerophospholipid metabolic process	60	0.0093	4	0.0078	0.1904223	D

<input type="radio"/>	GO:0000075	7,6	cell cycle checkpoint	53	0.0082	3	0.0059	0.1896665	D
<input type="radio"/>	GO:0051235	3,2	maintenance of localization	33	0.0051	1	0.0020	0.1879839	D
<input type="radio"/>	GO:0031505	6	chitin- and beta-glucan-containing cell wall organization and biogenesis	44	0.0068	2	0.0039	0.1871267	D
<input type="radio"/>	GO:0006752	6	group transfer coenzyme metabolic process	44	0.0068	2	0.0039	0.1871267	D
<input type="radio"/>	GO:0007052	5,4,9	mitotic spindle organization and biogenesis	44	0.0068	2	0.0039	0.1871267	D
<input type="radio"/>	GO:0050790	4	regulation of catalytic activity	45	0.0069	2	0.0039	0.1803635	D
<input type="radio"/>	GO:0006892	8,6,5,7	post-Golgi vesicle-mediated transport	69	0.0107	5	0.0098	0.1795488	D
<input type="radio"/>	GO:0006869	4,5	lipid transport	34	0.0053	1	0.0020	0.1783795	D
<input type="radio"/>	GO:0044264	5,6	cellular polysaccharide metabolic process	65	0.0100	4	0.0078	0.1753053	D
<input type="radio"/>	GO:0005976	5	polysaccharide metabolic process	65	0.0100	4	0.0078	0.1753053	D
<input type="radio"/>	GO:0043413	6	biopolymer glycosylation	73	0.0113	5	0.0098	0.1727811	D
<input type="radio"/>	GO:0006486	8,7,6	protein amino acid glycosylation	73	0.0113	5	0.0098	0.1727811	D
<input type="radio"/>	GO:0016567	9	protein ubiquitination	66	0.0102	4	0.0078	0.1718863	D
<input type="radio"/>	GO:0006623	9,8,7,6	protein targeting to vacuole	67	0.0103	4	0.0078	0.1683697	D
<input type="radio"/>	GO:0046467	6,5,7	membrane lipid biosynthetic process	78	0.0120	6	0.0118	0.1678527	D
<input type="radio"/>	GO:0007051	8	spindle organization and biogenesis	47	0.0073	2	0.0039	0.1670552	D
<input type="radio"/>	GO:0008654	7,6,8	phospholipid biosynthetic process	58	0.0090	3	0.0059	0.1655867	D
<input type="radio"/>	GO:0006457	6	protein folding	84	0.0130	6	0.0118	0.1623287	D
<input type="radio"/>	GO:0009101	7,5	glycoprotein biosynthetic process	78	0.0120	5	0.0098	0.1610184	D
<input type="radio"/>	GO:0006944	5	membrane fusion	59	0.0091	3	0.0059	0.1606759	D
<input type="radio"/>	GO:0009100	6	glycoprotein metabolic process	79	0.0122	5	0.0098	0.1583300	D
<input type="radio"/>	GO:0006512	8	ubiquitin cycle	88	0.0136	6	0.0118	0.1558073	D
<input type="radio"/>	GO:0007568	3	aging	49	0.0076	2	0.0039	0.1541484	D
<input type="radio"/>	GO:0007569	4	cell aging	49	0.0076	2	0.0039	0.1541484	D
<input type="radio"/>	GO:0000226	7	microtubule cytoskeleton organization and biogenesis	81	0.0125	5	0.0098	0.1526969	D
<input type="radio"/>	GO:0007264	6	small GTPase mediated signal transduction	61	0.0094	3	0.0059	0.1508808	D
<input type="radio"/>	GO:0007015	8	actin filament organization	61	0.0094	3	0.0059	0.1508808	D
<input type="radio"/>	GO:0016049	5,3,7,8	cell growth	102	0.0158	8	0.0157	0.1465382	D
<input type="radio"/>	GO:0030437	7,6	sporulation (sensu Fungi)	108	0.0167	8	0.0157	0.1437648	D
<input type="radio"/>	GO:0048622	6,5	reproductive sporulation	108	0.0167	8	0.0157	0.1437648	D
<input type="radio"/>	GO:0032446	8	protein modification by small protein conjugation	84	0.0130	5	0.0098	0.1437460	D
<input type="radio"/>	GO:0006090	7	pyruvate metabolic process	38	0.0059	1	0.0020	0.1434265	D
<input type="radio"/>	GO:0016485	8	protein processing	38	0.0059	1	0.0020	0.1434265	D
<input type="radio"/>	GO:0000122	10,9	negative regulation of transcription from RNA polymerase II promoter	63	0.0097	3	0.0059	0.1412033	D
<input type="radio"/>	GO:0019954	3	asexual reproduction	85	0.0131	5	0.0098	0.1406637	D
<input type="radio"/>	GO:0007114	5,4	cell budding	85	0.0131	5	0.0098	0.1406637	D
<input type="radio"/>	GO:0045893	9,8	positive regulation of transcription, DNA-dependent	95	0.0147	6	0.0118	0.1405236	D
<input type="radio"/>	GO:0042493	4	response to drug	121	0.0187	9	0.0176	0.1359059	D
<input type="radio"/>	GO:0006643	5,6	membrane lipid metabolic process	125	0.0193	9	0.0176	0.1324370	D
<input type="radio"/>	GO:0006006	7,8	glucose metabolic process	65	0.0100	3	0.0059	0.1317271	D
<input type="radio"/>	GO:0007067	8,6,7,5	mitosis	127	0.0196	10	0.0196	0.1316362	D
<input type="radio"/>	GO:0032787	6	monocarboxylic acid metabolic process	126	0.0195	9	0.0176	0.1313735	D
<input type="radio"/>	GO:0000087	7,5,6	M phase of mitotic cell cycle	129	0.0199	10	0.0196	0.1313690	D

<input type="radio"/>	GO:0006368	9,7,8	RNA elongation from RNA polymerase II promoter	53	0.0082	2	0.0039	0.1299290	D
<input type="radio"/>	GO:0007031	5	peroxisome organization and biogenesis	40	0.0062	1	0.0020	0.1280445	D
<input type="radio"/>	GO:0048308	5	organelle inheritance	40	0.0062	1	0.0020	0.1280445	D
<input type="radio"/>	GO:0006732	5	coenzyme metabolic process	136	0.0210	10	0.0196	0.1278221	D
<input type="radio"/>	GO:0009108	6	coenzyme biosynthetic process	66	0.0102	3	0.0059	0.1270864	D
<input type="radio"/>	GO:0045941	8,7	positive regulation of transcription	101	0.0156	6	0.0118	0.1250497	D
<input type="radio"/>	GO:0051188	5	cofactor biosynthetic process	79	0.0122	4	0.0078	0.1229091	D
<input type="radio"/>	GO:0030435	5	sporulation	123	0.0190	8	0.0157	0.1225557	D
<input type="radio"/>	GO:0048610	3,4	reproductive cellular process	149	0.0230	11	0.0216	0.1221873	D
<input type="radio"/>	GO:0022413	5,4	reproductive process in single-celled organism	149	0.0230	11	0.0216	0.1221873	D
<input type="radio"/>	GO:0007088	7,9,8,6	regulation of mitosis	55	0.0085	2	0.0039	0.1187439	D
<input type="radio"/>	GO:0006811	4,5	ion transport	115	0.0178	7	0.0137	0.1172722	D
<input type="radio"/>	GO:0006888	8,6,5,7	ER to Golgi vesicle-mediated transport	81	0.0125	4	0.0078	0.1154182	D
<input type="radio"/>	GO:0022414	3,2	reproductive process	183	0.0283	14	0.0275	0.1110984	D
<input type="radio"/>	GO:0045935	7,6	positive regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	108	0.0167	6	0.0118	0.1060549	D
<input type="radio"/>	GO:0006281	6,5	DNA repair	193	0.0298	14	0.0275	0.1057161	D
<input type="radio"/>	GO:0032505	4,3	reproduction of a single-celled organism	194	0.0300	14	0.0275	0.1049438	D
<input type="radio"/>	GO:0006812	5,6	cation transport	97	0.0150	5	0.0098	0.1028291	D
<input type="radio"/>	GO:0006644	6,7	phospholipid metabolic process	97	0.0150	5	0.0098	0.1028291	D
<input type="radio"/>	GO:0031167	8,9	rRNA methylation	44	0.0068	1	0.0020	0.1012965	D
<input type="radio"/>	GO:0006354	8,6,7	RNA elongation	59	0.0091	2	0.0039	0.0983832	D
<input type="radio"/>	GO:0051186	4	cofactor metabolic process	170	0.0263	11	0.0216	0.0970858	D
<input type="radio"/>	GO:0006312	7	mitotic recombination	45	0.0069	1	0.0020	0.0954004	D
<input type="radio"/>	GO:0048869	3	cellular developmental process	173	0.0267	11	0.0216	0.0924361	D
<input type="radio"/>	GO:0030154	4	cell differentiation	173	0.0267	11	0.0216	0.0924361	D
<input type="radio"/>	GO:0006468	8,7	protein amino acid phosphorylation	101	0.0156	5	0.0098	0.0908622	D
<input type="radio"/>	GO:0007034	7,5,6	vacuolar transport	114	0.0176	6	0.0118	0.0901070	D
<input type="radio"/>	GO:0007165	4	signal transduction	209	0.0323	14	0.0275	0.0896756	D
<input type="radio"/>	GO:0006357	9,8	regulation of transcription from RNA polymerase II promoter	221	0.0341	15	0.0294	0.0886499	D
<input type="radio"/>	GO:0045944	10,9	positive regulation of transcription from RNA polymerase II promoter	76	0.0117	3	0.0059	0.0855961	D
<input type="radio"/>	GO:0009893	5,4	positive regulation of metabolic process	116	0.0179	6	0.0118	0.0849964	D
<input type="radio"/>	GO:0031325	6,5	positive regulation of cellular metabolic process	116	0.0179	6	0.0118	0.0849964	D
<input type="radio"/>	GO:0048193	7,5,6	Golgi vesicle transport	166	0.0256	10	0.0196	0.0844445	D
<input type="radio"/>	GO:0009057	4	macromolecule catabolic process	345	0.0533	27	0.0529	0.0818700	D
<input type="radio"/>	GO:0043161	10,9,11	proteasomal ubiquitin-dependent protein catabolic process	63	0.0097	2	0.0039	0.0807358	D
<input type="radio"/>	GO:0007154	3	cell communication	240	0.0371	16	0.0314	0.0802248	D
<input type="radio"/>	GO:0006366	8,7	transcription from RNA polymerase II promoter	343	0.0530	25	0.0490	0.0775841	D
<input type="radio"/>	GO:0045045	7,5,4,6	secretory pathway	243	0.0375	16	0.0314	0.0768925	D
<input type="radio"/>	GO:0016197	7,5,6	endosome transport	49	0.0076	1	0.0020	0.0746893	D
<input type="radio"/>	GO:0016052	5	carbohydrate catabolic process	80	0.0124	3	0.0059	0.0719035	D
<input type="radio"/>	GO:0044275	6	cellular carbohydrate catabolic process	80	0.0124	3	0.0059	0.0719035	D
<input type="radio"/>	GO:0006796	5	phosphate metabolic process	212	0.0327	13	0.0255	0.0702464	D

<input type="checkbox"/>	GO:0006793	4	phosphorus metabolic process	212	0.0327	13	0.0255	0.0702464	D
<input type="checkbox"/>	GO:0046903	3,4	secretion	250	0.0386	16	0.0314	0.0689192	D
<input type="checkbox"/>	GO:0032940	6,4,5	secretion by cell	250	0.0386	16	0.0314	0.0689192	D
<input type="checkbox"/>	GO:0044248	4	cellular catabolic process	425	0.0656	31	0.0608	0.0687445	D
<input type="checkbox"/>	GO:0009056	3	catabolic process	438	0.0676	32	0.0627	0.0678107	D
<input type="checkbox"/>	GO:0006066	4	alcohol metabolic process	163	0.0252	9	0.0176	0.0675583	D
<input type="checkbox"/>	GO:0010324	5	membrane invagination	96	0.0148	4	0.0078	0.0668320	D
<input type="checkbox"/>	GO:0007005	5	mitochondrion organization and biogenesis	110	0.0170	5	0.0098	0.0667685	D
<input type="checkbox"/>	GO:0048518	4	positive regulation of biological process	124	0.0191	6	0.0118	0.0660553	D
<input type="checkbox"/>	GO:0048522	5,4	positive regulation of cellular process	124	0.0191	6	0.0118	0.0660553	D
<input type="checkbox"/>	GO:0051726	5,4	regulation of cell cycle	167	0.0258	9	0.0176	0.0606934	D
<input type="checkbox"/>	GO:0000074	6,5	regulation of progression through cell cycle	167	0.0258	9	0.0176	0.0606934	D
<input type="checkbox"/>	GO:0006974	4	response to DNA damage stimulus	234	0.0361	14	0.0275	0.0580372	D
<input type="checkbox"/>	GO:0019318	6,7	hexose metabolic process	85	0.0131	3	0.0059	0.0571902	D
<input type="checkbox"/>	GO:0006091	3	generation of precursor metabolites and energy	183	0.0283	10	0.0196	0.0563691	D
<input type="checkbox"/>	GO:0043687	7	post-translational protein modification	388	0.0599	26	0.0510	0.0550115	D
<input type="checkbox"/>	GO:0006897	6,5	endocytosis	86	0.0133	3	0.0059	0.0545564	D
<input type="checkbox"/>	GO:0015980	4	energy derivation by oxidation of organic compounds	145	0.0224	7	0.0137	0.0518837	D
<input type="checkbox"/>	GO:0006412	6,5	translation	688	0.1062	50	0.0980	0.0504314	D
<input type="checkbox"/>	GO:0009719	3	response to endogenous stimulus	243	0.0375	14	0.0275	0.0474061	D
<input type="checkbox"/>	GO:0006970	4	response to osmotic stress	89	0.0137	3	0.0059	0.0472408	D
<input type="checkbox"/>	GO:0045333	5	cellular respiration	89	0.0137	3	0.0059	0.0472408	D
<input type="checkbox"/>	GO:0005996	5,6	monosaccharide metabolic process	92	0.0142	3	0.0059	0.0407587	D
<input type="checkbox"/>	GO:0016051	5	carbohydrate biosynthetic process	77	0.0119	2	0.0039	0.0380477	D
<input type="checkbox"/>	GO:0043632	6	modification-dependent macromolecule catabolic process	155	0.0239	7	0.0137	0.0364890	D
<input type="checkbox"/>	GO:0045229	4	external encapsulating structure organization and biogenesis	200	0.0309	10	0.0196	0.0342127	D
<input type="checkbox"/>	GO:0007047	5	cell wall organization and biogenesis	200	0.0309	10	0.0196	0.0342127	D
<input type="checkbox"/>	GO:0050896	2	response to stimulus	763	0.1178	52	0.1020	0.0301448	D
<input type="checkbox"/>	GO:0009060	6	aerobic respiration	84	0.0130	2	0.0039	0.0253978	D
<input type="checkbox"/>	GO:0009059	4	macromolecule biosynthetic process	886	0.1368	60	0.1176	0.0232071	D
<input type="checkbox"/>	GO:0016044	4	membrane organization and biogenesis	188	0.0290	8	0.0157	0.0182716	D
<input type="checkbox"/>	GO:0006950	3	response to stress	488	0.0754	29	0.0569	0.0181288	D
<input type="checkbox"/>	GO:0009628	3	response to abiotic stimulus	117	0.0181	3	0.0059	0.0106242	D
<input type="checkbox"/>	GO:0019538	4	protein metabolic process	1547	0.2389	106	0.2078	0.0099763	D
<input type="checkbox"/>	GO:0016310	6	phosphorylation	155	0.0239	5	0.0098	0.0091177	D
<input type="checkbox"/>	GO:0044267	5	cellular protein metabolic process	1498	0.2313	101	0.1980	0.0077379	D
<input type="checkbox"/>	GO:0044260	4	cellular macromolecule metabolic process	1552	0.2397	105	0.2059	0.0075776	D
<input type="checkbox"/>	GO:0032196	3	transposition	105	0.0162	2	0.0039	0.0069692	D
<input type="checkbox"/>	GO:0044262	5	cellular carbohydrate metabolic process	213	0.0329	7	0.0137	0.0027947	D
<input type="checkbox"/>	GO:0019941	8,7,9	modification-dependent protein catabolic process	148	0.0229	3	0.0059	0.0016350	D
<input type="checkbox"/>	GO:0006511	9,8,10	ubiquitin-dependent protein catabolic process	148	0.0229	3	0.0059	0.0016350	D
<input type="checkbox"/>	GO:0016192	4,5	vesicle-mediated transport	328	0.0506	13	0.0255	0.0014590	D
<input type="checkbox"/>	GO:0051603	7,8	proteolysis involved in cellular protein catabolic process	151	0.0233	3	0.0059	0.0013521	D

<input type="checkbox"/>	GO:0030163	6,5	protein catabolic process	173	0.0267	4	0.0078	0.0012018	D
<input type="checkbox"/>	GO:0005975	4	carbohydrate metabolic process	233	0.0360	7	0.0137	0.0009876	D
<input type="checkbox"/>	GO:0044257	6,7	cellular protein catabolic process	160	0.0247	3	0.0059	0.0007588	D
<input type="checkbox"/>	GO:0006508	6	proteolysis	178	0.0275	3	0.0059	0.0002316	D
<input type="checkbox"/>	GO:0043284	5	biopolymer biosynthetic process	354	0.0547	4	0.0078	4.499779E-09	D
<input type="checkbox"/>	GO:0006414	7,6	translational elongation	313	0.0483	2	0.0039	1.439811E-09	D