

Module GO Enrichment

lightyellow enrichment (129 genes)

Over-represented GO terms:

category	num_in_subset	num_total	adj_pval	term	ontology
GO:0003735	27	161	0.0000000	structural constituent of ribosome	MF
GO:0005198	27	190	0.0000000	structural molecule activity	MF
GO:0005840	30	260	0.0000000	ribosome	CC
GO:0006412	28	243	0.0000000	translation	BP
GO:0043043	28	245	0.0000000	peptide biosynthetic process	BP
GO:0006518	28	252	0.0000000	peptide metabolic process	BP
GO:0009058	42	680	0.0000000	biosynthetic process	BP
GO:0043604	28	259	0.0000000	amide biosynthetic process	BP
GO:0043603	28	268	0.0000000	cellular amide metabolic process	BP
GO:1901566	33	399	0.0000000	organonitrogen compound biosynthetic process	BP
GO:0044249	40	657	0.0000000	cellular biosynthetic process	BP
GO:1990904	31	345	0.0000000	ribonucleoprotein complex	CC
GO:0044271	34	494	0.0000001	cellular nitrogen compound biosynthetic process	BP
GO:1901576	39	667	0.0000002	organic substance biosynthetic process	BP
GO:0034645	30	433	0.0000031	cellular macromolecule biosynthetic process	BP
GO:0009059	30	438	0.0000036	macromolecule biosynthetic process	BP
GO:1901564	40	921	0.0001648	organonitrogen compound metabolic process	BP
GO:0044391	15	142	0.0002268	ribosomal subunit	CC
GO:0034641	42	1006	0.0002632	cellular nitrogen compound metabolic process	BP
GO:0044237	54	1597	0.0009305	cellular metabolic process	BP
GO:0006733	7	36	0.0012185	oxidoreduction coenzyme metabolic process	BP
GO:0032991	41	1028	0.0028588	protein-containing complex	CC
GO:0015934	10	82	0.0039628	large ribosomal subunit	CC
GO:0009987	63	2144	0.0065162	cellular process	BP
GO:0005737	107	4374	0.0072243	cytoplasm	CC
GO:0044444	85	3008	0.0083317	cytoplasmic part	CC
GO:0044238	51	1630	0.0089353	primary metabolic process	BP
GO:0019538	31	763	0.0091452	protein metabolic process	BP
GO:0044267	29	673	0.0095362	cellular protein metabolic process	BP
GO:0006732	7	53	0.0127466	coenzyme metabolic process	BP

category	num_in_subset	num_total	adj_pval	term	ontology
GO:0010467	35	886	0.0141921	gene expression	BP
GO:0019843	4	11	0.0173635	rRNA binding	MF
GO:0008152	61	2137	0.0177609	metabolic process	BP
GO:0071704	56	1934	0.0235685	organic substance metabolic process	BP
GO:0019362	5	30	0.0279997	pyridine nucleotide metabolic process	BP
GO:0046496	5	30	0.0279997	nicotinamide nucleotide metabolic process	BP
GO:0006807	47	1532	0.0313548	nitrogen compound metabolic process	BP
GO:0072524	5	31	0.0320476	pyridine-containing compound metabolic process	BP
GO:0044281	15	305	0.0351167	small molecule metabolic process	BP
GO:0006091	6	53	0.0496410	generation of precursor metabolites and energy	BP

Under-represented GO terms:

category	num_in_subset	num_total	adj_pval	term	ontology
GO:0044430	0	659	0.0145493	cytoskeletal part	CC

greenyellow enrichment (251 genes)

Over-represented GO terms:

category	num_in_subset	num_total	adj_pval	term	ontology
GO:0005856	57	693	0.0012110	cytoskeleton	CC
GO:0044430	54	659	0.0012110	cytoskeletal part	CC
GO:0043228	75	1289	0.0015872	non-membrane-bounded organelle	CC
GO:0043232	75	1289	0.0015872	intracellular non-membrane-bounded organelle	CC
GO:0006928	21	125	0.0018341	movement of cell or subcellular component	BP
GO:0015630	35	344	0.0018341	microtubule cytoskeleton	CC
GO:0071103	7	22	0.0197493	DNA conformation change	BP
GO:0003774	15	77	0.0239083	motor activity	MF
GO:0003777	14	72	0.0366317	microtubule motor activity	MF
GO:0005875	14	82	0.0366317	microtubule associated complex	CC

magenta enrichment (264 genes)

Over-represented GO terms:

category	num_in_subset	num_total	adj_pval	term	ontology
GO:0005856	54	693	0.0003979	cytoskeleton	CC
GO:0005930	31	293	0.0003979	axoneme	CC
GO:0044430	52	659	0.0004082	cytoskeletal part	CC
GO:0005929	89	1558	0.0018070	cilium	CC
GO:0042995	89	1558	0.0018070	cell projection	CC
GO:0120025	89	1558	0.0018070	plasma membrane bounded cell projection	CC
GO:0044441	84	1464	0.0020837	ciliary part	CC
GO:0044463	84	1464	0.0020837	cell projection part	CC
GO:0120038	84	1464	0.0020837	plasma membrane bounded cell projection part	CC
GO:0043228	72	1289	0.0130204	non-membrane-bounded organelle	CC
GO:0043232	72	1289	0.0130204	intracellular non-membrane-bounded organelle	CC
GO:0004054	3	3	0.0182469	arginine kinase activity	MF
GO:0016775	3	3	0.0182469	phosphotransferase activity, nitrogenous group as acceptor	MF

black enrichment (438 genes)

Over-represented GO terms:

category	num_in_subset	num_total	adj_pval	term	ontology
GO:0044271	69	494	0.0000003	cellular nitrogen compound biosynthetic process	BP
GO:0016020	92	812	0.0000004	membrane	CC
GO:0009058	82	680	0.0000006	biosynthetic process	BP
GO:1901576	81	667	0.0000006	organic substance biosynthetic process	BP
GO:0044249	79	657	0.0000013	cellular biosynthetic process	BP
GO:0043043	42	245	0.0000052	peptide biosynthetic process	BP
GO:0043604	43	259	0.0000064	amide biosynthetic process	BP
GO:0006412	41	243	0.0000079	translation	BP
GO:0006518	42	252	0.0000079	peptide metabolic process	BP
GO:0044444	238	3008	0.0000079	cytoplasmic part	CC
GO:1901566	55	399	0.0000091	organonitrogen compound biosynthetic process	BP
GO:0043603	43	268	0.0000101	cellular amide metabolic process	BP
GO:0031966	34	212	0.0000944	mitochondrial membrane	CC
GO:0005740	34	216	0.0001360	mitochondrial envelope	CC
GO:1901564	91	921	0.0001360	organonitrogen compound metabolic process	BP

category	num_in_subset	num_total	adj_pval	term	ontology
GO:0044425	63	573	0.0002171	membrane part	CC
GO:0003735	30	161	0.0002241	structural constituent of ribosome	MF
GO:0016021	47	394	0.0004239	integral component of membrane	CC
GO:0031224	47	394	0.0004239	intrinsic component of membrane	CC
GO:0101031	6	9	0.0004816	chaperone complex	CC
GO:0044281	38	305	0.0013075	small molecule metabolic process	BP
GO:0019538	76	763	0.0013133	protein metabolic process	BP
GO:0004016	11	43	0.0017657	adenylate cyclase activity	MF
GO:0009975	11	43	0.0017657	cyclase activity	MF
GO:0008152	168	2137	0.0018345	metabolic process	BP
GO:0009187	12	52	0.0018345	cyclic nucleotide metabolic process	BP
GO:0009190	12	52	0.0018345	cyclic nucleotide biosynthetic process	BP
GO:0044267	69	673	0.0018345	cellular protein metabolic process	BP
GO:0016849	12	53	0.0022414	phosphorus-oxygen lyase activity	MF
GO:0031090	37	289	0.0024300	organelle membrane	CC
GO:0005198	30	190	0.0024755	structural molecule activity	MF
GO:0005777	24	158	0.0026918	peroxisome	CC
GO:0042579	24	158	0.0026918	microbody	CC
GO:0005832	5	8	0.0033944	chaperonin-containing T-complex	CC
GO:0055086	24	167	0.0042176	nucleobase-containing small molecule metabolic process	BP
GO:0020015	23	154	0.0047970	glycosome	CC
GO:0034645	49	433	0.0053470	cellular macromolecule biosynthetic process	BP
GO:0044238	132	1630	0.0053470	primary metabolic process	BP
GO:0005743	20	120	0.0061189	mitochondrial inner membrane	CC
GO:0008150	216	2974	0.0061189	biological_process	BP
GO:0009059	49	438	0.0061189	macromolecule biosynthetic process	BP
GO:0019866	20	120	0.0061189	organelle inner membrane	CC
GO:0044237	130	1597	0.0061189	cellular metabolic process	BP
GO:0071704	151	1934	0.0070658	organic substance metabolic process	BP
GO:0016829	15	87	0.0073759	lyase activity	MF
GO:0006807	124	1532	0.0105734	nitrogen compound metabolic process	BP
GO:0006753	20	138	0.0110370	nucleoside phosphate metabolic process	BP
GO:0055085	19	127	0.0139655	transmembrane transport	BP
GO:0009117	19	133	0.0191742	nucleotide metabolic process	BP
GO:0034641	88	1006	0.0196065	cellular nitrogen compound metabolic process	BP
GO:1901293	16	108	0.0281709	nucleoside phosphate biosynthetic process	BP
GO:0005742	4	7	0.0386128	mitochondrial outer membrane translocase complex	CC

category	num_in_subset	num_total	adj_pval	term	ontology
GO:0098799	4	7	0.0386128	outer mitochondrial membrane protein complex	CC
GO:0003674	233	3380	0.0395268	molecular_function	MF
GO:0006457	16	103	0.0400578	protein folding	BP
GO:0020022	9	43	0.0461871	acidocalcisome	CC
GO:0051082	12	68	0.0473986	unfolded protein binding	MF
GO:0009165	15	104	0.0499848	nucleotide biosynthetic process	BP
GO:0031967	38	359	0.0499848	organelle envelope	CC
GO:0031975	38	359	0.0499848	envelope	CC

Under-represented GO terms:

category	num_in_subset	num_total	adj_pval	term	ontology
GO:0044430	12	659	0.0003059	cytoskeletal part	CC
GO:0005856	14	693	0.0003853	cytoskeleton	CC
GO:0015630	3	344	0.0013839	microtubule cytoskeleton	CC

blue enrichment (614 genes)

Under-represented GO terms:

category	num_in_subset	num_total	adj_pval	term	ontology
GO:0006412	1	243	0.0000000	translation	BP
GO:0043043	1	245	0.0000000	peptide biosynthetic process	BP
GO:0043604	2	259	0.0000009	amide biosynthetic process	BP
GO:0006518	2	252	0.0000011	peptide metabolic process	BP
GO:0043603	3	268	0.0000026	cellular amide metabolic process	BP
GO:0003735	0	161	0.0000050	structural constituent of ribosome	MF
GO:1901566	10	399	0.0000131	organonitrogen compound biosynthetic process	BP
GO:0044271	15	494	0.0001405	cellular nitrogen compound biosynthetic process	BP
GO:0009058	29	680	0.0033229	biosynthetic process	BP
GO:0034641	49	1006	0.0033229	cellular nitrogen compound metabolic process	BP
GO:1901576	28	667	0.0033229	organic substance biosynthetic process	BP
GO:0044249	28	657	0.0041807	cellular biosynthetic process	BP
GO:1990904	13	345	0.0063849	ribonucleoprotein complex	CC
GO:0009059	17	438	0.0069189	macromolecule biosynthetic process	BP

category	num_in_subset	num_total	adj_pval	term	ontology
GO:0005730	9	307	0.0074725	nucleolus	CC
GO:0034645	17	433	0.0074725	cellular macromolecule biosynthetic process	BP
GO:0010467	47	886	0.0212876	gene expression	BP
GO:0003723	13	392	0.0223320	RNA binding	MF
GO:0005198	6	190	0.0281509	structural molecule activity	MF

turquoise enrichment (732 genes)

Over-represented GO terms:

category	num_in_subset	num_total	adj_pval	term	ontology
GO:0009986	15	30	0.0002395	cell surface	CC
GO:0016020	121	812	0.0002395	membrane	CC
GO:0044425	91	573	0.0002395	membrane part	CC
GO:0045121	9	11	0.0002395	membrane raft	CC
GO:0098589	9	11	0.0002395	membrane region	CC
GO:0098857	9	11	0.0002395	membrane microdomain	CC
GO:0016021	60	394	0.0158302	integral component of membrane	CC
GO:0031224	60	394	0.0158302	intrinsic component of membrane	CC

Under-represented GO terms:

category	num_in_subset	num_total	adj_pval	term	ontology
GO:0043228	64	1289	0.0000000	non-membrane-bounded organelle	CC
GO:0043232	64	1289	0.0000000	intracellular non-membrane-bounded organelle	CC
GO:0009987	156	2144	0.0103212	cellular process	BP
GO:0005730	13	307	0.0294454	nucleolus	CC

purple enrichment (251 genes)

Over-represented GO terms:

category	num_in_subset	num_total	adj_pval	term	ontology
GO:0098798	34	240	0.0000011	mitochondrial protein complex	CC

category	num_in_subset	num_total	adj_pval	term	ontology
GO:0005840	33	260	0.0002601	ribosome	CC
GO:1990904	36	345	0.0011188	ribonucleoprotein complex	CC
GO:0044429	54	714	0.0042343	mitochondrial part	CC
GO:0032991	65	1028	0.0081686	protein-containing complex	CC
GO:0000313	17	120	0.0085047	organellar ribosome	CC
GO:0005743	17	120	0.0085047	mitochondrial inner membrane	CC
GO:0019866	17	120	0.0085047	organelle inner membrane	CC
GO:0005761	16	114	0.0116451	mitochondrial ribosome	CC
GO:0003735	21	161	0.0185390	structural constituent of ribosome	MF
GO:0005762	12	70	0.0185390	mitochondrial large ribosomal subunit	CC
GO:0044391	18	142	0.0185390	ribosomal subunit	CC
GO:0005759	17	136	0.0190665	mitochondrial matrix	CC
GO:0000315	12	72	0.0218405	organellar large ribosomal subunit	CC
GO:0005739	81	1359	0.0218405	mitochondrion	CC

green enrichment (528 genes)

Under-represented GO terms:

category	num_in_subset	num_total	adj_pval	term	ontology
GO:0043228	56	1289	0.0090654	non-membrane-bounded organelle	CC
GO:0043232	56	1289	0.0090654	intracellular non-membrane-bounded organelle	CC

darkturquoise enrichment (100 genes)

Over-represented GO terms:

category	num_in_subset	num_total	adj_pval	term	ontology
GO:0016772	17	324	0.0181513	transferase activity, transferring phosphorus-containing groups	MF

brown enrichment (547 genes)

Over-represented GO terms:

category	num_in_subset	num_total	adj_pval	term	ontology
GO:0004016	10	43	0.0115138	adenylate cyclase activity	MF
GO:0009975	10	43	0.0115138	cyclase activity	MF
GO:0009187	10	52	0.0308189	cyclic nucleotide metabolic process	BP
GO:0009190	10	52	0.0308189	cyclic nucleotide biosynthetic process	BP
GO:0016849	10	53	0.0326296	phosphorus-oxygen lyase activity	MF

salmon enrichment (230 genes)

Over-represented GO terms:

category	num_in_subset	num_total	adj_pval	term	ontology
GO:0003723	33	392	0.002191	RNA binding	MF
GO:0003676	45	676	0.031293	nucleic acid binding	MF
GO:0016070	31	424	0.031293	RNA metabolic process	BP

red enrichment (460 genes)

Over-represented GO terms:

category	num_in_subset	num_total	adj_pval	term	ontology
GO:0044430	74	659	0.0007976	cytoskeletal part	CC
GO:0005856	74	693	0.0052547	cytoskeleton	CC
GO:0006260	14	57	0.0187719	DNA replication	BP
GO:0005815	31	231	0.0391543	microtubule organizing center	CC
GO:0005929	127	1558	0.0391543	cilium	CC
GO:0042995	127	1558	0.0391543	cell projection	CC
GO:0051276	15	74	0.0391543	chromosome organization	BP
GO:0120025	127	1558	0.0391543	plasma membrane bounded cell projection	CC
GO:0006259	22	140	0.0496745	DNA metabolic process	BP
GO:0015630	40	344	0.0496745	microtubule cytoskeleton	CC

Under-represented GO terms:

category	num_in_subset	num_total	adj_pval	term	ontology
GO:1990904	2	345	0.0303415	ribonucleoprotein complex	CC

pink enrichment (383 genes)

Over-represented GO terms:

category	num_in_subset	num_total	adj_pval	term	ontology
GO:0070069	5	8	0.049171	cytochrome complex	CC

tan enrichment (243 genes)

Over-represented GO terms:

category	num_in_subset	num_total	adj_pval	term	ontology
GO:0000922	5	13	0.0493009	spindle pole	CC
GO:0015630	25	344	0.0493009	microtubule cytoskeleton	CC

Total enriched GO terms

Total: 198 (Total $-\log_{10}(\text{adj.pval}) = 628.270773$)