

module	modSize	bkgrModSize	rank	enrichmer	Bonferoni	nModGε	bkgrTerr	termID	termName
black	599	511	1	4.41E-12	7.56E-08	19	79	GO:0006613	cotranslational protein targeting to membrane
black	599	511	2	9.00E-12	1.54E-07	19	82	GO:0045047	protein targeting to ER
black	599	511	3	1.32E-11	2.26E-07	18	74	GO:0006614	SRP-dependent cotranslational protein targeting to membrane
black	599	511	4	2.21E-11	3.79E-07	19	86	GO:0072599	establishment of protein localization to endoplasmic reticulum
black	599	511	5	1.97E-10	3.37E-06	20	108	GO:0070972	protein localization to endoplasmic reticulum
black	599	511	6	1.40E-09	2.39E-05	51	634	GO:0043604	amide biosynthetic process
black	599	511	7	1.46E-09	2.50E-05	54	694	GO:0006518	peptide metabolic process
black	599	511	8	1.54E-09	2.63E-05	457	12690	GO:0005622	intracellular
black	599	511	9	1.97E-09	3.37E-05	21	135	GO:0003735	structural constituent of ribosome
black	599	511	10	2.21E-09	3.78E-05	46	546	GO:0006412	translation
blue	3472	3025	1	4.41E-16	7.56E-12	117	301	GO:0043062	extracellular structure organization
blue	3472	3025	2	9.27E-16	1.59E-11	116	300	GO:0030198	extracellular matrix organization
blue	3472	3025	3	7.77E-15	1.33E-10	136	382	GO:0030055	cell-substrate junction
blue	3472	3025	4	1.21E-14	2.07E-10	899	3865	GO:0031982	vesicle
blue	3472	3025	5	1.71E-14	2.93E-10	133	374	GO:0005925	focal adhesion
blue	3472	3025	6	3.45E-14	5.91E-10	133	377	GO:0005924	cell-substrate adherens junction
blue	3472	3025	7	1.14E-13	1.95E-09	38	61	GO:0005518	collagen binding
blue	3472	3025	8	4.64E-13	7.95E-09	155	475	GO:0031012	extracellular matrix
blue	3472	3025	9	6.78E-13	1.16E-08	154	473	GO:0005912	adherens junction
blue	3472	3025	10	3.03E-12	5.19E-08	609	2533	GO:1903561	extracellular vesicle
brown	2419	1876	1	7.45E-05	1	102	600	GO:0043547	positive regulation of GTPase activity
brown	2419	1876	2	0.00015	1	49	246	GO:0005096	GTPase activator activity
brown	2419	1876	3	0.00022	1	107	653	GO:0043087	regulation of GTPase activity
brown	2419	1876	4	0.00035	1	52	275	GO:0030695	GTPase regulator activity
brown	2419	1876	5	0.00088	1	10	28	GO:0043368	positive T cell selection
brown	2419	1876	6	0.00093	1	5	8	GO:1903800	positive regulation of production of miRNAs involved in gene silencing by miRNA
brown	2419	1876	7	0.00163	1	3	3	GO:0018916	nitrobenzene metabolic process
brown	2419	1876	8	0.00163	1	3	3	GO:0046604	positive regulation of mitotic centrosome separation
brown	2419	1876	9	0.00163	1	3	3	GO:0051410	detoxification of nitrogen compound
brown	2419	1876	10	0.00163	1	3	3	GO:0061205	paramesonephric duct development
cyan	201	166	1	2.60E-16	4.44E-12	30	445	GO:0005743	mitochondrial inner membrane
cyan	201	166	2	6.00E-15	1.03E-10	30	500	GO:0019866	organelle inner membrane

cyan	201	166	3	4.51E-14	7.73E-10	33	662	GO:0005740	mitochondrial envelope
cyan	201	166	4	5.84E-14	9.99E-10	32	626	GO:0031966	mitochondrial membrane
cyan	201	166	5	9.23E-14	1.58E-09	20	215	GO:0046034	ATP metabolic process
cyan	201	166	6	1.46E-13	2.50E-09	50	1553	GO:0005739	mitochondrion
cyan	201	166	7	1.10E-12	1.88E-08	13	77	GO:0042775	mitochondrial ATP synthesis coupled electron transport
cyan	201	166	8	1.17E-12	2.00E-08	14	96	GO:0006119	oxidative phosphorylation
cyan	201	166	9	4.70E-12	8.04E-08	8	18	GO:0042776	mitochondrial ATP synthesis coupled proton transport
cyan	201	166	10	6.49E-12	1.11E-07	13	88	GO:1902600	hydrogen ion transmembrane transport
darkgrey	79	74	1	0.00027	1	7	272	GO:0008202	steroid metabolic process
darkgrey	79	74	2	0.00052	1	4	80	GO:0004497	monooxygenase activity
darkgrey	79	74	3	0.00059	1	2	8	GO:0052695	cellular glucuronidation
darkgrey	79	74	4	0.00127	1	3	46	GO:0016836	hydro-lyase activity
darkgrey	79	74	5	0.00136	1	2	12	GO:0031996	thioesterase binding
darkgrey	79	74	6	0.00143	1	31	4053	GO:0005576	extracellular region
darkgrey	79	74	7	0.00245	1	2	16	GO:0008392	arachidonic acid epoxygenase activity
darkgrey	79	74	8	0.00262	1	8	515	GO:0032787	monocarboxylic acid metabolic process
darkgrey	79	74	9	0.00357	1	3	66	GO:0019730	antimicrobial humoral response
darkgrey	79	74	10	0.00383	1	2	20	GO:0019373	epoxygenase P450 pathway
darkgrey	70	62	1	5.68E-05	0.97321	4	54	GO:0060291	long-term synaptic potentiation
darkgrey	70	62	2	0.00022	1	2	6	GO:0033211	adiponectin-activated signaling pathway
darkgrey	70	62	3	0.00032	1	4	84	GO:0005913	cell-cell adherens junction
darkgrey	70	62	4	0.00035	1	15	1453	GO:0007267	cell-cell signaling
darkgrey	70	62	5	0.00066	1	2	10	GO:0070254	mucus secretion
darkgrey	70	62	6	0.00071	1	10	769	GO:0010243	response to organonitrogen compound
darkgrey	70	62	7	0.00077	1	4	106	GO:0043200	response to amino acid
darkgrey	70	62	8	0.00082	1	13	1240	GO:0007155	cell adhesion
darkgrey	70	62	9	0.00096	1	2	12	GO:0006122	mitochondrial electron transport, ubiquinol to cytochrome c
darkgrey	70	62	10	0.00111	1	4	117	GO:0006633	fatty acid biosynthetic process
darkorange	39	28	1	0.00024	1	3	69	GO:0005905	clathrin-coated pit
darkorange	39	28	2	0.00102	1	2	27	GO:0031904	endosome lumen
darkorange	39	28	3	0.00176	1	1	1	GO:0033883	pyridoxal phosphatase activity
darkorange	39	28	4	0.00176	1	1	1	GO:0046570	methylthioribulose 1-phosphate dehydratase activity
darkorange	39	28	5	0.00269	1	2	44	GO:0036297	interstrand cross-link repair

darkora	39	28	6	0.00333	1	2	49	GO:0004402	histone acetyltransferase activity
darkora	39	28	7	0.00346	1	2	50	GO:0061733	peptide-lysine-N-acetyltransferase activity
darkora	39	28	8	0.00351	1	1	2	GO:0004174	electron-transferring-flavoprotein dehydrogenase activity
darkora	39	28	9	0.00351	1	1	2	GO:0042328	heparan sulfate N-acetylglucosaminyltransferase activity
darkora	39	28	10	0.00351	1	1	2	GO:0050509	N-acetylglucosaminyl-proteoglycan 4-beta-glucuronosyltransferase activity
darkred	100	85	1	2.81E-05	0.48166	2	2	GO:0030283	testosterone dehydrogenase [NAD(P)] activity
darkred	100	85	2	8.41E-05	1	2	3	GO:0018963	phthalate metabolic process
darkred	100	85	3	0.00017	1	2	4	GO:0018879	biphenyl metabolic process
darkred	100	85	4	0.00017	1	2	4	GO:0018894	dibenzo-p-dioxin metabolic process
darkred	100	85	5	0.00042	1	2	6	GO:0061370	testosterone biosynthetic process
darkred	100	85	6	0.00059	1	16	1210	GO:1902494	catalytic complex
darkred	100	85	7	0.00072	1	4	76	GO:0008080	N-acetyltransferase activity
darkred	100	85	8	0.00084	1	4	79	GO:0000123	histone acetyltransferase complex
darkred	100	85	9	0.00125	1	4	88	GO:0016410	N-acyltransferase activity
darkred	100	85	10	0.00148	1	4	92	GO:0016407	acetyltransferase activity
darkturc	74	50	1	3.09E-11	5.30E-07	5	9	GO:0042571	immunoglobulin complex, circulating
darkturc	74	50	2	1.93E-10	3.31E-06	5	12	GO:0034987	immunoglobulin receptor binding
darkturc	74	50	3	6.05E-08	0.00104	6	67	GO:0003823	antigen binding
darkturc	74	50	4	1.32E-07	0.00226	5	39	GO:0006958	complement activation, classical pathway
darkturc	74	50	5	3.44E-07	0.0059	5	47	GO:0002455	humoral immune response mediated by circulating immunoglobulin
darkturc	74	50	6	4.94E-07	0.00846	4	21	GO:0006910	phagocytosis, recognition
darkturc	74	50	7	1.19E-06	0.02036	5	60	GO:0006956	complement activation
darkturc	74	50	8	1.73E-06	0.02956	7	186	GO:0006959	humoral immune response
darkturc	74	50	9	5.25E-06	0.08993	4	37	GO:0006911	phagocytosis, engulfment
darkturc	74	50	10	9.65E-06	0.16528	2	2	GO:0071756	pentameric IgM immunoglobulin complex
green	1325	1065	1	2.61E-07	0.00446	121	1149	GO:0004872	receptor activity
green	1325	1065	2	6.53E-07	0.01118	25	125	GO:0015276	ligand-gated ion channel activity
green	1325	1065	3	1.09E-06	0.01873	90	810	GO:0004888	transmembrane signaling receptor activity
green	1325	1065	4	4.13E-06	0.07067	22	112	GO:0009593	detection of chemical stimulus
green	1325	1065	5	6.03E-06	0.10331	18	82	GO:0050907	detection of chemical stimulus involved in sensory perception
green	1325	1065	6	9.12E-06	0.15605	23	126	GO:0007606	sensory perception of chemical stimulus
green	1325	1065	7	9.12E-06	0.15605	23	126	GO:0050906	detection of stimulus involved in sensory perception
green	1325	1065	8	1.62E-05	0.27801	94	914	GO:0038023	signaling receptor activity

green	1325	1065	9	2.09E-05	0.35699	37	268	GO:0051606	detection of stimulus
green	1325	1065	10	3.40E-05	0.58284	16	76	GO:0030594	neurotransmitter receptor activity
greenye	268	242	1	1.81E-05	0.30979	6	37	GO:0042304	regulation of fatty acid biosynthetic process
greenye	268	242	2	2.51E-05	0.42943	50	1831	GO:0008283	cell proliferation
greenye	268	242	3	7.38E-05	1	14	272	GO:0008202	steroid metabolic process
greenye	268	242	4	8.31E-05	1	6	48	GO:0006695	cholesterol biosynthetic process
greenye	268	242	5	8.34E-05	1	17	384	GO:0005911	cell-cell junction
greenye	268	242	6	9.09E-05	1	7	70	GO:0000786	nucleosome
greenye	268	242	7	9.79E-05	1	88	4053	GO:0005576	extracellular region
greenye	268	242	8	0.00013	1	40	1439	GO:0042127	regulation of cell proliferation
greenye	268	242	9	0.00013	1	5	33	GO:0019731	antibacterial humoral response
greenye	268	242	10	0.00014	1	10	156	GO:0006694	steroid biosynthetic process
grey	1512	1214	1	0.00021	1	1014	12690	GO:0005622	intracellular
grey	1512	1214	2	0.00031	1	31	211	GO:0000075	cell cycle checkpoint
grey	1512	1214	3	0.00033	1	7	19	GO:0070987	error-free translesion synthesis
grey	1512	1214	4	0.00034	1	53	430	GO:0007067	mitotic nuclear division
grey	1512	1214	5	0.00071	1	92	868	GO:1903047	mitotic cell cycle process
grey	1512	1214	6	0.00072	1	73	658	GO:0070925	organelle assembly
grey	1512	1214	7	0.00074	1	99	948	GO:0000278	mitotic cell cycle
grey	1512	1214	8	0.00079	1	20	121	GO:0007062	sister chromatid cohesion
grey	1512	1214	9	0.00084	1	759	9276	GO:0044237	cellular metabolic process
grey	1512	1214	10	0.00098	1	109	1070	GO:0051276	chromosome organization
grey60	169	155	1	3.59E-06	0.06142	3	4	GO:0071953	elastic fiber
grey60	169	155	2	1.89E-05	0.32403	31	1439	GO:0042127	regulation of cell proliferation
grey60	169	155	3	2.95E-05	0.50477	14	392	GO:0006979	response to oxidative stress
grey60	169	155	4	0.0001	1	3	10	GO:0070102	interleukin-6-mediated signaling pathway
grey60	169	155	5	0.00011	1	4	26	GO:0071354	cellular response to interleukin-6
grey60	169	155	6	0.00014	1	34	1831	GO:0008283	cell proliferation
grey60	169	155	7	0.00019	1	3	12	GO:0006264	mitochondrial DNA replication
grey60	169	155	8	0.00019	1	4	30	GO:0070741	response to interleukin-6
grey60	169	155	9	0.00025	1	4	32	GO:0044091	membrane biogenesis
grey60	169	155	10	0.00028	1	2	3	GO:0090298	negative regulation of mitochondrial DNA replication
lightcyan	172	125	1	2.37E-05	0.40545	4	22	GO:0048679	regulation of axon regeneration

lightcyan	172	125	2	4.02E-05	0.68849	4	25	GO:0070570	regulation of neuron projection regeneration
lightcyan	172	125	3	9.85E-05	1	3	12	GO:0048681	negative regulation of axon regeneration
lightcyan	172	125	4	0.00013	1	3	13	GO:0070571	negative regulation of neuron projection regeneration
lightcyan	172	125	5	0.00027	1	4	40	GO:0031103	axon regeneration
lightcyan	172	125	6	0.00032	1	5	76	GO:0007098	centrosome cycle
lightcyan	172	125	7	0.00054	1	4	48	GO:0031102	neuron projection regeneration
lightcyan	172	125	8	0.0009	1	2	6	GO:0002318	myeloid progenitor cell differentiation
lightcyan	172	125	9	0.00125	1	2	7	GO:0035374	chondroitin sulfate binding
lightcyan	172	125	10	0.00133	1	4	61	GO:0048678	response to axon injury
lightgreen	168	150	1	8.20E-06	0.14047	11	222	GO:0060485	mesenchyme development
lightgreen	168	150	2	1.60E-05	0.2744	3	6	GO:0019237	centromeric DNA binding
lightgreen	168	150	3	0.0007	1	5	75	GO:0061333	renal tubule morphogenesis
lightgreen	168	150	4	0.00098	1	4	47	GO:0009948	anterior/posterior axis specification
lightgreen	168	150	5	0.00124	1	4	50	GO:0005876	spindle microtubule
lightgreen	168	150	6	0.00176	1	5	92	GO:0061326	renal tubule development
lightgreen	168	150	7	0.00179	1	2	7	GO:0014866	skeletal myofibril assembly
lightgreen	168	150	8	0.00179	1	2	7	GO:0003696	satellite DNA binding
lightgreen	168	150	9	0.00213	1	5	96	GO:0001657	ureteric bud development
lightgreen	168	150	10	0.00213	1	5	96	GO:0072163	mesonephric epithelium development
lightyellow	133	104	1	0.00025	1	2	4	GO:0061304	retinal blood vessel morphogenesis
lightyellow	133	104	2	0.00042	1	2	5	GO:0035426	extracellular matrix-cell signaling
lightyellow	133	104	3	0.00147	1	2	9	GO:0061299	retina vasculature morphogenesis in camera-type eye
lightyellow	133	104	4	0.00184	1	2	10	GO:0031987	locomotion involved in locomotory behavior
lightyellow	133	104	5	0.00223	1	2	11	GO:0005513	detection of calcium ion
lightyellow	133	104	6	0.00267	1	2	12	GO:0019215	intermediate filament binding
lightyellow	133	104	7	0.00365	1	2	14	GO:0042813	Wnt-activated receptor activity
lightyellow	133	104	8	0.0041	1	9	479	GO:0007423	sensory organ development
lightyellow	133	104	9	0.00419	1	2	15	GO:0001673	male germ cell nucleus
lightyellow	133	104	10	0.00477	1	2	16	GO:0061298	retina vasculature development in camera-type eye
magenta	530	478	1	1.86E-15	3.19E-11	144	2533	GO:1903561	extracellular vesicle
magenta	530	478	2	6.74E-15	1.15E-10	142	2520	GO:0070062	extracellular exosome
magenta	530	478	3	1.89E-13	3.24E-09	187	3865	GO:0031982	vesicle
magenta	530	478	4	1.55E-08	0.00027	169	3846	GO:0012505	endomembrane system

magenta	530	478	5	1.39E-07	0.00238	172	4053	GO:0005576	extracellular region
magenta	530	478	6	1.93E-07	0.00331	32	384	GO:0005911	cell-cell junction
magenta	530	478	7	1.43E-06	0.02445	283	7739	GO:0016020	membrane
magenta	530	478	8	4.10E-06	0.07012	73	1428	GO:0046903	secretion
magenta	530	478	9	4.65E-06	0.07969	7	24	GO:0032528	microvillus organization
magenta	530	478	10	6.70E-06	0.11473	31	431	GO:0050839	cell adhesion molecule binding
midnight	181	122	1	0.00017	1	2	3	GO:0005157	macrophage colony-stimulating factor receptor binding
midnight	181	122	2	0.00429	1	2	13	GO:0001741	XY body
midnight	181	122	3	0.00734	1	2	17	GO:0007026	negative regulation of microtubule depolymerization
midnight	181	122	4	0.00734	1	2	17	GO:0009264	deoxyribonucleotide catabolic process
midnight	181	122	5	0.00766	1	1	1	GO:0016077	snoRNA catabolic process
midnight	181	122	6	0.00766	1	1	1	GO:0033499	galactose catabolic process via UDP-galactose
midnight	181	122	7	0.00766	1	1	1	GO:0035863	dITP catabolic process
midnight	181	122	8	0.00766	1	1	1	GO:0055113	epiboly involved in gastrulation with mouth forming second
midnight	181	122	9	0.00766	1	1	1	GO:0070143	mitochondrial alanyl-tRNA aminoacylation
midnight	181	122	10	0.00766	1	1	1	GO:1901639	XDP catabolic process
orange	41	33	1	0.00085	1	2	21	GO:0046697	decidualization
orange	41	33	2	0.00199	1	2	32	GO:0001893	maternal placenta development
orange	41	33	3	0.00207	1	1	1	GO:0048685	negative regulation of collateral sprouting of intact axon in response to injury
orange	41	33	4	0.00207	1	1	1	GO:1902773	GTPase activator complex
orange	41	33	5	0.00207	1	1	1	GO:0001631	cysteinyl leukotriene receptor activity
orange	41	33	6	0.00207	1	1	1	GO:0004051	arachidonate 5-lipoxygenase activity
orange	41	33	7	0.00207	1	1	1	GO:0031682	G-protein gamma-subunit binding
orange	41	33	8	0.00207	1	1	1	GO:0047395	glycerophosphoinositol glycerophosphodiesterase activity
orange	41	33	9	0.00294	1	2	39	GO:0043551	regulation of phosphatidylinositol 3-kinase activity
orange	41	33	10	0.0034	1	2	42	GO:0007566	embryo implantation
pink	534	366	1	0.00053	1	2	2	GO:0036228	protein targeting to nuclear inner membrane
pink	534	366	2	0.00156	1	2	3	GO:0033693	neurofilament bundle assembly
pink	534	366	3	0.00156	1	2	3	GO:0016035	zeta DNA polymerase complex
pink	534	366	4	0.00173	1	3	11	GO:0000800	lateral element
pink	534	366	5	0.00258	1	7	81	GO:0000794	condensed nuclear chromosome
pink	534	366	6	0.0029	1	3	13	GO:0003906	DNA-(apurinic or apyrimidinic site) lyase activity
pink	534	366	7	0.00306	1	2	4	GO:1902953	positive regulation of ER to Golgi vesicle-mediated transport

pink	534	366	8	0.00363	1	3	14	GO:0055106	ubiquitin-protein transferase regulator activity
pink	534	366	9	0.00503	1	2	5	GO:0097418	neurofibrillary tangle
pink	534	366	10	0.00663	1	4	33	GO:0043928	exonucleolytic nuclear-transcribed mRNA catabolic process in deadenylation-dependent decay
purple	356	314	1	1.19E-06	0.02039	33	668	GO:0009986	cell surface
purple	356	314	2	1.30E-06	0.02231	42	971	GO:0048878	chemical homeostasis
purple	356	314	3	3.96E-06	0.06779	8	48	GO:0033762	response to glucagon
purple	356	314	4	8.59E-06	0.14713	36	835	GO:0033993	response to lipid
purple	356	314	5	2.23E-05	0.38115	180	7293	GO:0050896	response to stimulus
purple	356	314	6	2.40E-05	0.41041	118	4304	GO:0005886	plasma membrane
purple	356	314	7	3.15E-05	0.53883	112	4053	GO:0005576	extracellular region
purple	356	314	8	3.20E-05	0.54795	15	220	GO:0019932	second-messenger-mediated signaling
purple	356	314	9	4.85E-05	0.83075	45	1240	GO:0007155	cell adhesion
purple	356	314	10	4.91E-05	0.84023	52	1512	GO:0042592	homeostatic process
red	779	649	1	7.85E-05	1	7	27	GO:0007099	centriole replication
red	779	649	2	0.00013	1	7	29	GO:0098534	centriole assembly
red	779	649	3	0.00033	1	5	16	GO:0008392	arachidonic acid epoxygenase activity
red	779	649	4	0.00034	1	11	79	GO:0000123	histone acetyltransferase complex
red	779	649	5	0.00059	1	9	59	GO:0051298	centrosome duplication
red	779	649	6	0.00063	1	3	5	GO:0061743	motor learning
red	779	649	7	0.00099	1	10	76	GO:0007098	centrosome cycle
red	779	649	8	0.00103	1	5	20	GO:0019373	epoxygenase P450 pathway
red	779	649	9	0.00123	1	3	6	GO:1990316	ATG1/ULK1 kinase complex
red	779	649	10	0.00123	1	3	6	GO:0003836	beta-galactoside (CMP) alpha-2,3-sialyltransferase activity
royalblu	129	75	1	0.00077	1	2	9	GO:0018095	protein polyglutamylolation
royalblu	129	75	2	0.00123	1	3	45	GO:0032648	regulation of interferon-beta production
royalblu	129	75	3	0.0014	1	2	12	GO:0007342	fusion of sperm to egg plasma membrane
royalblu	129	75	4	0.0014	1	2	12	GO:0032688	negative regulation of interferon-beta production
royalblu	129	75	5	0.0014	1	3	47	GO:0032608	interferon-beta production
royalblu	129	75	6	0.00218	1	4	116	GO:0032479	regulation of type I interferon production
royalblu	129	75	7	0.00225	1	4	117	GO:0032606	type I interferon production
royalblu	129	75	8	0.00471	1	1	1	GO:0021813	cell-cell adhesion in neuronal-glia interactions in cerebral cortex radial glia guided migration
royalblu	129	75	9	0.00471	1	1	1	GO:0005503	all-trans retinal binding
royalblu	129	75	10	0.00471	1	1	1	GO:0015196	L-tryptophan transmembrane transporter activity

salmon	255	186	1	0.00014	1	2	2	GO:0004458	D-lactate dehydrogenase (cytochrome) activity
salmon	255	186	2	0.00021	1	64	3641	GO:0046872	metal ion binding
salmon	255	186	3	0.00036	1	16	515	GO:0016569	covalent chromatin modification
salmon	255	186	4	0.00038	1	64	3719	GO:0043169	cation binding
salmon	255	186	5	0.00039	1	14	416	GO:0016570	histone modification
salmon	255	186	6	0.0004	1	2	3	GO:0071001	U4/U6 snRNP
salmon	255	186	7	0.00063	1	4	34	GO:0017069	snRNA binding
salmon	255	186	8	0.00064	1	3	15	GO:0070816	phosphorylation of RNA polymerase II C-terminal domain
salmon	255	186	9	0.00132	1	3	19	GO:0071425	hematopoietic stem cell proliferation
salmon	255	186	10	0.00132	1	2	5	GO:0019323	pentose catabolic process
tan	261	198	1	1.89E-06	0.03238	3	3	GO:0001156	TFIIIC-class transcription factor binding
tan	261	198	2	1.86E-05	0.31786	3	5	GO:0001025	RNA polymerase III transcription factor binding
tan	261	198	3	0.00091	1	2	4	GO:0001032	RNA polymerase III type 3 promoter DNA binding
tan	261	198	4	0.0015	1	2	5	GO:0001030	RNA polymerase III type 1 promoter DNA binding
tan	261	198	5	0.0015	1	2	5	GO:0001031	RNA polymerase III type 2 promoter DNA binding
tan	261	198	6	0.0031	1	2	7	GO:0071233	cellular response to leucine
tan	261	198	7	0.0031	1	2	7	GO:0031931	TORC1 complex
tan	261	198	8	0.0031	1	2	7	GO:0070652	HAUS complex
tan	261	198	9	0.0031	1	2	7	GO:0001016	RNA polymerase III regulatory region DNA binding
tan	261	198	10	0.0031	1	2	7	GO:0008467	[heparan sulfate]-glucosamine 3-sulfotransferase 1 activity
turquoise	3906	3148	1	1.49E-06	0.02558	151	538	GO:0048812	neuron projection morphogenesis
turquoise	3906	3148	2	1.59E-06	0.02722	140	492	GO:0048667	cell morphogenesis involved in neuron differentiation
turquoise	3906	3148	3	1.93E-06	0.03308	154	553	GO:0048858	cell projection morphogenesis
turquoise	3906	3148	4	3.20E-06	0.0548	288	1150	GO:0030182	neuron differentiation
turquoise	3906	3148	5	6.05E-06	0.10358	156	572	GO:0032990	cell part morphogenesis
turquoise	3906	3148	6	8.83E-06	0.15118	478	2045	GO:0007399	nervous system development
turquoise	3906	3148	7	9.01E-06	0.1543	115	401	GO:0007409	axonogenesis
turquoise	3906	3148	8	1.92E-05	0.32875	231	916	GO:0048666	neuron development
turquoise	3906	3148	9	3.78E-05	0.64645	83	279	GO:0005261	cation channel activity
turquoise	3906	3148	10	6.14E-05	1	213	850	GO:0000902	cell morphogenesis
yellow	1731	1430	1	3.85E-08	0.00066	34	138	GO:0052652	cyclic purine nucleotide metabolic process
yellow	1731	1430	2	4.66E-08	0.0008	34	139	GO:0009190	cyclic nucleotide biosynthetic process
yellow	1731	1430	3	3.00E-07	0.00513	36	163	GO:0007187	G-protein coupled receptor signaling pathway, coupled to cyclic nucleotide second messenger



yellow	1731	1430	4	5.16E-07	0.00883	23	82	GO:0031279	regulation of cyclase activity
yellow	1731	1430	5	6.93E-07	0.01187	27	108	GO:0006171	cAMP biosynthetic process
yellow	1731	1430	6	8.75E-07	0.01498	69	425	GO:0004930	G-protein coupled receptor activity
yellow	1731	1430	7	1.64E-06	0.02804	26	106	GO:0030817	regulation of cAMP biosynthetic process
yellow	1731	1430	8	1.83E-06	0.03138	109	781	GO:0007186	G-protein coupled receptor signaling pathway
yellow	1731	1430	9	2.07E-06	0.0354	112	810	GO:0004888	transmembrane signaling receptor activity
yellow	1731	1430	10	2.31E-06	0.03957	47	259	GO:0034702	ion channel complex