

Tissue	Module	GO terms	Bonferroni p-value	p-value
Islet	blue	cellular metabolism	0.007669	1.80E-06
		metabolism	0.015245	3.58E-06
		primary metabolism	0.035455	8.32E-06
Islet	brown	cellular physiological process	8.95E-15	2.10E-18
		physiological process	4.02E-12	9.44E-16
		biological_process	7.94E-11	1.86E-14
		all	7.94E-11	1.86E-14
		cellular process	4.24E-09	9.95E-13
		metabolism	7.63E-07	1.79E-10
		transport	1.70E-06	4.00E-10
		protein localization	2.93E-06	6.88E-10
		establishment of protein localization	3.39E-06	7.95E-10
		primary metabolism	5.36E-06	1.26E-09
		protein transport	4.54E-05	1.07E-08
		cellular metabolism	4.75E-05	1.12E-08
		macromolecule metabolism	0.000120	2.81E-08
		intracellular protein transport	0.000444	1.04E-07
		localization	0.001537	3.61E-07
		secretory pathway	0.002319	5.44E-07
		establishment of localization	0.002753	6.46E-07
		secretion	0.004061	9.53E-07
		biopolymer metabolism	0.004220	9.91E-07
		intracellular transport	0.006137	1.44E-06
		establishment of cellular localization	0.008707	2.04E-06
		cellular localization	0.010698	2.51E-06
Islet	greenyellow	cell cycle	3.36E-49	7.88E-53
		M phase	9.60E-47	2.26E-50
		M phase of mitotic cell cycle	1.54E-45	3.63E-49
		mitosis	2.23E-44	5.25E-48
		mitotic cell cycle	3.35E-41	7.87E-45
		cell division	1.85E-26	4.34E-30
		regulation of progression through cell cycle	1.81E-24	4.25E-28
		cytokinesis	6.04E-24	1.42E-27
		DNA metabolism	9.75E-21	2.29E-24
		response to DNA damage stimulus	7.60E-19	1.78E-22
		chromosome segregation	1.14E-17	2.67E-21
		DNA replication	1.33E-16	3.13E-20
		meiosis	5.41E-16	1.27E-19
		meiotic cell cycle	5.41E-16	1.27E-19
		M phase of meiotic cell cycle	5.41E-16	1.27E-19
		response to endogenous stimulus	1.14E-13	2.69E-17
		biopolymer metabolism	3.08E-13	7.24E-17
		DNA repair	1.02E-12	2.39E-16
		microtubule-based process	2.69E-12	6.31E-16
		organelle organization and biogenesis	1.19E-11	2.79E-15
		DNA-dependent DNA replication	5.95E-08	1.40E-11
		regulation of cellular physiological process	1.11E-07	2.61E-11
		interphase of mitotic cell cycle	1.49E-07	3.50E-11
		interphase	1.49E-07	3.50E-11
		cell cycle checkpoint	1.80E-07	4.21E-11
		sister chromatid segregation	3.34E-07	7.84E-11
		mitotic sister chromatid segregation	3.34E-07	7.84E-11
		cellular physiological process	5.62E-07	1.32E-10
		cytoskeleton organization and biogenesis	5.87E-07	1.38E-10
		microtubule cytoskeleton organization and biogenesis	1.05E-06	2.46E-10
		regulation of cellular process	1.39E-06	3.25E-10
		regulation of physiological process	1.80E-06	4.23E-10
		G2/M transition of mitotic cell cycle	4.60E-06	1.08E-09
		microtubule organizing center organization and biogenesis	3.22E-05	7.55E-09
		centrosome organization and biogenesis	3.22E-05	7.55E-09
		centrosome cycle	3.22E-05	7.55E-09
		spindle organization and biogenesis	3.22E-05	7.55E-09
		meiotic spindle organization and biogenesis	4.02E-05	9.43E-09
		regulation of mitosis	6.14E-05	1.44E-08
		meiosis I	7.02E-05	1.65E-08

Tissue	Module	GO terms	Bonferroni p-value	p-value
Islet	grey60	cell adhesion	1.83E-07	4.29E-11
		cell-cell adhesion	0.000121	2.84E-08
		extracellular matrix organization and biogenesis	0.000126	2.96E-08
		extracellular structure organization and biogenesis	0.000132	3.10E-08
		biological_process	0.001740	4.08E-07
		all	0.001740	4.08E-07
		synapse organization and biogenesis	0.002030	4.77E-07
		cellular process	0.003588	8.42E-07
		organ development	0.007577	1.78E-06
		cell communication	0.022372	5.25E-06
Islet	lightyellow	nervous system development	0.066610	1.56E-05
		digestion	2.75E-12	6.47E-16
Islet	salmon	lipid catabolism	0.000151	3.56E-08
Islet	salmon	organ morphogenesis	3.01E-12	7.08E-16
		nervous system development	9.26E-12	2.17E-15
		morphogenesis	2.28E-11	5.35E-15
		organ development	3.65E-11	8.57E-15
		development	1.53E-09	3.59E-13
		neuron differentiation	6.00E-07	1.41E-10
		locomotory behavior	0.000272	6.39E-08
		behavior	0.000278	6.52E-08
		cell communication	0.000440	1.03E-07
		cell migration	0.001310	3.08E-07
		locomotion	0.002096	4.92E-07
		establishment of localization	0.002850	6.69E-07
		localization	0.004037	9.48E-07
		neuron development	0.005146	1.21E-06
		cell differentiation	0.016696	3.92E-06
Islet	tan	cellular morphogenesis during differentiation	0.017315	4.07E-06
Islet	turquoise	morphogenesis	0.042844	1.01E-05
Islet	turquoise	protein biosynthesis	3.77E-19	8.85E-23
		macromolecule biosynthesis	2.02E-16	4.75E-20
		cellular biosynthesis	2.49E-16	5.85E-20
		biosynthesis	1.22E-15	2.87E-19
		oxidative phosphorylation	3.91E-09	9.18E-13
		ribosome biogenesis	1.62E-07	3.81E-11
		nucleoside triphosphate metabolism	2.65E-07	6.22E-11
		ribosome biogenesis and assembly	2.98E-07	7.00E-11
		purine ribonucleoside triphosphate metabolism	3.60E-07	8.45E-11
		ribonucleoside triphosphate metabolism	4.75E-07	1.11E-10
		purine nucleoside triphosphate metabolism	4.75E-07	1.11E-10
		nucleoside triphosphate biosynthesis	1.43E-06	3.35E-10
		purine nucleoside triphosphate biosynthesis	4.24E-06	9.95E-10
		purine ribonucleoside triphosphate biosynthesis	4.24E-06	9.95E-10
		ribonucleoside triphosphate biosynthesis	5.65E-06	1.33E-09
		purine ribonucleotide metabolism	8.68E-06	2.04E-09
		ATP synthesis coupled electron transport	2.01E-05	4.71E-09
		ATP synthesis coupled electron transport (sensu Eukaryota)	2.01E-05	4.71E-09
		purine nucleotide metabolism	2.94E-05	6.91E-09
		purine ribonucleotide biosynthesis	5.56E-05	1.31E-08
		purine nucleotide biosynthesis	0.000133	3.13E-08
		cytoplasm organization and biogenesis	0.000155	3.64E-08
		protein metabolism	0.000179	4.21E-08
		ribonucleotide metabolism	0.000242	5.68E-08
		ribonucleotide biosynthesis	0.000245	5.75E-08
		ATP metabolism	0.000340	7.99E-08
		cellular protein metabolism	0.000365	8.57E-08
		cellular macromolecule metabolism	0.000991	2.33E-07
		macromolecule metabolism	0.002217	5.21E-07
		ATP biosynthesis	0.005471	1.28E-06
		nucleoside phosphate metabolism	0.005471	1.28E-06
		proton transport	0.006353	1.49E-06
		hydrogen transport	0.007454	1.75E-06

Tissue	Module	GO terms	Bonferroni p-value	p-value
Adipose	turquoise	cellular physiological process	2.24E-07	5.26E-11
		primary metabolism	4.03E-05	9.47E-09
		metabolism	8.78E-05	2.06E-08
		physiological process	0.000485	1.14E-07
		sterol biosynthesis	0.000513	1.21E-07
		cellular metabolism	0.000612	1.44E-07
		alcohol metabolism	0.000920	2.16E-07
		glucose catabolism	0.001464	3.44E-07
		cholesterol biosynthesis	0.001667	3.91E-07
		hexose catabolism	0.001746	4.10E-07
		monosaccharide catabolism	0.001746	4.10E-07
		cholesterol metabolism	0.002026	4.76E-07
		cellular process	0.002100	4.93E-07
		biological_process	0.002206	5.18E-07
		all	0.002206	5.18E-07
		alcohol catabolism	0.002459	5.77E-07
		sterol metabolism	0.003114	7.31E-07
		glycolysis	0.008495	1.99E-06
		cellular carbohydrate catabolism	0.009409	2.21E-06
		carbohydrate catabolism	0.009409	2.21E-06
Adipose	tan	generation of precursor metabolites and energy	1.38E-19	3.24E-23
		cofactor metabolism	6.12E-14	1.44E-17
		coenzyme metabolism	8.54E-14	2.00E-17
		energy derivation by oxidation of organic compounds	1.15E-11	2.70E-15
		aerobic respiration	6.52E-10	1.53E-13
		main pathways of carbohydrate metabolism	1.26E-09	2.96E-13
		cellular respiration	1.77E-09	4.16E-13
		acetyl-CoA metabolism	6.46E-09	1.52E-12
		tricarboxylic acid cycle	1.17E-08	2.74E-12
		acetyl-CoA catabolism	1.64E-08	3.86E-12
		electron transport	4.23E-08	9.92E-12
		coenzyme catabolism	7.29E-08	1.71E-11
		cofactor catabolism	1.97E-07	4.63E-11
		oxidative phosphorylation	1.28E-05	3.01E-09
		alcohol catabolism	1.28E-05	3.01E-09
		ATP synthesis coupled electron transport	7.01E-05	1.65E-08
		ATP synthesis coupled electron transport (sensu Eukaryota)	7.01E-05	1.65E-08
		cellular catabolism	0.000230	5.39E-08
		glucose catabolism	0.000336	7.89E-08
		monosaccharide catabolism	0.000375	8.81E-08
		hexose catabolism	0.000375	8.81E-08
		catabolism	0.001360	3.19E-07
		glycolysis	0.001874	4.40E-07
		cellular carbohydrate metabolism	0.002212	5.19E-07
		cellular metabolism	0.003606	8.47E-07
		metabolism	0.006876	1.61E-06
Adipose	salmon	branched chain family amino acid metabolism	5.60E-05	1.31E-08
		branched chain family amino acid catabolism	0.001643	3.86E-07
		nitrogen compound catabolism	0.008854	2.08E-06
		amine catabolism	0.008854	2.08E-06
		amino acid metabolism	0.012981	3.05E-06
		amino acid and derivative metabolism	0.013057	3.07E-06
		primary metabolism	0.013580	3.19E-06
		carboxylic acid metabolism	0.017752	4.17E-06
		organic acid metabolism	0.019573	4.60E-06
Adipose	purple	nucleosome assembly	7.57E-15	1.78E-18
		establishment and/or maintenance of chromatin architecture	2.19E-12	5.15E-16
		chromatin assembly	2.20E-12	5.16E-16
		chromosome organization and biogenesis (sensu Eukaryota)	2.57E-12	6.04E-16
		chromosome organization and biogenesis	5.22E-12	1.23E-15
		DNA packaging	5.40E-12	1.27E-15
		chromatin assembly or disassembly	4.51E-11	1.06E-14
		DNA metabolism	1.20E-08	2.81E-12
		cell-cell adhesion	2.13E-08	5.01E-12
		protein complex assembly	1.48E-07	3.48E-11
		cell adhesion	5.26E-06	1.23E-09
		biopolymer metabolism	2.12E-05	4.99E-09
		organelle organization and biogenesis	3.42E-05	8.03E-09

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		cellular process	6.43E-05	1.51E-08
		biological_process	7.56E-05	1.77E-08
		all	7.56E-05	1.77E-08
		nucleobase, nucleoside, nucleotide and nucleic acid metabolism	0.000778	1.83E-07
Adipose	lightgreen	DNA metabolism	1.05E-18	2.47E-22
		cell cycle	2.27E-16	5.33E-20
		DNA replication	4.24E-16	9.95E-20
		response to DNA damage stimulus	1.99E-14	4.67E-18
		mitotic cell cycle	1.21E-12	2.84E-16
		M phase	9.02E-12	2.12E-15
		mitosis	2.85E-11	6.69E-15
		M phase of mitotic cell cycle	3.94E-11	9.24E-15
		response to endogenous stimulus	4.95E-11	1.16E-14
		DNA repair	1.55E-10	3.64E-14
		cell division	5.05E-10	1.19E-13
		cytokinesis	2.30E-09	5.41E-13
		biopolymer metabolism	9.96E-08	2.34E-11
		microtubule-based process	3.58E-06	8.40E-10
		DNA replication initiation	2.52E-05	5.92E-09
		DNA-dependent DNA replication	2.56E-05	6.02E-09
		organelle organization and biogenesis	3.43E-05	8.06E-09
		DNA recombination	8.84E-05	2.08E-08
		microtubule cytoskeleton organization and biogenesis	0.000157	3.69E-08
		nucleobase, nucleoside, nucleotide and nucleic acid metabolism	0.000537	1.26E-07
		spindle organization and biogenesis	0.002422	5.69E-07
		regulation of progression through cell cycle	0.003047	7.15E-07
		chromosome segregation	0.005176	1.22E-06
		M phase of meiotic cell cycle	0.006178	1.45E-06
		meiotic cell cycle	0.006178	1.45E-06
		meiosis	0.006178	1.45E-06
		cell cycle checkpoint	0.008484	1.99E-06
		mitotic spindle organization and biogenesis	0.011277	2.65E-06
Adipose	grey60	generation of precursor metabolites and energy	2.62E-05	6.16E-09
		energy derivation by oxidation of organic compounds	0.007406	1.74E-06
		organic acid metabolism	0.011575	2.72E-06
		cofactor metabolism	0.012276	2.88E-06
		biosynthesis	0.014667	3.44E-06
		cellular metabolism	0.018202	4.27E-06
Adipose	cyan	generation of precursor metabolites and energy	1.37E-20	3.21E-24
		oxidative phosphorylation	3.68E-16	8.65E-20
		electron transport	1.21E-11	2.85E-15
		ATP synthesis coupled electron transport (sensu Eukaryota)	4.20E-11	9.85E-15
		ATP synthesis coupled electron transport	4.20E-11	9.85E-15
		mitochondrial electron transport, NADH to ubiquinone	1.08E-09	2.54E-13
		transport	5.89E-08	1.38E-11
		metabolism	7.79E-07	1.83E-10
		coenzyme metabolism	8.06E-07	1.89E-10
		aerobic respiration	2.71E-06	6.36E-10
		cofactor metabolism	5.49E-06	1.29E-09
		cellular respiration	5.77E-06	1.35E-09
		cellular metabolism	1.27E-05	2.99E-09
		phosphorylation	2.34E-05	5.50E-09
		acetyl-CoA metabolism	3.20E-05	7.52E-09
		energy derivation by oxidation of organic compounds	3.85E-05	9.04E-09
		tricarboxylic acid cycle	0.000127	2.98E-08
		acetyl-CoA catabolism	0.000160	3.75E-08
		coenzyme catabolism	0.000439	1.03E-07
		establishment of localization	0.000622	1.46E-07
		phosphate metabolism	0.000767	1.80E-07
		phosphorus metabolism	0.000767	1.80E-07
		localization	0.000860	2.02E-07
		cofactor catabolism	0.000866	2.03E-07
		carboxylic acid metabolism	0.001738	4.08E-07
		organic acid metabolism	0.001937	4.55E-07
		cellular physiological process	0.005147	1.21E-06
		tricarboxylic acid cycle intermediate metabolism	0.008642	2.03E-06
Adipose	brown	response to biotic stimulus	2.29E-42	5.38E-46
		immune response	2.77E-41	6.51E-45
		defense response	1.43E-40	3.35E-44

Tissue	Module	GO terms	Bonferroni p-value	p-value
		all	5.78E-28	1.36E-31
		biological_process	5.78E-28	1.36E-31
		response to external biotic stimulus	1.29E-25	3.03E-29
		response to pest, pathogen or parasite	3.00E-24	7.04E-28
		response to external stimulus	7.21E-24	1.69E-27
		cellular process	1.24E-23	2.92E-27
		immune cell activation	6.68E-23	1.57E-26
		cell activation	1.22E-22	2.87E-26
		physiological process	3.00E-21	7.05E-25
		lymphocyte activation	8.63E-20	2.03E-23
		response to stimulus	4.83E-19	1.13E-22
		organismal physiological process	6.72E-18	1.58E-21
		B cell activation	1.20E-17	2.81E-21
		intracellular signaling cascade	4.84E-17	1.14E-20
		response to wounding	4.87E-17	1.14E-20
		signal transduction	2.29E-16	5.37E-20
		response to stress	2.49E-16	5.85E-20
		humoral immune response	7.17E-16	1.68E-19
		hemopoiesis	8.95E-15	2.10E-18
		humoral defense mechanism (sensu Vertebrata)	1.54E-14	3.62E-18
		hemopoietic or lymphoid organ development	2.77E-14	6.51E-18
		cell communication	5.76E-14	1.35E-17
		phagocytosis	1.14E-13	2.67E-17
		cellular physiological process	4.64E-13	1.09E-16
		inflammatory response	2.16E-12	5.07E-16
		antimicrobial humoral response (sensu Vertebrata)	5.59E-12	1.31E-15
		B cell differentiation	5.59E-12	1.31E-15
		regulation of immune response	1.37E-11	3.21E-15
		antimicrobial humoral response	2.93E-11	6.89E-15
		lymphocyte differentiation	3.20E-11	7.51E-15
		regulation of biological process	3.89E-11	9.14E-15
		vesicle-mediated transport	1.44E-10	3.39E-14
		regulation of organismal physiological process	1.81E-10	4.26E-14
		endocytosis	3.62E-10	8.49E-14
		establishment of localization	3.79E-10	8.89E-14
		localization	3.81E-10	8.95E-14
		lymphocyte proliferation	6.40E-10	1.50E-13
		B cell proliferation	3.60E-09	8.45E-13
		transport	9.75E-09	2.29E-12
		T cell activation	1.00E-08	2.35E-12
		actin filament-based process	1.42E-08	3.34E-12
		regulation of lymphocyte activation	4.08E-08	9.58E-12
		negative regulation of biological process	7.87E-08	1.85E-11
		regulation of cell activation	8.62E-08	2.02E-11
		regulation of physiological process	8.77E-08	2.06E-11
		regulation of B cell activation	9.85E-08	2.31E-11
		regulation of apoptosis	3.07E-07	7.21E-11
		protein kinase cascade	3.62E-07	8.50E-11
		regulation of programmed cell death	3.76E-07	8.83E-11
		regulation of cellular process	5.99E-07	1.41E-10
		actin cytoskeleton organization and biogenesis	6.13E-07	1.44E-10
		apoptosis	1.40E-06	3.29E-10
		programmed cell death	2.24E-06	5.27E-10
		cellular defense response	2.99E-06	7.03E-10
		negative regulation of physiological process	3.13E-06	7.36E-10
		positive regulation of biological process	5.04E-06	1.18E-09
		cellular defense response (sensu Vertebrata)	6.21E-06	1.46E-09
		negative regulation of cellular process	1.09E-05	2.56E-09
		small GTPase mediated signal transduction	1.22E-05	2.86E-09
		regulation of cellular physiological process	1.54E-05	3.61E-09
		cell death	1.86E-05	4.36E-09
		death	1.88E-05	4.41E-09
		development	2.57E-05	6.03E-09
		positive regulation of immune response	2.65E-05	6.21E-09
		positive regulation of organismal physiological process	2.77E-05	6.51E-09
		anti-apoptosis	2.95E-05	6.93E-09
		negative regulation of cellular physiological process	3.69E-05	8.67E-09
		cytokine production	4.96E-05	1.16E-08
		cell-mediated immune response	5.16E-05	1.21E-08

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		cytoskeleton organization and biogenesis	7.00E-05	1.64E-08
		regulation of B cell differentiation	8.08E-05	1.90E-08
		T cell differentiation	9.45E-05	2.22E-08
		negative regulation of apoptosis	0.000110	2.59E-08
		cell surface receptor linked signal transduction	0.000131	3.08E-08
		negative regulation of programmed cell death	0.000133	3.12E-08
		cell differentiation	0.000159	3.72E-08
		organ development	0.000170	4.00E-08
		regulation of lymphocyte proliferation	0.000180	4.23E-08
		negative regulation of B cell activation	0.000245	5.76E-08
		I-kappaB kinase/NF-kappaB cascade	0.000336	7.88E-08
		regulation of protein metabolism	0.000555	1.30E-07
		macrophage activation	0.000569	1.34E-07
		positive regulation of cellular process	0.000659	1.55E-07
		cell proliferation	0.000808	1.90E-07
		myeloid cell differentiation	0.000901	2.12E-07
		positive regulation of physiological process	0.001512	3.55E-07
		negative regulation of B cell proliferation	0.001548	3.64E-07
		cytokine biosynthesis	0.001593	3.74E-07
		regulation of lymphocyte differentiation	0.001637	3.84E-07
		regulation of bone resorption	0.001778	4.18E-07
		integrin-mediated signaling pathway	0.001995	4.69E-07
		taxis	0.002016	4.73E-07
		chemotaxis	0.002016	4.73E-07
		cytokine metabolism	0.002123	4.98E-07
		actin polymerization and/or depolymerization	0.002303	5.41E-07
		negative regulation of organismal physiological process	0.003099	7.28E-07
		actin filament polymerization	0.003143	7.38E-07
		regulation of cytokine biosynthesis	0.003331	7.82E-07
		T cell proliferation	0.003976	9.34E-07
		regulation of B cell proliferation	0.007611	1.79E-06
		metabolism	0.008028	1.88E-06
		immune cell chemotaxis	0.009105	2.14E-06
		superoxide metabolism	0.009766	2.29E-06
		positive regulation of cellular physiological process	0.009917	2.33E-06
Adipose	blue	all	1.43E-16	3.36E-20
		biological_process	1.43E-16	3.36E-20
		cellular process	7.01E-16	1.65E-19
		cellular physiological process	1.33E-15	3.13E-19
		physiological process	5.93E-15	1.39E-18
		cellular metabolism	5.64E-10	1.33E-13
		metabolism	1.74E-09	4.09E-13
		primary metabolism	1.96E-08	4.60E-12
		macromolecule metabolism	8.67E-07	2.04E-10
		positive regulation of biological process	1.86E-06	4.38E-10
		death	1.99E-06	4.68E-10
		cell death	3.67E-06	8.61E-10
		cellular protein metabolism	9.92E-06	2.33E-09
		response to biotic stimulus	1.03E-05	2.43E-09
		protein metabolism	1.14E-05	2.67E-09
		cellular macromolecule metabolism	1.33E-05	3.13E-09
		response to stress	1.61E-05	3.77E-09
		programmed cell death	3.39E-05	7.96E-09
		positive regulation of cellular process	3.59E-05	8.43E-09
		defense response	8.86E-05	2.08E-08
		cell adhesion	0.000103	2.43E-08
		apoptosis	0.000126	2.97E-08
		positive regulation of physiological process	0.000135	3.16E-08
		positive regulation of cellular physiological process	0.000252	5.91E-08
		biopolymer modification	0.000399	9.37E-08
		cell communication	0.000410	9.62E-08
		regulation of biological process	0.000516	1.21E-07
		inflammatory response	0.000583	1.37E-07
		protein modification	0.000726	1.71E-07
		immune response	0.001244	2.92E-07
		intracellular signaling cascade	0.001794	4.21E-07
		response to external stimulus	0.001919	4.51E-07
		response to wounding	0.002482	5.83E-07
		regulation of cellular process	0.002497	5.86E-07

Tissue	Module	GO terms	Bonferroni p-value	p-value
		regulation of cellular physiological process	0.002520	5.92E-07
		cell proliferation	0.005642	1.32E-06
		regulation of physiological process	0.005850	1.37E-06
		biopolymer metabolism	0.008264	1.94E-06
		response to external biotic stimulus	0.009239	2.17E-06
		response to pest, pathogen or parasite	0.009520	2.24E-06
		localization	0.009635	2.26E-06
Adipose	black	metabolism	1.71E-06	4.03E-10
		cellular metabolism	1.11E-05	2.60E-09
		cellular physiological process	0.000122	2.86E-08
		all	0.001016	2.38E-07
		biological_process	0.001016	2.38E-07
		cellular process	0.001026	2.41E-07
		primary metabolism	0.003184	7.48E-07
		physiological process	0.004467	1.05E-06
		generation of precursor metabolites and energy	0.012026	2.82E-06

Tissue	Module	GO terms	Bonferroni p-value	p-value
Liver	yellow	metabolism	0.003465	8.14E-07
		cellular metabolism	0.007191	1.69E-06
		cellular process	0.009377	2.20E-06
		cellular physiological process	0.032893	7.72E-06
Liver	lightcyan	collagen fibril organization	5.04E-07	1.18E-10
		phosphate transport	7.51E-07	1.76E-10
		cell adhesion	6.34E-06	1.49E-09
		organ development	1.37E-05	3.22E-09
		morphogenesis	8.89E-05	2.09E-08
		cellular physiological process	0.000117	2.74E-08
		blood vessel development	0.000142	3.33E-08
		vasculature development	0.000146	3.43E-08
		organ morphogenesis	0.000233	5.48E-08
		extracellular matrix organization and biogenesis	0.000239	5.61E-08
		extracellular structure organization and biogenesis	0.000250	5.86E-08
		inorganic anion transport	0.000543	1.28E-07
		transmembrane receptor protein serine/threonine kinase signaling pathway	0.000819	1.92E-07
		blood vessel morphogenesis	0.000830	1.95E-07
		transforming growth factor beta receptor signaling pathway	0.001619	3.80E-07
		anion transport	0.002663	6.25E-07
		cellular process	0.003245	7.62E-07
		development	0.009097	2.14E-06
		physiological process	0.010346	2.43E-06
Liver	midnightblue	mitotic cell cycle	8.78E-42	2.06E-45
		M phase of mitotic cell cycle	8.90E-39	2.09E-42
		mitosis	2.66E-37	6.25E-41
		cell cycle	8.81E-37	2.07E-40
		M phase	4.21E-36	9.88E-40
		cell division	4.26E-19	1.00E-22
		regulation of progression through cell cycle	8.33E-19	1.96E-22
		cytokinesis	9.58E-19	2.25E-22
		chromosome segregation	1.19E-12	2.80E-16
		microtubule-based process	5.43E-12	1.27E-15
		microtubule cytoskeleton organization and biogenesis	7.27E-10	1.71E-13
		organelle organization and biogenesis	5.56E-09	1.31E-12
		cytoskeleton organization and biogenesis	4.21E-07	9.89E-11
		spindle organization and biogenesis	5.86E-07	1.38E-10
		interphase	4.28E-06	1.00E-09
		interphase of mitotic cell cycle	4.28E-06	1.00E-09
		M phase of meiotic cell cycle	5.37E-06	1.26E-09
		meiosis	5.37E-06	1.26E-09
		meiotic cell cycle	5.37E-06	1.26E-09
		regulation of cellular physiological process	1.78E-05	4.19E-09
		regulation of cellular process	2.62E-05	6.14E-09
		mitotic spindle organization and biogenesis	0.000106	2.48E-08
		regulation of physiological process	0.000109	2.55E-08
		cytokinesis after mitosis	0.000230	5.39E-08
		cell organization and biogenesis	0.000256	6.01E-08
		biological_process	0.000494	1.16E-07
		all	0.000494	1.16E-07
		regulation of biological process	0.000705	1.66E-07
		cellular physiological process	0.000764	1.79E-07
		G1/S transition of mitotic cell cycle	0.001198	2.81E-07
		sister chromatid segregation	0.003932	9.23E-07
		mitotic sister chromatid segregation	0.003932	9.23E-07
		physiological process	0.006751	1.59E-06
		cellular process	0.007128	1.67E-06
		cell proliferation	0.007493	1.76E-06
		mitotic metaphase	0.007950	1.87E-06
Liver	pink	macromolecule biosynthesis	0.000422	9.91E-08
		protein biosynthesis	0.001570	3.69E-07
		ribosome biogenesis	0.007987	1.88E-06
		cellular biosynthesis	0.018283	4.29E-06
		ribosome biogenesis and assembly	0.019821	4.65E-06
Liver	purple	protein biosynthesis	8.33E-09	1.95E-12
		macromolecule biosynthesis	4.58E-08	1.08E-11
		ribosome biogenesis and assembly	1.18E-07	2.78E-11
		cytoplasm organization and biogenesis	1.75E-06	4.10E-10
		ribosome biogenesis	2.21E-06	5.19E-10
		cellular biosynthesis	1.34E-05	3.16E-09
		biosynthesis	7.07E-05	1.66E-08

Tissue	Module	GO terms	Bonferroni p-value	p-value
Soleus	yellow	cellular process	1.37E-06	3.22E-10
		all	3.51E-05	8.25E-09
		biological_process	3.51E-05	8.25E-09
		cell-cell adhesion	0.000231	5.43E-08
		cell adhesion	0.000839	1.97E-07
		cellular physiological process	0.005935	1.39E-06
		morphogenesis	0.017720	4.16E-06
		organ development	0.024224	5.69E-06
		cytoskeleton organization and biogenesis	0.054923	1.29E-05
		organelle organization and biogenesis	0.063888	1.50E-05
		organ morphogenesis	0.075085	1.76E-05
		development	0.082620	1.94E-05
Soleus	black	morphogenesis	1.83E-05	4.29E-09
		development	0.000142	3.33E-08
		organ morphogenesis	0.001184	2.78E-07
		biological_process	0.004547	1.07E-06
		all	0.004547	1.07E-06
		blood vessel morphogenesis	0.005490	1.29E-06
		cell adhesion	0.008532	2.00E-06
		angiogenesis	0.011798	2.77E-06
		blood vessel development	0.012144	2.85E-06
		vasculature development	0.012488	2.93E-06
		cellular process	0.016486	3.87E-06
Soleus	blue	all	2.82E-20	6.63E-24
		biological_process	2.82E-20	6.63E-24
		cell adhesion	4.89E-20	1.15E-23
		development	2.74E-17	6.43E-21
		organ development	1.52E-16	3.56E-20
		cellular process	3.88E-16	9.11E-20
		cellular physiological process	4.31E-14	1.01E-17
		morphogenesis	1.29E-13	3.02E-17
		physiological process	8.73E-13	2.05E-16
		phosphate transport	9.22E-13	2.16E-16
		organ morphogenesis	1.64E-10	3.84E-14
		collagen fibril organization	3.13E-10	7.34E-14
		skeletal development	7.19E-09	1.69E-12
		cell proliferation	5.20E-08	1.22E-11
		extracellular matrix organization and biogenesis	3.83E-06	8.99E-10
		extracellular structure organization and biogenesis	4.14E-06	9.72E-10
		inorganic anion transport	1.67E-05	3.91E-09
		cell communication	2.46E-05	5.79E-09
		blood vessel development	4.70E-05	1.10E-08
		vasculature development	4.93E-05	1.16E-08
		bone remodeling	5.09E-05	1.20E-08
		biomineral formation	0.000102	2.41E-08
		ossification	0.000102	2.41E-08
		anion transport	0.000274	6.44E-08
		blood vessel morphogenesis	0.000464	1.09E-07
		muscle development	0.000753	1.77E-07
		actin cytoskeleton organization and biogenesis	0.001247	2.93E-07
		actin filament-based process	0.003202	7.52E-07
		histogenesis	0.005320	1.25E-06
		angiogenesis	0.011907	2.80E-06
Soleus	cyan	lipid metabolism	6.06E-10	1.42E-13
		fatty acid metabolism	1.87E-09	4.39E-13
		carboxylic acid metabolism	4.35E-07	1.02E-10
		organic acid metabolism	4.93E-07	1.16E-10
		cellular lipid metabolism	5.21E-07	1.22E-10
		fatty acid oxidation	8.95E-07	2.10E-10
		fatty acid beta-oxidation	8.44E-06	1.98E-09
Soleus	green	M phase of mitotic cell cycle	5.09E-38	1.19E-41
		mitosis	8.03E-37	1.89E-40
		M phase	2.66E-36	6.24E-40
		mitotic cell cycle	2.90E-35	6.82E-39
		cell cycle	3.58E-33	8.42E-37
		cytokinesis	7.71E-27	1.81E-30
		cell division	1.59E-26	3.74E-30
		regulation of progression through cell cycle	6.94E-18	1.63E-21

Tissue	Module	GO terms	Bonferroni p-value	p-value
		microtubule-based process	4.04E-17	9.49E-21
		chromosome segregation	6.03E-15	1.42E-18
		cytoskeleton organization and biogenesis	3.05E-12	7.15E-16
		M phase of meiotic cell cycle	9.71E-12	2.28E-15
		meiotic cell cycle	9.71E-12	2.28E-15
		meiosis	9.71E-12	2.28E-15
		microtubule cytoskeleton organization and biogenesis	6.17E-10	1.45E-13
		organelle organization and biogenesis	2.79E-09	6.54E-13
		G2/M transition of mitotic cell cycle	5.84E-08	1.37E-11
		spindle organization and biogenesis	2.24E-07	5.27E-11
		interphase of mitotic cell cycle	4.70E-07	1.10E-10
		interphase	4.70E-07	1.10E-10
		regulation of cellular physiological process	9.22E-07	2.17E-10
		regulation of physiological process	1.40E-06	3.29E-10
		cellular physiological process	4.69E-06	1.10E-09
		regulation of cellular process	8.95E-06	2.10E-09
		biological_process	1.29E-05	3.04E-09
		all	1.29E-05	3.04E-09
		regulation of biological process	4.14E-05	9.73E-09
		cell organization and biogenesis	9.22E-05	2.17E-08
		protein polymerization	0.000122	2.87E-08
		physiological process	0.000325	7.65E-08
		cellular process	0.000353	8.29E-08
		regulation of mitosis	0.000599	1.41E-07
		mitotic sister chromatid segregation	0.000726	1.71E-07
		sister chromatid segregation	0.000726	1.71E-07
		mitotic spindle organization and biogenesis	0.000965	2.27E-07
		cytokinesis after mitosis	0.001210	2.84E-07
		metaphase	0.001601	3.76E-07
		meiotic spindle organization and biogenesis	0.002502	5.88E-07
		response to DNA damage stimulus	0.004142	9.73E-07
		microtubule-based movement	0.005224	1.23E-06
		cytoskeleton-dependent intracellular transport	0.006670	1.57E-06
		cell cycle checkpoint	0.017816	4.18E-06
		cell proliferation	0.021556	5.06E-06
Soleus	red	protein metabolism	0.017513	4.11E-06
		cellular protein metabolism	0.034109	8.01E-06
		macromolecule metabolism	0.040166	9.43E-06
		cellular macromolecule metabolism	0.048743	1.14E-05
Soleus	salmon	protein biosynthesis	0.000272	6.40E-08
		ribosome biogenesis	0.000315	7.41E-08
		ribosome biogenesis and assembly	0.000623	1.46E-07
		macromolecule biosynthesis	0.000756	1.78E-07
		cytoplasm organization and biogenesis	0.003302	7.75E-07
		cellular biosynthesis	0.022792	5.35E-06
Soleus	turquoise	cellular physiological process	8.11E-07	1.90E-10
		biological_process	5.12E-05	1.20E-08
		all	5.12E-05	1.20E-08
		cellular process	6.74E-05	1.58E-08
		physiological process	0.001067	2.51E-07
		cellular metabolism	0.010218	2.40E-06
		primary metabolism	0.015104	3.55E-06
		metabolism	0.024844	5.83E-06

Tissue	Module	GO terms	Bonferroni p-value	p-value
Gastroc	yellow	sensory perception of chemical stimulus	1.59E-06	3.74E-10
		sensory perception of smell	3.75E-06	8.81E-10
		G-protein coupled receptor protein signaling pathway	5.83E-06	1.37E-09
		sensory perception	4.87E-05	1.14E-08
		neurophysiological process	5.37E-05	1.26E-08
Gastroc	black	all	1.32E-08	3.10E-12
		biological_process	1.32E-08	3.10E-12
		cellular process	3.62E-07	8.51E-11
		cellular physiological process	7.85E-05	1.84E-08
		physiological process	0.000112	2.64E-08
		development	0.000127	2.98E-08
		organ development	0.010268	2.41E-06
		cell adhesion	0.013791	3.24E-06
Gastroc	blue	all	5.03E-08	1.18E-11
		biological_process	5.03E-08	1.18E-11
		cell adhesion	5.33E-08	1.25E-11
		development	9.62E-07	2.26E-10
		cellular process	2.14E-06	5.02E-10
		morphogenesis	1.46E-05	3.43E-09
		cellular physiological process	2.91E-05	6.84E-09
		organ development	0.000294	6.91E-08
		organ morphogenesis	0.001106	2.60E-07
		physiological process	0.003810	8.95E-07
		cell communication	0.004791	1.12E-06
		nervous system development	0.020463	4.80E-06
Gastroc	brown	sensory perception of chemical stimulus	1.25E-08	2.94E-12
		sensory perception	2.16E-08	5.07E-12
		sensory perception of smell	1.93E-07	4.52E-11
		G-protein coupled receptor protein signaling pathway	7.30E-07	1.71E-10
		neurophysiological process	1.08E-06	2.53E-10
		cell surface receptor linked signal transduction	0.000535	1.26E-07
		response to stimulus	0.000847	1.99E-07
		calcium ion homeostasis	0.005233	1.23E-06
		organismal physiological process	0.005345	1.26E-06
		metal ion homeostasis	0.005607	1.32E-06
		cell ion homeostasis	0.006138	1.44E-06
		cell homeostasis	0.007590	1.78E-06
		cation homeostasis	0.008774	2.06E-06
		ion homeostasis	0.009654	2.27E-06
Gastroc	cyan	mitotic cell cycle	1.24E-19	2.92E-23
		mitosis	3.67E-19	8.63E-23
		M phase of mitotic cell cycle	6.18E-19	1.45E-22
		M phase	1.78E-16	4.18E-20
		cell cycle	3.70E-14	8.69E-18
		cytokinesis	3.72E-12	8.74E-16
		cell division	3.45E-11	8.11E-15
		chromosome segregation	5.72E-08	1.34E-11
		interphase of mitotic cell cycle	4.25E-06	9.98E-10
		interphase	4.25E-06	9.98E-10
		G2/M transition of mitotic cell cycle	4.89E-06	1.15E-09
		regulation of progression through cell cycle	1.06E-05	2.48E-09
		microtubule-based process	2.26E-05	5.30E-09
		cellular physiological process	4.46E-05	1.05E-08
		microtubule cytoskeleton organization and biogenesis	0.000191	4.49E-08
		cellular process	0.002520	5.92E-07
		regulation of cyclin dependent protein kinase activity	0.007228	1.70E-06
		regulation of cellular physiological process	0.011295	2.65E-06
		sister chromatid segregation	0.011812	2.77E-06
		mitotic sister chromatid segregation	0.011812	2.77E-06
		regulation of cellular process	0.019355	4.54E-06
		biological_process	0.033474	7.86E-06
		all	0.033474	7.86E-06
		regulation of physiological process	0.055568	1.30E-05
		physiological process	0.072891	1.71E-05
		G1/S transition of mitotic cell cycle	0.104691	2.46E-05
Gastroc	lightyellow	morphogenesis	0.001680	3.94E-07
		cell adhesion	0.011086	2.60E-06
		development	0.059565	1.40E-05

Tissue	Module	GO terms	Bonferroni p-value	p-value
Gastroc	pink	cellular morphogenesis	0.071830	1.69E-05
		cell organization and biogenesis	0.094507	2.22E-05
		cell adhesion	3.63E-19	8.52E-23
		development	3.40E-18	7.99E-22
		phosphate transport	4.39E-18	1.03E-21
		organ development	2.83E-16	6.64E-20
		morphogenesis	5.23E-15	1.23E-18
		all	5.78E-15	1.36E-18
		biological_process	5.78E-15	1.36E-18
		skeletal development	5.48E-14	1.29E-17
		cellular process	3.08E-13	7.23E-17
		inorganic anion transport	8.87E-12	2.08E-15
		organ morphogenesis	1.48E-11	3.47E-15
		anion transport	4.07E-10	9.55E-14
		collagen fibril organization	1.19E-09	2.79E-13
		physiological process	2.75E-08	6.47E-12
		cellular physiological process	4.18E-08	9.83E-12
		bone remodeling	8.36E-07	1.96E-10
		histogenesis	1.05E-06	2.47E-10
		cell communication	1.09E-06	2.56E-10
		extracellular matrix organization and biogenesis	8.00E-06	1.88E-09
		extracellular structure organization and biogenesis	8.57E-06	2.01E-09
		ossification	2.28E-05	5.35E-09
		biomineral formation	2.28E-05	5.35E-09
		ion transport	5.75E-05	1.35E-08
		vasculature development	0.000179	4.20E-08
		muscle development	0.000310	7.28E-08
		blood vessel development	0.001141	2.68E-07
		negative regulation of angiogenesis	0.002523	5.92E-07
		blood vessel morphogenesis	0.002611	6.13E-07
		actin cytoskeleton organization and biogenesis	0.005901	1.39E-06
Gastroc	purple	RNA metabolism	0.006149	0.000001
		mRNA metabolism	0.499943	0.000117
		RNA processing	0.674904	0.000158
		translation	1.169159	0.000275
		mRNA processing	1.260536	0.000296
		tRNA aminoacylation	1.300783	0.000305
		tRNA aminoacylation for protein translation	1.300783	0.000305
Gastroc	tan	development	0.002145	5.04E-07
		muscle development	0.002472	5.80E-07
		organ development	0.005842	1.37E-06
		biological_process	0.011726	2.75E-06
		all	0.011726	2.75E-06
		cellular physiological process	0.012897	3.03E-06
		physiological process	0.024529	5.76E-06
		striated muscle contraction	0.035145	8.25E-06

Tissue	Module	GO terms	Bonferroni p-value	p-value
Hypothal	magenta	establishment and/or maintenance of chromatin architecture	4.20E-06	9.85E-10
		DNA packaging	6.33E-06	1.49E-09
		chromosome organization and biogenesis (sensu Eukaryota)	1.47E-05	3.44E-09
		chromosome organization and biogenesis	2.00E-05	4.69E-09
		nucleosome assembly	2.43E-05	5.70E-09
		chromatin assembly	0.000218	5.11E-08
		DNA metabolism	0.000300	7.05E-08
Hypothal	red	chromatin assembly or disassembly	0.000714	1.68E-07
		development	0.010447	2.45E-06
		morphogenesis	0.037846	8.89E-06
		nervous system development	0.055949	1.31E-05
Hypothal	turquoise	organ morphogenesis	0.060350	1.42E-05
		morphogenesis	1.37E-10	3.22E-14
		all	8.21E-10	1.93E-13
		biological_process	8.21E-10	1.93E-13
		nerve ensheathment	3.12E-09	7.33E-13
		physiological process	3.23E-09	7.59E-13
		cellular physiological process	3.85E-09	9.05E-13
		development	1.32E-08	3.09E-12
		nerve maturation	4.74E-08	1.11E-11
		organ morphogenesis	5.27E-08	1.24E-11
		organ development	8.59E-08	2.02E-11
		cellular process	1.05E-07	2.47E-11
		cell maturation	8.92E-06	2.09E-09
		glial cell differentiation	3.67E-05	8.62E-09
		cell adhesion	6.78E-05	1.59E-08
		nervous system development	0.000116	2.73E-08
		cell organization and biogenesis	0.000404	9.50E-08
		myelination	0.000463	1.09E-07
		ionic insulation of neurons by glial cells	0.000463	1.09E-07
		cellular nerve ensheathment	0.000463	1.09E-07
		gliogenesis	0.001116	2.62E-07
		lipid biosynthesis	0.005596	1.31E-06
		organelle organization and biogenesis	0.009902	2.32E-06