GO ID	robust pval.	normal pval.	GO Name	process type
Altzheimer Intersect:				
GO:0005344	0.00014656	2.5249e-13	oxygen transporter activity	`molecular_function`
GO:0005833	0.00014656	2.5249e-13	hemoglobin complex	`cellular_component`
GO:0015669	0.00023572	1.1502e-12	gas transport	`biological_process`
GO:0015671	0.00014656	2.5249e-13	oxygen transport	`biological_process`
GO:0019825	0.0010499	3.3415e-08	oxygen binding	`molecular_function`
GO:0020037	0.0056749	1.2689e-05	heme binding	`molecular_function`
GO:0030185	0.002101	0.0018265	nitric oxide transport	`biological_process`
GO:0030492	0.011594	0.011505	hemoglobin binding	`molecular_function`
GO:0046906	0.0056749	1.2689e-05	tetrapyrrole binding	`molecular_function`
Differences:				
GO:0045429	0.036103		positive regulation of nitric oxide biosynthetic process	`biological_process`
GO:0051173	0.036541		positive regulation of nitrogen compound metabolic process	`biological_process`
GO:0005506		0.0048786	iron ion binding	`molecular_function`
GO:0005882		0.050402	intermediate filament	`cellular_component`
GO:0005883		9.3124e-08	neurofilament	`cellular_component`
GO:0006113		0.015933	fermentation	`biological_process`
GO:0006114		0.015933	glycerol biosynthetic process	`biological_process`
GO:0006810		0.011699	transport	`biological_process`
GO:0007017		0.027231	microtubule-based process	`biological_process`
GO:0007018		0.017842	microtubule-based movement	`biological_process`
GO:0007399		0.001582	nervous system development	`biological_process`
GO:0008088		0.030413	axon cargo transport	`biological_process`
GO:0008089		0.014422	anterograde axon cargo transport	`biological_process`

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GO ID	robust pval.	normal pval.	GO Name	process type
GO:0008090		0.070899	retrograde axon cargo transport	`biological_process`
GO:0014012		0.00021099	axon regeneration in the peripheral nervous system	`biological_process`
GO:0019896		0.0053856	axon transport of mitochondrion	`biological_process`
GO:0030424		2.144e-05	axon	`cellular_component`
GO:0030705		0.073521	cytoskeleton-dependent intracellular transport	`biological_process`
GO:0031099		0.059309	regeneration	`biological_process`
GO:0031102		0.011505	neuron projection regeneration	`biological_process`
GO:0031103		0.011505	axon regeneration	`biological_process`
GO:0031133		1.2689e-05	regulation of axon diameter	`biological_process`
GO:0031346		0.083158	positive regulation of cell projection organization	`biological_process`
GO:0032393		0.055117	MHC class I receptor activity	`molecular_function`
GO:0033596		0.0033421	TSC1-TSC2 complex	`cellular_component`
GO:0033693		0.00021099	neurofilament bundle assembly	`biological_process`
GO:0042995		8.1736e-05	cell projection	`cellular_component`
GO:0043005		0.00021099	neuron projection	`cellular_component`
GO:0043234		0.011699	protein complex	`cellular_component`
GO:0044430		0.0028739	cytoskeletal part	`cellular_component`
GO:0044445		9.064e-06	cytosolic part	`cellular_component`
GO:0045103		3.2157e-05	intermediate filament-based process	`biological_process`
GO:0045104		2.144e-05	intermediate filament cytoskeleton organization	`biological_process`
GO:0045109		1.6453e-07	intermediate filament organization	`biological_process`
GO:0045110		2.3144e-09	intermediate filament bundle assembly	`biological_process`
GO:0045111		0.073521	intermediate filament cytoskeleton	`cellular_component`
GO:0045202		0.060963	synapse	`cellular_component`
GO:0048306		0.012452	calcium-dependent protein binding	`molecular_function`

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GO ID	robust pval.	normal pval.	GO Name	process type
GO:0048678		0.017842	response to axon injury	`biological_process`
GO:0060052		4.8678e-08	neurofilament cytoskeleton organization	`biological_process`
GO:0060053		1.4301e-05	neurofilament cytoskeleton	`cellular_component`
Arabidopsis Salinity Time course Intersect:				
GO:0000160	0.021089	0.021547	two-component signal transduction system (phosphorelay)	`biological_process`
GO:0000302	3.6315e-05	3.5484e-06	response to reactive oxygen species	`biological_process`
GO:0004497	4.302e-05	2.7043e-06	monooxygenase activity	`molecular_function`
GO:0004553	0.023191	0.025158	hydrolase activity, hydrolyzing O-glycosyl compounds	`molecular_function`
GO:0004601	0.022751	0.042495	peroxidase activity	`molecular_function`
GO:0005199	0.0148	9.554e-06	structural constituent of cell wall	`molecular_function`
GO:0005506	0.00025155	4.7519e-06	iron ion binding	`molecular_function`
GO:0005576	3.9806e-05	3.43e-09	extracellular region	`cellular_component`
GO:0005618	0.00049794	2.8254e-06	cell wall	`cellular_component`
GO:0005975	0.002922	0.0054155	carbohydrate metabolic process	`biological_process`
GO:0005976	0.0059941	0.0061248	polysaccharide metabolic process	`biological_process`
GO:0006073	0.0003911	0.0049279	cellular glucan metabolic process	`biological_process`
GO:0006091	0.010538	0.0089474	generation of precursor metabolites and energy	`biological_process`
GO:0006811	0.032707	0.015892	ion transport	`biological_process`
GO:0006950	6.8309e-19	1.5097e-23	response to stress	`biological_process`
GO:0006952	0.0067397	1.104e-05	defense response	`biological_process`
GO:0006970	0.0016523	0.0018341	response to osmotic stress	`biological_process`
GO:0006972	0.0020291	0.0082019	hyperosmotic response	`biological_process`
GO:0006979	1.5388e-05	7.4694e-09	response to oxidative stress	`biological_process`
GO:0007047	2.9135e-06	4.4562e-09	cell wall organization	`biological_process`
GO:0009055	9.1798e-05	3.1166e-06	electron carrier activity	`molecular_function`

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GO ID	robust pval.	normal pval.	GO Name	process type
GO:0009266	8.4911e-12	5.2456e-15	response to temperature stimulus	`biological_process`
GO:0009314	0.024072	0.00014325	response to radiation	`biological_process`
GO:0009408	3.2058e-11	3.2655e-12	response to heat	`biological_process`
GO:0009409	0.00045245	3.5484e-06	response to cold	`biological_process`
GO:0009414	8.3106e-13	3.2029e-13	response to water deprivation	`biological_process`
GO:0009415	8.3106e-13	3.9798e-13	response to water	`biological_process`
GO:0009416	0.017893	7.8078e-05	response to light stimulus	`biological_process`
GO:0009521	3.2058e-11	2.5605e-16	photosystem	`cellular_component`
GO:0009522	1.5046e-08	5.2814e-09	photosystem I	`cellular_component`
GO:0009523	0.00029875	1.9035e-08	photosystem II	`cellular_component`
GO:0009534	5.6158e-08	4.8028e-12	chloroplast thylakoid	`cellular_component`
GO:0009535	5.3901e-09	4.1612e-13	chloroplast thylakoid membrane	`cellular_component`
GO:0009538	0.0093701	0.0010077	photosystem I reaction center	`cellular_component`
GO:0009579	2.3662e-06	1.0006e-09	thylakoid	`cellular_component`
GO:0009607	0.032248	0.0012923	response to biotic stimulus	`biological_process`
GO:0009611	0.036813	0.0004346	response to wounding	`biological_process`
GO:0009628	3.2058e-11	4.1804e-14	response to abiotic stimulus	`biological_process`
GO:0009631	0.000798	0.0026302	cold acclimation	`biological_process`
GO:0009642	0.00045245	1.0479e-07	response to light intensity	`biological_process`
GO:0009644	0.0020291	6.7229e-07	response to high light intensity	`biological_process`
GO:0009651	0.024072	0.031454	response to salt stress	`biological_process`
GO:0009664	0.0019086	4.4562e-09	plant-type cell wall organization	`biological_process`
GO:0009719	6.0828e-08	3.1566e-09	response to endogenous stimulus	`biological_process`
GO:0009723	0.017273	0.021971	response to ethylene stimulus	`biological_process`
GO:0009725	5.9445e-07	3.1529e-08	response to hormone stimulus	`biological_process`

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GO ID	robust pval.	normal pval.	GO Name	process type
GO:0009737	8.8952e-09	3.5764e-10	response to abscisic acid stimulus	`biological_process`
GO:0009743	1.1835e-08	1.4129e-09	response to carbohydrate stimulus	`biological_process`
GO:0009765	3.3015e-07	2.6278e-06	photosynthesis, light harvesting	`biological_process`
GO:0009768	0.0148	0.021701	photosynthesis, light harvesting in photosystem I	`biological_process`
GO:0009873	0.040421	0.021971	ethylene mediated signaling pathway	`biological_process`
GO:0010033	1.61e-08	2.1919e-09	response to organic substance	`biological_process`
GO:0010196	0.00024861	0.00045844	nonphotochemical quenching	`biological_process`
GO:0010200	7.656e-13	3.9798e-13	response to chitin	`biological_process`
GO:0010286	0.0060808	0.013326	heat acclimation	`biological_process`
GO:0010287	1.1642e-05	4.5163e-08	plastoglobule	`cellular_component`
GO:0010683	0.029915	0.040144	tricyclic triterpenoid metabolic process	`biological_process`
GO:0012505	0.00020405	3.1773e-06	endomembrane system	`cellular_component`
GO:0015979	4.752e-11	1.4605e-14	photosynthesis	`biological_process`
GO:0016137	0.018276	0.002145	glycoside metabolic process	`biological_process`
GO:0016138	0.0024779	0.0011001	glycoside biosynthetic process	`biological_process`
GO:0016168	2.9721e-06	1.3954e-05	chlorophyll binding	`molecular_function`
GO:0016209	0.049913	0.089657	antioxidant activity	`molecular_function`
GO:0016491	2.3985e-05	6.5941e-09	oxidoreductase activity	`molecular_function`
GO:0016563	0.0027044	0.0080159	transcription activator activity	`molecular_function`
GO:0016684	0.022751	0.042495	oxidoreductase activity, acting on peroxide as acceptor	`molecular_function`
GO:0016709	0.0062227	0.0060306	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, NADH or NADPH as one donor, and incorporation of one atom of oxygen	`molecular_function`
GO:0016758	0.018276	0.030378	transferase activity, transferring hexosyl groups	`molecular_function`
GO:0016762	4.4807e-06	3.0214e-05	xyloglucan:xyloglucosyl transferase activity	`molecular_function`
GO:0016798	0.043662	0.044959	hydrolase activity, acting on glycosyl bonds	`molecular_function`
GO:0019684	4.2212e-07	3.6128e-08	photosynthesis, light reaction	`biological_process`

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GO ID	robust pval.	normal pval.	GO Name	process type
GO:0019748	0.0067397	1.104e-05	secondary metabolic process	`biological_process`
GO:0019757	0.018276	0.002145	glycosinolate metabolic process	`biological_process`
GO:0019758	0.0024779	0.0011001	glycosinolate biosynthetic process	`biological_process`
GO:0019760	0.018276	0.002145	glucosinolate metabolic process	`biological_process`
GO:0019761	0.0024779	0.0011001	glucosinolate biosynthetic process	`biological_process`
GO:0019825	0.00085293	5.941e-05	oxygen binding	`molecular_function`
GO:0020037	1.2209e-05	2.2927e-07	heme binding	`molecular_function`
GO:0030076	2.9721e-06	1.3954e-05	light-harvesting complex	`cellular_component`
GO:0031090	0.016086	0.0064177	organelle membrane	`cellular_component`
GO:0031347	0.037694	0.031454	regulation of defense response	`biological_process`
GO:0031976	6.7792e-08	6.6965e-12	plastid thylakoid	`cellular_component`
GO:0031984	7.8091e-08	8.1937e-12	organelle subcompartment	`cellular_component`
GO:0034357	5.3901e-09	5.1073e-13	photosynthetic membrane	`cellular_component`
GO:0042221	1.7686e-13	3.6796e-17	response to chemical stimulus	`biological_process`
GO:0042538	0.0067397	0.021971	hyperosmotic salinity response	`biological_process`
GO:0042542	8.3222e-06	2.7543e-06	response to hydrogen peroxide	`biological_process`
GO:0042651	1.1835e-08	1.3568e-12	thylakoid membrane	`cellular_component`
GO:0042742	0.034251	0.0070216	defense response to bacterium	`biological_process`
GO:0042744	0.040811	0.048572	hydrogen peroxide catabolic process	`biological_process`
GO:0043167	0.015367	0.018222	ion binding	`molecular_function`
GO:0043169	0.037694	0.031454	cation binding	`molecular_function`
GO:0044042	0.0034564	0.013775	glucan metabolic process	`biological_process`
GO:0044262	0.00045884	0.00043376	cellular carbohydrate metabolic process	`biological_process`
GO:0044264	0.0024287	0.022942	cellular polysaccharide metabolic process	`biological_process`
GO:0044436	1.1787e-07	1.4675e-11	thylakoid part	`cellular_component`

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GO ID	robust pval.	normal pval.	GO Name	process type
GO:0045229	9.3008e-06	2.2672e-08	external encapsulating structure organization	`biological_process`
GO:0046872	0.014039	0.014011	metal ion binding	`molecular_function`
GO:0046906	7.5103e-10	1.5857e-11	tetrapyrrole binding	`molecular_function`
GO:0048046	0.0044855	0.00074784	apoplast	`cellular_component`
GO:0050832	0.044236	0.052885	defense response to fungus	`biological_process`
GO:0050896	2.0051e-18	1.7108e-23	response to stimulus	`biological_process`
GO:0055035	5.3901e-09	4.1612e-13	plastid thylakoid membrane	`cellular_component`
GO:0055114	0.00045245	6.3304e-06	oxidation reduction	`biological_process`
GO:0080003	0.0148	0.021701	thalianol metabolic process	`biological_process`
Differences:				
GO:0016564	0.030549		transcription repressor activity	`molecular_function`
GO:0016757	0.047558		transferase activity, transferring glycosyl groups	`molecular_function`
GO:0001871		0.082711	pattern binding	`molecular_function`
GO:0003978		0.048553	UDP-glucose 4-epimerase activity	`molecular_function`
GO:0004364		0.057508	glutathione transferase activity	`molecular_function`
GO:0004657		0.073204	proline dehydrogenase activity	`molecular_function`
GO:0005215		0.057577	transporter activity	`molecular_function`
GO:0005342		0.034732	organic acid transmembrane transporter activity	`molecular_function`
GO:0005509		0.031454	calcium ion binding	`molecular_function`
GO:0006470		0.027178	protein amino acid dephosphorylation	`biological_process`
GO:0006569		0.073204	tryptophan catabolic process	`biological_process`
GO:0006812		0.037346	cation transport	`biological_process`
GO:0006949		0.003653	syncytium formation	`biological_process`
GO:0006955		0.0061248	immune response	`biological_process`
GO:0009404		0.040144	toxin metabolic process	`biological_process`
GO:0009407		0.040144	toxin catabolic process	`biological_process`

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GO ID	robust pval.	normal pval.	GO Name	process type
GO:0009512		0.073204	cytochrome b6f complex	`cellular_component`
GO:0009533		0.040144	chloroplast stromal thylakoid	`cellular_component`
GO:0009543		0.0061248	chloroplast thylakoid lumen	`cellular_component`
GO:0009605		0.025158	response to external stimulus	`biological_process`
GO:0009617		0.016067	response to bacterium	`biological_process`
GO:0009636		0.051383	response to toxin	`biological_process`
GO:0009654		0.030697	oxygen evolving complex	`cellular_component`
GO:0009700		0.025158	indole phytoalexin biosynthetic process	`biological_process`
GO:0009738		0.044837	abscisic acid mediated signaling	`biological_process`
GO:0009755		0.06861	hormone-mediated signaling	`biological_process`
GO:0009767		0.012546	photosynthetic electron transport chain	`biological_process`
GO:0009783		0.073204	photosystem II antenna complex	`cellular_component`
GO:0009825		0.094331	multidimensional cell growth	`biological_process`
GO:0009826		0.033768	unidimensional cell growth	`biological_process`
GO:0009827		0.00013246	plant-type cell wall modification	`biological_process`
GO:0009828		2.1751e-05	plant-type cell wall loosening	`biological_process`
GO:0009831		0.031906	plant-type cell wall modification during multidimensional cell growth	`biological_process`
GO:0010120		0.016903	camalexin biosynthetic process	`biological_process`
GO:0010177		0.073204	methylthioalkylmalate synthase activity	`molecular_function`
GO:0010205		0.099777	photoinhibition	`biological_process`
GO:0010242		0.073204	oxygen evolving activity	`molecular_function`
GO:0015103		0.082711	inorganic anion transmembrane transporter activity	`molecular_function`
GO:0015140		0.073204	malate transmembrane transporter activity	`molecular_function`
GO:0015291		0.05095	secondary active transmembrane transporter activity	`molecular_function`
GO:0015849		0.06861	organic acid transport	`biological_process`

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GO ID	robust pval.	normal pval.	GO Name	process type
GO:0016020		0.00094685	membrane	`cellular_component`
GO:0016021		0.0037111	integral to membrane	`cellular_component`
GO:0016051		0.040144	carbohydrate biosynthetic process	`biological_process`
GO:0016311		0.026315	dephosphorylation	`biological_process`
GO:0016620		0.065324	oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor	`molecular_function`
GO:0016705		0.0038847	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen	`molecular_function`
GO:0022857		0.030244	transmembrane transporter activity	`molecular_function`
GO:0022891		0.031454	substrate-specific transmembrane transporter activity	`molecular_function`
GO:0030001		0.026158	metal ion transport	`biological_process`
GO:0030095		7.463e-05	chloroplast photosystem II	`cellular_component`
GO:0030145		0.041456	manganese ion binding	`molecular_function`
GO:0030247		0.082711	polysaccharide binding	`molecular_function`
GO:0031224		0.00054999	intrinsic to membrane	`cellular_component`
GO:0031977		0.0064177	thylakoid lumen	`cellular_component`
GO:0031978		0.0061248	plastid thylakoid lumen	`cellular_component`
GO:0034637		0.096967	cellular carbohydrate biosynthetic process	`biological_process`
GO:0035303		0.073204	regulation of dephosphorylation	`biological_process`
GO:0035304		0.073204	regulation of protein amino acid dephosphorylation	`biological_process`
GO:0042431		0.025158	indole metabolic process	`biological_process`
GO:0042436		0.073204	indole derivative catabolic process	`biological_process`
GO:0042545		0.0038577	cell wall modification	`biological_process`
GO:0042547		0.044914	cell wall modification during multidimensional cell growth	`biological_process`
GO:0042548		0.082711	regulation of photosynthesis, light reaction	`biological_process`
GO:0042743		0.082711	hydrogen peroxide metabolic process	`biological_process`
GO:0043155		0.099777	negative regulation of photosynthesis, light reaction	`biological_process`

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GO ID	robust pval.	normal pval.	GO Name	process type
GO:0043467		0.030697	regulation of generation of precursor metabolites and energy	biological_process
GO:0044425		0.00087869	membrane part	cellular_component
GO:0044434		0.018203	chloroplast part	cellular_component
GO:0044435		0.033205	plastid part	cellular_component
GO:0045087		0.021971	innate immune response	biological_process
GO:0046217		0.025158	indole phytoalexin metabolic process	biological_process
GO:0046218		0.073204	indolalkylamine catabolic process	biological_process
GO:0046914		0.073204	transition metal ion binding	molecular_function
GO:0046942		0.06861	carboxylic acid transport	biological_process
GO:0046943		0.034732	carboxylic acid transmembrane transporter activity	molecular_function
GO:0048583		0.095377	regulation of response to stimulus	biological_process
GO:0050691		0.073204	regulation of defense response to virus by host	biological_process
GO:0051707		0.0098105	response to other organism	biological_process
GO:0052314		0.025158	phytoalexin metabolic process	biological_process
GO:0052315		0.025158	phytoalexin biosynthetic process	biological_process
GO:0052317		0.016903	camalexin metabolic process	biological_process
GO:0080134		0.042508	regulation of response to stress	biological_process
Arabidopsis Selenate Intersect:				
GO:0000103	0.00022269	0.00025683	sulfate assimilation	biological_process
GO:0000160	2.6264e-06	1.5281e-05	two-component signal transduction system (phosphorelay)	biological_process
GO:0000302	1.0105e-09	4.2155e-10	response to reactive oxygen species	biological_process
GO:0002252	0.00090649	0.0010982	immune effector process	biological_process
GO:0002679	0.0063967	0.007273	respiratory burst during defense response	biological_process
GO:0003700	1.7691e-06	6.342e-07	transcription factor activity	molecular_function
GO:0004089	0.0073223	0.063592	carbonate dehydratase activity	molecular_function

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GO ID	robust pval.	normal pval.	GO Name	process type
GO:0004601	1.6022e-05	9.102e-05	peroxidase activity	`molecular_function`
GO:0004779	0.049817	0.05546	sulfate adenylyltransferase activity	`molecular_function`
GO:0004781	0.049817	0.05546	sulfate adenylyltransferase (ATP) activity	`molecular_function`
GO:0005199	0.000888	6.664e-06	structural constituent of cell wall	`molecular_function`
GO:0005488	0.049031	0.063298	binding	`molecular_function`
GO:0005506	0.0052749	0.0062578	iron ion binding	`molecular_function`
GO:0005509	4.0189e-06	1.6728e-06	calcium ion binding	`molecular_function`
GO:0005516	0.0025843	0.00058199	calmodulin binding	`molecular_function`
GO:0005576	3.0915e-10	2.5406e-12	extracellular region	`cellular_component`
GO:0005618	4.8063e-05	1.5586e-05	cell wall	`cellular_component`
GO:0006091	0.0059635	0.037782	generation of precursor metabolites and energy	`biological_process`
GO:0006350	0.00033599	0.00093706	transcription	`biological_process`
GO:0006351	0.0021164	0.0019332	transcription, DNA-dependent	`biological_process`
GO:0006355	0.001342	0.00080442	regulation of transcription, DNA-dependent	`biological_process`
GO:0006534	0.040227	0.0474	cysteine metabolic process	`biological_process`
GO:0006791	0.00035044	0.00043315	sulfur utilization	`biological_process`
GO:0006800	1.0496e-05	6.0165e-05	oxygen and reactive oxygen species metabolic process	`biological_process`
GO:0006950	8.6946e-38	2.5848e-38	response to stress	`biological_process`
GO:0006952	1.1204e-20	3.1159e-21	defense response	`biological_process`
GO:0006955	5.6872e-11	1.6185e-10	immune response	`biological_process`
GO:0006970	1.2343e-05	4.8435e-06	response to osmotic stress	`biological_process`
GO:0006979	1.2717e-12	1.0037e-12	response to oxidative stress	`biological_process`
GO:0007047	0.0012019	9.9898e-05	cell wall organization	`biological_process`
GO:0007165	0.029727	0.017231	signal transduction	`biological_process`
GO:0007242	0.033641	0.09436	intracellular signaling cascade	`biological_process`

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GO ID	robust pval.	normal pval.	GO Name	process type
GO:0008152	3.1415e-07	0.00015091	metabolic process	`biological_process`
GO:0008271	0.010301	0.099475	secondary active sulfate transmembrane transporter activity	`molecular_function`
GO:0008453	0.022511	0.024866	alanine-glyoxylate transaminase activity	`molecular_function`
GO:0009055	2.3164e-05	1.4254e-05	electron carrier activity	`molecular_function`
GO:0009266	2.434e-10	2.2726e-11	response to temperature stimulus	`biological_process`
GO:0009408	3.8034e-10	1.6185e-10	response to heat	`biological_process`
GO:0009409	0.00024995	6.8689e-05	response to cold	`biological_process`
GO:0009414	1.624e-08	1.1889e-07	response to water deprivation	`biological_process`
GO:0009415	7.297e-08	5.2208e-07	response to water	`biological_process`
GO:0009521	3.3908e-14	8.9676e-13	photosystem	`cellular_component`
GO:0009522	5.429e-11	1.5799e-09	photosystem I	`cellular_component`
GO:0009523	9.0676e-07	1.1867e-06	photosystem II	`cellular_component`
GO:0009534	3.0638e-07	9.0564e-08	chloroplast thylakoid	`cellular_component`
GO:0009535	4.721e-08	3.5682e-08	chloroplast thylakoid membrane	`cellular_component`
GO:0009538	5.0528e-05	0.0013081	photosystem I reaction center	`cellular_component`
GO:0009579	2.8767e-05	2.9034e-05	thylakoid	`cellular_component`
GO:0009605	1.4986e-06	3.103e-06	response to external stimulus	`biological_process`
GO:0009607	6.7191e-08	8.8468e-08	response to biotic stimulus	`biological_process`
GO:0009611	6.0258e-14	2.351e-14	response to wounding	`biological_process`
GO:0009617	0.0041138	0.015381	response to bacterium	`biological_process`
GO:0009620	0.0088177	0.0013859	response to fungus	`biological_process`
GO:0009626	0.00058248	0.00078946	plant-type hypersensitive response	`biological_process`
GO:0009628	1.0431e-11	6.0696e-12	response to abiotic stimulus	`biological_process`
GO:0009642	3.4217e-06	9.7198e-07	response to light intensity	`biological_process`
GO:0009644	0.00010606	2.3435e-05	response to high light intensity	`biological_process`

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GO ID	robust pval.	normal pval.	GO Name	process type
GO:0009646	0.048563	0.054489	response to absence of light	`biological_process`
GO:0009651	2.6528e-05	1.016e-05	response to salt stress	`biological_process`
GO:0009664	0.021749	0.00066361	plant-type cell wall organization	`biological_process`
GO:0009694	0.00030827	0.00039489	jasmonic acid metabolic process	`biological_process`
GO:0009695	0.00022269	0.00025683	jasmonic acid biosynthetic process	`biological_process`
GO:0009700	0.0021869	0.0025524	indole phytoalexin biosynthetic process	`biological_process`
GO:0009719	1.881e-11	3.1644e-12	response to endogenous stimulus	`biological_process`
GO:0009723	5.0563e-10	3.7863e-10	response to ethylene stimulus	`biological_process`
GO:0009725	7.2189e-08	1.5394e-08	response to hormone stimulus	`biological_process`
GO:0009737	4.0158e-07	2.7379e-07	response to abscisic acid stimulus	`biological_process`
GO:0009743	1.7361e-28	1.0915e-29	response to carbohydrate stimulus	`biological_process`
GO:0009751	7.8269e-05	4.0603e-05	response to salicylic acid stimulus	`biological_process`
GO:0009753	4.2806e-11	8.806e-11	response to jasmonic acid stimulus	`biological_process`
GO:0009755	0.00022269	0.00042848	hormone-mediated signaling	`biological_process`
GO:0009765	6.7196e-06	9.2006e-07	photosynthesis, light harvesting	`biological_process`
GO:0009814	0.0021869	0.0092421	defense response, incompatible interaction	`biological_process`
GO:0009861	0.0010381	0.0012846	jasmonic acid and ethylene-dependent systemic resistance	`biological_process`
GO:0009867	0.0091985	0.011644	jasmonic acid mediated signaling pathway	`biological_process`
GO:0009873	1.7756e-06	9.2006e-07	ethylene mediated signaling pathway	`biological_process`
GO:0009889	7.8269e-05	0.00015404	regulation of biosynthetic process	`biological_process`
GO:0009973	0.0063967	0.007273	adenylyl-sulfate reductase activity	`molecular_function`
GO:0009987	0.00076815	0.0031673	cellular process	`biological_process`
GO:0010033	4.1075e-28	2.6999e-29	response to organic substance	`biological_process`
GO:0010120	0.00116	0.0013081	camalexin biosynthetic process	`biological_process`
GO:0010200	5.1364e-39	8.8755e-41	response to chitin	`biological_process`

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GO ID	robust pval.	normal pval.	GO Name	process type
GO:0010287	1.7756e-06	1.5297e-05	plastoglobule	`cellular_component`
GO:0010468	0.00023091	0.00044378	regulation of gene expression	`biological_process`
GO:0010556	7.0782e-05	0.00013765	regulation of macromolecule biosynthetic process	`biological_process`
GO:0010941	0.049607	0.057633	regulation of cell death	`biological_process`
GO:0012505	0.00030827	4.8865e-05	endomembrane system	`cellular_component`
GO:0015116	0.00022269	0.0027205	sulfate transmembrane transporter activity	`molecular_function`
GO:0015979	5.6872e-11	2.4935e-09	photosynthesis	`biological_process`
GO:0016020	0.018711	0.063298	membrane	`cellular_component`
GO:0016168	2.6264e-06	2.4955e-07	chlorophyll binding	`molecular_function`
GO:0016209	2.3164e-05	0.00012227	antioxidant activity	`molecular_function`
GO:0016491	0.00024407	0.00022252	oxidoreductase activity	`molecular_function`
GO:0016563	0.00024812	0.00011704	transcription activator activity	`molecular_function`
GO:0016671	0.0036527	0.0046005	oxidoreductase activity, acting on sulfur group of donors, disulfide as acceptor	`molecular_function`
GO:0016684	1.6022e-05	9.102e-05	oxidoreductase activity, acting on peroxide as acceptor	`molecular_function`
GO:0016762	1.0722e-05	1.7442e-06	xyloglucan:xyloglucosyl transferase activity	`molecular_function`
GO:0016829	0.018022	0.016108	lyase activity	`molecular_function`
GO:0019219	0.0001185	0.00022484	regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	`biological_process`
GO:0019222	0.00023091	0.00069882	regulation of metabolic process	`biological_process`
GO:0019344	0.024195	0.028786	cysteine biosynthetic process	`biological_process`
GO:0019684	3.2368e-05	1.1405e-05	photosynthesis, light reaction	`biological_process`
GO:0019748	0.0028905	0.0026524	secondary metabolic process	`biological_process`
GO:0020037	3.1965e-05	1.2039e-05	heme binding	`molecular_function`
GO:0030076	0.00030827	4.119e-05	light-harvesting complex	`cellular_component`
GO:0030528	2.8767e-05	2.2381e-05	transcription regulator activity	`molecular_function`
GO:0031224	0.0018273	0.007273	intrinsic to membrane	`cellular_component`

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GO ID	robust pval.	normal pval.	GO Name	process type
GO:0031225	0.022193	0.033538	anchored to membrane	`cellular_component`
GO:0031323	1.728e-05	6.0165e-05	regulation of cellular metabolic process	`biological_process`
GO:0031326	7.8269e-05	0.00015404	regulation of cellular biosynthetic process	`biological_process`
GO:0031347	0.0036527	0.019591	regulation of defense response	`biological_process`
GO:0031407	0.0012242	0.0014831	oxylipin metabolic process	`biological_process`
GO:0031408	0.00090649	0.0010982	oxylipin biosynthetic process	`biological_process`
GO:0031976	3.9256e-07	1.1809e-07	plastid thylakoid	`cellular_component`
GO:0031977	0.041808	0.0054095	thylakoid lumen	`cellular_component`
GO:0031984	4.5439e-07	1.3755e-07	organelle subcompartment	`cellular_component`
GO:0032774	0.0021869	0.0020352	RNA biosynthetic process	`biological_process`
GO:0033741	0.0063967	0.007273	adenylyl-sulfate reductase (glutathione) activity	`molecular_function`
GO:0034050	0.00069609	0.0009331	host programmed cell death induced by symbiont	`biological_process`
GO:0034357	5.4796e-08	4.2951e-08	photosynthetic membrane	`cellular_component`
GO:0042221	9.0523e-30	5.6525e-31	response to chemical stimulus	`biological_process`
GO:0042431	0.0021869	0.0025524	indole metabolic process	`biological_process`
GO:0042542	4.2468e-10	1.6185e-10	response to hydrogen peroxide	`biological_process`
GO:0042651	1.1342e-07	9.0564e-08	thylakoid membrane	`cellular_component`
GO:0042742	0.0028905	0.011422	defense response to bacterium	`biological_process`
GO:0042743	2.6264e-06	1.8745e-05	hydrogen peroxide metabolic process	`biological_process`
GO:0042744	3.2069e-06	5.1931e-06	hydrogen peroxide catabolic process	`biological_process`
GO:0043067	0.049607	0.057633	regulation of programmed cell death	`biological_process`
GO:0043167	0.00014224	0.00012556	ion binding	`molecular_function`
GO:0043169	0.00058885	0.0004546	cation binding	`molecular_function`
GO:0044237	1.8052e-06	0.00013524	cellular metabolic process	`biological_process`
GO:0044248	0.0036527	0.0091848	cellular catabolic process	`biological_process`

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GO ID	robust pval.	normal pval.	GO Name	process type
GO:0044425	0.0036527	0.020849	membrane part	`cellular_component`
GO:0044436	7.262e-07	2.2552e-07	thylakoid part	`cellular_component`
GO:0045087	1.0679e-08	2.6442e-08	innate immune response	`biological_process`
GO:0045229	0.0030875	0.00030363	external encapsulating structure organization	`biological_process`
GO:0045449	5.8991e-05	0.00011704	regulation of transcription	`biological_process`
GO:0045730	0.00049194	0.00056143	respiratory burst	`biological_process`
GO:0045735	0.0018273	0.0024393	nutrient reservoir activity	`molecular_function`
GO:0046217	0.0021869	0.0025524	indole phytoalexin metabolic process	`biological_process`
GO:0046872	0.00049134	0.00041368	metal ion binding	`molecular_function`
GO:0046906	1.4218e-08	1.4698e-09	tetrapyrrole binding	`molecular_function`
GO:0046914	0.018172	0.025775	transition metal ion binding	`molecular_function`
GO:0048046	4.3021e-05	2.5916e-06	apoplast	`cellular_component`
GO:0050776	0.01422	0.017316	regulation of immune response	`biological_process`
GO:0050794	0.0003693	0.00050349	regulation of cellular process	`biological_process`
GO:0050832	0.00030827	0.00011704	defense response to fungus	`biological_process`
GO:0050896	4.4899e-36	2.0145e-37	response to stimulus	`biological_process`
GO:0051252	0.0015833	0.00093768	regulation of RNA metabolic process	`biological_process`
GO:0051707	9.8042e-07	1.06e-06	response to other organism	`biological_process`
GO:0051865	0.0063967	0.007273	protein autoubiquitination	`biological_process`
GO:0052314	0.0021869	0.0025524	phytoalexin metabolic process	`biological_process`
GO:0052315	0.0021869	0.0025524	phytoalexin biosynthetic process	`biological_process`
GO:0052317	0.00116	0.0013081	camalexin metabolic process	`biological_process`
GO:0055035	4.721e-08	3.5682e-08	plastid thylakoid membrane	`cellular_component`
GO:0055114	8.52e-07	1.8845e-05	oxidation reduction	`biological_process`
GO:0060255	0.0010957	0.0020837	regulation of macromolecule metabolic process	`biological_process`

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GO ID	robust pval.	normal pval.	GO Name	process type
GO:0080090	0.00040937	0.00081487	regulation of primary metabolic process	biological_process
GO:0080134	0.0014826	0.0079542	regulation of response to stress	biological_process
Differences:				
GO:0008272	0.022511		sulfate transport	biological_process
GO:0015698	0.0081482		inorganic anion transport	biological_process
GO:0022900	0.024195		electron transport chain	biological_process
GO:0000249		0.09436	C-22 sterol desaturase activity	molecular_function
GO:0003677		0.088459	DNA binding	molecular_function
GO:0005776		0.09436	autophagic vacuole	cellular_component
GO:0006073		0.044276	cellular glucan metabolic process	biological_process
GO:0007154		0.054489	cell communication	biological_process
GO:0009505		0.085469	plant-type cell wall	cellular_component
GO:0009543		0.015381	chloroplast thylakoid lumen	cellular_component
GO:0009783		0.09436	photosystem II antenna complex	cellular_component
GO:0009853		0.099475	photorespiration	biological_process
GO:0010193		0.082048	response to ozone	biological_process
GO:0010604		0.080518	positive regulation of macromolecule metabolic process	biological_process
GO:0010942		0.09436	positive regulation of cell death	biological_process
GO:0016137		0.088459	glycoside metabolic process	biological_process
GO:0016667		0.070288	oxidoreductase activity, acting on sulfur group of donors	molecular_function
GO:0019757		0.088459	glycosinolate metabolic process	biological_process
GO:0019760		0.088459	glucosinolate metabolic process	biological_process
GO:0019825		0.018015	oxygen binding	molecular_function
GO:0030095		0.012362	chloroplast photosystem II	cellular_component
GO:0031978		0.015381	plastid thylakoid lumen	cellular_component
GO:0042430		0.088459	indole and derivative metabolic process	biological_process

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GO ID	robust pval.	normal pval.	GO Name	process type
GO:0042434		0.088459	indole derivative metabolic process	`biological_process`
GO:0042435		0.065676	indole derivative biosynthetic process	`biological_process`
GO:0043068		0.09436	positive regulation of programmed cell death	`biological_process`
GO:0044042		0.049983	glucan metabolic process	`biological_process`
GO:0050691		0.09436	regulation of defense response to virus by host	`biological_process`
GO:0051245		0.09436	negative regulation of cellular defense response	`biological_process`
Zebrafish Retina regeneration Time course				
Intersect:				
GO:0001654	0.040761	0.076172	eye development	`biological_process`
GO:0004872	0.042374	0.076172	receptor activity	`molecular_function`
GO:0005488	0.042374	0.076172	binding	`molecular_function`
GO:0005515	0.045764	0.092211	protein binding	`molecular_function`
GO:0006464	0.040761	0.076172	protein modification process	`biological_process`
GO:0009628	0.034686	0.076172	response to abiotic stimulus	`biological_process`
GO:0009653	0.042374	0.076172	anatomical structure morphogenesis	`biological_process`
GO:0016020	0.041817	0.084725	membrane	`cellular_component`
GO:0048598	0.034686	0.076172	embryonic morphogenesis	`biological_process`
GO:0048731	0.045764	0.076172	system development	`biological_process`
GO:0050896	0.045764	0.076172	response to stimulus	`biological_process`
Differences:				
GO:0006575	0.049925		amino acid derivative metabolic process	`biological_process`
GO:0003824		0.084725	catalytic activity	`molecular_function`
GO:0004871		0.076172	signal transducer activity	`molecular_function`
GO:0006950		0.079018	response to stress	`biological_process`
GO:0007369		0.092211	gastrulation	`biological_process`
GO:0009887		0.079018	organ morphogenesis	`biological_process`

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GO ID	robust pval.	normal pval.	GO Name	process type
GO:0016021		0.076172	integral to membrane	`cellular_component`
GO:0031101		0.076172	fin regeneration	`biological_process`
GO:0031224		0.076172	intrinsic to membrane	`cellular_component`
GO:0042398		0.093715	amino acid derivative biosynthetic process	`biological_process`
GO:0043412		0.076172	biopolymer modification	`biological_process`
GO:0043687		0.079018	post-translational protein modification	`biological_process`
GO:0048513		0.076172	organ development	`biological_process`
GO:0048589		0.076172	developmental growth	`biological_process`
Drosophila Sleep deprivation final time point				
Intersect:				
GO:0005550	0.0019151	7.4072e-05	pheromone binding	`molecular_function`
GO:0005576	8.4384e-06	1.8262e-07	extracellular region	`cellular_component`
GO:0006950	0.044448	0.00019272	response to stress	`biological_process`
GO:0006952	0.0042644	2.7658e-05	defense response	`biological_process`
GO:0009607	0.034943	4.7894e-06	response to biotic stimulus	`biological_process`
GO:0019731	0.0025782	4.3872e-08	antibacterial humoral response	`biological_process`
GO:0042742	0.034943	1.1129e-05	defense response to bacterium	`biological_process`
GO:0045087	0.0025782	3.4806e-06	innate immune response	`biological_process`
GO:0050877	0.019917	5.3476e-08	neurological system process	`biological_process`
GO:0050896	0.0042644	3.4153e-08	response to stimulus	`biological_process`
GO:0051707	0.033148	1.1129e-05	response to other organism	`biological_process`
Differences:				
GO:0000902		0.00069781	cell morphogenesis	`biological_process`
GO:0000904		0.0038533	cell morphogenesis involved in differentiation	`biological_process`
GO:0001505		2.523e-05	regulation of neurotransmitter levels	`biological_process`
GO:0001654		0.077565	eye development	`biological_process`

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GO ID	robust pval.	normal pval.	GO Name	process type
GO:0003001		1.5661e-05	generation of a signal involved in cell-cell signaling	`biological_process`
GO:0005488		0.0032219	binding	`molecular_function`
GO:0005515		0.065238	protein binding	`molecular_function`
GO:0005543		0.028447	phospholipid binding	`molecular_function`
GO:0005615		0.0004054	extracellular space	`cellular_component`
GO:0005886		0.025691	plasma membrane	`cellular_component`
GO:0006457		0.043831	protein folding	`biological_process`
GO:0006528		0.030401	asparagine metabolic process	`biological_process`
GO:0006805		0.083966	xenobiotic metabolic process	`biological_process`
GO:0006810		0.0002194	transport	`biological_process`
GO:0006836		3.8341e-05	neurotransmitter transport	`biological_process`
GO:0006887		4.773e-05	exocytosis	`biological_process`
GO:0006928		0.024209	cell motion	`biological_process`
GO:0006955		6.9138e-06	immune response	`biological_process`
GO:0006959		5.5458e-06	humoral immune response	`biological_process`
GO:0007154		4.8172e-05	cell communication	`biological_process`
GO:0007165		0.087542	signal transduction	`biological_process`
GO:0007267		5.5458e-06	cell-cell signaling	`biological_process`
GO:0007268		1.5264e-06	synaptic transmission	`biological_process`
GO:0007269		1.1129e-05	neurotransmitter secretion	`biological_process`
GO:0007399		0.023472	nervous system development	`biological_process`
GO:0007409		0.0033055	axonogenesis	`biological_process`
GO:0007411		0.0090787	axon guidance	`biological_process`
GO:0007600		0.070891	sensory perception	`biological_process`
GO:0007610		0.00029095	behavior	`biological_process`

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GO ID	robust pval.	normal pval.	GO Name	process type
GO:0007626		0.009215	locomotory behavior	`biological_process`
GO:0008021		0.0046242	synaptic vesicle	`cellular_component`
GO:0008037		0.086247	cell recognition	`biological_process`
GO:0008038		0.086247	neuron recognition	`biological_process`
GO:0008145		0.0075403	phenylalkylamine binding	`molecular_function`
GO:0008200		0.074291	ion channel inhibitor activity	`molecular_function`
GO:0008344		0.037775	adult locomotory behavior	`biological_process`
GO:0009410		0.083966	response to xenobiotic stimulus	`biological_process`
GO:0009617		3.3425e-05	response to bacterium	`biological_process`
GO:0009620		0.017372	response to fungus	`biological_process`
GO:0009653		0.00036691	anatomical structure morphogenesis	`biological_process`
GO:0009987		0.00015176	cellular process	`biological_process`
GO:0016023		0.0057769	cytoplasmic membrane-bounded vesicle	`cellular_component`
GO:0016043		0.0073154	cellular component organization	`biological_process`
GO:0016079		0.00037357	synaptic vesicle exocytosis	`biological_process`
GO:0016192		4.3475e-05	vesicle-mediated transport	`biological_process`
GO:0016248		0.074291	channel inhibitor activity	`molecular_function`
GO:0016601		0.074291	Rac protein signal transduction	`biological_process`
GO:0019226		1.9611e-06	transmission of nerve impulse	`biological_process`
GO:0019730		3.4888e-06	antimicrobial humoral response	`biological_process`
GO:0022008		0.016578	neurogenesis	`biological_process`
GO:0030030		0.053352	cell projection organization	`biological_process`
GO:0030135		0.023472	coated vesicle	`cellular_component`
GO:0030136		0.0072519	clathrin-coated vesicle	`cellular_component`
GO:0030154		0.0013513	cell differentiation	`biological_process`

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GO ID	robust pval.	normal pval.	GO Name	process type
GO:0030182		0.0032704	neuron differentiation	`biological_process`
GO:0030534		0.016578	adult behavior	`biological_process`
GO:0031175		0.014918	neuron projection development	`biological_process`
GO:0031225		0.083966	anchored to membrane	`cellular_component`
GO:0031410		0.00905	cytoplasmic vesicle	`cellular_component`
GO:0031982		0.012177	vesicle	`cellular_component`
GO:0031988		0.0072588	membrane-bounded vesicle	`cellular_component`
GO:0032268		0.041707	regulation of cellular protein metabolic process	`biological_process`
GO:0032269		0.077565	negative regulation of cellular protein metabolic process	`biological_process`
GO:0032940		7.4072e-05	secretion by cell	`biological_process`
GO:0032989		0.0010944	cellular component morphogenesis	`biological_process`
GO:0032990		0.0075403	cell part morphogenesis	`biological_process`
GO:0035249		0.030401	synaptic transmission, glutamatergic	`biological_process`
GO:0044267		0.066721	cellular protein metabolic process	`biological_process`
GO:0044421		0.0028613	extracellular region part	`cellular_component`
GO:0044456		0.0010944	synapse part	`cellular_component`
GO:0044459		0.047621	plasma membrane part	`cellular_component`
GO:0045202		0.0010272	synapse	`cellular_component`
GO:0046903		0.00015176	secretion	`biological_process`
GO:0048468		0.00038287	cell development	`biological_process`
GO:0048489		0.00043998	synaptic vesicle transport	`biological_process`
GO:0048666		0.0065646	neuron development	`biological_process`
GO:0048667		0.014918	cell morphogenesis involved in neuron differentiation	`biological_process`
GO:0048699		0.013696	generation of neurons	`biological_process`
GO:0048731		0.023138	system development	`biological_process`

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GO ID	robust pval.	normal pval.	GO Name	process type
GO:0048812		0.014918	neuron projection morphogenesis	`biological_process`
GO:0048856		0.00249	anatomical structure development	`biological_process`
GO:0048858		0.014918	cell projection morphogenesis	`biological_process`
GO:0048869		0.0010944	cellular developmental process	`biological_process`
GO:0050794		0.075408	regulation of cellular process	`biological_process`
GO:0050803		0.070891	regulation of synapse structure and activity	`biological_process`
GO:0050807		0.070891	regulation of synapse organization	`biological_process`
GO:0050808		0.074291	synapse organization	`biological_process`
GO:0050829		0.0065037	defense response to Gram-negative bacterium	`biological_process`
GO:0050832		0.013696	defense response to fungus	`biological_process`
GO:0050890		0.015205	cognition	`biological_process`
GO:0051128		0.048846	regulation of cellular component organization	`biological_process`
GO:0051246		0.060193	regulation of protein metabolic process	`biological_process`
GO:0051248		0.083441	negative regulation of protein metabolic process	`biological_process`
GO:0051641		0.00019272	cellular localization	`biological_process`
GO:0051649		0.00053303	establishment of localization in cell	`biological_process`
GO:0060341		0.06175	regulation of cellular localization	`biological_process`
Drosophila Sleep deprivation Time course Intersect:				
Differences:				
GO:0050896		0.021692	response to stimulus	`biological_process`
GO:0009607		0.03978	response to biotic stimulus	`biological_process`
GO:0006959		0.064406	humoral immune response	`biological_process`
GO:0019730		0.064406	antimicrobial humoral response	`biological_process`
GO:0050829		0.064406	defense response to Gram-negative bacterium	`biological_process`
GO:0019731		0.087727	antibacterial humoral response	`biological_process`

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GO ID	robust pval.	normal pval.	GO Name	process type
Melanoma Intersect:				
GO:0001501	0.024728	0.0080717	skeletal system development	`biological_process`
GO:0001533	0.016028	0.00019421	cornified envelope	`cellular_component`
GO:0001568	0.0096322	0.00093373	blood vessel development	`biological_process`
GO:0001725	0.012909	0.0020237	stress fiber	`cellular_component`
GO:0001871	0.0078725	0.0028527	pattern binding	`molecular_function`
GO:0001944	0.012292	0.0010636	vasculature development	`biological_process`
GO:0003700	0.016047	0.0032525	transcription factor activity	`molecular_function`
GO:0003779	5.5779e-05	1.2702e-10	actin binding	`molecular_function`
GO:0003824	5.7114e-05	2.4672e-05	catalytic activity	`molecular_function`
GO:0004601	0.046389	0.034847	peroxidase activity	`molecular_function`
GO:0004867	0.019228	0.00073666	serine-type endopeptidase inhibitor activity	`molecular_function`
GO:0005083	0.013729	0.075565	GTPase regulator activity	`molecular_function`
GO:0005488	6.3558e-16	2.5389e-14	binding	`molecular_function`
GO:0005515	1.401e-25	4.7468e-19	protein binding	`molecular_function`
GO:0005523	0.018767	0.0069864	tropomyosin binding	`molecular_function`
GO:0005539	0.0030331	0.0016837	glycosaminoglycan binding	`molecular_function`
GO:0005578	2.5365e-05	2.4587e-11	proteinaceous extracellular matrix	`cellular_component`
GO:0005622	1.3247e-27	1.9857e-17	intracellular	`cellular_component`
GO:0005623	4.6945e-28	5.9428e-25	cell	`cellular_component`
GO:0005737	4.6945e-28	2.7456e-22	cytoplasm	`cellular_component`
GO:0005783	0.00010324	1.9045e-05	endoplasmic reticulum	`cellular_component`
GO:0005789	0.03432	0.003914	endoplasmic reticulum membrane	`cellular_component`
GO:0005792	0.030739	0.00076587	microsome	`cellular_component`
GO:0005794	0.019228	0.044551	Golgi apparatus	`cellular_component`

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GO ID	robust pval.	normal pval.	GO Name	process type
GO:0005856	6.2203e-07	1.9795e-11	cytoskeleton	cellular_component
GO:0005886	0.030739	8.9844e-06	plasma membrane	cellular_component
GO:0005911	0.019228	0.0001477	cell-cell junction	cellular_component
GO:0006357	0.0068187	0.00019421	regulation of transcription from RNA polymerase II promoter	biological_process
GO:0006583	0.044308	0.022925	melanin biosynthetic process from tyrosine	biological_process
GO:0006629	0.0017817	2.7834e-07	lipid metabolic process	biological_process
GO:0006633	0.017151	0.00013602	fatty acid biosynthetic process	biological_process
GO:0006886	0.0022669	0.062815	intracellular protein transport	biological_process
GO:0006915	3.3485e-05	4.1551e-06	apoptosis	biological_process
GO:0006917	0.049852	0.023913	induction of apoptosis	biological_process
GO:0006928	0.018385	5.5735e-06	cell motion	biological_process
GO:0006996	0.00043199	1.256e-05	organelle organization	biological_process
GO:0006997	0.013729	0.098938	nucleus organization	biological_process
GO:0007010	0.0029771	1.6689e-06	cytoskeleton organization	biological_process
GO:0007049	0.015498	0.0026147	cell cycle	biological_process
GO:0007154	0.030739	0.00018275	cell communication	biological_process
GO:0007155	0.0012167	9.1889e-10	cell adhesion	biological_process
GO:0007165	0.017474	0.00012793	signal transduction	biological_process
GO:0007167	0.0032023	2.3212e-05	enzyme linked receptor protein signaling pathway	biological_process
GO:0007242	0.017151	0.050892	intracellular signaling cascade	biological_process
GO:0007264	0.00079839	0.0066498	GTPase mediated signal transduction	biological_process
GO:0007265	0.0040106	0.06814	Ras protein signal transduction	biological_process
GO:0007266	0.0098047	0.06814	Rho protein signal transduction	biological_process
GO:0007275	2.3813e-05	3.4457e-14	multicellular organismal development	biological_process
GO:0007398	2.1202e-07	1.7237e-10	ectoderm development	biological_process

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GO ID	robust pval.	normal pval.	GO Name	process type
GO:0007517	0.044584	0.012147	muscle organ development	`biological_process`
GO:0008092	0.00023672	5.3518e-10	cytoskeletal protein binding	`molecular_function`
GO:0008134	0.045268	0.033169	transcription factor binding	`molecular_function`
GO:0008152	0.0095231	0.044551	metabolic process	`biological_process`
GO:0008201	0.0020008	0.02615	heparin binding	`molecular_function`
GO:0008219	2.3813e-05	6.2358e-06	cell death	`biological_process`
GO:0008283	0.00062726	2.8978e-07	cell proliferation	`biological_process`
GO:0008360	0.015687	0.0073298	regulation of cell shape	`biological_process`
GO:0008544	2.0941e-08	1.9795e-11	epidermis development	`biological_process`
GO:0008565	0.024728	0.041134	protein transporter activity	`molecular_function`
GO:0008610	0.0065878	0.00023875	lipid biosynthetic process	`biological_process`
GO:0008656	0.020959	0.069964	caspase activator activity	`molecular_function`
GO:0009653	2.3975e-05	1.347e-10	anatomical structure morphogenesis	`biological_process`
GO:0009887	0.00016587	1.9682e-09	organ morphogenesis	`biological_process`
GO:0009888	1.6983e-07	3.9027e-10	tissue development	`biological_process`
GO:0009892	0.028478	0.015972	negative regulation of metabolic process	`biological_process`
GO:0009966	0.0022101	0.038301	regulation of signal transduction	`biological_process`
GO:0009987	6.8382e-14	1.043e-14	cellular process	`biological_process`
GO:0010558	0.021834	0.012035	negative regulation of macromolecule biosynthetic process	`biological_process`
GO:0010605	0.0099447	0.0073177	negative regulation of macromolecule metabolic process	`biological_process`
GO:0010628	0.015329	0.0073177	positive regulation of gene expression	`biological_process`
GO:0010629	0.012835	0.0085589	negative regulation of gene expression	`biological_process`
GO:0010646	0.0036495	0.028544	regulation of cell communication	`biological_process`
GO:0010941	0.0055189	0.00020796	regulation of cell death	`biological_process`
GO:0012501	3.1644e-05	4.2586e-06	programmed cell death	`biological_process`

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GO ID	robust pval.	normal pval.	GO Name	process type
GO:0012505	0.00027034	0.00018393	endomembrane system	`cellular_component`
GO:0014896	0.024432	0.0037176	muscle hypertrophy	`biological_process`
GO:0015629	0.030739	0.0031793	actin cytoskeleton	`cellular_component`
GO:0016020	5.1704e-09	1.621e-15	membrane	`cellular_component`
GO:0016023	0.024432	0.0032375	cytoplasmic membrane-bounded vesicle	`cellular_component`
GO:0016043	0.0001645	0.00019981	cellular component organization	`biological_process`
GO:0016265	2.3813e-05	7.0843e-06	death	`biological_process`
GO:0016323	0.017474	1.8953e-05	basolateral plasma membrane	`cellular_component`
GO:0016477	0.010945	5.2407e-05	cell migration	`biological_process`
GO:0016481	0.016047	0.0071099	negative regulation of transcription	`biological_process`
GO:0016504	0.012034	0.024018	peptidase activator activity	`molecular_function`
GO:0016564	0.0036495	0.00020796	transcription repressor activity	`molecular_function`
GO:0016614	0.035228	0.0018884	oxidoreductase activity, acting on CH-OH group of donors	`molecular_function`
GO:0016616	0.029322	0.00092026	oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor	`molecular_function`
GO:0016684	0.046389	0.034847	oxidoreductase activity, acting on peroxide as acceptor	`molecular_function`
GO:0018149	0.033894	0.0034832	peptide cross-linking	`biological_process`
GO:0019199	0.032359	0.0075747	transmembrane receptor protein kinase activity	`molecular_function`
GO:0019838	0.016047	4.402e-05	growth factor binding	`molecular_function`
GO:0030029	0.0057118	2.5986e-06	actin filament-based process	`biological_process`
GO:0030036	0.0037466	7.7719e-07	actin cytoskeleton organization	`biological_process`
GO:0030154	0.0011891	2.885e-09	cell differentiation	`biological_process`
GO:0030216	1.1363e-05	2.6023e-08	keratinocyte differentiation	`biological_process`
GO:0030234	0.0012341	1.3974e-05	enzyme regulator activity	`molecular_function`
GO:0030246	0.0011978	0.00016573	carbohydrate binding	`molecular_function`
GO:0030247	0.0033382	0.00087921	polysaccharide binding	`molecular_function`

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GO ID	robust pval.	normal pval.	GO Name	process type
GO:0030262	0.018607	0.017517	apoptotic nuclear changes	`biological_process`
GO:0031012	4.9892e-06	3.2982e-12	extracellular matrix	`cellular_component`
GO:0031090	0.0011978	0.0076113	organelle membrane	`cellular_component`
GO:0031324	0.046591	0.022589	negative regulation of cellular metabolic process	`biological_process`
GO:0031325	0.032499	0.0012484	positive regulation of cellular metabolic process	`biological_process`
GO:0031410	0.015687	0.001102	cytoplasmic vesicle	`cellular_component`
GO:0031424	0.018767	1.5673e-05	keratinization	`biological_process`
GO:0031982	0.0050707	0.00019421	vesicle	`cellular_component`
GO:0031988	0.016028	0.0015381	membrane-bounded vesicle	`cellular_component`
GO:0032432	0.012909	0.0020237	actin filament bundle	`cellular_component`
GO:0032787	0.033522	1.9609e-05	monocarboxylic acid metabolic process	`biological_process`
GO:0034613	0.00095828	0.033138	cellular protein localization	`biological_process`
GO:0042127	0.044438	3.5019e-05	regulation of cell proliferation	`biological_process`
GO:0042175	0.049994	0.0074351	nuclear envelope-endoplasmic reticulum network	`cellular_component`
GO:0042221	0.024974	5.1668e-06	response to chemical stimulus	`biological_process`
GO:0042246	0.020959	0.069964	tissue regeneration	`biological_process`
GO:0042470	0.0012167	0.00031354	melanosome	`cellular_component`
GO:0042598	0.029552	0.00040633	vesicular fraction	`cellular_component`
GO:0042641	0.0037425	0.00070586	actomyosin	`cellular_component`
GO:0042692	0.02393	0.0011767	muscle cell differentiation	`biological_process`
GO:0042803	0.034283	0.090127	protein homodimerization activity	`molecular_function`
GO:0042981	0.0058774	0.0001689	regulation of apoptosis	`biological_process`
GO:0043066	0.049852	0.038655	negative regulation of apoptosis	`biological_process`
GO:0043067	0.0060006	0.00019421	regulation of programmed cell death	`biological_process`
GO:0043069	0.045453	0.045748	negative regulation of programmed cell death	`biological_process`

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GO ID	robust pval.	normal pval.	GO Name	process type
GO:0043227	2.6397e-08	0.0055873	membrane-bounded organelle	`cellular_component`
GO:0043229	1.1535e-10	5.9763e-05	intracellular organelle	`cellular_component`
GO:0043231	2.9439e-08	0.005301	intracellular membrane-bounded organelle	`cellular_component`
GO:0043473	0.002726	0.001473	pigmentation	`biological_process`
GO:0044255	0.017151	7.3897e-05	cellular lipid metabolic process	`biological_process`
GO:0044420	0.0012167	1.3951e-05	extracellular matrix part	`cellular_component`
GO:0044421	0.00064603	5.6187e-12	extracellular region part	`cellular_component`
GO:0044424	2.3943e-25	1.0078e-15	intracellular part	`cellular_component`
GO:0044425	0.02393	2.7249e-05	membrane part	`cellular_component`
GO:0044430	0.0033119	0.0002563	cytoskeletal part	`cellular_component`
GO:0044432	0.0068187	0.00093236	endoplasmic reticulum part	`cellular_component`
GO:0044444	6.5303e-07	0.00019421	cytoplasmic part	`cellular_component`
GO:0044464	4.6945e-28	5.9428e-25	cell part	`cellular_component`
GO:0045892	0.017314	0.017	negative regulation of transcription, DNA-dependent	`biological_process`
GO:0045893	0.0036389	0.0019197	positive regulation of transcription, DNA-dependent	`biological_process`
GO:0045941	0.0071374	0.0032375	positive regulation of transcription	`biological_process`
GO:0046456	0.047514	0.0012223	icosanoid biosynthetic process	`biological_process`
GO:0046907	0.024728	0.044241	intracellular transport	`biological_process`
GO:0046983	0.00011396	0.0032902	protein dimerization activity	`molecular_function`
GO:0048066	0.0029771	0.0001438	pigmentation during development	`biological_process`
GO:0048513	8.6678e-08	2.5182e-14	organ development	`biological_process`
GO:0048522	1.0093e-05	1.3077e-07	positive regulation of cellular process	`biological_process`
GO:0048523	0.0078355	7.2318e-05	negative regulation of cellular process	`biological_process`
GO:0048731	2.1202e-07	1.621e-15	system development	`biological_process`
GO:0048770	0.0012167	0.00031354	pigment granule	`cellular_component`

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GO ID	robust pval.	normal pval.	GO Name	process type
GO:0048856	2.1351e-08	6.0781e-17	anatomical structure development	`biological_process`
GO:0048869	0.00016939	1.7237e-10	cellular developmental process	`biological_process`
GO:0048870	0.019228	0.0001477	cell motility	`biological_process`
GO:0050793	0.0005152	8.7014e-06	regulation of developmental process	`biological_process`
GO:0050794	0.0047627	3.908e-05	regulation of cellular process	`biological_process`
GO:0051094	0.044308	0.0030064	positive regulation of developmental process	`biological_process`
GO:0051253	0.025424	0.02615	negative regulation of RNA metabolic process	`biological_process`
GO:0051254	0.0055011	0.0026629	positive regulation of RNA metabolic process	`biological_process`
GO:0051301	0.030739	0.017246	cell division	`biological_process`
GO:0060548	0.045453	0.045748	negative regulation of cell death	`biological_process`
GO:0060589	0.015727	0.075773	nucleoside-triphosphatase regulator activity	`molecular_function`
Differences:				
GO:0001783	0.044308		B cell apoptosis	`biological_process`
GO:0005085	0.0045106		guanyl-nucleotide exchange factor activity	`molecular_function`
GO:0005088	0.012378		Ras guanyl-nucleotide exchange factor activity	`molecular_function`
GO:0005089	0.018371		Rho guanyl-nucleotide exchange factor activity	`molecular_function`
GO:0005581	0.014943		collagen	`cellular_component`
GO:0005583	0.0099447		fibrillar collagen	`cellular_component`
GO:0005634	0.032359		nucleus	`cellular_component`
GO:0005874	0.030739		microtubule	`cellular_component`
GO:0008104	0.016028		protein localization	`biological_process`
GO:0009249	0.016028		protein lipoylation	`biological_process`
GO:0015031	0.0092493		protein transport	`biological_process`
GO:0016505	0.020673		apoptotic protease activator activity	`molecular_function`
GO:0022604	0.030739		regulation of cell morphogenesis	`biological_process`
GO:0030140	0.0063582		trans-Golgi network transport vesicle	`cellular_component`

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GO ID	robust pval.	normal pval.	GO Name	process type
GO:0030695	0.01751		GTPase regulator activity	`molecular_function`
GO:0031970	0.041629		organelle envelope lumen	`cellular_component`
GO:0035023	0.018607		regulation of Rho protein signal transduction	`biological_process`
GO:0043588	0.014943		skin development	`biological_process`
GO:0044419	0.018607		interspecies interaction between organisms	`biological_process`
GO:0044446	0.0028032		intracellular organelle part	`cellular_component`
GO:0045184	0.010945		establishment of protein localization	`biological_process`
GO:0046578	0.016047		regulation of Ras protein signal transduction	`biological_process`
GO:0050650	0.029766		chondroitin sulfate proteoglycan biosynthetic process	`biological_process`
GO:0050654	0.029766		chondroitin sulfate proteoglycan metabolic process	`biological_process`
GO:0051056	0.0027566		regulation of GTPase mediated signal transduction	`biological_process`
GO:0000085		0.038368	G2 phase of mitotic cell cycle	`biological_process`
GO:0000122		0.01517	negative regulation of transcription from RNA polymerase II promoter	`biological_process`
GO:0000267		0.055741	cell fraction	`cellular_component`
GO:0000307		0.042764	cyclin-dependent protein kinase holoenzyme complex	`cellular_component`
GO:0000902		0.048162	cell morphogenesis	`biological_process`
GO:0000910		0.0074351	cytokinesis	`biological_process`
GO:0001516		0.042764	prostaglandin biosynthetic process	`biological_process`
GO:0001525		0.011613	angiogenesis	`biological_process`
GO:0001527		0.011511	microfibril	`cellular_component`
GO:0001558		0.015884	regulation of cell growth	`biological_process`
GO:0001666		0.080718	response to hypoxia	`biological_process`
GO:0001709		0.098938	cell fate determination	`biological_process`
GO:0001818		0.08995	negative regulation of cytokine production	`biological_process`
GO:0001934		0.033138	positive regulation of protein amino acid phosphorylation	`biological_process`

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GO ID	robust pval.	normal pval.	GO Name	process type
GO:0001959		0.031988	regulation of cytokine-mediated signaling pathway	`biological_process`
GO:0002250		0.080477	adaptive immune response	`biological_process`
GO:0002327		0.049808	immature B cell differentiation	`biological_process`
GO:0002329		0.049808	pre-B cell differentiation	`biological_process`
GO:0002376		0.06814	immune system process	`biological_process`
GO:0002424		0.081989	T cell mediated immune response to tumor cell	`biological_process`
GO:0002504		0.014714	antigen processing and presentation of peptide or polysaccharide antigen via MHC class II	`biological_process`
GO:0002682		0.035941	regulation of immune system process	`biological_process`
GO:0002840		0.081989	regulation of T cell mediated immune response to tumor cell	`biological_process`
GO:0002842		0.081989	positive regulation of T cell mediated immune response to tumor cell	`biological_process`
GO:0002902		0.044551	regulation of B cell apoptosis	`biological_process`
GO:0002904		0.049808	positive regulation of B cell apoptosis	`biological_process`
GO:0003714		0.056028	transcription corepressor activity	`molecular_function`
GO:0004364		0.0078478	glutathione transferase activity	`molecular_function`
GO:0004664		0.049808	prephenate dehydratase activity	`molecular_function`
GO:0004714		0.049808	transmembrane receptor protein tyrosine kinase activity	`molecular_function`
GO:0004857		0.00021548	enzyme inhibitor activity	`molecular_function`
GO:0004864		0.017147	phosphoprotein phosphatase inhibitor activity	`molecular_function`
GO:0004866		0.00054248	endopeptidase inhibitor activity	`molecular_function`
GO:0005001		0.090377	transmembrane receptor protein tyrosine phosphatase activity	`molecular_function`
GO:0005104		0.010598	fibroblast growth factor receptor binding	`molecular_function`
GO:0005152		0.022925	interleukin-1 receptor antagonist activity	`molecular_function`
GO:0005200		0.044551	structural constituent of cytoskeleton	`molecular_function`
GO:0005509		0.023	calcium ion binding	`molecular_function`
GO:0005520		0.009712	insulin-like growth factor binding	`molecular_function`

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GO ID	robust pval.	normal pval.	GO Name	process type
GO:0005576		1.1367e-09	extracellular region	`cellular_component`
GO:0005604		0.00031753	basement membrane	`cellular_component`
GO:0005615		4.01e-05	extracellular space	`cellular_component`
GO:0005819		0.0083005	spindle	`cellular_component`
GO:0005876		0.022428	spindle microtubule	`cellular_component`
GO:0005882		0.00016491	intermediate filament	`cellular_component`
GO:0005884		0.052383	actin filament	`cellular_component`
GO:0005896		0.081989	interleukin-6 receptor complex	`cellular_component`
GO:0005901		0.049808	caveola	`cellular_component`
GO:0005912		0.0053658	adherens junction	`cellular_component`
GO:0005924		0.00059803	cell-substrate adherens junction	`cellular_component`
GO:0005925		0.00070931	focal adhesion	`cellular_component`
GO:0005938		0.038301	cell cortex	`cellular_component`
GO:0006082		0.0013467	organic acid metabolic process	`biological_process`
GO:0006366		0.0042863	transcription from RNA polymerase II promoter	`biological_process`
GO:0006509		0.0093687	membrane protein ectodomain proteolysis	`biological_process`
GO:0006516		0.017655	glycoprotein catabolic process	`biological_process`
GO:0006631		0.00022512	fatty acid metabolic process	`biological_process`
GO:0006690		0.0020237	icosanoid metabolic process	`biological_process`
GO:0006691		0.029222	leukotriene metabolic process	`biological_process`
GO:0006692		0.010114	prostanoid metabolic process	`biological_process`
GO:0006693		0.010114	prostaglandin metabolic process	`biological_process`
GO:0006726		0.049808	eye pigment biosynthetic process	`biological_process`
GO:0006892		0.055098	post-Golgi vesicle-mediated transport	`biological_process`
GO:0006903		0.055098	vesicle targeting	`biological_process`

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GO ID	robust pval.	normal pval.	GO Name	process type
GO:0006916		0.012035	anti-apoptosis	`biological_process`
GO:0006950		0.0071908	response to stress	`biological_process`
GO:0006954		0.052183	inflammatory response	`biological_process`
GO:0006979		0.068895	response to oxidative stress	`biological_process`
GO:0006986		0.049808	response to unfolded protein	`biological_process`
GO:0007015		0.0083882	actin filament organization	`biological_process`
GO:0007051		0.049808	spindle organization	`biological_process`
GO:0007166		0.0090853	cell surface receptor linked signal transduction	`biological_process`
GO:0007169		0.0083005	transmembrane receptor protein tyrosine kinase signaling pathway	`biological_process`
GO:0007178		0.030272	transmembrane receptor protein serine/threonine kinase signaling pathway	`biological_process`
GO:0007179		0.084588	transforming growth factor beta receptor signaling pathway	`biological_process`
GO:0007219		0.022925	Notch signaling pathway	`biological_process`
GO:0007220		0.081989	Notch receptor processing	`biological_process`
GO:0007399		0.0036584	nervous system development	`biological_process`
GO:0007507		0.080718	heart development	`biological_process`
GO:0008013		0.043987	beta-catenin binding	`molecular_function`
GO:0008045		0.023991	motor axon guidance	`biological_process`
GO:0008047		0.08995	enzyme activator activity	`molecular_function`
GO:0008131		0.081989	amine oxidase activity	`molecular_function`
GO:0008139		0.047448	nuclear localization sequence binding	`molecular_function`
GO:0008195		0.042764	phosphatidate phosphatase activity	`molecular_function`
GO:0008233		0.08995	peptidase activity	`molecular_function`
GO:0008236		0.032354	serine-type peptidase activity	`molecular_function`
GO:0008285		0.0028174	negative regulation of cell proliferation	`biological_process`
GO:0008289		0.062918	lipid binding	`molecular_function`

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GO ID	robust pval.	normal pval.	GO Name	process type
GO:0008361		0.0013052	regulation of cell size	`biological_process`
GO:0008624		0.051283	induction of apoptosis by extracellular signals	`biological_process`
GO:0008637		0.033138	apoptotic mitochondrial changes	`biological_process`
GO:0009056		0.046818	catabolic process	`biological_process`
GO:0009094		0.049808	L-phenylalanine biosynthetic process	`biological_process`
GO:0009605		5.9763e-05	response to external stimulus	`biological_process`
GO:0009611		0.00019421	response to wounding	`biological_process`
GO:0009719		0.08995	response to endogenous stimulus	`biological_process`
GO:0009725		0.027529	response to hormone stimulus	`biological_process`
GO:0009790		0.062918	embryonic development	`biological_process`
GO:0009792		0.045533	embryonic development ending in birth or egg hatching	`biological_process`
GO:0009880		0.041134	embryonic pattern specification	`biological_process`
GO:0009890		0.044551	negative regulation of biosynthetic process	`biological_process`
GO:0009891		0.021072	positive regulation of biosynthetic process	`biological_process`
GO:0009893		0.0075203	positive regulation of metabolic process	`biological_process`
GO:0009913		0.0014784	epidermal cell differentiation	`biological_process`
GO:0009986		0.0055873	cell surface	`cellular_component`
GO:0010466		0.029913	negative regulation of peptidase activity	`biological_process`
GO:0010557		0.061385	positive regulation of macromolecule biosynthetic process	`biological_process`
GO:0010562		0.0098522	positive regulation of phosphorus metabolic process	`biological_process`
GO:0010604		0.01249	positive regulation of macromolecule metabolic process	`biological_process`
GO:0010613		0.081989	positive regulation of cardiac muscle hypertrophy	`biological_process`
GO:0010942		0.034666	positive regulation of cell death	`biological_process`
GO:0012502		0.022859	induction of programmed cell death	`biological_process`
GO:0014706		0.048481	striated muscle tissue development	`biological_process`

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GO ID	robust pval.	normal pval.	GO Name	process type
GO:0014742		0.081989	positive regulation of muscle hypertrophy	`biological_process`
GO:0014866		0.081989	skeletal myofibril assembly	`biological_process`
GO:0015166		0.081989	polyol transmembrane transporter activity	`molecular_function`
GO:0015630		0.08986	microtubule cytoskeleton	`cellular_component`
GO:0015665		0.081989	alcohol transmembrane transporter activity	`molecular_function`
GO:0016021		0.0075324	integral to membrane	`cellular_component`
GO:0016049		0.0020237	cell growth	`biological_process`
GO:0016053		0.0020237	organic acid biosynthetic process	`biological_process`
GO:0016055		0.0031177	Wnt receptor signaling pathway	`biological_process`
GO:0016209		0.029303	antioxidant activity	`molecular_function`
GO:0016327		0.04948	apicolateral plasma membrane	`cellular_component`
GO:0016337		0.037898	cell-cell adhesion	`biological_process`
GO:0016485		0.042639	protein processing	`biological_process`
GO:0016491		0.0010514	oxidoreductase activity	`molecular_function`
GO:0016563		0.052383	transcription activator activity	`molecular_function`
GO:0016566		0.038655	specific transcriptional repressor activity	`molecular_function`
GO:0016600		0.044551	flotillin complex	`cellular_component`
GO:0016615		0.062918	malate dehydrogenase activity	`molecular_function`
GO:0016620		0.052183	oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor	`molecular_function`
GO:0016765		0.098938	transferase activity, transferring alkyl or aryl (other than methyl) groups	`molecular_function`
GO:0016787		0.0018288	hydrolase activity	`molecular_function`
GO:0016791		0.086799	phosphatase activity	`molecular_function`
GO:0017171		0.042017	serine hydrolase activity	`molecular_function`
GO:0019198		0.090377	transmembrane receptor protein phosphatase activity	`molecular_function`
GO:0019212		0.02531	phosphatase inhibitor activity	`molecular_function`

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GO ID	robust pval.	normal pval.	GO Name	process type
GO:0019221		0.013834	cytokine-mediated signaling pathway	`biological_process`
GO:0019319		0.049808	hexose biosynthetic process	`biological_process`
GO:0019369		0.049808	arachidonic acid metabolic process	`biological_process`
GO:0019370		0.017655	leukotriene biosynthetic process	`biological_process`
GO:0019752		0.0010636	carboxylic acid metabolic process	`biological_process`
GO:0019888		0.081989	protein phosphatase regulator activity	`molecular_function`
GO:0022008		0.0083005	neurogenesis	`biological_process`
GO:0022402		0.025999	cell cycle process	`biological_process`
GO:0022403		0.01249	cell cycle phase	`biological_process`
GO:0022409		0.028544	positive regulation of cell-cell adhesion	`biological_process`
GO:0030016		0.02256	myofibril	`cellular_component`
GO:0030017		0.04948	sarcomere	`cellular_component`
GO:0030018		0.066652	Z disc	`cellular_component`
GO:0030054		0.042298	cell junction	`cellular_component`
GO:0030055		0.00089134	cell-substrate junction	`cellular_component`
GO:0030057		0.023991	desmosome	`cellular_component`
GO:0030100		0.030621	regulation of endocytosis	`biological_process`
GO:0030323		0.072841	respiratory tube development	`biological_process`
GO:0030353		0.022925	fibroblast growth factor receptor antagonist activity	`molecular_function`
GO:0030414		0.00044684	peptidase inhibitor activity	`molecular_function`
GO:0030435		0.049808	sporulation resulting in formation of a cellular spore	`biological_process`
GO:0030509		0.044551	BMP signaling pathway	`biological_process`
GO:0030510		0.073724	regulation of BMP signaling pathway	`biological_process`
GO:0030514		0.062918	negative regulation of BMP signaling pathway	`biological_process`
GO:0030528		0.04948	transcription regulator activity	`molecular_function`

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GO ID	robust pval.	normal pval.	GO Name	process type
GO:0030595		0.018573	leukocyte chemotaxis	`biological_process`
GO:0031032		0.042017	actomyosin structure organization	`biological_process`
GO:0031105		0.0086449	septin complex	`cellular_component`
GO:0031175		0.0075203	neuron projection development	`biological_process`
GO:0031224		0.0066363	intrinsic to membrane	`cellular_component`
GO:0031327		0.046117	negative regulation of cellular biosynthetic process	`biological_process`
GO:0031328		0.0076113	positive regulation of cellular biosynthetic process	`biological_process`
GO:0031401		0.090701	positive regulation of protein modification process	`biological_process`
GO:0031528		0.049808	microvillus membrane	`cellular_component`
GO:0031674		0.029303	I band	`cellular_component`
GO:0031941		0.028544	filamentous actin	`cellular_component`
GO:0032103		0.054301	positive regulation of response to external stimulus	`biological_process`
GO:0032156		0.0086449	septin cytoskeleton	`cellular_component`
GO:0032395		0.065361	MHC class II receptor activity	`molecular_function`
GO:0032465		0.062918	regulation of cytokinesis	`biological_process`
GO:0032526		0.052183	response to retinoic acid	`biological_process`
GO:0032594		0.049808	protein transport within lipid bilayer	`biological_process`
GO:0032595		0.049808	B cell receptor transport within lipid bilayer	`biological_process`
GO:0032596		0.049808	protein transport into membrane raft	`biological_process`
GO:0032597		0.049808	B cell receptor transport into membrane raft	`biological_process`
GO:0032599		0.049808	protein transport out of membrane raft	`biological_process`
GO:0032600		0.049808	chemokine receptor transport out of membrane raft	`biological_process`
GO:0032907		0.049808	transforming growth factor-beta3 production	`biological_process`
GO:0032910		0.049808	regulation of transforming growth factor-beta3 production	`biological_process`
GO:0032913		0.049808	negative regulation of transforming growth factor-beta3 production	`biological_process`

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GO ID	robust pval.	normal pval.	GO Name	process type
GO:0032989		0.025109	cellular component morphogenesis	`biological_process`
GO:0033162		0.031988	melanosome membrane	`cellular_component`
GO:0033189		0.075565	response to vitamin A	`biological_process`
GO:0033606		0.049808	chemokine receptor transport within lipid bilayer	`biological_process`
GO:0033619		0.0093687	membrane protein proteolysis	`biological_process`
GO:0033622		0.049808	integrin activation	`biological_process`
GO:0033623		0.049808	regulation of integrin activation	`biological_process`
GO:0033625		0.049808	positive regulation of integrin activation	`biological_process`
GO:0033632		0.053319	regulation of cell-cell adhesion mediated by integrin	`biological_process`
GO:0033634		0.049808	positive regulation of cell-cell adhesion mediated by integrin	`biological_process`
GO:0034102		0.049808	erythrocyte clearance	`biological_process`
GO:0034106		0.049808	regulation of erythrocyte clearance	`biological_process`
GO:0034107		0.049808	negative regulation of erythrocyte clearance	`biological_process`
GO:0034110		0.049808	regulation of homotypic cell-cell adhesion	`biological_process`
GO:0034111		0.049808	negative regulation of homotypic cell-cell adhesion	`biological_process`
GO:0034117		0.049808	erythrocyte aggregation	`biological_process`
GO:0034118		0.049808	regulation of erythrocyte aggregation	`biological_process`
GO:0034119		0.049808	negative regulation of erythrocyte aggregation	`biological_process`
GO:0034637		0.044241	cellular carbohydrate biosynthetic process	`biological_process`
GO:0035295		0.013309	tube development	`biological_process`
GO:0040007		5.0646e-05	growth	`biological_process`
GO:0040008		0.063146	regulation of growth	`biological_process`
GO:0040011		0.0019324	locomotion	`biological_process`
GO:0042060		0.015591	wound healing	`biological_process`
GO:0042103		0.049808	positive regulation of T cell homeostatic proliferation	`biological_process`

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GO ID	robust pval.	normal pval.	GO Name	process type
GO:0042327		0.022403	positive regulation of phosphorylation	`biological_process`
GO:0042438		0.038368	melanin biosynthetic process	`biological_process`
GO:0042441		0.049808	eye pigment metabolic process	`biological_process`
GO:0042445		0.0053453	hormone metabolic process	`biological_process`
GO:0042578		0.028544	phosphoric ester hydrolase activity	`molecular_function`
GO:0042802		0.0036389	identical protein binding	`molecular_function`
GO:0042987		0.016162	amyloid precursor protein catabolic process	`biological_process`
GO:0043009		0.038301	chordate embryonic development	`biological_process`
GO:0043065		0.028976	positive regulation of apoptosis	`biological_process`
GO:0043068		0.03226	positive regulation of programmed cell death	`biological_process`
GO:0043121		0.015998	neurotrophin binding	`molecular_function`
GO:0043154		0.047448	negative regulation of caspase activity	`biological_process`
GO:0043232		0.03455	intracellular non-membrane-bounded organelle	`cellular_component`
GO:0043292		0.033138	contractile fiber	`cellular_component`
GO:0043296		0.049808	apical junction complex	`cellular_component`
GO:0043449		0.043987	cellular alkene metabolic process	`biological_process`
GO:0043450		0.017655	alkene biosynthetic process	`biological_process`
GO:0043616		0.042764	keratinocyte proliferation	`biological_process`
GO:0044449		0.084756	contractile fiber part	`cellular_component`
GO:0044459		0.062956	plasma membrane part	`cellular_component`
GO:0045009		0.031988	chitosome	`cellular_component`
GO:0045111		0.00031086	intermediate filament cytoskeleton	`cellular_component`
GO:0045445		0.0090853	myoblast differentiation	`biological_process`
GO:0045595		0.017655	regulation of cell differentiation	`biological_process`
GO:0045597		0.022611	positive regulation of cell differentiation	`biological_process`

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GO ID	robust pval.	normal pval.	GO Name	process type
GO:0045639		0.075773	positive regulation of myeloid cell differentiation	`biological_process`
GO:0045667		0.023	regulation of osteoblast differentiation	`biological_process`
GO:0045669		0.075565	positive regulation of osteoblast differentiation	`biological_process`
GO:0045785		0.033593	positive regulation of cell adhesion	`biological_process`
GO:0045934		0.077145	negative regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	`biological_process`
GO:0045935		0.023333	positive regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	`biological_process`
GO:0045937		0.0098522	positive regulation of phosphate metabolic process	`biological_process`
GO:0045944		0.031901	positive regulation of transcription from RNA polymerase II promoter	`biological_process`
GO:0046014		0.049808	negative regulation of T cell homeostatic proliferation	`biological_process`
GO:0046165		0.04948	alcohol biosynthetic process	`biological_process`
GO:0046364		0.033341	monosaccharide biosynthetic process	`biological_process`
GO:0046394		0.0020237	carboxylic acid biosynthetic process	`biological_process`
GO:0046457		0.042764	prostanoid biosynthetic process	`biological_process`
GO:0048069		0.081989	eye pigmentation	`biological_process`
GO:0048468		0.00035904	cell development	`biological_process`
GO:0048514		0.013822	blood vessel morphogenesis	`biological_process`
GO:0048589		0.05276	developmental growth	`biological_process`
GO:0048646		0.0023009	anatomical structure formation involved in morphogenesis	`biological_process`
GO:0048699		0.060094	generation of neurons	`biological_process`
GO:0048729		0.004153	tissue morphogenesis	`biological_process`
GO:0048730		0.046111	epidermis morphogenesis	`biological_process`
GO:0050661		0.081989	NADP or NADPH binding	`molecular_function`
GO:0050673		0.077145	epithelial cell proliferation	`biological_process`
GO:0050679		0.0093687	positive regulation of epithelial cell proliferation	`biological_process`
GO:0050729		0.097725	positive regulation of inflammatory response	`biological_process`

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GO ID	robust pval.	normal pval.	GO Name	process type
GO:0050896		0.035699	response to stimulus	`biological_process`
GO:0050900		0.0015094	leukocyte migration	`biological_process`
GO:0051015		0.012385	actin filament binding	`molecular_function`
GO:0051043		0.073752	regulation of membrane protein ectodomain proteolysis	`biological_process`
GO:0051093		0.055098	negative regulation of developmental process	`biological_process`
GO:0051128		0.001559	regulation of cellular component organization	`biological_process`
GO:0051287		0.041134	NAD or NADH binding	`molecular_function`
GO:0051302		0.042764	regulation of cell division	`biological_process`
GO:0051319		0.038368	G2 phase	`biological_process`
GO:0051325		0.097208	interphase	`biological_process`
GO:0051329		0.099609	interphase of mitotic cell cycle	`biological_process`
GO:0051346		0.059695	negative regulation of hydrolase activity	`biological_process`
GO:0051604		0.019244	protein maturation	`biological_process`
GO:0051641		0.043987	cellular localization	`biological_process`
GO:0051648		0.049808	vesicle localization	`biological_process`
GO:0051649		0.061484	establishment of localization in cell	`biological_process`
GO:0051650		0.049808	establishment of vesicle localization	`biological_process`
GO:0051789		0.067857	response to protein stimulus	`biological_process`
GO:0055008		0.064644	cardiac muscle tissue morphogenesis	`biological_process`
GO:0055114		0.0011851	oxidation reduction	`biological_process`
GO:0060170		0.011511	cilium membrane	`cellular_component`
GO:0060326		0.018573	cell chemotaxis	`biological_process`
GO:0060415		0.064644	muscle tissue morphogenesis	`biological_process`
GO:0060537		0.049808	muscle tissue development	`biological_process`
GO:0070161		0.00044684	anchoring junction	`cellular_component`

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GO ID	robust pval.	normal pval.	GO Name	process type
GO:0070228		0.044551	regulation of lymphocyte apoptosis	`biological_process`
GO:0070230		0.049808	positive regulation of lymphocyte apoptosis	`biological_process`
Mouse diet Intersect:				
GO:0000267	1.544e-05	0.00011191	cell fraction	`cellular_component`
GO:0000271	0.0052759	0.018715	polysaccharide biosynthetic process	`biological_process`
GO:0001523	0.0019709	0.006675	retinoid metabolic process	`biological_process`
GO:0001775	0.018754	0.0016109	cell activation	`biological_process`
GO:0001823	0.018754	0.035681	mesonephros development	`biological_process`
GO:0003824	2.8037e-05	5.5659e-05	catalytic activity	`molecular_function`
GO:0003912	0.013324	0.027248	DNA nucleotidylexotransferase activity	`molecular_function`
GO:0004112	0.01227	0.03695	cyclic-nucleotide phosphodiesterase activity	`molecular_function`
GO:0004114	0.010227	0.034468	3',5'-cyclic-nucleotide phosphodiesterase activity	`molecular_function`
GO:0004115	0.012452	0.032387	3',5'-cyclic-AMP phosphodiesterase activity	`molecular_function`
GO:0004163	0.0032521	0.006675	diphosphomevalonate decarboxylase activity	`molecular_function`
GO:0004340	0.0032521	0.006675	glucokinase activity	`molecular_function`
GO:0004497	8.0857e-08	8.9886e-09	monooxygenase activity	`molecular_function`
GO:0005488	0.026686	0.00017416	binding	`molecular_function`
GO:0005506	0.0019828	0.013212	iron ion binding	`molecular_function`
GO:0005536	0.0075962	0.016117	glucose binding	`molecular_function`
GO:0005622	0.019664	0.0054674	intracellular	`cellular_component`
GO:0005623	0.0026032	0.00021339	cell	`cellular_component`
GO:0005624	4.3087e-05	0.00021339	membrane fraction	`cellular_component`
GO:0005626	8.1139e-05	0.00044226	insoluble fraction	`cellular_component`
GO:0005737	4.7655e-05	7.2718e-05	cytoplasm	`cellular_component`
GO:0005783	0.00012891	6.7444e-05	endoplasmic reticulum	`cellular_component`

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GO ID	robust pval.	normal pval.	GO Name	process type
GO:0005789	0.0001628	7.2718e-05	endoplasmic reticulum membrane	`cellular_component`
GO:0005792	1.8583e-05	3.2254e-05	microsome	`cellular_component`
GO:0005975	0.010222	0.032387	carbohydrate metabolic process	`biological_process`
GO:0005977	0.014669	0.045614	glycogen metabolic process	`biological_process`
GO:0005978	0.00064562	0.0022807	glycogen biosynthetic process	`biological_process`
GO:0005979	0.018754	0.035681	regulation of glycogen biosynthetic process	`biological_process`
GO:0005996	0.0062129	0.045614	monosaccharide metabolic process	`biological_process`
GO:0006066	2.7044e-06	2.147e-05	cellular alcohol metabolic process	`biological_process`
GO:0006073	0.014669	0.045614	cellular glucan metabolic process	`biological_process`
GO:0006112	0.021904	0.073408	energy reserve metabolic process	`biological_process`
GO:0006629	8.0857e-08	1.3218e-07	lipid metabolic process	`biological_process`
GO:0006694	3.1658e-05	7.2718e-05	steroid biosynthetic process	`biological_process`
GO:0006695	0.0019431	0.0006738	cholesterol biosynthetic process	`biological_process`
GO:0006720	2.9104e-05	3.2254e-05	isoprenoid metabolic process	`biological_process`
GO:0006721	0.00015861	5.8615e-05	terpenoid metabolic process	`biological_process`
GO:0006733	0.018792	0.061942	oxidoreduction coenzyme metabolic process	`biological_process`
GO:0006766	1.8583e-05	0.0001742	vitamin metabolic process	`biological_process`
GO:0006775	0.00026011	0.001246	fat-soluble vitamin metabolic process	`biological_process`
GO:0006776	0.0024012	0.0080022	vitamin A metabolic process	`biological_process`
GO:0008152	1.8583e-05	5.8615e-05	metabolic process	`biological_process`
GO:0008202	1.8583e-05	8.8091e-05	steroid metabolic process	`biological_process`
GO:0008203	0.00015861	0.00021339	cholesterol metabolic process	`biological_process`
GO:0008356	0.041481	0.079664	asymmetric cell division	`biological_process`
GO:0008610	1.8583e-05	7.9007e-05	lipid biosynthetic process	`biological_process`
GO:0009055	9.7669e-06	3.3849e-06	electron carrier activity	`molecular_function`

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GO ID	robust pval.	normal pval.	GO Name	process type
GO:0009250	0.00064562	0.0022807	glucan biosynthetic process	biological_process
GO:0009730	0.0032521	0.006675	detection of carbohydrate stimulus	biological_process
GO:0009732	0.0032521	0.006675	detection of hexose stimulus	biological_process
GO:0009968	0.035175	0.020348	negative regulation of signal transduction	biological_process
GO:0009987	0.0032521	0.00013683	cellular process	biological_process
GO:0010466	0.0019709	0.068864	negative regulation of peptidase activity	biological_process
GO:0010677	0.013324	0.027248	negative regulation of cellular carbohydrate metabolic process	biological_process
GO:0010962	0.018754	0.035681	regulation of glucan biosynthetic process	biological_process
GO:0016051	0.0003999	0.0045325	carbohydrate biosynthetic process	biological_process
GO:0016101	0.0019709	0.006675	diterpenoid metabolic process	biological_process
GO:0016125	3.1658e-05	7.2718e-05	sterol metabolic process	biological_process
GO:0016126	0.000265	0.00016288	sterol biosynthetic process	biological_process
GO:0016491	8.4262e-05	0.00063668	oxidoreductase activity	molecular_function
GO:0016705	8.0857e-08	8.9886e-09	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen	molecular_function
GO:0016712	0.0012347	0.0057106	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, reduced flavin or flavoprotein as one donor, and incorporation of one atom of oxygen	molecular_function
GO:0016713	0.033663	0.064573	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, reduced iron-sulfur protein as one donor, and incorporation of one atom of oxygen	molecular_function
GO:0017022	0.0032521	6.5303e-05	myosin binding	molecular_function
GO:0017159	0.0075962	0.016117	pantetheine hydrolase activity	molecular_function
GO:0018685	0.0032521	0.006675	alkane 1-monooxygenase activity	molecular_function
GO:0019318	0.0057182	0.043488	hexose metabolic process	biological_process
GO:0019362	0.0076517	0.027591	pyridine nucleotide metabolic process	biological_process
GO:0019748	0.0021271	0.0008694	secondary metabolic process	biological_process
GO:0020037	2.3534e-06	9.3744e-06	heme binding	molecular_function
GO:0030497	0.018754	0.035681	fatty acid elongation	biological_process
GO:0032020	0.041481	0.079664	ISG15-protein conjugation	biological_process

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GO ID	robust pval.	normal pval.	GO Name	process type
GO:0032881	0.025306	0.04762	regulation of polysaccharide metabolic process	`biological_process`
GO:0032885	0.018754	0.035681	regulation of polysaccharide biosynthetic process	`biological_process`
GO:0033089	0.041481	0.079664	positive regulation of T cell differentiation in the thymus	`biological_process`
GO:0033692	0.0038307	0.014719	cellular polysaccharide biosynthetic process	`biological_process`
GO:0034235	0.018754	0.035681	GPI anchor binding	`molecular_function`
GO:0034287	0.0032521	0.006675	detection of monosaccharide stimulus	`biological_process`
GO:0035110	0.018754	0.035681	leg morphogenesis	`biological_process`
GO:0042078	0.0075962	0.016117	germ-line stem cell division	`biological_process`
GO:0042175	0.00019902	8.5011e-05	nuclear envelope-endoplasmic reticulum network	`cellular_component`
GO:0042445	0.0047774	0.032387	hormone metabolic process	`biological_process`
GO:0042572	0.00015861	0.00053592	retinol metabolic process	`biological_process`
GO:0042598	2.9104e-05	5.5659e-05	vesicular fraction	`cellular_component`
GO:0043154	0.0019709	0.068864	negative regulation of caspase activity	`biological_process`
GO:0043281	0.018795	0.079142	regulation of caspase activity	`biological_process`
GO:0044042	0.014669	0.045614	glucan metabolic process	`biological_process`
GO:0044237	0.0044923	0.005986	cellular metabolic process	`biological_process`
GO:0044238	0.0040214	0.035681	primary metabolic process	`biological_process`
GO:0044255	8.0857e-08	6.7282e-07	cellular lipid metabolic process	`biological_process`
GO:0044262	0.0015083	0.02228	cellular carbohydrate metabolic process	`biological_process`
GO:0044424	0.020899	0.0041512	intracellular part	`cellular_component`
GO:0044432	0.00019902	8.5011e-05	endoplasmic reticulum part	`cellular_component`
GO:0044444	0.026686	0.0089799	cytoplasmic part	`cellular_component`
GO:0044464	0.0026032	0.00021339	cell part	`cellular_component`
GO:0045321	0.012105	0.0006738	leukocyte activation	`biological_process`
GO:0045721	0.0075962	0.016117	negative regulation of gluconeogenesis	`biological_process`

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GO ID	robust pval.	normal pval.	GO Name	process type
GO:0045725	0.018754	0.035681	positive regulation of glycogen biosynthetic process	`biological_process`
GO:0045912	0.013324	0.027248	negative regulation of carbohydrate metabolic process	`biological_process`
GO:0046649	0.018795	0.011265	lymphocyte activation	`biological_process`
GO:0046906	2.3534e-06	9.3744e-06	tetrapyrrole binding	`molecular_function`
GO:0048029	0.037071	0.091746	monosaccharide binding	`molecular_function`
GO:0048133	0.0075962	0.016117	male germ-line stem cell division	`biological_process`
GO:0051156	0.0075962	0.016117	glucose 6-phosphate metabolic process	`biological_process`
GO:0051594	0.0032521	0.006675	detection of glucose	`biological_process`
GO:0052547	0.019664	0.082043	regulation of peptidase activity	`biological_process`
GO:0052548	0.019302	0.07969	regulation of endopeptidase activity	`biological_process`
GO:0055114	4.3479e-05	0.00021339	oxidation reduction	`biological_process`
Differences:				
GO:0004683	0.044602		calmodulin-dependent protein kinase activity	`molecular_function`
GO:0006006	0.041481		glucose metabolic process	`biological_process`
GO:0006732	0.0047774		coenzyme metabolic process	`biological_process`
GO:0006739	0.018754		NADP metabolic process	`biological_process`
GO:0006769	0.0057068		nicotinamide metabolic process	`biological_process`
GO:0010941	0.041464		regulation of cell death	`biological_process`
GO:0016790	0.025306		thiolester hydrolase activity	`molecular_function`
GO:0032787	0.012105		monocarboxylic acid metabolic process	`biological_process`
GO:0034637	0.0068583		cellular carbohydrate biosynthetic process	`biological_process`
GO:0042981	0.037659		regulation of apoptosis	`biological_process`
GO:0043067	0.041464		regulation of programmed cell death	`biological_process`
GO:0044264	0.033202		cellular polysaccharide metabolic process	`biological_process`
GO:0046165	0.027388		alcohol biosynthetic process	`biological_process`
GO:0046364	0.020899		monosaccharide biosynthetic process	`biological_process`

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GO ID	robust pval.	normal pval.	GO Name	process type
GO:0051186	0.016229		cofactor metabolic process	`biological_process`
GO:0051346	0.014669		negative regulation of hydrolase activity	`biological_process`
GO:0000723		0.04762	telomere maintenance	`biological_process`
GO:0002526		0.032247	acute inflammatory response	`biological_process`
GO:0004022		0.096293	alcohol dehydrogenase activity	`molecular_function`
GO:0004452		0.016117	isopentenyl-diphosphate delta-isomerase activity	`molecular_function`
GO:0005576		0.095157	extracellular region	`cellular_component`
GO:0005615		0.040165	extracellular space	`cellular_component`
GO:0006909		0.057616	phagocytosis	`biological_process`
GO:0006916		0.098142	anti-apoptosis	`biological_process`
GO:0007041		0.084649	lysosomal transport	`biological_process`
GO:0008299		0.018715	isoprenoid biosynthetic process	`biological_process`
GO:0008333		0.032387	endosome to lysosome transport	`biological_process`
GO:0008398		0.016117	sterol 14-demethylase activity	`molecular_function`
GO:0008499		0.017537	UDP-galactose:beta-N-acetylglucosamine beta-1,3-galactosyltransferase activity	`molecular_function`
GO:0009266		0.073408	response to temperature stimulus	`biological_process`
GO:0009311		0.035681	oligosaccharide metabolic process	`biological_process`
GO:0009312		0.013304	oligosaccharide biosynthetic process	`biological_process`
GO:0009408		0.0251	response to heat	`biological_process`
GO:0010648		0.032387	negative regulation of cell communication	`biological_process`
GO:0016108		0.04762	tetraterpenoid metabolic process	`biological_process`
GO:0016109		0.035681	tetraterpenoid biosynthetic process	`biological_process`
GO:0016114		0.035681	terpenoid biosynthetic process	`biological_process`
GO:0016116		0.04762	carotenoid metabolic process	`biological_process`
GO:0016117		0.035681	carotenoid biosynthetic process	`biological_process`

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GO ID	robust pval.	normal pval.	GO Name	process type
GO:0016566		0.035681	specific transcriptional repressor activity	molecular_function
GO:0016709		8.8091e-05	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, NADH or NADPH as one donor, and incorporation of one atom of oxygen	molecular_function
GO:0016860		0.064573	intramolecular oxidoreductase activity	molecular_function
GO:0016863		0.023417	intramolecular oxidoreductase activity, transposing C=C bonds	molecular_function
GO:0019882		0.095157	antigen processing and presentation	biological_process
GO:0031225		0.04382	anchored to membrane	cellular_component
GO:0032200		0.04762	telomere organization	biological_process
GO:0035034		0.027248	histone acetyltransferase regulator activity	molecular_function
GO:0043167		0.032387	ion binding	molecular_function
GO:0046627		0.096293	negative regulation of insulin receptor signaling pathway	biological_process
GO:0046872		0.020348	metal ion binding	molecular_function
GO:0046914		0.069318	transition metal ion binding	molecular_function
GO:0048531		0.027004	beta-1,3-galactosyltransferase activity	molecular_function
Mouse glycerol Intersect:				
GO:0000307	0.02936	0.040664	cyclin-dependent protein kinase holoenzyme complex	cellular_component
GO:0003824	3.9491e-05	7.7587e-11	catalytic activity	molecular_function
GO:0004370	0.001043	0.0017282	glycerol kinase activity	molecular_function
GO:0004648	0.0071501	0.0091411	O-phospho-L-serine:2-oxoglutarate aminotransferase activity	molecular_function
GO:0006066	0.00049411	8.9891e-05	cellular alcohol metabolic process	biological_process
GO:0006071	0.00039298	9.5165e-05	glycerol metabolic process	biological_process
GO:0006072	2.0894e-05	6.5376e-05	glycerol-3-phosphate metabolic process	biological_process
GO:0006082	0.0016293	0.00018486	organic acid metabolic process	biological_process
GO:0009055	0.022491	8.9891e-05	electron carrier activity	molecular_function
GO:0009987	0.044168	0.065729	cellular process	biological_process
GO:0010811	0.039535	0.015717	positive regulation of cell-substrate adhesion	biological_process

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GO ID	robust pval.	normal pval.	GO Name	process type
GO:0015362	0.032872	0.029543	high affinity sodium:dicarboxylate symporter activity	`molecular_function`
GO:0016290	0.0021651	0.065729	palmitoyl-CoA hydrolase activity	`molecular_function`
GO:0016291	0.0035196	0.084848	acyl-CoA thioesterase activity	`molecular_function`
GO:0016491	0.00091826	1.1325e-05	oxidoreductase activity	`molecular_function`
GO:0019751	3.9491e-05	6.5376e-05	polyol metabolic process	`biological_process`
GO:0019752	0.0016293	0.00018486	carboxylic acid metabolic process	`biological_process`
GO:0019867	0.0041465	0.03093	outer membrane	`cellular_component`
GO:0020037	0.032872	7.6409e-05	heme binding	`molecular_function`
GO:0031968	0.0040298	0.029186	organelle outer membrane	`cellular_component`
GO:0032787	0.0082978	0.007854	monocarboxylic acid metabolic process	`biological_process`
GO:0046906	0.032872	7.6409e-05	tetrapyrrole binding	`molecular_function`
GO:0051786	0.0071501	0.0091411	all-trans-retinol 13,14-reductase activity	`molecular_function`
GO:0055114	3.9491e-05	3.8524e-08	oxidation reduction	`biological_process`
Differences:				
GO:0006637	0.0071501		acyl-CoA metabolic process	`biological_process`
GO:0016289	0.0081003		CoA hydrolase activity	`molecular_function`
GO:0000064		0.00048185	L-ornithine transmembrane transporter activity	`molecular_function`
GO:0000267		0.01938	cell fraction	`cellular_component`
GO:0002526		0.034897	acute inflammatory response	`biological_process`
GO:0002532		0.01938	production of molecular mediator of acute inflammatory response	`biological_process`
GO:0002537		0.0042124	production of nitric oxide during acute inflammatory response	`biological_process`
GO:0004091		0.012269	carboxylesterase activity	`molecular_function`
GO:0004252		0.098068	serine-type endopeptidase activity	`molecular_function`
GO:0004368		0.074414	glycerol-3-phosphate dehydrogenase activity	`molecular_function`
GO:0004497		0.00018749	monooxygenase activity	`molecular_function`
GO:0004798		0.01938	thymidylate kinase activity	`molecular_function`

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GO ID	robust pval.	normal pval.	GO Name	process type
GO:0004833		0.01938	tryptophan 2,3-dioxygenase activity	`molecular_function`
GO:0004867		0.025549	serine-type endopeptidase inhibitor activity	`molecular_function`
GO:0005287		0.00048185	high affinity basic amino acid transmembrane transporter activity	`molecular_function`
GO:0005289		0.00048185	high affinity arginine transmembrane transporter activity	`molecular_function`
GO:0005342		0.024374	organic acid transmembrane transporter activity	`molecular_function`
GO:0005488		0.061169	binding	`molecular_function`
GO:0005496		0.025008	steroid binding	`molecular_function`
GO:0005506		0.005756	iron ion binding	`molecular_function`
GO:0005576		0.00085871	extracellular region	`cellular_component`
GO:0005604		0.034389	basement membrane	`cellular_component`
GO:0005624		0.034793	membrane fraction	`cellular_component`
GO:0005626		0.056788	insoluble fraction	`cellular_component`
GO:0005792		0.0032866	microsome	`cellular_component`
GO:0006233		0.01938	dTDP biosynthetic process	`biological_process`
GO:0006519		0.005304	cellular amino acid and derivative metabolic process	`biological_process`
GO:0006520		0.095282	amino acid metabolic process	`biological_process`
GO:0006559		0.074414	L-phenylalanine catabolic process	`biological_process`
GO:0006572		0.060532	tyrosine catabolic process	`biological_process`
GO:0006575		0.016339	amino acid derivative metabolic process	`biological_process`
GO:0006576		0.005215	biogenic amine metabolic process	`biological_process`
GO:0006584		0.079006	catecholamine metabolic process	`biological_process`
GO:0006629		0.02137	lipid metabolic process	`biological_process`
GO:0006725		0.00074218	cellular aromatic compound metabolic process	`biological_process`
GO:0006807		8.341e-06	nitrogen compound metabolic process	`biological_process`
GO:0006809		0.087147	nitric oxide biosynthetic process	`biological_process`

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GO ID	robust pval.	normal pval.	GO Name	process type
GO:0006814		0.095282	sodium ion transport	`biological_process`
GO:0006929		0.087147	substrate-bound cell migration	`biological_process`
GO:0006931		0.0091411	substrate-bound cell migration, cell attachment to substrate	`biological_process`
GO:0007586		0.070397	digestion	`biological_process`
GO:0008152		6.5376e-05	metabolic process	`biological_process`
GO:0008278		0.043643	cohesin complex	`cellular_component`
GO:0008289		0.01938	lipid binding	`molecular_function`
GO:0008483		0.06791	transaminase activity	`molecular_function`
GO:0009063		0.040977	amino acid catabolic process	`biological_process`
GO:0009072		0.025549	aromatic amino acid family metabolic process	`biological_process`
GO:0009074		0.0013217	aromatic amino acid family catabolic process	`biological_process`
GO:0009133		0.029543	nucleoside diphosphate biosynthetic process	`biological_process`
GO:0009138		0.01938	pyrimidine nucleoside diphosphate metabolic process	`biological_process`
GO:0009139		0.01938	pyrimidine nucleoside diphosphate biosynthetic process	`biological_process`
GO:0009189		0.01938	deoxyribonucleoside diphosphate biosynthetic process	`biological_process`
GO:0009196		0.01938	pyrimidine deoxyribonucleoside diphosphate metabolic process	`biological_process`
GO:0009197		0.01938	pyrimidine deoxyribonucleoside diphosphate biosynthetic process	`biological_process`
GO:0009308		0.0013914	cellular amine metabolic process	`biological_process`
GO:0009310		0.06791	amine catabolic process	`biological_process`
GO:0010466		0.079006	negative regulation of peptidase activity	`biological_process`
GO:0010810		0.073875	regulation of cell-substrate adhesion	`biological_process`
GO:0015174		0.01165	basic amino acid transmembrane transporter activity	`molecular_function`
GO:0015181		0.0042124	arginine transmembrane transporter activity	`molecular_function`
GO:0015189		0.00096837	L-lysine transmembrane transporter activity	`molecular_function`
GO:0015802		0.01165	basic amino acid transport	`biological_process`

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GO ID	robust pval.	normal pval.	GO Name	process type
GO:0015809		0.0073768	arginine transport	`biological_process`
GO:0015819		0.00096837	lysine transport	`biological_process`
GO:0015822		0.00048185	ornithine transport	`biological_process`
GO:0015849		0.022284	organic acid transport	`biological_process`
GO:0016151		0.023666	nickel ion binding	`molecular_function`
GO:0016705		0.00018486	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen	`molecular_function`
GO:0016712		0.00070967	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, reduced flavin or flavoprotein as one donor, and incorporation of one atom of oxygen	`molecular_function`
GO:0016787		0.004327	hydrolase activity	`molecular_function`
GO:0016788		0.06791	hydrolase activity, acting on ester bonds	`molecular_function`
GO:0016810		0.095856	hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds	`molecular_function`
GO:0016829		0.02137	lyase activity	`molecular_function`
GO:0017159		0.01938	pantetheine hydrolase activity	`molecular_function`
GO:0018958		0.081591	phenol metabolic process	`biological_process`
GO:0019439		0.0023853	aromatic compound catabolic process	`biological_process`
GO:0019441		0.087147	tryptophan catabolic process to kynurenine	`biological_process`
GO:0019842		0.031655	vitamin binding	`molecular_function`
GO:0022904		0.005756	respiratory electron transport chain	`biological_process`
GO:0030170		0.024374	pyridoxal phosphate binding	`molecular_function`
GO:0030857		0.087147	negative regulation of epithelial cell differentiation	`biological_process`
GO:0031402		0.027713	sodium ion binding	`molecular_function`
GO:0031589		0.02137	cell-substrate adhesion	`biological_process`
GO:0033089		0.087147	positive regulation of T cell differentiation in the thymus	`biological_process`
GO:0034235		0.043643	GPI anchor binding	`molecular_function`
GO:0034641		6.5376e-05	cellular nitrogen compound metabolic process	`biological_process`
GO:0042116		0.094795	macrophage activation	`biological_process`

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GO ID	robust pval.	normal pval.	GO Name	process type
GO:0042598		0.0050221	vesicular fraction	`cellular_component`
GO:0043129		0.087147	surfactant homeostasis	`biological_process`
GO:0043154		0.079006	negative regulation of caspase activity	`biological_process`
GO:0043394		0.060532	proteoglycan binding	`molecular_function`
GO:0043395		0.060532	heparan sulfate proteoglycan binding	`molecular_function`
GO:0043618		0.060532	regulation of transcription from RNA polymerase II promoter in response to stress	`biological_process`
GO:0043619		0.060532	regulation of transcription from RNA polymerase II promoter in response to oxidative stress	`biological_process`
GO:0043620		0.060532	regulation of transcription in response to stress	`biological_process`
GO:0044237		0.074414	cellular metabolic process	`biological_process`
GO:0044255		0.039195	cellular lipid metabolic process	`biological_process`
GO:0044270		0.06791	nitrogen compound catabolic process	`biological_process`
GO:0044271		0.02611	nitrogen compound biosynthetic process	`biological_process`
GO:0044420		0.08244	extracellular matrix part	`cellular_component`
GO:0045333		0.024356	cellular respiration	`biological_process`
GO:0045682		0.069815	regulation of epidermis development	`biological_process`
GO:0045785		0.073875	positive regulation of cell adhesion	`biological_process`
GO:0046072		0.01938	dTDP metabolic process	`biological_process`
GO:0046165		0.098331	alcohol biosynthetic process	`biological_process`
GO:0046209		0.087147	nitric oxide metabolic process	`biological_process`
GO:0046942		0.02137	carboxylic acid transport	`biological_process`
GO:0046943		0.023666	carboxylic acid transmembrane transporter activity	`molecular_function`
GO:0048875		0.087147	chemical homeostasis within a tissue	`biological_process`
GO:0070279		0.024374	vitamin B6 binding	`molecular_function`
Rat liver				
Intersect:				
GO:0000267	0.0067958	0.0080526	cell fraction	`cellular_component`

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GO ID	robust pval.	normal pval.	GO Name	process type
GO:0001523	0.029115	0.037422	retinoid metabolic process	`biological_process`
GO:0003824	1.5283e-06	6.2778e-09	catalytic activity	`molecular_function`
GO:0004091	0.011616	6.2234e-05	carboxylesterase activity	`molecular_function`
GO:0004497	0.011743	0.00071695	monooxygenase activity	`molecular_function`
GO:0004745	0.033978	0.039649	retinol dehydrogenase activity	`molecular_function`
GO:0005344	1.4005e-05	1.9639e-05	oxygen transporter activity	`molecular_function`
GO:0005488	0.0072849	0.00043611	binding	`molecular_function`
GO:0005506	2.1042e-05	2.8949e-05	iron ion binding	`molecular_function`
GO:0005622	0.0071437	0.00042455	intracellular	`cellular_component`
GO:0005623	0.017435	0.0059457	cell	`cellular_component`
GO:0005737	0.011575	7.8519e-05	cytoplasm	`cellular_component`
GO:0005783	0.026047	0.0045545	endoplasmic reticulum	`cellular_component`
GO:0005792	0.00026228	0.0001016	microsome	`cellular_component`
GO:0005829	0.048962	0.0095421	cytosol	`cellular_component`
GO:0005833	1.7755e-06	2.4498e-06	hemoglobin complex	`cellular_component`
GO:0006066	0.00017065	1.1721e-08	cellular alcohol metabolic process	`biological_process`
GO:0006082	1.3569e-09	2.0475e-09	organic acid metabolic process	`biological_process`
GO:0006519	7.763e-05	0.011316	cellular amino acid and derivative metabolic process	`biological_process`
GO:0006520	0.002817	0.024923	amino acid metabolic process	`biological_process`
GO:0006536	0.0050106	0.0063112	glutamate metabolic process	`biological_process`
GO:0006629	1.2696e-08	8.1389e-14	lipid metabolic process	`biological_process`
GO:0006631	3.5153e-06	1.2438e-07	fatty acid metabolic process	`biological_process`
GO:0006633	9.9389e-05	3.668e-05	fatty acid biosynthetic process	`biological_process`
GO:0006720	0.010439	0.0019314	isoprenoid metabolic process	`biological_process`
GO:0006721	0.00028473	0.00043611	terpenoid metabolic process	`biological_process`

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GO ID	robust pval.	normal pval.	GO Name	process type
GO:0006732	0.025564	0.051141	coenzyme metabolic process	`biological_process`
GO:0006807	1.5283e-06	0.00019266	nitrogen compound metabolic process	`biological_process`
GO:0006950	0.0051164	0.00089658	response to stress	`biological_process`
GO:0007584	4.4722e-05	0.00017311	response to nutrient	`biological_process`
GO:0008152	0.00013201	2.4498e-06	metabolic process	`biological_process`
GO:0008202	0.0086333	9.4581e-05	steroid metabolic process	`biological_process`
GO:0008395	0.036915	0.047895	steroid hydroxylase activity	`molecular_function`
GO:0008610	0.00014857	4.9533e-06	lipid biosynthetic process	`biological_process`
GO:0009308	1.7755e-06	0.00034398	cellular amine metabolic process	`biological_process`
GO:0009309	0.041778	0.064213	amine biosynthetic process	`biological_process`
GO:0009605	0.0076655	0.00029397	response to external stimulus	`biological_process`
GO:0009719	4.5409e-05	9.7621e-09	response to endogenous stimulus	`biological_process`
GO:0009725	2.0359e-05	6.7519e-09	response to hormone stimulus	`biological_process`
GO:0009987	0.036613	0.029435	cellular process	`biological_process`
GO:0009991	1.8789e-05	6.6213e-06	response to extracellular stimulus	`biological_process`
GO:0010033	0.00053523	6.2316e-05	response to organic substance	`biological_process`
GO:0010035	0.023236	0.021708	response to inorganic substance	`biological_process`
GO:0014070	0.002817	0.0023991	response to organic cyclic substance	`biological_process`
GO:0015669	7.4346e-05	6.4493e-06	gas transport	`biological_process`
GO:0015671	2.3817e-05	3.668e-05	oxygen transport	`biological_process`
GO:0016053	2.9641e-05	1.2597e-05	organic acid biosynthetic process	`biological_process`
GO:0016101	0.029115	0.037422	diterpenoid metabolic process	`biological_process`
GO:0016125	0.017435	0.00022003	sterol metabolic process	`biological_process`
GO:0016491	9.6343e-05	2.0416e-05	oxidoreductase activity	`molecular_function`
GO:0016614	0.023567	0.0099493	oxidoreductase activity, acting on CH-OH group of donors	`molecular_function`

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GO ID	robust pval.	normal pval.	GO Name	process type
GO:0016616	0.019404	0.0080096	oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor	`molecular_function`
GO:0016705	0.00019726	2.4097e-05	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen	`molecular_function`
GO:0016712	0.040247	0.057023	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, reduced flavin or flavoprotein as one donor, and incorporation of one atom of oxygen	`molecular_function`
GO:0016717	0.020252	0.023235	oxidoreductase activity, acting on paired donors, with oxidation of a pair of donors resulting in the reduction of molecular oxygen to two molecules of water	`molecular_function`
GO:0016787	0.032351	0.0052192	hydrolase activity	`molecular_function`
GO:0016788	0.00067376	0.00019266	hydrolase activity, acting on ester bonds	`molecular_function`
GO:0016829	0.0012273	3.668e-05	lyase activity	`molecular_function`
GO:0019748	3.7266e-05	6.656e-05	secondary metabolic process	`biological_process`
GO:0019752	1.3569e-09	2.0475e-09	carboxylic acid metabolic process	`biological_process`
GO:0019825	0.0012314	0.0018614	oxygen binding	`molecular_function`
GO:0019842	0.0058611	0.0027052	vitamin binding	`molecular_function`
GO:0020037	1.6499e-06	9.0717e-07	heme binding	`molecular_function`
GO:0031667	2.1042e-05	2.8949e-05	response to nutrient levels	`biological_process`
GO:0031960	2.0359e-05	4.4273e-08	response to corticosteroid stimulus	`biological_process`
GO:0032355	0.013227	0.02195	response to estradiol stimulus	`biological_process`
GO:0032787	1.5441e-06	1.4569e-08	monocarboxylic acid metabolic process	`biological_process`
GO:0032868	0.032538	0.00020349	response to insulin stimulus	`biological_process`
GO:0032870	0.0013845	6.3639e-06	cellular response to hormone stimulus	`biological_process`
GO:0034641	2.4919e-06	0.00045331	cellular nitrogen compound metabolic process	`biological_process`
GO:0042221	6.0412e-06	6.7519e-09	response to chemical stimulus	`biological_process`
GO:0042493	0.013569	0.0059457	response to drug	`biological_process`
GO:0042598	0.00040327	0.0001653	vesicular fraction	`cellular_component`
GO:0043167	0.031157	0.010325	ion binding	`molecular_function`
GO:0043434	0.00025689	2.0416e-05	response to peptide hormone stimulus	`biological_process`
GO:0043627	0.026822	0.00105	response to estrogen stimulus	`biological_process`

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GO ID	robust pval.	normal pval.	GO Name	process type
GO:0044237	0.0010286	3.8401e-05	cellular metabolic process	`biological_process`
GO:0044238	0.0024476	6.2234e-05	primary metabolic process	`biological_process`
GO:0044255	7.0914e-08	3.3477e-12	cellular lipid metabolic process	`biological_process`
GO:0044262	0.02646	0.00020423	cellular carbohydrate metabolic process	`biological_process`
GO:0044424	0.0020725	6.0378e-05	intracellular part	`cellular_component`
GO:0044444	0.017296	0.00049702	cytoplasmic part	`cellular_component`
GO:0044464	0.017435	0.0059457	cell part	`cellular_component`
GO:0046394	2.9641e-05	1.2597e-05	carboxylic acid biosynthetic process	`biological_process`
GO:0046872	0.017296	0.0047434	metal ion binding	`molecular_function`
GO:0046906	1.6499e-06	9.0717e-07	tetrapyrrole binding	`molecular_function`
GO:0048037	0.013436	0.00036061	cofactor binding	`molecular_function`
GO:0048545	2.0359e-05	6.2778e-09	response to steroid hormone stimulus	`biological_process`
GO:0050896	4.4041e-05	3.257e-07	response to stimulus	`biological_process`
GO:0051186	0.0075282	0.01829	cofactor metabolic process	`biological_process`
GO:0051384	6.6643e-06	9.7621e-09	response to glucocorticoid stimulus	`biological_process`
GO:0051412	0.036915	0.047895	response to corticosterone stimulus	`biological_process`
GO:0051716	0.011539	0.00040727	cellular response to stimulus	`biological_process`
GO:0055114	7.3198e-05	8.7085e-06	oxidation reduction	`biological_process`
Differences:				
GO:0006575	0.025564		amino acid derivative metabolic process	`biological_process`
GO:0016407	0.040643		acetyltransferase activity	`molecular_function`
GO:0019966	0.010261		interleukin-1 binding	`molecular_function`
GO:0004056		0.057344	argininosuccinate lyase activity	`molecular_function`
GO:0004313		0.057344	[acyl-carrier-protein] S-acetyltransferase activity	`molecular_function`
GO:0004315		0.057344	3-oxoacyl-[acyl-carrier-protein] synthase activity	`molecular_function`
GO:0004316		0.057344	3-oxoacyl-[acyl-carrier-protein] reductase activity	`molecular_function`

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GO ID	robust pval.	normal pval.	GO Name	process type
GO:0004317		0.057344	3-hydroxypalmitoyl-[acyl-carrier-protein] dehydratase activity	`molecular_function`
GO:0004319		0.057344	enoyl-[acyl-carrier-protein] reductase (NADPH, B-specific) activity	`molecular_function`
GO:0004806		0.023235	triacylglycerol lipase activity	`molecular_function`
GO:0005549		0.0015416	odorant binding	`molecular_function`
GO:0005550		0.00015736	pheromone binding	`molecular_function`
GO:0005789		0.047895	endoplasmic reticulum membrane	`cellular_component`
GO:0005865		0.080306	striated muscle thin filament	`cellular_component`
GO:0005975		0.003431	carbohydrate metabolic process	`biological_process`
GO:0005977		0.047895	glycogen metabolic process	`biological_process`
GO:0005996		0.010453	monosaccharide metabolic process	`biological_process`
GO:0006006		0.030157	glucose metabolic process	`biological_process`
GO:0006073		0.047895	cellular glucan metabolic process	`biological_process`
GO:0006112		0.069411	energy reserve metabolic process	`biological_process`
GO:0006694		0.0343	steroid biosynthetic process	`biological_process`
GO:0006695		0.069411	cholesterol biosynthetic process	`biological_process`
GO:0006766		0.099553	vitamin metabolic process	`biological_process`
GO:0006776		0.068522	vitamin A metabolic process	`biological_process`
GO:0006790		0.031348	sulfur metabolic process	`biological_process`
GO:0007586		3.8899e-05	digestion	`biological_process`
GO:0008203		0.00095834	cholesterol metabolic process	`biological_process`
GO:0008645		0.064213	hexose transport	`biological_process`
GO:0008652		0.080306	amino acid biosynthetic process	`biological_process`
GO:0009055		0.081653	electron carrier activity	`molecular_function`
GO:0009056		3.1646e-05	catabolic process	`biological_process`
GO:0009058		0.047895	biosynthetic process	`biological_process`

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GO ID	robust pval.	normal pval.	GO Name	process type
GO:0009628		0.031313	response to abiotic stimulus	`biological_process`
GO:0015749		0.064213	monosaccharide transport	`biological_process`
GO:0015758		0.057344	glucose transport	`biological_process`
GO:0016042		6.2234e-05	lipid catabolic process	`biological_process`
GO:0016114		0.057344	terpenoid biosynthetic process	`biological_process`
GO:0016126		0.015479	sterol biosynthetic process	`biological_process`
GO:0016298		0.019357	lipase activity	`molecular_function`
GO:0016418		0.057344	S-acetyltransferase activity	`molecular_function`
GO:0016631		0.057344	enoyl-[acyl-carrier-protein] reductase activity	`molecular_function`
GO:0016709		0.00076464	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, NADH or NADPH as one donor, and incorporation of one atom of oxygen	`molecular_function`
GO:0016835		0.091747	carbon-oxygen lyase activity	`molecular_function`
GO:0016836		0.057023	hydro-lyase activity	`molecular_function`
GO:0016840		0.080306	carbon-nitrogen lyase activity	`molecular_function`
GO:0019171		0.057344	3-hydroxyacyl-[acyl-carrier-protein] dehydratase activity	`molecular_function`
GO:0019318		0.026963	hexose metabolic process	`biological_process`
GO:0030299		0.039649	intestinal cholesterol absorption	`biological_process`
GO:0032269		0.077944	negative regulation of cellular protein metabolic process	`biological_process`
GO:0032869		0.0028996	cellular response to insulin stimulus	`biological_process`
GO:0042175		0.030157	nuclear envelope-endoplasmic reticulum network	`cellular_component`
GO:0042450		0.057344	arginine biosynthetic process via ornithine	`biological_process`
GO:0043169		0.021902	cation binding	`molecular_function`
GO:0043177		0.057344	organic acid binding	`molecular_function`
GO:0043227		0.03219	membrane-bounded organelle	`cellular_component`
GO:0043229		0.014828	intracellular organelle	`cellular_component`
GO:0043231		0.030157	intracellular membrane-bounded organelle	`cellular_component`

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GO ID	robust pval.	normal pval.	GO Name	process type
GO:0044042		0.047895	glucan metabolic process	`biological_process`
GO:0044240		0.057344	multicellular organismal lipid catabolic process	`biological_process`
GO:0044241		0.0032335	lipid digestion	`biological_process`
GO:0044248		0.0093903	cellular catabolic process	`biological_process`
GO:0044249		0.034219	cellular biosynthetic process	`biological_process`
GO:0044432		0.023235	endoplasmic reticulum part	`cellular_component`
GO:0046165		0.089578	alcohol biosynthetic process	`biological_process`
GO:0046470		0.068522	phosphatidylcholine metabolic process	`biological_process`
GO:0046914		0.057344	transition metal ion binding	`molecular_function`
GO:0048002		0.018625	antigen processing and presentation of peptide antigen	`biological_process`
GO:0050662		0.057344	coenzyme binding	`molecular_function`
GO:0050667		0.057344	homocysteine metabolic process	`biological_process`
GO:0051248		0.091747	negative regulation of protein metabolic process	`biological_process`
GO:0051258		0.091534	protein polymerization	`biological_process`
Rat obesity Intersect:				
GO:0005488	0.0040334	2.5184e-05	binding	`molecular_function`
GO:0005515	0.0040334	0.00020715	protein binding	`molecular_function`
GO:0005622	0.0057218	5.0024e-06	intracellular	`cellular_component`
GO:0005623	0.0013386	1.4395e-06	cell	`cellular_component`
GO:0005737	0.013155	3.0132e-06	cytoplasm	`cellular_component`
GO:0005996	0.032849	0.018653	monosaccharide metabolic process	`biological_process`
GO:0006006	0.015818	0.0096188	glucose metabolic process	`biological_process`
GO:0008152	0.03209	1.1047e-05	metabolic process	`biological_process`
GO:0009987	0.030044	1.0462e-05	cellular process	`biological_process`
GO:0019318	0.031394	0.016118	hexose metabolic process	`biological_process`

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GO ID	robust pval.	normal pval.	GO Name	process type
GO:0032787	0.013155	0.00070822	monocarboxylic acid metabolic process	`biological_process`
GO:0044424	0.0049752	1.4395e-06	intracellular part	`cellular_component`
GO:0044464	0.0013386	1.4395e-06	cell part	`cellular_component`
GO:0050794	0.041882	9.5471e-05	regulation of cellular process	`biological_process`
Differences:				
GO:0000003		0.091011	reproduction	`biological_process`
GO:0000267		0.023063	cell fraction	`cellular_component`
GO:0000323		0.0059477	lytic vacuole	`cellular_component`
GO:0001501		0.010074	skeletal system development	`biological_process`
GO:0001503		0.022761	ossification	`biological_process`
GO:0001726		0.083962	ruffle	`cellular_component`
GO:0001775		0.013549	cell activation	`biological_process`
GO:0001794		0.013549	type IIa hypersensitivity	`biological_process`
GO:0001796		0.013549	regulation of type IIa hypersensitivity	`biological_process`
GO:0001798		0.013549	positive regulation of type IIa hypersensitivity	`biological_process`
GO:0001802		0.0071134	type III hypersensitivity	`biological_process`
GO:0001803		0.0071134	regulation of type III hypersensitivity	`biological_process`
GO:0001805		0.0071134	positive regulation of type III hypersensitivity	`biological_process`
GO:0001810		0.013549	regulation of type I hypersensitivity	`biological_process`
GO:0001812		0.0071134	positive regulation of type I hypersensitivity	`biological_process`
GO:0001816		0.0014324	cytokine production	`biological_process`
GO:0001817		0.0028419	regulation of cytokine production	`biological_process`
GO:0001894		0.0071134	tissue homeostasis	`biological_process`
GO:0002250		0.059205	adaptive immune response	`biological_process`
GO:0002252		0.013023	immune effector process	`biological_process`
GO:0002274		8.0938e-05	myeloid leukocyte activation	`biological_process`

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GO ID	robust pval.	normal pval.	GO Name	process type
GO:0002367		0.002002	cytokine production during immune response	`biological_process`
GO:0002438		0.031401	acute inflammatory response to antigenic stimulus	`biological_process`
GO:0002440		0.00081624	production of molecular mediator of immune response	`biological_process`
GO:0002443		0.015369	leukocyte mediated immunity	`biological_process`
GO:0002444		0.0087171	myeloid leukocyte mediated immunity	`biological_process`
GO:0002445		0.013549	type II hypersensitivity	`biological_process`
GO:0002448		0.065241	mast cell mediated immunity	`biological_process`
GO:0002449		0.052343	lymphocyte mediated immunity	`biological_process`
GO:0002460		0.059205	adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	`biological_process`
GO:0002495		0.077624	antigen processing and presentation of peptide antigen via MHC class II	`biological_process`
GO:0002524		0.031401	hypersensitivity	`biological_process`
GO:0002526		0.00046634	acute inflammatory response	`biological_process`
GO:0002673		0.01243	regulation of acute inflammatory response	`biological_process`
GO:0002675		0.002002	positive regulation of acute inflammatory response	`biological_process`
GO:0002682		0.015369	regulation of immune system process	`biological_process`
GO:0002683		0.013549	negative regulation of immune system process	`biological_process`
GO:0002684		0.024698	positive regulation of immune system process	`biological_process`
GO:0002694		0.026112	regulation of leukocyte activation	`biological_process`
GO:0002695		0.031796	negative regulation of leukocyte activation	`biological_process`
GO:0002697		0.00093293	regulation of immune effector process	`biological_process`
GO:0002699		0.050993	positive regulation of immune effector process	`biological_process`
GO:0002700		0.00015552	regulation of production of molecular mediator of immune response	`biological_process`
GO:0002702		0.052735	positive regulation of production of molecular mediator of immune response	`biological_process`
GO:0002703		0.0017097	regulation of leukocyte mediated immunity	`biological_process`
GO:0002705		0.022911	positive regulation of leukocyte mediated immunity	`biological_process`

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GO ID	robust pval.	normal pval.	GO Name	process type
GO:0002706		0.0090308	regulation of lymphocyte mediated immunity	`biological_process`
GO:0002708		0.022911	positive regulation of lymphocyte mediated immunity	`biological_process`
GO:0002712		0.00093293	regulation of B cell mediated immunity	`biological_process`
GO:0002714		0.0029588	positive regulation of B cell mediated immunity	`biological_process`
GO:0002718		0.0011475	regulation of cytokine production during immune response	`biological_process`
GO:0002819		0.010656	regulation of adaptive immune response	`biological_process`
GO:0002821		0.02061	positive regulation of adaptive immune response	`biological_process`
GO:0002822		0.010656	regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	`biological_process`
GO:0002824		0.02061	positive regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	`biological_process`
GO:0002861		0.077624	regulation of inflammatory response to antigenic stimulus	`biological_process`
GO:0002863		0.031401	positive regulation of inflammatory response to antigenic stimulus	`biological_process`
GO:0002864		0.031401	regulation of acute inflammatory response to antigenic stimulus	`biological_process`
GO:0002866		0.013549	positive regulation of acute inflammatory response to antigenic stimulus	`biological_process`
GO:0002883		0.031401	regulation of hypersensitivity	`biological_process`
GO:0002885		0.013549	positive regulation of hypersensitivity	`biological_process`
GO:0002886		0.0042953	regulation of myeloid leukocyte mediated immunity	`biological_process`
GO:0002888		0.013549	positive regulation of myeloid leukocyte mediated immunity	`biological_process`
GO:0002889		0.00093293	regulation of immunoglobulin mediated immune response	`biological_process`
GO:0002891		0.0029588	positive regulation of immunoglobulin mediated immune response	`biological_process`
GO:0002892		0.013549	regulation of type II hypersensitivity	`biological_process`
GO:0002894		0.013549	positive regulation of type II hypersensitivity	`biological_process`
GO:0003824		0.028456	catalytic activity	`molecular_function`
GO:0005215		0.018653	transporter activity	`molecular_function`
GO:0005319		0.00091731	lipid transporter activity	`molecular_function`
GO:0005324		0.013549	long-chain fatty acid transporter activity	`molecular_function`

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GO ID	robust pval.	normal pval.	GO Name	process type
GO:0005391		0.052735	sodium:potassium-exchanging ATPase activity	`molecular_function`
GO:0005504		0.089091	fatty acid binding	`molecular_function`
GO:0005506		0.083045	iron ion binding	`molecular_function`
GO:0005576		3.3213e-08	extracellular region	`cellular_component`
GO:0005615		8.0938e-05	extracellular space	`cellular_component`
GO:0005764		0.0059477	lysosome	`cellular_component`
GO:0005773		0.0091108	vacuole	`cellular_component`
GO:0005783		0.0030661	endoplasmic reticulum	`cellular_component`
GO:0005792		0.012203	microsome	`cellular_component`
GO:0005886		0.089793	plasma membrane	`cellular_component`
GO:0006066		0.00093293	cellular alcohol metabolic process	`biological_process`
GO:0006082		0.0023368	organic acid metabolic process	`biological_process`
GO:0006090		0.077624	pyruvate metabolic process	`biological_process`
GO:0006094		0.050993	gluconeogenesis	`biological_process`
GO:0006629		1.4629e-05	lipid metabolic process	`biological_process`
GO:0006631		0.0327	fatty acid metabolic process	`biological_process`
GO:0006643		0.077624	membrane lipid metabolic process	`biological_process`
GO:0006644		0.042714	phospholipid metabolic process	`biological_process`
GO:0006650		0.053642	glycerophospholipid metabolic process	`biological_process`
GO:0006656		0.0087171	phosphatidylcholine biosynthetic process	`biological_process`
GO:0006700		0.089793	C21-steroid hormone biosynthetic process	`biological_process`
GO:0006810		0.009203	transport	`biological_process`
GO:0006869		0.00081624	lipid transport	`biological_process`
GO:0006909		0.0062207	phagocytosis	`biological_process`
GO:0006911		0.052735	phagocytosis, engulfment	`biological_process`

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GO ID	robust pval.	normal pval.	GO Name	process type
GO:0006915		0.017935	apoptosis	`biological_process`
GO:0006950		0.003137	response to stress	`biological_process`
GO:0006952		7.4448e-05	defense response	`biological_process`
GO:0006954		1.2698e-05	inflammatory response	`biological_process`
GO:0006955		0.051207	immune response	`biological_process`
GO:0006996		0.040046	organelle organization	`biological_process`
GO:0007154		0.0087312	cell communication	`biological_process`
GO:0007165		0.0076533	signal transduction	`biological_process`
GO:0007275		0.01243	multicellular organismal development	`biological_process`
GO:0007584		0.030377	response to nutrient	`biological_process`
GO:0007586		0.068809	digestion	`biological_process`
GO:0008191		0.04207	metalloendopeptidase inhibitor activity	`molecular_function`
GO:0008202		0.0071134	steroid metabolic process	`biological_process`
GO:0008219		0.022361	cell death	`biological_process`
GO:0008233		0.01817	peptidase activity	`molecular_function`
GO:0008289		0.063796	lipid binding	`molecular_function`
GO:0008610		0.03108	lipid biosynthetic process	`biological_process`
GO:0009056		0.0045609	catabolic process	`biological_process`
GO:0009058		0.0030923	biosynthetic process	`biological_process`
GO:0009266		0.068275	response to temperature stimulus	`biological_process`
GO:0009605		9.8153e-05	response to external stimulus	`biological_process`
GO:0009611		6.2026e-05	response to wounding	`biological_process`
GO:0009719		0.00081624	response to endogenous stimulus	`biological_process`
GO:0009725		0.00028224	response to hormone stimulus	`biological_process`
GO:0009888		0.088247	tissue development	`biological_process`

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GO ID	robust pval.	normal pval.	GO Name	process type
GO:0009889		0.044421	regulation of biosynthetic process	`biological_process`
GO:0009894		0.086638	regulation of catabolic process	`biological_process`
GO:0009897		0.039858	external side of plasma membrane	`cellular_component`
GO:0009966		0.096366	regulation of signal transduction	`biological_process`
GO:0009986		0.0076533	cell surface	`cellular_component`
GO:0009991		0.033722	response to extracellular stimulus	`biological_process`
GO:0010033		0.00074869	response to organic substance	`biological_process`
GO:0010035		0.019462	response to inorganic substance	`biological_process`
GO:0010522		0.01243	regulation of calcium ion transport into cytosol	`biological_process`
GO:0010524		0.065241	positive regulation of calcium ion transport into cytosol	`biological_process`
GO:0010556		0.077624	regulation of macromolecule biosynthetic process	`biological_process`
GO:0010576		0.04207	metalloenzyme regulator activity	`molecular_function`
GO:0010646		0.09582	regulation of cell communication	`biological_process`
GO:0010769		0.050022	regulation of cell morphogenesis involved in differentiation	`biological_process`
GO:0010941		0.024302	regulation of cell death	`biological_process`
GO:0010959		0.083225	regulation of metal ion transport	`biological_process`
GO:0012501		0.018653	programmed cell death	`biological_process`
GO:0014070		0.013549	response to organic cyclic substance	`biological_process`
GO:0015245		0.022361	fatty acid transporter activity	`molecular_function`
GO:0015248		0.089793	sterol transporter activity	`molecular_function`
GO:0015908		0.089793	fatty acid transport	`biological_process`
GO:0015909		0.065241	long-chain fatty acid transport	`biological_process`
GO:0015914		0.015569	phospholipid transport	`biological_process`
GO:0016020		0.0059385	membrane	`cellular_component`
GO:0016042		0.036136	lipid catabolic process	`biological_process`

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GO ID	robust pval.	normal pval.	GO Name	process type
GO:0016043		0.00020237	cellular component organization	`biological_process`
GO:0016064		0.013549	immunoglobulin mediated immune response	`biological_process`
GO:0016068		0.013549	type I hypersensitivity	`biological_process`
GO:0016125		0.056715	sterol metabolic process	`biological_process`
GO:0016265		0.022951	death	`biological_process`
GO:0016491		0.0071134	oxidoreductase activity	`molecular_function`
GO:0016614		0.065241	oxidoreductase activity, acting on CH-OH group of donors	`molecular_function`
GO:0016616		0.059205	oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor	`molecular_function`
GO:0016705		0.026112	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen	`molecular_function`
GO:0016712		0.04675	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, reduced flavin or flavoprotein as one donor, and incorporation of one atom of oxygen	`molecular_function`
GO:0016787		0.049722	hydrolase activity	`molecular_function`
GO:0017127		0.089793	cholesterol transporter activity	`molecular_function`
GO:0017147		0.031401	Wnt-protein binding	`molecular_function`
GO:0019216		0.056715	regulation of lipid metabolic process	`biological_process`
GO:0019222		0.0052684	regulation of metabolic process	`biological_process`
GO:0019319		0.068809	hexose biosynthetic process	`biological_process`
GO:0019724		0.013549	B cell mediated immunity	`biological_process`
GO:0019752		0.0023026	carboxylic acid metabolic process	`biological_process`
GO:0019763		0.022361	immunoglobulin receptor activity	`molecular_function`
GO:0019864		0.022361	IgG binding	`molecular_function`
GO:0019865		0.052735	immunoglobulin binding	`molecular_function`
GO:0019886		0.077624	antigen processing and presentation of exogenous peptide antigen via MHC class II	`biological_process`
GO:0019953		0.098929	sexual reproduction	`biological_process`
GO:0022414		0.086638	reproductive process	`biological_process`
GO:0022600		0.028988	digestive system process	`biological_process`

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GO ID	robust pval.	normal pval.	GO Name	process type
GO:0022607		0.074674	cellular component assembly	`biological_process`
GO:0022892		0.058427	substrate-specific transporter activity	`molecular_function`
GO:0030017		0.089421	sarcomere	`cellular_component`
GO:0030018		0.018653	Z disc	`cellular_component`
GO:0030100		0.027632	regulation of endocytosis	`biological_process`
GO:0030279		0.077624	negative regulation of ossification	`biological_process`
GO:0030282		0.007417	bone mineralization	`biological_process`
GO:0030336		0.059205	negative regulation of cell migration	`biological_process`
GO:0031012		0.013549	extracellular matrix	`cellular_component`
GO:0031099		0.0089813	regeneration	`biological_process`
GO:0031100		0.0096861	organ regeneration	`biological_process`
GO:0031214		0.010656	biomineral formation	`biological_process`
GO:0031323		0.002002	regulation of cellular metabolic process	`biological_process`
GO:0031326		0.042714	regulation of cellular biosynthetic process	`biological_process`
GO:0031347		0.0087171	regulation of defense response	`biological_process`
GO:0031349		0.042302	positive regulation of defense response	`biological_process`
GO:0031430		0.022361	M band	`cellular_component`
GO:0031667		0.024276	response to nutrient levels	`biological_process`
GO:0031672		0.052735	A band	`cellular_component`
GO:0031674		0.031152	I band	`cellular_component`
GO:0032101		0.009203	regulation of response to external stimulus	`biological_process`
GO:0032103		0.013549	positive regulation of response to external stimulus	`biological_process`
GO:0032403		0.086599	protein complex binding	`molecular_function`
GO:0032502		0.0014654	developmental process	`biological_process`
GO:0032640		0.077624	tumor necrosis factor production	`biological_process`

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GO ID	robust pval.	normal pval.	GO Name	process type
GO:0032680		0.077624	regulation of tumor necrosis factor production	biological_process
GO:0032762		0.0071134	mast cell cytokine production	biological_process
GO:0032763		0.0071134	regulation of mast cell cytokine production	biological_process
GO:0032844		0.0024515	regulation of homeostatic process	biological_process
GO:0032846		0.0023026	positive regulation of homeostatic process	biological_process
GO:0033003		0.052735	regulation of mast cell activation	biological_process
GO:0033273		0.053642	response to vitamin	biological_process
GO:0033700		0.065241	phospholipid efflux	biological_process
GO:0034105		0.042302	positive regulation of tissue remodeling	biological_process
GO:0034405		0.089793	response to fluid shear stress	biological_process
GO:0035020		0.065241	regulation of Rac protein signal transduction	biological_process
GO:0042035		0.050993	regulation of cytokine biosynthetic process	biological_process
GO:0042089		0.074074	cytokine biosynthetic process	biological_process
GO:0042107		0.074074	cytokine metabolic process	biological_process
GO:0042127		0.089091	regulation of cell proliferation	biological_process
GO:0042221		1.2698e-05	response to chemical stimulus	biological_process
GO:0042493		9.1253e-05	response to drug	biological_process
GO:0042590		0.013549	antigen processing and presentation of exogenous peptide antigen via MHC class I	biological_process
GO:0042592		0.0023026	homeostatic process	biological_process
GO:0042598		0.013549	vesicular fraction	cellular_component
GO:0042981		0.022951	regulation of apoptosis	biological_process
GO:0042995		0.005855	cell projection	cellular_component
GO:0043005		0.091329	neuron projection	cellular_component
GO:0043066		0.041318	negative regulation of apoptosis	biological_process
GO:0043067		0.024091	regulation of programmed cell death	biological_process

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GO ID	robust pval.	normal pval.	GO Name	process type
GO:0043069		0.041318	negative regulation of programmed cell death	`biological_process`
GO:0043169		0.071747	cation binding	`molecular_function`
GO:0043170		0.069775	macromolecule metabolic process	`biological_process`
GO:0043227		9.5471e-05	membrane-bounded organelle	`cellular_component`
GO:0043229		1.7021e-05	intracellular organelle	`cellular_component`
GO:0043231		9.3512e-05	intracellular membrane-bounded organelle	`cellular_component`
GO:0043269		0.094946	regulation of ion transport	`biological_process`
GO:0043270		0.093137	positive regulation of ion transport	`biological_process`
GO:0043299		0.089793	leukocyte degranulation	`biological_process`
GO:0043300		0.04207	regulation of leukocyte degranulation	`biological_process`
GO:0043303		0.065241	mast cell degranulation	`biological_process`
GO:0043304		0.04207	regulation of mast cell degranulation	`biological_process`
GO:0043434		0.052735	response to peptide hormone stimulus	`biological_process`
GO:0044237		0.00081624	cellular metabolic process	`biological_process`
GO:0044238		0.00027216	primary metabolic process	`biological_process`
GO:0044248		0.096366	cellular catabolic process	`biological_process`
GO:0044249		0.0025277	cellular biosynthetic process	`biological_process`
GO:0044255		6.2026e-05	cellular lipid metabolic process	`biological_process`
GO:0044262		0.072789	cellular carbohydrate metabolic process	`biological_process`
GO:0044421		3.0132e-06	extracellular region part	`cellular_component`
GO:0044425		0.0091108	membrane part	`cellular_component`
GO:0044444		8.0938e-05	cytoplasmic part	`cellular_component`
GO:0044459		0.024698	plasma membrane part	`cellular_component`
GO:0045321		0.086638	leukocyte activation	`biological_process`
GO:0045453		0.012985	bone resorption	`biological_process`

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GO ID	robust pval.	normal pval.	GO Name	process type
GO:0045576		0.0015398	mast cell activation	`biological_process`
GO:0045780		0.04207	positive regulation of bone resorption	`biological_process`
GO:0045807		0.022911	positive regulation of endocytosis	`biological_process`
GO:0046364		0.089091	monosaccharide biosynthetic process	`biological_process`
GO:0046470		0.018182	phosphatidylcholine metabolic process	`biological_process`
GO:0046474		0.064695	glycerophospholipid biosynthetic process	`biological_process`
GO:0046486		0.039858	glycerolipid metabolic process	`biological_process`
GO:0046849		0.0049973	bone remodeling	`biological_process`
GO:0046852		0.028988	positive regulation of bone remodeling	`biological_process`
GO:0046914		0.070471	transition metal ion binding	`molecular_function`
GO:0048468		0.044421	cell development	`biological_process`
GO:0048513		0.0327	organ development	`biological_process`
GO:0048522		0.036074	positive regulation of cellular process	`biological_process`
GO:0048523		0.00057217	negative regulation of cellular process	`biological_process`
GO:0048545		0.035873	response to steroid hormone stimulus	`biological_process`
GO:0048551		0.04207	metalloenzyme inhibitor activity	`molecular_function`
GO:0048583		0.0034247	regulation of response to stimulus	`biological_process`
GO:0048584		0.02007	positive regulation of response to stimulus	`biological_process`
GO:0048585		0.047354	negative regulation of response to stimulus	`biological_process`
GO:0048679		0.022361	regulation of axon regeneration	`biological_process`
GO:0048731		0.013549	system development	`biological_process`
GO:0048771		0.0046586	tissue remodeling	`biological_process`
GO:0048856		0.019671	anatomical structure development	`biological_process`
GO:0048869		0.077624	cellular developmental process	`biological_process`
GO:0048871		0.0071134	multicellular organismal homeostasis	`biological_process`

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GO ID	robust pval.	normal pval.	GO Name	process type
GO:0048872		0.016118	homeostasis of number of cells	`biological_process`
GO:0050727		0.017856	regulation of inflammatory response	`biological_process`
GO:0050729		0.018182	positive regulation of inflammatory response	`biological_process`
GO:0050764		0.00081624	regulation of phagocytosis	`biological_process`
GO:0050766		0.0071134	positive regulation of phagocytosis	`biological_process`
GO:0050776		0.00070822	regulation of immune response	`biological_process`
GO:0050778		0.013549	positive regulation of immune response	`biological_process`
GO:0050793		0.093261	regulation of developmental process	`biological_process`
GO:0050865		0.029924	regulation of cell activation	`biological_process`
GO:0050866		0.039858	negative regulation of cell activation	`biological_process`
GO:0050892		0.089793	intestinal absorption	`biological_process`
GO:0050896		0.00020981	response to stimulus	`biological_process`
GO:0050994		0.052735	regulation of lipid catabolic process	`biological_process`
GO:0051049		0.0054944	regulation of transport	`biological_process`
GO:0051050		0.0080584	positive regulation of transport	`biological_process`
GO:0051093		0.012203	negative regulation of developmental process	`biological_process`
GO:0051128		0.015369	regulation of cellular component organization	`biological_process`
GO:0051130		0.013549	positive regulation of cellular component organization	`biological_process`
GO:0051234		0.0096481	establishment of localization	`biological_process`
GO:0051271		0.077624	negative regulation of cell motion	`biological_process`
GO:0055066		0.074346	di-, tri-valent inorganic cation homeostasis	`biological_process`
GO:0055080		0.047726	cation homeostasis	`biological_process`
GO:0055114		0.0054944	oxidation reduction	`biological_process`
GO:0060249		0.04207	anatomical structure homeostasis	`biological_process`
GO:0060255		0.0030989	regulation of macromolecule metabolic process	`biological_process`

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GO ID	robust pval.	normal pval.	GO Name	process type
GO:0060284		0.042302	regulation of cell development	`biological_process`
GO:0060341		0.036136	regulation of cellular localization	`biological_process`
GO:0060348		0.022761	bone development	`biological_process`
GO:0060401		0.028988	cytosolic calcium ion transport	`biological_process`
GO:0060402		0.028988	calcium ion transport into cytosol	`biological_process`
GO:0060548		0.041318	negative regulation of cell death	`biological_process`
GO:0070011		0.039858	peptidase activity, acting on L-amino acid peptides	`molecular_function`
GO:0070570		0.022361	regulation of neuron projection regeneration	`biological_process`
GO:0080090		0.0045609	regulation of primary metabolic process	`biological_process`
GO:0080134		0.018653	regulation of response to stress	`biological_process`

Table 0.1: Table of GO terms and their p-values, shared by the methods or differing between methods