

Positive Loadings

Negative Loadings

Adipose

term	N-term	N-query	overlap	p_value	domain	term	N-term	N-query	overlap	p_value	domain
cell migration	1500	140	43	1.2e-16	GO:BP	branched-chain amino acid catabolic process	19	140	8	6.3e-11	GO:BP
cell motility	1800	140	43	1.7e-14	GO:BP	branched-chain amino acid metabolic process	22	140	8	2.6e-10	GO:BP
immune system process	2800	140	49	3.9e-11	GO:BP	valine, leucine and isoleucine degradation	56	67	9	1.4e-08	KEGG
intracellular signal transduction	2600	140	47	4.5e-11	GO:BP	organic acid catabolic process	260	140	15	1.8e-08	GO:BP
locomotion	1300	140	33	4.7e-11	GO:BP	carboxylic acid catabolic process	260	140	15	1.8e-08	GO:BP
regulation of cellular component organization	2500	140	46	8.3e-11	GO:BP	small molecule metabolic process	1800	140	35	3.1e-08	GO:BP
cell surface receptor signaling pathway	2800	140	48	8.6e-11	GO:BP	mitochondrion	1900	140	34	9.3e-08	GO:CC
positive regulation of response to stimulus	2400	140	44	1.2e-10	GO:BP	carboxylic acid metabolic process	940	140	24	2.9e-07	GO:BP
vesicle-mediated transport	1500	140	35	2e-10	GO:BP	small molecule catabolic process	390	140	16	4.3e-07	GO:BP
regulation of cell motility	1000	140	29	4.2e-10	GO:BP	oxoacid metabolic process	960	140	24	4.5e-07	GO:BP

Islet

term	N-term	N-query	overlap	p_value	domain	term	N-term	N-query	overlap	p_value	domain
mitotic cell cycle process	720	140	31	2.1e-16	GO:BP	ribosome biogenesis	320	150	23	5e-16	GO:BP
mitotic cell cycle	850	140	31	2.7e-14	GO:BP	small-subunit processome	73	150	10	2.2e-09	GO:CC
cell cycle process	1300	140	34	4.1e-12	GO:BP	preribosome	110	150	11	4.3e-09	GO:CC
regulation of cell cycle process	730	140	26	2.2e-11	GO:BP	nuclear protein-containing complex	2400	150	41	4.4e-09	GO:CC
mitotic nuclear division	270	140	17	1.3e-10	GO:BP	rrna metabolic process	250	150	15	1.4e-08	GO:BP
regulation of cell cycle	1000	140	29	3.9e-10	GO:BP	rrna processing	210	150	14	2.3e-08	GO:BP
organelle fission	500	140	21	4.7e-10	GO:BP	nucleocytoplasmic transport	360	150	17	2.4e-08	GO:BP
nuclear division	440	140	20	4.7e-10	GO:BP	nuclear transport	360	150	17	2.4e-08	GO:BP
cell cycle	1800	140	37	1.1e-09	GO:BP	fibrillar center	150	150	10	3.5e-06	GO:CC
sister chromatid segregation	220	140	15	1.2e-09	GO:BP	ncrna metabolic process	640	150	19	3.6e-06	GO:BP

Liver

term	N-term	N-query	overlap	p_value	domain	term	N-term	N-query	overlap	p value	domain
small molecule metabolic process	1800	140	39	1e-10	GO:BP	positive regulation of nitrogen compound metabolic...	2900	150	65	2.1e-21	GO:BP
monocarboxylic acid metabolic process	700	140	24	8.5e-10	GO:BP	positive regulation of nucleobase-containing compo...	2100	150	55	8.3e-21	GO:BP
oxoacid metabolic process	960	140	27	3.1e-09	GO:BP	transcription by rna polymerase ii	2600	150	59	1.2e-19	GO:BP
organic acid metabolic process	970	140	27	3.6e-09	GO:BP	regulation of transcription by rna polymerase ii	2500	150	57	9.1e-19	GO:BP
organophosphate metabolic process	1000	140	27	1e-08	GO:BP	positive regulation of rna metabolic process	1900	150	50	1.3e-18	GO:BP
carboxylic acid metabolic process	940	140	26	1.2e-08	GO:BP	positive regulation of dna-templated transcription...	1700	150	48	1.9e-18	GO:BP
catabolic process	2500	140	42	2e-08	GO:BP	positive regulation of rna biosynthetic process	1700	150	48	2e-18	GO:BP
carbohydrate derivative metabolic process	1100	140	27	5.2e-08	GO:BP	positive regulation of macromolecule biosynthetic ...	2700	150	57	4.7e-17	GO:BP
organic substance catabolic process	2100	140	37	9.4e-08	GO:BP	protein-dna complex	860	150	33	1.4e-16	GO:CC
lipid metabolic process	1400	140	30	1.6e-07	GO:BP	positive regulation of cellular biosynthetic proce...	2800	150	57	2.7e-16	GO:BP

Muscle

term	N-term	N-query	overlap	p value	domain	term	N-term	N-query	overlap	p value	domain
anatomical structure formation involved in morphog...	1200	150	34	6.3e-12	GO:BP	cytosolic ribosome	130	150	16	4.8e-15	GO:CC
anatomical structure morphogenesis	2800	150	50	1.7e-11	GO:BP	cytoplasmic translation	160	150	16	6.8e-13	GO:BP
circulatory system development	1200	150	33	3.6e-11	GO:BP	ribosomal subunit	200	150	16	5.6e-12	GO:CC
tube development	1200	150	30	3.5e-09	GO:BP	cytosolic small ribosomal subunit	45	150	10	1.2e-11	GO:CC
tube morphogenesis	930	150	26	1.5e-08	GO:BP	ribosome	170	85	16	1.6e-10	KEGG
blood vessel development	760	150	23	6.2e-08	GO:BP	small ribosomal subunit	81	150	11	2e-10	GO:CC
vasculature development	790	150	23	1.4e-07	GO:BP	translation at presynapse	51	150	10	2.8e-10	GO:BP
intracellular signal transduction	2600	150	42	2.1e-07	GO:BP	translation at synapse	52	150	10	3.5e-10	GO:BP
cell migration	1500	150	31	4.9e-07	GO:BP	translation at postsynapse	52	150	10	3.5e-10	GO:BP
angiogenesis	560	150	19	5.5e-07	GO:BP	coronavirus disease - covid-19	240	85	18	3.5e-10	KEGG