

GeDiPNet Cluster 522 -- Enriched GO Terms (Biological Process)

GO term enrichment: Biological Process terms (gene2go, human/tax_id=9606 only), upper-tail hypergeometric test, fold enrichment = (overlap / cluster gene count) / (term gene count / universe size), Benjamini-Hochberg FDR-corrected. Top 15 terms per cluster by q-value. See scripts/build_cluster_go_enrichment.php on gedipnet.bicnirrh.res.in. Data as of: 2026-10-20 03:23:13. · Rows: 15 · Generated: 2026-10-20 00:00:45

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
negative regulation of lipid catabolic process	GO:0050995	3	CIDEA, ADRA2A, BSCL2	21	22	121.34	1.858e-6	1.428e-4
nuclear envelope organization	GO:0006998	3	LMNA, ZMPSTE24, LMNB2	24	22	106.18	2.821e-6	1.997e-4
lipid metabolic process	GO:0006629	8	LIPE, PLIN1, AGPAT2, BSCL2, ZMPSTE24, PCYT1A, PLAAT3, EPHX1	840	22	8.09	2.938e-6	2.063e-4
lipid storage	GO:0019915	3	CIDEA, CAV1, BSCL2	32	22	79.63	6.871e-6	4.058e-4
lipid catabolic process	GO:0016042	4	LIPE, PLIN1, BSCL2, PLAAT3	119	22	28.55	1.046e-5	5.634e-4
nuclear pore localization	GO:0051664	2	LMNA, LMNB2	5	22	339.76	1.320e-5	6.742e-4
ether lipid metabolic process	GO:0046485	2	LIPE, PLAAT3	6	22	283.14	1.979e-5	9.161e-4
protein localization to nuclear envelope	GO:0090435	2	LMNA, LMNB2	8	22	212.35	3.689e-5	1.466e-3
phospholipid biosynthetic process	GO:0008654	3	AGPAT2, PCYT1A, PLAAT3	58	22	43.93	4.190e-5	1.614e-3
negative regulation of cardiac muscle hypertrophy in response to stress	GO:1903243	2	LMNA, PPARG	11	22	154.44	7.230e-5	2.427e-3
lipid droplet organization	GO:0034389	2	CIDEA, BSCL2	18	22	94.38	2.001e-4	5.089e-3
regulation of smooth muscle contraction	GO:0006940	2	ADRA2A, CAV1	21	22	80.90	2.741e-4	6.351e-3
nuclear migration	GO:0007097	2	LMNA, LMNB2	22	22	77.22	3.013e-4	6.803e-3
positive regulation of cell motility	GO:2000147	2	AKT2, CAVIN1	23	22	73.86	3.298e-4	7.164e-3
positive regulation of cholesterol efflux	GO:0010875	2	CAV1, PPARG	27	22	62.92	4.562e-4	8.934e-3