

GeDiPNet Cluster 585 -- 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 03:23:14. · Rows: 15 · Generated: 2026-10-19 23:18:29

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
positive regulation of cholesterol efflux	GO:0010875	2	CAV1, PPARG	27	9	153.80	7.192e-5	2.419e-3
response to progesterone	GO:0032570	2	CAV1, FOS	31	9	133.96	9.519e-5	2.978e-3
lipid storage	GO:0019915	2	BSCL2, CAV1	32	9	129.77	1.015e-4	3.131e-3
positive regulation of miRNA transcription	GO:1902895	2	FOS, PPARG	56	9	74.15	3.133e-4	6.998e-3
phospholipid biosynthetic process	GO:0008654	2	AGPAT2, PCYT1A	58	9	71.60	3.361e-4	7.266e-3
negative regulation of MAPK cascade	GO:0043409	2	CAV1, PPARG	64	9	64.89	4.093e-4	8.311e-3
cellular response to transforming growth factor beta stimulus	GO:0071560	2	CAV1, FOS	67	9	61.98	4.486e-4	8.828e-3
medium-term memory	GO:0072375	1	FOS	1	9	2076.33	4.816e-4	9.241e-3
cellular response to prolactin	GO:1990646	1	FOS	1	9	2076.33	4.816e-4	9.241e-3
negative regulation of BMP signaling pathway	GO:0030514	2	CAV1, PPARG	75	9	55.37	5.618e-4	1.025e-2
negative regulation of connective tissue replacement involved in inflammatory response wound healing	GO:1904597	1	PPARG	2	9	1038.17	9.630e-4	1.423e-2
regulation of the force of heart contraction by chemical signal	GO:0003057	1	CAV1	2	9	1038.17	9.630e-4	1.423e-2
response to forskolin	GO:1904321	1	FOS	2	9	1038.17	9.630e-4	1.423e-2
positive regulation of cold-induced thermogenesis	GO:0120162	2	BSCL2, CAV1	102	9	40.71	1.036e-3	1.498e-2
protein localization to basolateral plasma membrane	GO:1903361	1	CAV1	3	9	692.11	1.444e-3	1.794e-2