

GeDiPNet Cluster 63 -- 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: 2026-10-08 03:23:04. · Rows: 15 · Generated: 2026-10-08 08:45:38

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 connective tissue replacement involved in inflammatory response wound healing	GO:1904597	2	PPARG, AGER	2	49	381.37	6.736e-6	3.882e-4
positive regulation of miRNA transcription	GO:1902895	4	FOS, PPARG, TP53, NOTCH3	56	49	27.24	1.386e-5	6.845e-4
negative regulation of miRNA processing	GO:1903799	2	TP53, ZMPSTE24	3	49	254.24	2.017e-5	9.186e-4
negative regulation of lipid catabolic process	GO:0050995	3	BSCL2, CIDEC, ADRA2A	21	49	54.48	2.180e-5	9.740e-4
nuclear envelope organization	GO:0006998	3	LMNB2, LMNA, ZMPSTE24	24	49	47.67	3.299e-5	1.331e-3
immature T cell proliferation in thymus	GO:0033080	2	ERBB2, WNT4	5	49	152.55	6.702e-5	2.290e-3
nuclear pore localization	GO:0051664	2	LMNB2, LMNA	5	49	152.55	6.702e-5	2.290e-3
lipid storage	GO:0019915	3	BSCL2, CAV1, CIDEC	32	49	35.75	7.966e-5	2.615e-3
positive regulation of DNA metabolic process	GO:0051054	2	AGER, ATAD5	6	49	127.12	1.004e-4	3.100e-3
ether lipid metabolic process	GO:0046485	2	LIPE, PLAAT3	6	49	127.12	1.004e-4	3.100e-3
positive regulation of cell migration	GO:0030335	6	AKT2, CAV1, AGER, PPP3CA, SYNPO2, ADRA2A	292	49	7.84	1.099e-4	3.312e-3
regulation of DNA damage response, signal transduction by p53 class mediator	GO:0043516	2	TP53, ZMPSTE24	7	49	108.96	1.403e-4	3.974e-3
protein localization to nuclear envelope	GO:0090435	2	LMNB2, LMNA	8	49	95.34	1.867e-4	4.920e-3
protein import into nucleus	GO:0006606	4	KPNB1, PPP3CA, TP53, LMNA	110	49	13.87	1.964e-4	5.097e-3
epidermis development	GO:0008544	4	AGPAT2, CCN2, PPP3CA, ZMPSTE24	114	49	13.38	2.252e-4	5.585e-3