

GeDiPNet Cluster 362 -- 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 06:35:57

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 wound healing, spreading of epidermal cells	GO:1903690	2	PTEN, CLASP1	5	5	1494.96	5.726e-7	5.294e-5
phosphatidylinositol 3-kinase/protein kinase B signal transduction	GO:0043491	3	PIK3CD, PIK3R1, PTEN	92	5	121.87	1.147e-6	9.353e-5
negative regulation of stress fiber assembly	GO:0051497	2	PIK3R1, CLASP1	33	5	226.51	3.014e-5	1.239e-3
cell migration	GO:0016477	3	PIK3CD, PTEN, KNSTRN	303	5	37.00	4.120e-5	1.586e-3
phosphatidylinositol phosphate biosynthetic process	GO:0046854	2	PIK3CD, PIK3R1	43	5	173.83	5.149e-5	1.875e-3
T cell differentiation	GO:0030217	2	PIK3CD, PIK3R1	54	5	138.42	8.151e-5	2.662e-3
B cell differentiation	GO:0030183	2	PIK3CD, PIK3R1	80	5	93.44	1.795e-4	4.778e-3
negative regulation of cell communication	GO:0010648	1	PTEN	1	5	3737.40	2.676e-4	6.316e-3
negative regulation of synaptic vesicle clustering	GO:2000808	1	PTEN	1	5	3737.40	2.676e-4	6.316e-3
positive regulation of endoplasmic reticulum unfolded protein response	GO:1900103	1	PIK3R1	2	5	1868.70	5.351e-4	1.019e-2
natural killer cell chemotaxis	GO:0035747	1	PIK3CD	2	5	1868.70	5.351e-4	1.019e-2
negative regulation of keratinocyte migration	GO:0051548	1	PTEN	2	5	1868.70	5.351e-4	1.019e-2
positive regulation of basement membrane assembly involved in embryonic body morphogenesis	GO:1904261	1	CLASP1	2	5	1868.70	5.351e-4	1.019e-2
negative regulation of microtubule polymerization or depolymerization	GO:0031111	1	CLASP1	2	5	1868.70	5.351e-4	1.019e-2
microtubule cytoskeleton organization	GO:0000226	2	KNSTRN, CLASP1	149	5	50.17	6.216e-4	1.135e-2