

GeDiPNet Cluster 61 -- 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 04:18:31

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 epithelial cell proliferation	GO:0050679	6	ERBB2, TCF7L2, EGFR, HRAS, TGFA, TGFB1	73	67	22.92	2.383e-7	2.549e-5
ERBB2-EGFR signaling pathway	GO:0038134	3	ERBB2, EGFR, TGFA	8	67	104.59	2.435e-6	1.721e-4
regulation of cell population proliferation	GO:0042127	7	ERBB2, PTGS2, SMAD4, TBX19, EGFR, HRAS, TGFB1	201	67	9.71	7.558e-6	4.270e-4
positive regulation of fibroblast proliferation	GO:0048146	4	CDKN1A, EGFR, HRAS, TGFB1	55	67	20.28	4.485e-5	1.693e-3
positive regulation of miRNA transcription	GO:1902895	4	SMAD4, TERT, EGFR, TGFB1	56	67	19.92	4.817e-5	1.778e-3
response to UV-A	GO:0070141	2	CCND1, EGFR	4	67	139.46	7.563e-5	2.513e-3
negative regulation of apoptotic process	GO:0043066	9	BAG1, ERBB2, PTGS2, SOD2, TERT, EGFR, AAMDC, CRYAB, HSPB1	524	67	4.79	1.007e-4	3.110e-3
cellular response to gamma radiation	GO:0071480	3	CDKN1A, HRAS, CRYAB	28	67	29.88	1.353e-4	3.867e-3
cellular response to hypoxia	GO:0071456	5	ATF4, PTGS2, TERT, TGFB1, AQP3	139	67	10.03	1.413e-4	4.000e-3
cellular response to growth factor stimulus	GO:0071363	4	ERBB2, SMAD4, EGFR, TGFB1	76	67	14.68	1.595e-4	4.378e-3
gamma-aminobutyric acid signaling pathway	GO:0007214	3	ATF4, GABBR2, GABRA3	30	67	27.89	1.669e-4	4.522e-3
positive regulation of vascular endothelial growth factor production	GO:0010575	3	ATF4, PTGS2, TGFB1	32	67	26.15	2.028e-4	5.209e-3
oncogene-induced cell senescence	GO:0090402	2	CDKN1A, HRAS	7	67	79.69	2.629e-4	6.233e-3
cell population proliferation	GO:0008283	6	ERBB2, SMAD4, CCND1, EGFR, ODC1, TGFB1	263	67	6.36	3.571e-4	7.749e-3
cell surface receptor signaling pathway	GO:0007166	7	BAG1, CD274, ERBB2, TNFRSF10B, EGFR, HRAS, TGFA	373	67	5.23	3.708e-4	7.973e-3