

GeDiPNet Cluster 381 -- 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: 2026-10-07 03:23:06. · Rows: 15 · Generated: 2026-10-07 09:46:33

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 bone resorption	GO:0045780	3	LTBP3, SPP1, TNFSF11	15	51	73.28	8.514e-6	4.600e-4
stem cell proliferation	GO:0072089	4	PRRX1, CD109, KDR, TGFB1	54	51	27.14	1.407e-5	6.816e-4
positive regulation of phosphatidylinositol 3-kinase/protein kinase B signal transduction	GO:0051897	6	KDR, MFHAS1, RELN, SEMA4D, TGFB1, TNFSF11	217	51	10.13	2.665e-5	1.117e-3
regulation of miRNA transcription	GO:1902893	2	SMAD3, TGFB1	4	51	183.21	4.366e-5	1.629e-3
osteoclast proliferation	GO:0002158	2	CSF1, TNFSF11	5	51	146.56	7.264e-5	2.385e-3
embryonic cranial skeleton morphogenesis	GO:0048701	3	PRRX1, IRX5, SMAD3	31	51	35.46	8.156e-5	2.596e-3
regulation of striated muscle tissue development	GO:0016202	2	SMAD3, TGFB1	6	51	122.14	1.088e-4	3.216e-3
positive regulation of cell migration	GO:0030335	6	CSF1, KDR, PREX1, SEMA4D, SMAD3, TGFB1	292	51	7.53	1.379e-4	3.839e-3
positive regulation of mesenchymal stem cell proliferation	GO:1902462	2	LTBP3, TGFB1	7	51	104.69	1.520e-4	4.136e-3
positive regulation of stem cell proliferation	GO:2000648	3	PRRX1, KDR, TGFB1	41	51	26.81	1.897e-4	4.875e-3
protein autophosphorylation	GO:0046777	4	MAK, KDR, MEX3B, PEAK1	113	51	12.97	2.545e-4	5.993e-3
positive regulation of extracellular matrix assembly	GO:1901203	2	SMAD3, TGFB1	9	51	81.42	2.597e-4	6.076e-3
osteoclast differentiation	GO:0030316	3	CSF1, TGFB1, TNFSF11	49	51	22.43	3.229e-4	7.058e-3
positive regulation of positive chemotaxis	GO:0050927	2	KDR, SMAD3	11	51	66.62	3.954e-4	8.137e-3
transforming growth factor beta receptor superfamily signaling pathway	GO:0141091	2	SMAD3, TGFB1	11	51	66.62	3.954e-4	8.137e-3