

GeDiPNet Cluster 316 -- 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 03:34:01

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
cell-cell adhesion mediated by cadherin	GO:0044331	4	CDH1, CTNND1, PLEKHA7, DCHS2	42	11	161.79	7.190e-9	1.253e-6
cell-cell adhesion	GO:0098609	4	CDH1, CTNND1, PLEKHA7, DCHS2	218	11	31.17	5.576e-6	3.342e-4
negative regulation of blood vessel branching	GO:1905554	1	CTNND1	1	11	1698.82	5.886e-4	1.091e-2
negative regulation of miRNA catabolic process	GO:2000626	1	TENT2	2	11	849.41	1.177e-3	1.702e-2
ureteric bud invasion	GO:0072092	1	KIF26B	2	11	849.41	1.177e-3	1.702e-2
positive regulation of protein localization to cell-cell junction	GO:0150107	1	CTNND1	3	11	566.27	1.765e-3	2.164e-2
condensed mesenchymal cell proliferation	GO:0072137	1	DCHS2	3	11	566.27	1.765e-3	2.164e-2
zonula adherens maintenance	GO:0045218	1	PLEKHA7	3	11	566.27	1.765e-3	2.164e-2
response to heparin	GO:0071503	1	CDH1	3	11	566.27	1.765e-3	2.164e-2
regulation of protein catabolic process at postsynapse, modulating synaptic transmission	GO:0099576	1	CDH1	4	11	424.70	2.353e-3	2.546e-2
target-directed miRNA degradation	GO:0140958	1	TENT2	4	11	424.70	2.353e-3	2.546e-2
cellular response to indole-3-methanol	GO:0071681	1	CDH1	5	11	339.76	2.940e-3	2.858e-2
response to Gram-positive bacterium	GO:0140459	1	CDH1	6	11	283.14	3.527e-3	3.150e-2
negative regulation of D-glucose transmembrane transport	GO:0010829	1	CTNND1	7	11	242.69	4.114e-3	3.375e-2
desmosome assembly	GO:0002159	1	CDH1	7	11	242.69	4.114e-3	3.375e-2