

GeDiPNet Cluster 165 -- 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 06:32:01

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	16	111.23	3.933e-8	5.536e-6
cell-cell adhesion	GO:0098609	5	CDH1, CTNND1, MYH9, PLEKHA7, DCHS2	218	16	26.79	8.119e-7	7.003e-5
negative regulation of blood vessel branching	GO:1905554	1	CTNND1	1	16	1167.94	8.562e-4	1.360e-2
regulation of systemic arterial blood pressure by circulatory renin-angiotensin	GO:0001991	1	AGTR2	1	16	1167.94	8.562e-4	1.360e-2
G protein-coupled receptor signaling pathway coupled to cGMP nucleotide second messenger	GO:0007199	1	AGTR2	2	16	583.97	1.712e-3	2.068e-2
regulation of metanephros size	GO:0035566	1	AGTR2	2	16	583.97	1.712e-3	2.068e-2
negative regulation of miRNA catabolic process	GO:2000626	1	TENT2	2	16	583.97	1.712e-3	2.068e-2
brain renin-angiotensin system	GO:0002035	1	AGTR2	2	16	583.97	1.712e-3	2.068e-2
ureteric bud invasion	GO:0072092	1	KIF26B	2	16	583.97	1.712e-3	2.068e-2
uropod organization	GO:0032796	1	MYH9	2	16	583.97	1.712e-3	2.068e-2
positive regulation of protein processing in phagocytic vesicle	GO:1903923	1	MYH9	2	16	583.97	1.712e-3	2.068e-2
cortical granule exocytosis	GO:0060471	1	MYH9	2	16	583.97	1.712e-3	2.068e-2
positive regulation of mast cell differentiation	GO:0060376	1	STAT5A	2	16	583.97	1.712e-3	2.068e-2
negative regulation of actin filament severing	GO:1903919	1	MYH9	2	16	583.97	1.712e-3	2.068e-2
cell adhesion	GO:0007155	4	CDH1, CTNND1, MYH9, DCHS2	665	16	7.03	2.055e-3	2.295e-2