

GeDiPNet Cluster 455 -- 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: 2026-10-20 03:23:14. · Rows: 15 · Generated: 2026-10-20 00:01:16

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
cell migration involved in coronary angiogenesis	GO:0060981	1	PDGFRB	1	21	889.86	1.124e-3	1.550e-2
metanephric glomerular mesangial cell proliferation involved in metanephros development	GO:0072262	1	PDGFRB	1	21	889.86	1.124e-3	1.550e-2
glomerular epithelium development	GO:0072010	1	FOXC1	1	21	889.86	1.124e-3	1.550e-2
positive regulation of hematopoietic stem cell differentiation	GO:1902038	1	FOXC1	1	21	889.86	1.124e-3	1.550e-2
beta-catenin-TCF complex assembly	GO:1904837	1	KMT2D	1	21	889.86	1.124e-3	1.550e-2
visual learning	GO:0008542	2	BRAF, TUBA1A	54	21	32.96	1.662e-3	1.931e-2
pattern specification process	GO:0007389	2	MID1, ZIC1	60	21	29.66	2.047e-3	2.148e-2
cell migration involved in vasculogenesis	GO:0035441	1	PDGFRB	2	21	444.93	2.246e-3	2.244e-2
smooth muscle cell chemotaxis	GO:0071670	1	PDGFRB	2	21	444.93	2.246e-3	2.244e-2
apoptotic process involved in outflow tract morphogenesis	GO:0003275	1	FOXC1	2	21	444.93	2.246e-3	2.244e-2
negative regulation of apoptotic process involved in outflow tract morphogenesis	GO:1902257	1	FOXC1	2	21	444.93	2.246e-3	2.244e-2
maintenance of cell number	GO:0098727	1	ZIC1	2	21	444.93	2.246e-3	2.244e-2
cilium assembly	GO:0060271	3	PIBF1, ARMC9, HYLS1	237	21	11.26	2.263e-3	2.256e-2
hippocampus development	GO:0021766	2	TUBA1A, ZIC1	74	21	24.05	3.094e-3	2.654e-2
positive T cell selection	GO:0043368	1	BRAF	3	21	296.62	3.368e-3	2.763e-2