

GeDiPNet Cluster 457 -- 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: 2026-10-19 23:18:31

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
carbon dioxide transport	GO:0015670	4	HBB, HBG2, HBD, HBG1	13	7	821.41	4.921e-12	2.005e-9
oxygen transport	GO:0015671	4	HBB, HBG2, HBD, HBG1	17	7	628.13	1.637e-11	5.929e-9
erythrocyte development	GO:0048821	4	HBB, HBG2, HBD, HBG1	32	7	333.70	2.469e-10	6.879e-8
regulation of timing of catagen	GO:0051794	1	TGFB2	1	7	2669.57	3.746e-4	7.813e-3
positive regulation of activation-induced cell death of T cells	GO:0070237	1	TGFB2	1	7	2669.57	3.746e-4	7.813e-3
regulation of apoptotic process involved in outflow tract morphogenesis	GO:1902256	1	TGFB2	1	7	2669.57	3.746e-4	7.813e-3
negative regulation of epithelial to mesenchymal transition involved in endocardial cushion formation	GO:1905006	1	TGFB2	1	7	2669.57	3.746e-4	7.813e-3
uterine wall breakdown	GO:0042704	1	TGFB2	2	7	1334.79	7.491e-4	1.230e-2
substantia propria of cornea development	GO:1903701	1	TGFB2	2	7	1334.79	7.491e-4	1.230e-2
positive regulation of timing of catagen	GO:0051795	1	TGFB2	3	7	889.86	1.123e-3	1.550e-2
cardioblast differentiation	GO:0010002	1	TGFB2	3	7	889.86	1.123e-3	1.550e-2
positive regulation of integrin biosynthetic process	GO:0045726	1	TGFB2	3	7	889.86	1.123e-3	1.550e-2
positive regulation of cardioblast differentiation	GO:0051891	1	TGFB2	4	7	667.39	1.498e-3	1.821e-2
regulation of transforming growth factor beta2 production	GO:0032909	1	TGFB2	4	7	667.39	1.498e-3	1.821e-2
ascending aorta morphogenesis	GO:0035910	1	TGFB2	4	7	667.39	1.498e-3	1.821e-2