

GeDiPNet Cluster 560 -- 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
ossification involved in bone maturation	GO:0043931	2	RHOA, RYR1	12	11	283.14	2.072e-5	9.507e-4
endothelial cell migration	GO:0043542	2	PIK3CA, RHOA	48	11	70.78	3.501e-4	7.487e-3
angiotensin-mediated vasoconstriction involved in regulation of systemic arterial blood pressure	GO:0001998	1	RHOA	1	11	1698.82	5.886e-4	1.058e-2
alpha-beta T cell lineage commitment	GO:0002363	1	RHOA	1	11	1698.82	5.886e-4	1.058e-2
mitotic cleavage furrow formation	GO:1903673	1	RHOA	1	11	1698.82	5.886e-4	1.058e-2
regulation of ERBB signaling pathway	GO:1901184	1	SH3TC2	1	11	1698.82	5.886e-4	1.058e-2
response to butyrate	GO:1903544	1	PIK3CA	1	11	1698.82	5.886e-4	1.058e-2
regulation of membrane potential	GO:0042391	2	PIEZO2, SCN1A	85	11	39.97	1.095e-3	1.537e-2
aortic valve formation	GO:0003189	1	RHOA	2	11	849.41	1.177e-3	1.592e-2
endothelial tube lumen extension	GO:0097498	1	RHOA	2	11	849.41	1.177e-3	1.592e-2
skeletal muscle satellite cell migration	GO:1902766	1	RHOA	2	11	849.41	1.177e-3	1.592e-2
positive regulation of vascular associated smooth muscle contraction	GO:1904695	1	RHOA	2	11	849.41	1.177e-3	1.592e-2
microvillus organization	GO:0032528	1	GLDN	2	11	849.41	1.177e-3	1.592e-2
response to muscle inactivity	GO:0014870	1	PIK3CA	2	11	849.41	1.177e-3	1.592e-2
phosphatidylinositol 3-kinase/protein kinase B signal transduction	GO:0043491	2	PIK3CA, COL6A3	92	11	36.93	1.281e-3	1.669e-2