

GeDiPNet Cluster 553 -- 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 23:19:09

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
molybdopterin cofactor biosynthetic process	GO:0032324	2	MOCS1, MOCS2	4	4	2335.88	2.062e-7	2.318e-5
Mo-molybdopterin cofactor biosynthetic process	GO:0006777	2	MOCS1, MOCS2	6	4	1557.25	5.153e-7	4.996e-5
hypotonic response	GO:0006971	1	ITGA2	3	4	1557.25	6.421e-4	1.113e-2
regulation of non-canonical Wnt signaling pathway	GO:2000050	1	DAAM2	3	4	1557.25	6.421e-4	1.113e-2
response to L-ascorbic acid	GO:0033591	1	ITGA2	4	4	1167.94	8.560e-4	1.331e-2
response to parathyroid hormone	GO:0071107	1	ITGA2	5	4	934.35	1.070e-3	1.514e-2
collagen-activated signaling pathway	GO:0038065	1	ITGA2	6	4	778.63	1.284e-3	1.669e-2
positive regulation of transmission of nerve impulse	GO:0051971	1	ITGA2	6	4	778.63	1.284e-3	1.669e-2
podocyte cell migration	GO:0090521	1	DAAM2	7	4	667.39	1.498e-3	1.821e-2
dorsal spinal cord development	GO:0021516	1	DAAM2	8	4	583.97	1.711e-3	1.958e-2
substrate-dependent cell migration	GO:0006929	1	ITGA2	8	4	583.97	1.711e-3	1.958e-2
positive regulation of cell projection organization	GO:0031346	1	ITGA2	8	4	583.97	1.711e-3	1.958e-2
response to amine	GO:0014075	1	ITGA2	10	4	467.18	2.139e-3	2.189e-2
positive regulation of positive chemotaxis	GO:0050927	1	ITGA2	11	4	424.70	2.353e-3	2.301e-2
positive regulation of phagocytosis, engulfment	GO:0060100	1	ITGA2	12	4	389.31	2.566e-3	2.402e-2