

GeDiPNet Cluster 249 -- 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 11:05:27

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
endothelium development	GO:0003158	3	KRIT1, CCM2, PDCD10	10	13	431.24	3.147e-8	4.570e-6
regulation of angiogenesis	GO:0045765	3	KRIT1, CCM2, PDCD10	43	13	100.29	3.194e-6	2.101e-4
angiogenesis	GO:0001525	4	KRIT1, PDCD10, PIK3CA, RASA1	284	13	20.25	3.352e-5	1.332e-3
negative regulation of nitric oxide biosynthetic process	GO:0045019	2	GLA, PTGIS	15	13	191.66	4.667e-5	1.706e-3
vasculature development	GO:0001944	2	CCM2, PIK3CA	33	13	87.12	2.330e-4	5.619e-3
organophosphate catabolic process	GO:0046434	1	PON1	1	13	1437.46	6.957e-4	1.192e-2
response to butyrate	GO:1903544	1	PIK3CA	1	13	1437.46	6.957e-4	1.192e-2
vasculogenesis	GO:0001570	2	CCM2, RASA1	63	13	45.63	8.519e-4	1.360e-2
blood vessel development	GO:0001568	2	CCM2, MAP3K3	70	13	41.07	1.051e-3	1.558e-2
negative regulation of nitric-oxide synthase activity	GO:0051001	1	GLA	2	13	718.73	1.391e-3	1.837e-2
response to muscle inactivity	GO:0014870	1	PIK3CA	2	13	718.73	1.391e-3	1.837e-2
glycosylceramide catabolic process	GO:0046477	1	GLA	3	13	479.15	2.086e-3	2.313e-2
cellular response to hydrostatic pressure	GO:0071464	1	PIK3CA	3	13	479.15	2.086e-3	2.313e-2
negative regulation of plasma lipoprotein oxidation	GO:0034445	1	PON1	3	13	479.15	2.086e-3	2.313e-2
intrinsic apoptotic signaling pathway in response to hydrogen peroxide	GO:0036481	1	PDCD10	3	13	479.15	2.086e-3	2.313e-2