

GeDiPNet Cluster 560 -- Enriched Pathways

Pathway enrichment: KEGG + Reactome, upper-tail hypergeometric test, Benjamini-Hochberg FDR-corrected. Fold enrichment = (overlap / cluster gene count) / (pathway gene count / universe size). Top 15 pathways per cluster by q-value. See scripts/build_cluster_enrichment.php on gedipnet.bicnirrh.res.in. Data as of: 2026-10-20 03:30:09. · Rows: 15 · Generated: 2026-10-20 00:02:53

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
PI3K/AKT activation	Reactome	2	PIK3CA, RHOA	9	11	242.63	2.736e-5	6.732e-4
GPVI-mediated activation cascade	Reactome	2	PIK3CA, RHOA	34	11	64.22	4.211e-4	5.847e-3
Focal adhesion	KEGG	3	PIK3CA, RHOA, COL6A3	203	11	16.14	7.103e-4	8.740e-3
Assembly of collagen fibrils and other multimeric structures	Reactome	2	COL6A3, DST	51	11	42.82	9.489e-4	1.089e-2
VEGFA-VEGFR2 Pathway	Reactome	2	PIK3CA, RHOA	62	11	35.22	1.400e-3	1.462e-2
Bacterial invasion of epithelial cells	KEGG	2	PIK3CA, RHOA	78	11	28.00	2.205e-3	2.046e-2
Colorectal cancer	KEGG	2	PIK3CA, RHOA	87	11	25.10	2.735e-3	2.390e-2
Axonal growth stimulation	Reactome	1	RHOA	4	11	272.95	3.659e-3	2.935e-2
SLIT2:ROBO1 increases RHOA activity	Reactome	1	RHOA	4	11	272.95	3.659e-3	2.935e-2
C-type lectin receptor signaling pathway	KEGG	2	PIK3CA, RHOA	105	11	20.80	3.955e-3	3.109e-2
RHO GTPases Activate ROCKs	Reactome	1	RHOA	5	11	218.36	4.572e-3	3.438e-2
Leukocyte transendothelial migration	KEGG	2	PIK3CA, RHOA	116	11	18.82	4.805e-3	3.559e-2
Neurotrophin signaling pathway	KEGG	2	PIK3CA, RHOA	120	11	18.20	5.134e-3	3.717e-2
Sphingolipid signaling pathway	KEGG	2	PIK3CA, RHOA	122	11	17.90	5.302e-3	3.795e-2
T cell receptor signaling pathway	KEGG	2	PIK3CA, RHOA	122	11	17.90	5.302e-3	3.795e-2