

GeDiPNet Cluster 329 -- 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: 2026-10-07 03:30:09. · Rows: 15 · Generated: 2026-10-07 21:41:00

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Nef mediated downregulation of MHC class I complex cell surface expression	Reactome	1	AP1S2	10	14	85.79	1.160e-2	7.504e-2
CD28 dependent Vav1 pathway	Reactome	1	PAK3	12	14	71.49	1.391e-2	8.315e-2
Sema3A PAK dependent Axon repulsion	Reactome	1	PAK3	15	14	57.19	1.735e-2	9.505e-2
Major pathway of rRNA processing in the nucleolus and cytosol	Reactome	2	LAS1L, RPL10	184	14	9.32	1.882e-2	9.943e-2
Ephrin signaling	Reactome	1	PAK3	19	14	45.15	2.193e-2	1.084e-1
CD209 (DC-SIGN) signaling	Reactome	1	PAK3	21	14	40.85	2.422e-2	1.147e-1
Human immunodeficiency virus 1 infection	KEGG	2	AP1S2, PAK3	213	14	8.05	2.476e-2	1.157e-1
Downregulation of SMAD2/3:SMAD4 transcriptional activity	Reactome	1	USP9X	22	14	38.99	2.536e-2	1.173e-1
RHO GTPases activate PAKs	Reactome	1	PAK3	23	14	37.30	2.649e-2	1.203e-1
Dopamine Neurotransmitter Release Cycle	Reactome	1	CASK	23	14	37.30	2.649e-2	1.203e-1
VEGFR2 mediated vascular permeability	Reactome	1	PAK3	29	14	29.58	3.330e-2	1.369e-1
Synthesis of active ubiquitin: roles of E1 and E2 enzymes	Reactome	1	USP9X	30	14	28.60	3.443e-2	1.393e-1
Generation of second messenger molecules	Reactome	1	PAK3	31	14	27.67	3.556e-2	1.422e-1
Neurexins and neuroligins	Reactome	1	CASK	32	14	26.81	3.668e-2	1.445e-1
Lysosome Vesicle Biogenesis	Reactome	1	AP1S2	35	14	24.51	4.006e-2	1.519e-1