

GeDiPNet Cluster 278 -- 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 03:09:29

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Late Phase of HIV Life Cycle	Reactome	1	NMT1	1	15	800.67	1.249e-3	1.600e-2
Cellular response to hypoxia	Reactome	1	EPAS1	3	15	266.89	3.743e-3	3.593e-2
Activation, myristoylation of BID and translocation to mitochondria	Reactome	1	NMT1	4	15	200.17	4.987e-3	4.365e-2
PTK6 Expression	Reactome	1	EPAS1	5	15	160.13	6.230e-3	5.059e-2
FGFR1b ligand binding and activation	Reactome	1	FGF3	6	15	133.44	7.472e-3	5.688e-2
FGFR2b ligand binding and activation	Reactome	1	FGF3	10	15	80.07	1.242e-2	7.776e-2
Regulation of gene expression by Hypoxia-inducible Factor	Reactome	1	EPAS1	11	15	72.79	1.366e-2	8.229e-2
FGFRL1 modulation of FGFR1 signaling	Reactome	1	FGF3	13	15	61.59	1.612e-2	9.107e-2
Phospholipase C-mediated cascade: FGFR1	Reactome	1	FGF3	16	15	50.04	1.981e-2	1.022e-1
Transcriptional regulation of pluripotent stem cells	Reactome	1	EPAS1	17	15	47.10	2.104e-2	1.058e-1
Activated point mutants of FGFR2	Reactome	1	FGF3	17	15	47.10	2.104e-2	1.058e-1
Phospholipase C-mediated cascade; FGFR2	Reactome	1	FGF3	18	15	44.48	2.226e-2	1.093e-1
Downstream signaling of activated FGFR1	Reactome	1	FGF3	18	15	44.48	2.226e-2	1.093e-1
PI-3K cascade:FGFR1	Reactome	1	FGF3	21	15	38.13	2.592e-2	1.188e-1
SHC-mediated cascade:FGFR1	Reactome	1	FGF3	21	15	38.13	2.592e-2	1.188e-1