

GeDiPNet Cluster 453 -- 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](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 00:03:00

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Defective SLC4A4 causes renal tubular acidosis, proximal, with ocular abnormalities and mental retardation (pRTA-OA)	Reactome	1	SLC4A4	1	16	750.63	1.332e-3	1.409e-2
Toxicity of botulinum toxin type B (BoNT/B)	Reactome	1	SYT1	3	16	250.21	3.992e-3	3.122e-2
SMAD4 MH2 Domain Mutants in Cancer	Reactome	1	SMAD2	3	16	250.21	3.992e-3	3.122e-2
SMAD2/3 MH2 Domain Mutants in Cancer	Reactome	1	SMAD2	3	16	250.21	3.992e-3	3.122e-2
Regulation of commissural axon pathfinding by SLIT and ROBO	Reactome	1	ROBO1	3	16	250.21	3.992e-3	3.122e-2
Toxicity of botulinum toxin type G (BoNT/G)	Reactome	1	SYT1	3	16	250.21	3.992e-3	3.122e-2
Role of ABL in ROBO-SLIT signaling	Reactome	1	ROBO1	4	16	187.66	5.319e-3	3.801e-2
SLIT2:ROBO1 increases RHOA activity	Reactome	1	ROBO1	4	16	187.66	5.319e-3	3.801e-2
Signaling by NODAL	Reactome	1	SMAD2	6	16	125.10	7.968e-3	4.940e-2
RUNX1 regulates transcription of genes involved in differentiation of keratinocytes	Reactome	1	CTSK	6	16	125.10	7.968e-3	4.940e-2
SMAD2/3 Phosphorylation Motif Mutants in Cancer	Reactome	1	SMAD2	6	16	125.10	7.968e-3	4.940e-2
TGFBR1 KD Mutants in Cancer	Reactome	1	SMAD2	6	16	125.10	7.968e-3	4.940e-2
Regulation of expression of SLITs and ROBOs	Reactome	1	ROBO1	8	16	93.83	1.061e-2	5.902e-2
Bicarbonate transporters	Reactome	1	SLC4A4	10	16	75.06	1.325e-2	6.742e-2
FOXO-mediated transcription of cell cycle genes	Reactome	1	SMAD2	11	16	68.24	1.456e-2	7.132e-2