

GeDiPNet Cluster 123 -- 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 17:18:39

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Negative regulation of TCF-dependent signaling by WNT ligand antagonists	Reactome	2	LRP5, SOST	8	9	333.61	1.395e-5	4.419e-4
Vitamin D (calciferol) metabolism	Reactome	2	LRP2, VDR	11	9	242.63	2.736e-5	7.707e-4
Parathyroid hormone synthesis, secretion and action	KEGG	3	LRP5, SOST, VDR	115	9	34.81	6.889e-5	1.654e-3
Regulation of FZD by ubiquitination	Reactome	2	LRP5, LGR4	21	9	127.09	1.041e-4	2.327e-3
Wnt signaling pathway	KEGG	3	LRP5, LGR4, SOST	174	9	23.01	2.355e-4	4.443e-3
Influenza Virus Induced Apoptosis	Reactome	1	TGFB1	2	9	667.22	1.498e-3	1.846e-2
TGFBR2 MSI Frameshift Mutants in Cancer	Reactome	1	TGFB1	2	9	667.22	1.498e-3	1.846e-2
TGFBR2 Kinase Domain Mutants in Cancer	Reactome	1	TGFB1	3	9	444.81	2.247e-3	2.484e-2
TGFBR1 LBD Mutants in Cancer	Reactome	1	TGFB1	4	9	333.61	2.995e-3	3.068e-2
Misspliced LRP5 mutants have enhanced beta-catenin-dependent signaling	Reactome	1	LRP5	6	9	222.41	4.489e-3	4.079e-2
SMAD2/3 Phosphorylation Motif Mutants in Cancer	Reactome	1	TGFB1	6	9	222.41	4.489e-3	4.079e-2
TGFBR1 KD Mutants in Cancer	Reactome	1	TGFB1	6	9	222.41	4.489e-3	4.079e-2
RUNX3 regulates CDKN1A transcription	Reactome	1	TGFB1	7	9	190.63	5.235e-3	4.504e-2
Gastric cancer	KEGG	2	LRP5, TGFB1	150	9	17.79	5.266e-3	4.526e-2
Efferocytosis	KEGG	2	TGFB1, PLA2G6	157	9	17.00	5.756e-3	4.811e-2