

GeDiPNet Cluster 90 -- 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 03:57:06

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
FGFR1c ligand binding and activation	Reactome	3	FGF8, ANOS1, FGFR1	12	53	56.65	1.736e-5	5.323e-4
PI3K Cascade	Reactome	4	FGFR2, FGF8, FGFR1, KLB	39	53	23.24	2.479e-5	7.122e-4
COPI-independent Golgi-to-ER retrograde traffic	Reactome	4	RAB18, RAB3GAP1, RAB3GAP2, TUBB3	51	53	17.77	7.244e-5	1.722e-3
Negative regulation of FGFR1 signaling	Reactome	3	FGF8, ANOS1, FGFR1	26	53	26.15	1.964e-4	3.848e-3
Constitutive Signaling by Aberrant PI3K in Cancer	Reactome	4	FGFR2, FGF8, FGFR1, KLB	75	53	12.09	3.258e-4	5.725e-3
Ligand-receptor interactions	Reactome	2	GAS1, PTCH1	7	53	64.74	3.956e-4	6.654e-3
PIP3 activates AKT signaling	Reactome	4	FGFR2, FGF8, FGFR1, KLB	93	53	9.75	7.382e-4	1.081e-2
Signaling by activated point mutants of FGFR1	Reactome	2	FGF8, FGFR1	11	53	41.20	1.025e-3	1.380e-2
PI5P, PP2A and IER3 Regulate PI3K/AKT Signaling	Reactome	4	FGFR2, FGF8, FGFR1, KLB	103	53	8.80	1.082e-3	1.440e-2
FGFR2c ligand binding and activation	Reactome	2	FGFR2, FGF8	13	53	34.86	1.445e-3	1.793e-2
Phospholipase C-mediated cascade; FGFR4	Reactome	2	FGF8, KLB	15	53	30.21	1.934e-3	2.222e-2
RAF/MAP kinase cascade	Reactome	4	FGFR2, FGF8, FGFR1, KLB	124	53	7.31	2.145e-3	2.404e-2
Phospholipase C-mediated cascade: FGFR1	Reactome	2	FGF8, FGFR1	16	53	28.33	2.204e-3	2.450e-2
Activated point mutants of FGFR2	Reactome	2	FGFR2, FGF8	17	53	26.66	2.491e-3	2.686e-2
Activation of SMO	Reactome	2	GAS1, PTCH1	18	53	25.18	2.794e-3	2.922e-2