

GeDiPNet Cluster 426 -- 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 21:40:04

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Smooth Muscle Contraction	Reactome	5	ACTG2, MYH11, LMOD1, MYL9, MYLK	34	20	88.31	2.012e-9	2.063e-7
Vascular smooth muscle contraction	KEGG	5	ACTG2, MYH11, MYL9, MYLK, EDN3	134	20	22.41	2.174e-6	9.443e-5
RHO GTPases activate PAKs	Reactome	3	MYH11, MYL9, MYLK	23	20	78.33	6.847e-6	2.445e-4
GRB7 events in ERBB2 signaling	Reactome	2	ERBB3, ERBB2	5	20	240.20	2.627e-5	7.466e-4
Tight junction	KEGG	4	MYH11, MYL9, GATA4, ERBB2	170	20	14.13	1.573e-4	3.227e-3
Downregulation of ERBB2:ERBB3 signaling	Reactome	2	ERBB3, ERBB2	13	20	92.38	2.033e-4	3.951e-3
ERBB2 Activates PTK6 Signaling	Reactome	2	ERBB3, ERBB2	13	20	92.38	2.033e-4	3.951e-3
Constitutive Signaling by Aberrant PI3K in Cancer	Reactome	3	PTPN11, ERBB3, ERBB2	75	20	24.02	2.470e-4	4.604e-3
Motor proteins	KEGG	4	ACTG2, MYH11, MYL9, KIF26B	194	20	12.38	2.611e-4	4.810e-3
ERBB2 Regulates Cell Motility	Reactome	2	ERBB3, ERBB2	15	20	80.07	2.731e-4	4.982e-3
TFAP2 (AP-2) family regulates transcription of growth factors and their receptors	Reactome	2	TFAP2B, ERBB2	15	20	80.07	2.731e-4	4.982e-3
PI3K events in ERBB2 signaling	Reactome	2	ERBB3, ERBB2	16	20	75.06	3.118e-4	5.526e-3
SHC1 events in ERBB2 signaling	Reactome	2	ERBB3, ERBB2	17	20	70.65	3.530e-4	6.090e-3
Signaling by ERBB2	Reactome	2	ERBB3, ERBB2	18	20	66.72	3.967e-4	6.664e-3
PIP3 activates AKT signaling	Reactome	3	PTPN11, ERBB3, ERBB2	93	20	19.37	4.658e-4	7.547e-3