

GeDiPNet Cluster 420 -- 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 03:10:42

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Regulation of KIT signaling	Reactome	1	KIT	14	1	857.86	1.166e-3	1.522e-2
TFAP2 (AP-2) family regulates transcription of growth factors and their receptors	Reactome	1	KIT	15	1	800.67	1.249e-3	1.600e-2
Signaling by SCF-KIT	Reactome	1	KIT	37	1	324.59	3.081e-3	3.132e-2
Acute myeloid leukemia	KEGG	1	KIT	68	1	176.62	5.662e-3	4.751e-2
Central carbon metabolism in cancer	KEGG	1	KIT	71	1	169.15	5.912e-3	4.892e-2
Constitutive Signaling by Aberrant PI3K in Cancer	Reactome	1	KIT	75	1	160.13	6.245e-3	5.066e-2
PIP3 activates AKT signaling	Reactome	1	KIT	93	1	129.14	7.744e-3	5.842e-2
Hematopoietic cell lineage	KEGG	1	KIT	100	1	120.10	8.326e-3	6.117e-2
Melanogenesis	KEGG	1	KIT	101	1	118.91	8.410e-3	6.167e-2
PI5P, PP2A and IER3 Regulate PI3K/AKT Signaling	Reactome	1	KIT	103	1	116.60	8.576e-3	6.254e-2
RAF/MAP kinase cascade	Reactome	1	KIT	124	1	96.85	1.032e-2	7.008e-2
Breast cancer	KEGG	1	KIT	148	1	81.15	1.232e-2	7.753e-2
Phospholipase D signaling pathway	KEGG	1	KIT	149	1	80.60	1.241e-2	7.776e-2
Rap1 signaling pathway	KEGG	1	KIT	211	1	56.92	1.757e-2	9.585e-2
Ras signaling pathway	KEGG	1	KIT	237	1	50.68	1.973e-2	1.022e-1