

GeDiPNet Cluster 314 -- 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: 2026-10-09 03:30:08. · Rows: 15 · Generated: 2026-10-09 11:16:43

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Transcriptional misregulation in cancer	KEGG	5	FLI1, ERG, EWSR1, ETV1, ETV4	198	30	10.11	1.180e-4	2.492e-3
Glucagon-type ligand receptors	Reactome	2	ADCYAP1R1, GHRHR	33	30	24.26	3.035e-3	3.082e-2
MASTL Facilitates Mitotic Progression	Reactome	1	ENSA	3	30	133.44	7.476e-3	5.710e-2
Electric Transmission Across Gap Junctions	Reactome	1	GJD2	5	30	80.07	1.243e-2	7.935e-2
Activation of NOXA and translocation to mitochondria	Reactome	1	TFDP2	5	30	80.07	1.243e-2	7.935e-2
Insulin secretion	KEGG	2	ADCYAP1R1, KCNMB2	86	30	9.31	1.936e-2	1.033e-1
Platelet homeostasis	Reactome	1	P2RX4	8	30	50.04	1.982e-2	1.044e-1
Ca2+ activated K+ channels	Reactome	1	KCNMB2	9	30	44.48	2.227e-2	1.115e-1
Activation of PUMA and translocation to mitochondria	Reactome	1	TFDP2	9	30	44.48	2.227e-2	1.115e-1
Pyrimidine salvage	Reactome	1	UPP2	11	30	36.39	2.715e-2	1.246e-1
Pyrimidine catabolism	Reactome	1	UPP2	11	30	36.39	2.715e-2	1.246e-1
The activation of arylsulfatases	Reactome	1	SUMF1	13	30	30.79	3.201e-2	1.371e-1
Elevation of cytosolic Ca2+ levels	Reactome	1	P2RX4	13	30	30.79	3.201e-2	1.371e-1
Transcriptional regulation of granulopoiesis	Reactome	1	TFDP2	14	30	28.60	3.443e-2	1.424e-1
N-Glycan antennae elongation	Reactome	1	MGAT4A	15	30	26.69	3.684e-2	1.480e-1