

GeDiPNet Cluster 582 -- 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: 2026-10-20 03:30:09. · Rows: 15 · Generated: 2026-10-20 00:03:13

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Gap junction	KEGG	4	PDGFB, PDGFRB, DRD2, HTR2A	89	22	24.54	1.861e-5	4.909e-4
Dopamine receptors	Reactome	2	DRD2, DRD3	5	22	218.36	3.193e-5	7.637e-4
DDX58/IFIH1-mediated induction of interferon-alpha/beta	Reactome	2	IFIH1, ISG15	17	22	64.22	4.284e-4	5.929e-3
Negative regulators of DDX58/IFIH1 signaling	Reactome	2	IFIH1, ISG15	27	22	40.44	1.094e-3	1.212e-2
Downstream signal transduction	Reactome	2	PDGFB, PDGFRB	29	22	37.65	1.262e-3	1.353e-2
Signaling by PDGF	Reactome	2	PDGFB, PDGFRB	33	22	33.09	1.634e-3	1.642e-2
Defective SLC20A2 causes idiopathic basal ganglia calcification 1 (IBGC1)	Reactome	1	SLC20A2	1	22	545.91	1.832e-3	1.781e-2
JAK-STAT signaling pathway	KEGG	3	PDGFB, PDGFRB, PRL	168	22	9.75	3.405e-3	2.786e-2
Sodium-coupled phosphate cotransporters	Reactome	1	SLC20A2	2	22	272.95	3.660e-3	2.935e-2
Neuroactive ligand-receptor interaction	KEGG	4	DRD2, DRD3, HTR2A, PRL	370	22	5.90	4.175e-3	3.219e-2
Rap1 signaling pathway	KEGG	3	PDGFB, PDGFRB, DRD2	211	22	7.76	6.435e-3	4.304e-2
Hormone signaling	KEGG	3	DRD2, DRD3, PRL	219	22	7.48	7.131e-3	4.600e-2
RIG-I-like receptor signaling pathway	KEGG	2	IFIH1, ISG15	72	22	15.16	7.577e-3	4.777e-2
Melanoma	KEGG	2	PDGFB, PDGFRB	73	22	14.96	7.781e-3	4.870e-2
Constitutive Signaling by Aberrant PI3K in Cancer	Reactome	2	PDGFB, PDGFRB	75	22	14.56	8.198e-3	5.037e-2