

GeDiPNet Cluster 411 -- 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 03:09:26

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	20	26.99	1.247e-5	4.032e-4
Dopamine receptors	Reactome	2	DRD2, DRD3	5	20	240.20	2.627e-5	7.466e-4
Downstream signal transduction	Reactome	2	PDGFB, PDGFRB	29	20	41.41	1.041e-3	1.398e-2
Signaling by PDGF	Reactome	2	PDGFB, PDGFRB	33	20	36.39	1.349e-3	1.696e-2
Defective SLC20A2 causes idiopathic basal ganglia calcification 1 (IBGC1)	Reactome	1	SLC20A2	1	20	600.50	1.665e-3	1.998e-2
JAK-STAT signaling pathway	KEGG	3	PDGFB, PDGFRB, PRL	168	20	10.72	2.573e-3	2.755e-2
Neuroactive ligand-receptor interaction	KEGG	4	DRD2, DRD3, HTR2A, PRL	370	20	6.49	2.903e-3	3.009e-2
Sodium-coupled phosphate cotransporters	Reactome	1	SLC20A2	2	20	300.25	3.328e-3	3.313e-2
Rap1 signaling pathway	KEGG	3	PDGFB, PDGFRB, DRD2	211	20	8.54	4.888e-3	4.326e-2
Hormone signaling	KEGG	3	DRD2, DRD3, PRL	219	20	8.23	5.422e-3	4.618e-2
Melanoma	KEGG	2	PDGFB, PDGFRB	73	20	16.45	6.451e-3	5.179e-2
Constitutive Signaling by Aberrant PI3K in Cancer	Reactome	2	PDGFB, PDGFRB	75	20	16.01	6.798e-3	5.360e-2
Glioma	KEGG	2	PDGFB, PDGFRB	76	20	15.80	6.975e-3	5.451e-2
EGFR tyrosine kinase inhibitor resistance	KEGG	2	PDGFB, PDGFRB	80	20	15.01	7.703e-3	5.821e-2
Calcium signaling pathway	KEGG	3	PDGFB, PDGFRB, HTR2A	254	20	7.09	8.166e-3	6.057e-2