

GeDiPNet Cluster 157 -- 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 14:41:46

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Vitamin B2 (riboflavin) metabolism	Reactome	2	SLC52A3, SLC52A2	7	37	92.74	1.921e-4	3.787e-3
Defective SLC17A8 causes autosomal dominant deafness 25 (DFNA25)	Reactome	1	SLC17A8	1	37	324.59	3.081e-3	3.132e-2
Defective SLC26A4 causes Pendred syndrome (PDS)	Reactome	1	SLC26A4	1	37	324.59	3.081e-3	3.132e-2
Regulation of Apoptosis	Reactome	1	OPA1	2	37	162.30	6.152e-3	5.022e-2
Nicotine addiction	KEGG	2	CACNA1A, SLC17A8	41	37	15.83	7.022e-3	5.474e-2
TBC/RABGAPs	Reactome	2	RAB33A, TBC1D24	46	37	14.11	8.778e-3	6.342e-2
Parkinson disease	KEGG	4	KIF5A, MFN2, ND6, TUBB4A	268	37	4.84	8.979e-3	6.424e-2
RHO GTPases Activate Formins	Reactome	3	DIAPH3, DIAPH1, TUBB4A	140	37	6.96	9.018e-3	6.446e-2
Electron transport from NADPH to Ferredoxin	Reactome	1	FDXR	3	37	108.20	9.215e-3	6.532e-2
Potassium transport channels	Reactome	1	KCNJ10	3	37	108.20	9.215e-3	6.532e-2
Spinocerebellar ataxia	KEGG	3	CACNA1A, OPA1, TWNK	144	37	6.76	9.737e-3	6.752e-2
Retrograde endocannabinoid signaling	KEGG	3	CACNA1A, ND6, SLC17A8	149	37	6.54	1.068e-2	7.152e-2
Defective CYP11A1 causes Adrenal insufficiency, congenital, with 46,XY sex reversal (AICSR)	Reactome	1	FDXR	4	37	81.15	1.227e-2	7.741e-2
Kinesins	Reactome	2	KIF5A, TUBB4A	59	37	11.00	1.415e-2	8.408e-2
Huntington disease	KEGG	4	KIF5A, ND6, TUBB4A, KCNJ10	308	37	4.22	1.440e-2	8.516e-2