

GeDiPNet Cluster 252 -- 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 13:00:06

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Parkinson disease	KEGG	4	GNAS, KIF5C, TUBA8, MFN2	268	15	11.95	2.726e-4	4.980e-3
Signaling by SCF-KIT	Reactome	2	FER, PTPN11	37	15	43.28	9.455e-4	1.301e-2
Motor proteins	KEGG	3	ACTR1B, KIF5C, TUBA8	194	15	12.38	1.636e-3	1.973e-2
Collagen degradation	Reactome	2	COL7A1, MMP1	52	15	30.79	1.862e-3	2.163e-2
Pathways of neurodegeneration - multiple diseases	KEGG	4	ACTR1B, KIF5C, TUBA8, MFN2	480	15	6.67	2.420e-3	2.625e-2
Salmonella infection	KEGG	3	ACTR1B, KIF5C, TUBA8	248	15	9.69	3.293e-3	3.291e-2
Gap junction	KEGG	2	GNAS, TUBA8	89	15	17.99	5.355e-3	4.576e-2
Huntington disease	KEGG	3	ACTR1B, KIF5C, TUBA8	308	15	7.80	6.044e-3	4.959e-2
MET activates PTPN11	Reactome	1	PTPN11	5	15	160.13	6.230e-3	5.059e-2
Parathyroid hormone synthesis, secretion and action	KEGG	2	GNAS, MAFB	115	15	13.92	8.798e-3	6.352e-2
Amyotrophic lateral sclerosis	KEGG	3	ACTR1B, KIF5C, TUBA8	368	15	6.53	9.870e-3	6.808e-2
MHC class II antigen presentation	Reactome	2	ACTR1B, TUBA8	123	15	13.02	1.001e-2	6.848e-2
Relaxin signaling pathway	KEGG	2	MMP1, GNAS	130	15	12.32	1.113e-2	7.325e-2
MAPK1 (ERK2) activation	Reactome	1	PTPN11	9	15	88.96	1.119e-2	7.338e-2
Dopaminergic synapse	KEGG	2	GNAS, KIF5C	132	15	12.13	1.146e-2	7.448e-2