

GeDiPNet Cluster 222 -- 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: 2026-10-08 03:30:07. · Rows: 15 · Generated: 2026-10-08 20:35:35

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Pathways of neurodegeneration - multiple diseases	KEGG	3	APP, PSEN1, LRRK2	480	4	18.77	2.463e-4	4.650e-3
Amyloid fiber formation	Reactome	2	APP, TTR	109	4	55.09	4.839e-4	7.935e-3
PTK6 promotes HIF1A stabilization	Reactome	1	LRRK2	6	4	500.42	1.997e-3	2.322e-2
Advanced glycosylation endproduct receptor signaling	Reactome	1	APP	8	4	375.31	2.662e-3	2.882e-2
Noncanonical activation of NOTCH3	Reactome	1	PSEN1	8	4	375.31	2.662e-3	2.882e-2
Formyl peptide receptors bind formyl peptides and many other ligands	Reactome	1	APP	8	4	375.31	2.662e-3	2.882e-2
Regulated proteolysis of p75NTR	Reactome	1	PSEN1	11	4	272.95	3.659e-3	3.598e-2
Retinoid cycle disease events	Reactome	1	TTR	13	4	230.96	4.323e-3	4.039e-2
The NLRP3 inflammasome	Reactome	1	APP	15	4	200.17	4.987e-3	4.437e-2
NRIF signals cell death from the nucleus	Reactome	1	PSEN1	15	4	200.17	4.987e-3	4.437e-2
Deregulated CDK5 triggers multiple neurodegenerative pathways in Alzheimer's disease models	Reactome	1	APP	16	4	187.66	5.319e-3	4.649e-2
Insertion of tail-anchored proteins into the endoplasmic reticulum membrane	Reactome	1	APP	16	4	187.66	5.319e-3	4.649e-2
Alzheimer disease	KEGG	2	APP, PSEN1	388	4	15.48	5.982e-3	5.030e-2
NOTCH3 Activation and Transmission of Signal to the Nucleus	Reactome	1	PSEN1	19	4	158.03	6.314e-3	5.220e-2
The canonical retinoid cycle in rods (twilight vision)	Reactome	1	TTR	20	4	150.13	6.645e-3	5.398e-2