

GeDiPNet Cluster 484 -- 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 00:02:19

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Resolution of AP sites via the single-nucleotide replacement pathway	Reactome	1	LIG3	3	6	667.22	1.498e-3	1.536e-2
APEX1-Independent Resolution of AP Sites via the Single Nucleotide Replacement Pathway	Reactome	1	LIG3	7	6	285.95	3.493e-3	2.829e-2
Advanced glycosylation endproduct receptor signaling	Reactome	1	APP	8	6	250.21	3.991e-3	3.122e-2
Formyl peptide receptors bind formyl peptides and many other ligands	Reactome	1	APP	8	6	250.21	3.991e-3	3.122e-2
HDR through MMEJ (alt-NHEJ)	Reactome	1	LIG3	10	6	200.17	4.986e-3	3.635e-2
Synthesis of PIPs at the late endosome membrane	Reactome	1	FIG4	10	6	200.17	4.986e-3	3.635e-2
Pyrimidine salvage	Reactome	1	TYMP	11	6	181.97	5.484e-3	3.872e-2
Pyrimidine catabolism	Reactome	1	TYMP	11	6	181.97	5.484e-3	3.872e-2
Heme biosynthesis	Reactome	1	HMBS	14	6	142.98	6.975e-3	4.528e-2
The NLRP3 inflammasome	Reactome	1	APP	15	6	133.44	7.472e-3	4.730e-2
Synthesis of PIPs at the early endosome membrane	Reactome	1	FIG4	15	6	133.44	7.472e-3	4.730e-2
Deregulated CDK5 triggers multiple neurodegenerative pathways in Alzheimer's disease models	Reactome	1	APP	16	6	125.10	7.968e-3	4.940e-2
Insertion of tail-anchored proteins into the endoplasmic reticulum membrane	Reactome	1	APP	16	6	125.10	7.968e-3	4.940e-2
Synthesis of PIPs at the Golgi membrane	Reactome	1	FIG4	18	6	111.20	8.961e-3	5.313e-2
Cytosolic tRNA aminoacylation	Reactome	1	AARS1	24	6	83.40	1.193e-2	6.320e-2