

GeDiPNet Cluster 330 -- 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: 2026-10-09 03:30:08. · Rows: 15 · Generated: 2026-10-09 03:18:27

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Complex I biogenesis	Reactome	4	ND1, NDUFAF6, NDUFB3, NDUFS4	55	54	16.18	1.050e-4	2.279e-3
Retrograde endocannabinoid signaling	KEGG	4	GNB1, ND1, NDUFB3, NDUFS4	149	54	5.97	4.448e-3	4.053e-2
Loss of MECP2 binding ability to 5hmC-DNA	Reactome	1	MECP2	1	54	222.41	4.496e-3	4.076e-2
Inhibition of PKR	Reactome	1	EIF2AK2	1	54	222.41	4.496e-3	4.076e-2
MPS IIIA - Sanfilippo syndrome A	Reactome	1	SGSH	1	54	222.41	4.496e-3	4.076e-2
Respiratory electron transport	Reactome	3	ND1, NDUFB3, NDUFS4	83	54	8.04	6.126e-3	5.021e-2
Loss of MECP2 binding ability to 5mC-DNA	Reactome	1	MECP2	3	54	74.14	1.343e-2	8.298e-2
Breakdown of the nuclear lamina	Reactome	1	LMNA	3	54	74.14	1.343e-2	8.298e-2
Regulation of commissural axon pathfinding by SLIT and ROBO	Reactome	1	ROBO2	3	54	74.14	1.343e-2	8.298e-2
MECP2 regulates neuronal receptors and channels	Reactome	1	MECP2	4	54	55.60	1.787e-2	9.875e-2
Chemical carcinogenesis - reactive oxygen species	KEGG	4	ND1, NDUFB3, NDUFS4, MGST2	227	54	3.92	1.881e-2	1.017e-1
Thermogenesis	KEGG	4	ND1, NDUFAF6, NDUFB3, NDUFS4	234	54	3.80	2.077e-2	1.074e-1
RUNX1 regulates transcription of genes involved in interleukin signaling	Reactome	1	LIFR	5	54	44.48	2.228e-2	1.115e-1
Oxidative phosphorylation	KEGG	3	ND1, NDUFB3, NDUFS4	137	54	4.87	2.360e-2	1.153e-1
Ca2+ pathway	Reactome	2	GNB1, WNT5A	56	54	7.94	2.617e-2	1.222e-1