

GeDiPNet Cluster 120 -- 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 12:26:57

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Defective MAOA causes Brunner syndrome (BRUNS)	Reactome	1	MAOA	1	35	343.14	2.914e-3	3.012e-2
Interleukin-4 and Interleukin-13 signaling	Reactome	3	MAOA, OPRD1, OPRM1	108	35	9.53	3.755e-3	3.601e-2
Tyrosine metabolism	KEGG	2	MAOA, DBH	36	35	19.06	4.885e-3	4.325e-2
G alpha (i) signalling events	Reactome	4	DRD4, HTR1B, OPRD1, OPRM1	249	35	5.51	5.700e-3	4.778e-2
Enzymatic degradation of Dopamine by monoamine oxidase	Reactome	1	MAOA	2	35	171.57	5.820e-3	4.843e-2
Metabolism of serotonin	Reactome	1	MAOA	2	35	171.57	5.820e-3	4.843e-2
Biogenic amines are oxidatively deaminated to aldehydes by MAOA and MAOB	Reactome	1	MAOA	2	35	171.57	5.820e-3	4.843e-2
Tryptophan metabolism	KEGG	2	MAOA, GCDH	42	35	16.34	6.603e-3	5.268e-2
Mitotic Telophase/Cytokinesis	Reactome	1	KIF23	3	35	114.38	8.718e-3	6.306e-2
Enzymatic degradation of dopamine by COMT	Reactome	1	MAOA	3	35	114.38	8.718e-3	6.306e-2
IRE1alpha activates chaperones	Reactome	1	HSPA5	3	35	114.38	8.718e-3	6.306e-2
Opioid Signalling	Reactome	1	OPRM1	3	35	114.38	8.718e-3	6.306e-2
Catecholamine biosynthesis	Reactome	1	DBH	4	35	85.79	1.161e-2	7.504e-2
ATF6 (ATF6-alpha) activates chaperones	Reactome	1	HSPA5	4	35	85.79	1.161e-2	7.504e-2
IRAK4 deficiency (TLR5)	Reactome	1	IRAK4	4	35	85.79	1.161e-2	7.504e-2