

GeDiPNet Cluster 443 -- 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: 2026-10-19 23:19:58

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Toxoplasmosis	KEGG	3	MAPK14, NOS2, PPIF	112	17	18.92	4.881e-4	6.562e-3
activated TAK1 mediates p38 MAPK activation	Reactome	2	MAPK14, NOD2	24	17	58.87	5.111e-4	6.776e-3
Other interleukin signaling	Reactome	2	STX3, STXBP2	24	17	58.87	5.111e-4	6.776e-3
NOD1/2 Signaling Pathway	Reactome	2	MAPK14, NOD2	36	17	39.25	1.155e-3	1.265e-2
Tuberculosis	KEGG	3	MAPK14, NOD2, NOS2	181	17	11.71	1.959e-3	1.879e-2
SDK interactions	Reactome	1	SDK2	2	17	353.24	2.829e-3	2.444e-2
Peroxisomal protein import	Reactome	2	ACOT8, NOS2	63	17	22.43	3.501e-3	2.832e-2
Pathways of neurodegeneration - multiple diseases	KEGG	4	MAPK14, DDIT3, NOS2, PPIF	480	17	5.89	3.960e-3	3.111e-2
Inhibition of nitric oxide production	Reactome	1	NOS2	3	17	235.49	4.241e-3	3.256e-2
Nitric oxide stimulates guanylate cyclase	Reactome	1	NOS2	3	17	235.49	4.241e-3	3.256e-2
Pertussis	KEGG	2	MAPK14, NOS2	78	17	18.11	5.316e-3	3.801e-2
Leishmaniasis	KEGG	2	MAPK14, NOS2	78	17	18.11	5.316e-3	3.801e-2
Peroxisome	KEGG	2	ACOT8, NOS2	83	17	17.02	6.000e-3	4.105e-2
Prion disease	KEGG	3	MAPK14, DDIT3, PPIF	275	17	7.71	6.365e-3	4.277e-2
Chagas disease	KEGG	2	MAPK14, NOS2	103	17	13.72	9.109e-3	5.370e-2