

GeDiPNet Cluster 476 -- 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: 10 · Generated: 2026-10-20 00:02:55

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Tryptophan catabolism	Reactome	2	KYNU, HAAO	11	5	436.73	7.615e-6	2.329e-4
Biosynthesis of cofactors	KEGG	3	KYNU, HAAO, NADSYN1	154	5	46.79	2.029e-5	5.276e-4
Tryptophan metabolism	KEGG	2	KYNU, HAAO	42	5	114.38	1.186e-4	2.165e-3
Metabolic pathways	KEGG	4	KYNU, TGDS, HAAO, NADSYN1	1563	5	6.15	1.281e-3	1.370e-2
Nicotinate metabolism	Reactome	1	NADSYN1	12	5	200.17	4.987e-3	3.635e-2
Biosynthesis of various nucleotide sugars	KEGG	1	TGDS	15	5	160.13	6.230e-3	4.212e-2
Biosynthesis of nucleotide sugars	KEGG	1	TGDS	37	5	64.92	1.531e-2	7.347e-2
Nicotinate and nicotinamide metabolism	KEGG	1	NADSYN1	38	5	63.21	1.572e-2	7.460e-2
Spliceosome	KEGG	1	WBP11	162	5	14.83	6.566e-2	1.692e-1
mRNA Splicing - Major Pathway	Reactome	1	WBP11	183	5	13.13	7.391e-2	1.814e-1