

GeDiPNet Cluster 199 -- 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 08:31:34

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Tyrosine catabolism	Reactome	3	FAH, HPD, TAT	5	9	800.67	2.908e-9	2.901e-7
Tyrosine metabolism	KEGG	3	FAH, HPD, TAT	36	9	111.20	2.052e-6	8.987e-5
Ubiquinone and other terpenoid-quinone biosynthesis	KEGG	2	HPD, TAT	12	9	222.41	3.282e-5	9.001e-4
Phenylalanine metabolism	KEGG	2	HPD, TAT	16	9	166.81	5.958e-5	1.472e-3
Lysosomal oligosaccharide catabolism	Reactome	1	MANBA	4	9	333.61	2.995e-3	3.068e-2
Phenylalanine, tyrosine and tryptophan biosynthesis	KEGG	1	TAT	6	9	222.41	4.489e-3	4.079e-2
Lysine catabolism	Reactome	1	GCDH	12	9	111.20	8.960e-3	6.417e-2
Other glycan degradation	KEGG	1	MANBA	18	9	74.14	1.341e-2	8.136e-2
Metabolic pathways	KEGG	4	FAH, HPD, TAT, GCDH	1563	9	3.42	2.093e-2	1.055e-1
Tryptophan metabolism	KEGG	1	GCDH	42	9	31.77	3.105e-2	1.313e-1
Fatty acid degradation	KEGG	1	GCDH	43	9	31.03	3.178e-2	1.331e-1
Cysteine and methionine metabolism	KEGG	1	TAT	52	9	25.66	3.831e-2	1.480e-1
Lysine degradation	KEGG	1	GCDH	63	9	21.18	4.625e-2	1.643e-1
RAB GEFs exchange GTP for GDP on RABs	Reactome	1	ALS2	90	9	14.83	6.548e-2	1.975e-1
Lysosome	KEGG	1	MANBA	133	9	10.03	9.539e-2	2.414e-1