

GeDiPNet Cluster 526 -- 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: 2026-10-20 00:02:55

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Ethanol oxidation	Reactome	3	ADH5, ALDH2, ADH1B	12	9	333.61	6.381e-8	3.773e-6
Fatty acid degradation	KEGG	3	ADH5, ALDH2, ADH1B	43	9	93.10	3.538e-6	1.229e-4
Pyruvate metabolism	KEGG	3	ADH5, ALDH2, ADH1B	47	9	85.18	4.641e-6	1.547e-4
Glycolysis / Gluconeogenesis	KEGG	3	ADH5, ALDH2, ADH1B	67	9	59.75	1.361e-5	3.763e-4
Alcoholic liver disease	KEGG	3	ADH5, ALDH2, ADH1B	144	9	27.80	1.345e-4	2.394e-3
Tyrosine metabolism	KEGG	2	ADH5, ADH1B	36	9	74.14	3.104e-4	4.621e-3
Retinol metabolism	KEGG	2	ADH5, ADH1B	68	9	39.25	1.108e-3	1.224e-2
Drug metabolism - cytochrome P450	KEGG	2	ADH5, ADH1B	73	9	36.56	1.276e-3	1.366e-2
Metabolism of xenobiotics by cytochrome P450	KEGG	2	ADH5, ADH1B	79	9	33.78	1.493e-3	1.535e-2
Metabolism of serotonin	Reactome	1	ALDH2	2	9	667.22	1.498e-3	1.536e-2
Interferon gamma signaling	Reactome	2	HLA-DQB1, IRF4	87	9	30.68	1.807e-3	1.768e-2
Th17 cell differentiation	KEGG	2	HLA-DQB1, IRF4	109	9	24.49	2.819e-3	2.438e-2
Translocation of ZAP-70 to Immunological synapse	Reactome	1	HLA-DQB1	19	9	70.23	1.415e-2	7.004e-2
Pantothenate and CoA biosynthesis	KEGG	1	ALDH2	21	9	63.54	1.563e-2	7.438e-2
Histidine metabolism	KEGG	1	ALDH2	22	9	60.66	1.637e-2	7.625e-2