

GeDiPNet Cluster 230 -- 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: 2026-10-08 03:30:07. · Rows: 15 · Generated: 2026-10-08 12:16:44

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Pyrimidine biosynthesis	Reactome	3	CAD, DHODH, UMPS	3	91	131.98	4.209e-7	2.301e-5
Biosynthesis of cofactors	KEGG	7	ALAD, CAD, DHODH, GCH1, HMBS, UMPS, MOCS1	154	91	6.00	1.635e-4	3.358e-3
Alternative complement activation	Reactome	2	C3, CFB	5	91	52.79	5.595e-4	8.868e-3
Fluid shear stress and atherosclerosis	KEGG	6	GSTT1, NFE2L2, NOS3, TNF, VCAM1, HMOX1	141	91	5.62	6.922e-4	1.048e-2
AGE-RAGE signaling pathway in diabetic complications	KEGG	5	NOS3, TNF, VCAM1, VEGFC, COL4A3	101	91	6.53	9.994e-4	1.390e-2
Lipid and atherosclerosis	KEGG	7	APOB, NFE2L2, NOS3, TNF, VCAM1, CYP2B6, ABCA1	216	91	4.28	1.245e-3	1.643e-2
Activation of C3 and C5	Reactome	2	C3, CFB	8	91	32.99	1.543e-3	1.932e-2
African trypanosomiasis	KEGG	3	HBB, TNF, VCAM1	37	91	10.70	2.714e-3	2.920e-2
CYP2E1 reactions	Reactome	2	CYP2C19, CYP2B6	11	91	24.00	2.987e-3	3.114e-2
Tetrahydrobiopterin (BH4) synthesis, recycling, salvage and regulation	Reactome	2	GCH1, NOS3	11	91	24.00	2.987e-3	3.114e-2
Scavenging of heme from plasma	Reactome	2	HBB, HP	13	91	20.30	4.195e-3	3.951e-2
Heme biosynthesis	Reactome	2	ALAD, HMBS	14	91	18.85	4.870e-3	4.377e-2
Porphyrin metabolism	KEGG	3	ALAD, HMBS, HMOX1	46	91	8.61	5.049e-3	4.480e-2
Malaria	KEGG	3	HBB, TNF, VCAM1	50	91	7.92	6.378e-3	5.252e-2
Pyrimidine metabolism	KEGG	3	CAD, DHODH, UMPS	58	91	6.83	9.615e-3	6.836e-2