

GeDiPNet Cluster 318 -- 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 00:03:09

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
ABO blood group biosynthesis	Reactome	1	ABO	3	7	571.90	1.748e-3	2.112e-2
Biosynthesis of protectins	Reactome	1	CYP1A1	4	7	428.93	2.330e-3	2.607e-2
Synthesis of 5-eicosatetraenoic acids	Reactome	1	PON1	6	7	285.95	3.493e-3	3.476e-2
Synthesis of epoxy (EET) and dihydroxyeicosatrienoic acids (DHET)	Reactome	1	CYP1A1	8	7	214.46	4.655e-3	4.241e-2
Synthesis of (16-20)-hydroxyeicosatetraenoic acids (HETE)	Reactome	1	CYP1A1	9	7	190.63	5.235e-3	4.595e-2
Gamma-carboxylation of protein precursors	Reactome	1	PROC	9	7	190.63	5.235e-3	4.595e-2
Transport of gamma-carboxylated protein precursors from the endoplasmic reticulum to the Golgi apparatus	Reactome	1	PROC	9	7	190.63	5.235e-3	4.595e-2
Removal of aminoterminal propeptides from gamma-carboxylated proteins	Reactome	1	PROC	10	7	171.57	5.815e-3	4.945e-2
Glycosphingolipid biosynthesis - globo and isoglobo series	KEGG	1	ABO	16	7	107.23	9.291e-3	6.693e-2
Common Pathway of Fibrin Clot Formation	Reactome	1	PROC	22	7	77.99	1.276e-2	8.117e-2
Intrinsic Pathway of Fibrin Clot Formation	Reactome	1	PROC	23	7	74.60	1.333e-2	8.341e-2
Xenobiotics	Reactome	1	CYP1A1	24	7	71.49	1.391e-2	8.546e-2
Glycosphingolipid biosynthesis - lacto and neolacto series	KEGG	1	ABO	28	7	61.28	1.621e-2	9.420e-2
SMAD2/SMAD3:SMAD4 heterotrimer regulates transcription	Reactome	1	CDKN2B	32	7	53.62	1.851e-2	1.016e-1
Oncogene Induced Senescence	Reactome	1	CDKN2B	33	7	51.99	1.908e-2	1.033e-1