

GeDiPNet Cluster 305 -- 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: 7 · Generated: 2026-10-07 22:10:52

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Rhesus blood group biosynthesis	Reactome	2	RHD, RHCE	2	5	2402.00	1.387e-7	8.728e-6
Defective RHAG causes regulator type Rh-null hemolytic anemia (RHN)	Reactome	1	RHAG	1	5	2402.00	4.163e-4	7.053e-3
Rhesus glycoproteins mediate ammonium transport.	Reactome	1	RHAG	3	5	800.67	1.249e-3	1.645e-2
Erythrocytes take up oxygen and release carbon dioxide	Reactome	1	RHAG	9	5	266.89	3.742e-3	3.650e-2
Erythrocytes take up carbon dioxide and release oxygen	Reactome	1	RHAG	13	5	184.77	5.401e-3	4.703e-2
Platelet degranulation	Reactome	1	SERPINA3	123	5	19.53	5.018e-2	1.747e-1
Neutrophil degranulation	Reactome	1	SERPINA3	480	5	5.00	1.845e-1	3.507e-1