

GeDiPNet Cluster 311 -- 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: 2026-10-09 03:30:08. · Rows: 15 · Generated: 2026-10-08 22:43:41

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Glycolysis	Reactome	6	PKLR, GPI, HK1, PGK1, TPI1, BPGM	28	63	40.85	5.622e-9	5.037e-7
Glycolysis / Gluconeogenesis	KEGG	6	PKLR, GPI, HK1, PGK1, TPI1, BPGM	67	63	17.07	1.270e-6	5.775e-5
Erythrocytes take up oxygen and release carbon dioxide	Reactome	3	HBB, RHAG, SLC4A1	9	63	63.54	1.130e-5	3.598e-4
Glutathione metabolism	KEGG	5	G6PD, GSR, GSS, GCLC, GPX1	59	63	16.16	1.361e-5	4.221e-4
Rhesus blood group biosynthesis	Reactome	2	RHCE, RHD	2	63	190.63	2.708e-5	7.502e-4
Defective ABCG8 causes gallbladder disease 4 and sitosterolemia	Reactome	2	ABCG5, ABCG8	2	63	190.63	2.708e-5	7.502e-4
Defective ABCG5 causes sitosterolemia	Reactome	2	ABCG5, ABCG8	2	63	190.63	2.708e-5	7.502e-4
Carbon metabolism	KEGG	6	G6PD, PKLR, GPI, HK1, PGK1, TPI1	115	63	9.95	2.946e-5	8.053e-4
Interaction between L1 and Ankyrins	Reactome	3	ANK1, SPTA1, SPTB	13	63	43.99	3.790e-5	9.903e-4
Erythrocytes take up carbon dioxide and release oxygen	Reactome	3	HBB, RHAG, SLC4A1	13	63	43.99	3.790e-5	9.903e-4
Gluconeogenesis	Reactome	3	GPI, PGK1, TPI1	34	63	16.82	7.330e-4	1.059e-2
Ferroptosis	KEGG	3	GSS, GCLC, HMOX1	42	63	13.62	1.365e-3	1.706e-2
Purine catabolism	Reactome	2	ITPA, GPX1	12	63	31.77	1.728e-3	2.048e-2
Glutathione synthesis and recycling	Reactome	2	GSS, GCLC	12	63	31.77	1.728e-3	2.048e-2
Type II diabetes mellitus	KEGG	3	PKLR, HK1, PRKCZ	47	63	12.17	1.892e-3	2.193e-2