

GeDiPNet Cluster 520 -- 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 00:02:39

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Synthesis, secretion, and inactivation of Glucose-dependent Insulinotropic Polypeptide (GIP)	Reactome	2	ISL1, GATA4	7	17	201.85	3.944e-5	9.047e-4
Physiological factors	Reactome	2	NKX2-5, GATA4	12	17	117.75	1.234e-4	2.235e-3
YAP1- and WWTR1 (TAZ)-stimulated gene expression	Reactome	2	NKX2-5, GATA4	14	17	100.92	1.699e-4	2.893e-3
Metabolism of folate and pterines	Reactome	2	MTHFR, SLC19A1	17	17	83.11	2.533e-4	3.951e-3
Antifolate resistance	KEGG	2	MTHFR, SLC19A1	30	17	47.10	8.015e-4	9.570e-3
Folate transport and metabolism	KEGG	2	MTHFR, SLC19A1	31	17	45.58	8.560e-4	1.007e-2
Cytokine-cytokine receptor interaction	KEGG	3	GDF1, ACVR1B, BMP2	298	17	7.11	7.945e-3	4.940e-2
Factors involved in megakaryocyte development and platelet production	Reactome	2	ZFPM2, GATA4	99	17	14.27	8.440e-3	5.123e-2
TGF-beta signaling pathway	KEGG	2	ACVR1B, BMP2	108	17	13.08	9.978e-3	5.673e-2
Thyroid hormone signaling pathway	KEGG	2	GATA4, MED13L	122	17	11.58	1.260e-2	6.547e-2
CD28 co-stimulation	Reactome	1	YES1	9	17	78.50	1.267e-2	6.569e-2
Signaling by Activin	Reactome	1	ACVR1B	11	17	64.22	1.547e-2	7.389e-2
Transcriptional regulation by RUNX2	Reactome	1	BMP2	12	17	58.87	1.686e-2	7.778e-2
FCGR activation	Reactome	1	YES1	12	17	58.87	1.686e-2	7.778e-2
PECAM1 interactions	Reactome	1	YES1	12	17	58.87	1.686e-2	7.778e-2