

GeDiPNet Cluster 557 -- 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 00:03:00

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Thyroid hormone synthesis	KEGG	9	PAX8, SLC26A4, TSHR, TSHB, DUOX2, DUOX2, IYD, SLC5A5, TPO	75	30	48.04	1.134e-13	2.647e-11
Thyroxine biosynthesis	Reactome	5	TSHB, DUOX2, IYD, SLC5A5, TPO	7	30	285.95	1.433e-12	2.628e-10
Autoimmune thyroid disease	KEGG	4	TSHR, TSHB, TPO, FASLG	54	30	29.65	9.172e-6	2.714e-4
Multifunctional anion exchangers	Reactome	2	SLC26A4, SLC26A7	9	30	88.96	2.148e-4	3.474e-3
Glycoprotein hormones	Reactome	2	TSHB, INHBB	12	30	66.72	3.920e-4	5.533e-3
Hormone ligand-binding receptors	Reactome	2	TSHR, TSHB	12	30	66.72	3.920e-4	5.533e-3
Defective SLC26A4 causes Pendred syndrome (PDS)	Reactome	1	SLC26A4	1	30	400.33	2.498e-3	2.231e-2
Defective SLC5A5 causes thyroid dysharmonogenesis 1 (TDH1)	Reactome	1	SLC5A5	1	30	400.33	2.498e-3	2.231e-2
HSP90 chaperone cycle for steroid hormone receptors (SHR)	Reactome	2	TUBB1, FKBP4	55	30	14.56	8.251e-3	5.049e-2
Regulation of lipolysis in adipocytes	KEGG	2	TSHR, TSHB	59	30	13.57	9.448e-3	5.493e-2
Antagonism of Activin by Follistatin	Reactome	1	INHBB	4	30	100.08	9.956e-3	5.666e-2
HHAT G278V abrogates palmitoylation of Hh-Np	Reactome	1	SHH	4	30	100.08	9.956e-3	5.666e-2
Long-term potentiation	KEGG	2	GRIN2B, PPP3CA	67	30	11.95	1.206e-2	6.366e-2
FasL/ CD95L signaling	Reactome	1	FASLG	5	30	80.07	1.243e-2	6.493e-2
Amphetamine addiction	KEGG	2	GRIN2B, PPP3CA	69	30	11.60	1.276e-2	6.573e-2