

GeDiPNet Cluster 282 -- 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: 2026-10-07 03:30:09. · Rows: 15 · Generated: 2026-10-07 10:41:11

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Defective SLC9A6 causes X-linked, syndromic mental retardation,, Christianson type (MRXSCH)	Reactome	1	SLC9A6	1	31	387.42	2.581e-3	2.760e-2
Calcium signaling pathway	KEGG	4	CACNA1E, CACNA1F, CAMK1D, GRIN2B	254	31	6.10	3.923e-3	3.725e-2
Transcriptional regulation by the AP-2 (TFAP2) family of transcription factors	Reactome	1	TFAP2A	3	31	129.14	7.724e-3	5.831e-2
TFAP2 (AP-2) family regulates transcription of other transcription factors	Reactome	1	TFAP2A	4	31	96.85	1.029e-2	6.995e-2
Inflammatory bowel disease	KEGG	2	HLA-DQA2, TLR4	66	31	11.74	1.248e-2	7.799e-2
TFAP2 (AP-2) family regulates transcription of cell cycle factors	Reactome	1	TFAP2A	5	31	77.48	1.284e-2	7.922e-2
Melanin biosynthesis	Reactome	1	OCA2	5	31	77.48	1.284e-2	7.922e-2
TFAP2A acts as a transcriptional repressor during retinoic acid induced cell differentiation	Reactome	1	TFAP2A	5	31	77.48	1.284e-2	7.922e-2
Assembly and cell surface presentation of NMDA receptors	Reactome	1	GRIN2B	6	31	64.57	1.539e-2	8.841e-2
Switching of origins to a post-replicative state	Reactome	1	MCM7	6	31	64.57	1.539e-2	8.841e-2
Leishmaniasis	KEGG	2	HLA-DQA2, TLR4	78	31	9.93	1.714e-2	9.461e-2
MyD88-independent TLR4 cascade	Reactome	1	TLR4	7	31	55.35	1.793e-2	9.703e-2
cAMP signaling pathway	KEGG	3	CACNA1F, CNGB1, GRIN2B	226	31	5.14	2.006e-2	1.029e-1
Relaxin receptors	Reactome	1	INSL5	8	31	48.43	2.047e-2	1.042e-1
Cardiac muscle contraction	KEGG	2	CACNA1F, SLC9A6	87	31	8.91	2.105e-2	1.058e-1