

GeDiPNet Cluster 489 -- 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 00:02:37

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Ion homeostasis	Reactome	2	CASQ1, STIM1	54	6	74.14	2.942e-4	4.444e-3
Defective GNE causes sialuria, Nonaka myopathy and inclusion body myopathy 2	Reactome	1	GNE	1	6	2001.67	4.996e-4	6.672e-3
Calcium signaling pathway	KEGG	2	CASQ1, STIM1	254	6	15.76	6.318e-3	4.251e-2
Biosynthesis of various nucleotide sugars	KEGG	1	GNE	15	6	133.44	7.472e-3	4.730e-2
HSF1-dependent transactivation	Reactome	1	HSPB8	19	6	105.35	9.457e-3	5.493e-2
Antigen activates B Cell Receptor (BCR) leading to generation of second messengers	Reactome	1	STIM1	23	6	87.03	1.144e-2	6.180e-2
TRP channels	Reactome	1	TRPM7	28	6	71.49	1.391e-2	6.943e-2
Sialic acid metabolism	Reactome	1	GNE	33	6	60.66	1.638e-2	7.625e-2
Biosynthesis of nucleotide sugars	KEGG	1	GNE	37	6	54.10	1.835e-2	8.162e-2
Processing of Capped Intron-Containing Pre-mRNA	Reactome	1	HNRNPA2B1	37	6	54.10	1.835e-2	8.162e-2
Amino sugar and nucleotide sugar metabolism	KEGG	1	GNE	38	6	52.68	1.884e-2	8.276e-2
Gene and protein expression by JAK-STAT signaling after Interleukin-12 stimulation	Reactome	1	HNRNPA2B1	38	6	52.68	1.884e-2	8.276e-2
Mineral absorption	KEGG	1	TRPM7	61	6	32.81	3.010e-2	1.084e-1
Stimuli-sensing channels	Reactome	1	CASQ1	79	6	25.34	3.883e-2	1.255e-1
Platelet activation	KEGG	1	STIM1	126	6	15.89	6.133e-2	1.626e-1