

GeDiPNet Cluster 363 -- 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: 2026-10-10 03:30:08. · Rows: 12 · Generated: 2026-10-10 02:45:34

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Platelet homeostasis	Reactome	1	P2RX7	8	2	750.63	1.332e-3	1.749e-2
Elevation of cytosolic Ca2+ levels	Reactome	1	P2RX7	13	2	461.92	2.164e-3	2.511e-2
Thiamine metabolism	KEGG	1	ALPL	15	2	400.33	2.496e-3	2.775e-2
The NLRP3 inflammasome	Reactome	1	P2RX7	15	2	400.33	2.496e-3	2.775e-2
Purinergic signaling in leishmaniasis infection	Reactome	1	P2RX7	24	2	250.21	3.993e-3	3.872e-2
Folate biosynthesis	KEGG	1	ALPL	28	2	214.46	4.658e-3	4.313e-2
Post-translational modification: synthesis of GPI-anchored proteins	Reactome	1	ALPL	66	2	90.98	1.096e-2	7.498e-2
Biosynthesis of cofactors	KEGG	1	ALPL	154	2	38.99	2.548e-2	1.229e-1
NOD-like receptor signaling pathway	KEGG	1	P2RX7	187	2	32.11	3.090e-2	1.364e-1
Calcium signaling pathway	KEGG	1	P2RX7	254	2	23.64	4.185e-2	1.605e-1
Neuroactive ligand-receptor interaction	KEGG	1	P2RX7	370	2	16.23	6.067e-2	1.950e-1
Metabolic pathways	KEGG	1	ALPL	1563	2	3.84	2.434e-1	4.160e-1