

GeDiPNet Cluster 406 -- 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 20:46:24

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
MyD88 deficiency (TLR2/4)	Reactome	1	BTK	10	2	600.50	1.665e-3	1.998e-2
IRAK4 deficiency (TLR2/4)	Reactome	1	BTK	11	2	545.91	1.831e-3	2.135e-2
G beta:gamma signalling through BTK	Reactome	1	BTK	18	2	333.61	2.995e-3	3.068e-2
MyD88:MAL(TIRAP) cascade initiated on plasma membrane	Reactome	1	BTK	19	2	316.05	3.162e-3	3.196e-2
Antigen activates B Cell Receptor (BCR) leading to generation of second messengers	Reactome	1	BTK	23	2	261.09	3.827e-3	3.654e-2
FCERI mediated Ca+2 mobilization	Reactome	1	BTK	29	2	207.07	4.824e-3	4.284e-2
DAP12 signaling	Reactome	1	BTK	30	2	200.17	4.990e-3	4.365e-2
ER-Phagosome pathway	Reactome	1	BTK	30	2	200.17	4.990e-3	4.365e-2
RHO GTPases Activate WASPs and WAVES	Reactome	1	BTK	36	2	166.81	5.986e-3	4.925e-2
Primary immunodeficiency	KEGG	1	BTK	38	2	158.03	6.318e-3	5.105e-2
FCGR3A-mediated phagocytosis	Reactome	1	BTK	59	2	101.78	9.801e-3	6.778e-2
Regulation of actin dynamics for phagocytic cup formation	Reactome	1	BTK	60	2	100.08	9.967e-3	6.823e-2
Fc epsilon RI signaling pathway	KEGG	1	BTK	69	2	87.03	1.146e-2	7.445e-2
G alpha (12/13) signalling events	Reactome	1	BTK	80	2	75.06	1.328e-2	8.084e-2
B cell receptor signaling pathway	KEGG	1	BTK	91	2	65.99	1.510e-2	8.724e-2