

GeDiPNet Cluster 436 -- 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 00:02:55

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Primary immunodeficiency	KEGG	3	CD19, TNFRSF13C, ICOS	38	5	189.63	2.910e-7	1.425e-5
Regulation of Complement cascade	Reactome	3	CD19, CD81, CR2	47	5	153.32	5.587e-7	2.513e-5
B cell receptor signaling pathway	KEGG	3	CD19, CD81, CR2	91	5	79.19	4.163e-6	1.409e-4
Intestinal immune network for IgA production	KEGG	2	TNFRSF13C, ICOS	50	5	96.08	1.685e-4	2.875e-3
Constitutive Signaling by Aberrant PI3K in Cancer	Reactome	2	CD19, ICOS	75	5	64.05	3.801e-4	5.403e-3
PIP3 activates AKT signaling	Reactome	2	CD19, ICOS	93	5	51.66	5.843e-4	7.528e-3
Hematopoietic cell lineage	KEGG	2	CD19, CR2	100	5	48.04	6.753e-4	8.402e-3
PI5P, PP2A and IER3 Regulate PI3K/AKT Signaling	Reactome	2	CD19, ICOS	103	5	46.64	7.163e-4	8.804e-3
Immunoregulatory interactions between a Lymphoid and a non-Lymphoid cell	Reactome	2	CD19, CD81	130	5	36.95	1.138e-3	1.250e-2
Epstein-Barr virus infection	KEGG	2	CD19, CR2	204	5	23.55	2.776e-3	2.411e-2
Costimulation by the CD28 family	Reactome	1	ICOS	11	5	218.36	4.572e-3	3.438e-2
TNF receptor superfamily (TNFSF) members mediating non-canonical NF-kB pathway	Reactome	1	TNFRSF13C	18	5	133.44	7.473e-3	4.730e-2
Antigen activates B Cell Receptor (BCR) leading to generation of second messengers	Reactome	1	CD19	23	5	104.43	9.540e-3	5.527e-2
Virion - Hepatitis viruses	KEGG	1	CD81	48	5	50.04	1.983e-2	8.517e-2
Malaria	KEGG	1	CD81	50	5	48.04	2.065e-2	8.746e-2