

GeDiPNet Cluster 316 -- 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: 2026-10-08 03:30:07. · Rows: 15 · Generated: 2026-10-07 23:04:31

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
InIA-mediated entry of Listeria monocytogenes into host cells	Reactome	2	CDH1, CTNND1	9	11	242.63	2.736e-5	7.882e-4
Adherens junction	KEGG	3	CDH1, CTNND1, ARHGAP29	93	11	35.22	7.091e-5	1.713e-3
Adherens junctions interactions	Reactome	2	CDH1, CTNND1	32	11	68.24	3.727e-4	6.461e-3
Apoptotic cleavage of cell adhesion proteins	Reactome	1	CDH1	11	11	99.26	1.003e-2	7.007e-2
Rap1 signaling pathway	KEGG	2	CDH1, CTNND1	211	11	10.35	1.522e-2	9.042e-2
FGFR2 alternative splicing	Reactome	1	ESRP2	26	11	41.99	2.357e-2	1.165e-1
Hippo signaling pathway - multiple species	KEGG	1	DCHS2	29	11	37.65	2.625e-2	1.238e-1
VEGFR2 mediated vascular permeability	Reactome	1	CTNND1	29	11	37.65	2.625e-2	1.238e-1
RHO GTPases activate IQGAPs	Reactome	1	CDH1	32	11	34.12	2.893e-2	1.299e-1
Detoxification of Reactive Oxygen Species	Reactome	1	GPX6	34	11	32.11	3.072e-2	1.344e-1
Thyroid cancer	KEGG	1	CDH1	37	11	29.51	3.338e-2	1.404e-1
Bladder cancer	KEGG	1	CDH1	41	11	26.63	3.693e-2	1.481e-1
Synthesis of PIPs at the plasma membrane	Reactome	1	PLEKHA5	51	11	21.41	4.575e-2	1.664e-1
Glutathione metabolism	KEGG	1	GPX6	59	11	18.51	5.275e-2	1.794e-1
Endometrial cancer	KEGG	1	CDH1	59	11	18.51	5.275e-2	1.794e-1