

GeDiPNet Cluster 418 -- 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: 7 · Generated: 2026-10-07 06:19:18

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Notch signaling pathway	KEGG	1	DLL3	62	5	38.74	2.555e-2	1.179e-1
Th1 and Th2 cell differentiation	KEGG	1	DLL3	93	5	25.83	3.813e-2	1.477e-1
Endocrine resistance	KEGG	1	DLL3	99	5	24.26	4.055e-2	1.528e-1
ATP-dependent chromatin remodeling	KEGG	1	PHF6	117	5	20.53	4.778e-2	1.674e-1
Breast cancer	KEGG	1	DLL3	148	5	16.23	6.013e-2	1.886e-1
Chemical carcinogenesis - receptor activation	KEGG	1	DLL3	215	5	11.17	8.637e-2	2.287e-1
Pathways in cancer	KEGG	1	DLL3	533	5	4.51	2.031e-1	3.669e-1