

GeDiPNet Cluster 285 -- 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: 9 · Generated: 2026-10-07 03:59:21

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Metabolism of polyamines	Reactome	1	SMS	4	5	600.50	1.664e-3	1.998e-2
Arginine and proline metabolism	KEGG	1	SMS	50	5	48.04	2.065e-2	1.047e-1
Cysteine and methionine metabolism	KEGG	1	SMS	52	5	46.19	2.147e-2	1.071e-1
Amino acids regulate mTORC1	Reactome	1	FLCN	55	5	43.67	2.269e-2	1.105e-1
Glutathione metabolism	KEGG	1	SMS	59	5	40.71	2.433e-2	1.150e-1
Renal cell carcinoma	KEGG	1	FLCN	70	5	34.31	2.881e-2	1.261e-1
mTOR signaling pathway	KEGG	1	FLCN	158	5	15.20	6.408e-2	1.950e-1
Endocytosis	KEGG	1	IQSEC2	250	5	9.61	9.985e-2	2.478e-1
Metabolic pathways	KEGG	1	SMS	1563	5	1.54	5.020e-1	6.444e-1