

GeDiPNet Cluster 380 -- 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: 4 · Generated: 2026-10-07 08:04:07

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Creatine metabolism	Reactome	3	GAMT, GATM, SLC6A8	11	3	1091.82	5.716e-10	6.803e-8
Glycine, serine and threonine metabolism	KEGG	2	GAMT, GATM	40	3	200.17	3.238e-5	8.900e-4
Arginine and proline metabolism	KEGG	2	GAMT, GATM	50	3	160.13	5.083e-5	1.295e-3
Metabolic pathways	KEGG	2	GAMT, GATM	1563	3	5.12	4.638e-2	1.646e-1