

GeDiPNet Cluster 585 -- 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 00:02:58

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Extra-nuclear estrogen signaling	Reactome	2	CAV1, GNG3	58	9	46.02	8.074e-4	9.618e-3
Circadian entrainment	KEGG	2	FOS, GNG3	97	9	27.51	2.240e-3	2.072e-2
Choline metabolism in cancer	KEGG	2	FOS, PCYT1A	99	9	26.96	2.332e-3	2.130e-2
Glycerophospholipid metabolism	KEGG	2	AGPAT2, PCYT1A	102	9	26.17	2.473e-3	2.223e-2
Cholinergic synapse	KEGG	2	FOS, GNG3	115	9	23.21	3.132e-3	2.626e-2
NOSTRIN mediated eNOS trafficking	Reactome	1	CAV1	5	9	266.89	3.742e-3	2.976e-2
Relaxin signaling pathway	KEGG	2	FOS, GNG3	130	9	20.53	3.983e-3	3.122e-2
Dopaminergic synapse	KEGG	2	FOS, GNG3	132	9	20.22	4.103e-3	3.185e-2
Phosphonate and phosphinate metabolism	KEGG	1	PCYT1A	6	9	222.41	4.489e-3	3.394e-2
Fluid shear stress and atherosclerosis	KEGG	2	CAV1, FOS	141	9	18.93	4.668e-3	3.485e-2
Osteoclast differentiation	KEGG	2	FOS, PPARG	142	9	18.79	4.733e-3	3.521e-2
Non-alcoholic fatty liver disease	KEGG	2	FOS, PPARG	157	9	17.00	5.756e-3	4.010e-2
Pathways in cancer	KEGG	3	FOS, PPARG, GNG3	533	9	7.51	5.974e-3	4.097e-2
Activation of the AP-1 family of transcription factors	Reactome	1	FOS	10	9	133.44	7.471e-3	4.730e-2
FOXO-mediated transcription of cell cycle genes	Reactome	1	CAV1	11	9	121.31	8.216e-3	5.037e-2