

GeDiPNet Cluster 328 -- 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: 15 · Generated: 2026-10-07 20:45:45

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Oxytocin signaling pathway	KEGG	3	PRKAG2, ADCY9, KCNJ6	154	8	29.25	1.105e-4	2.432e-3
Longevity regulating pathway - multiple species	KEGG	2	PRKAG2, ADCY9	62	8	48.43	7.197e-4	1.059e-2
GABAergic synapse	KEGG	2	ADCY9, KCNJ6	89	8	33.74	1.477e-3	1.826e-2
Longevity regulating pathway	KEGG	2	PRKAG2, ADCY9	90	8	33.36	1.510e-3	1.856e-2
Morphine addiction	KEGG	2	ADCY9, KCNJ6	91	8	32.99	1.543e-3	1.886e-2
Circadian entrainment	KEGG	2	ADCY9, KCNJ6	97	8	30.95	1.751e-3	2.071e-2
Hypertrophic cardiomyopathy	KEGG	2	MYH6, PRKAG2	99	8	30.33	1.824e-3	2.135e-2
Dilated cardiomyopathy	KEGG	2	MYH6, ADCY9	105	8	28.60	2.048e-3	2.323e-2
Progesterone-mediated oocyte maturation	KEGG	2	ADCY9, PKMYT1	110	8	27.30	2.245e-3	2.484e-2
Cholinergic synapse	KEGG	2	ADCY9, KCNJ6	115	8	26.11	2.451e-3	2.654e-2
G2/M DNA replication checkpoint	Reactome	1	PKMYT1	5	8	300.25	3.327e-3	3.313e-2
Oocyte meiosis	KEGG	2	ADCY9, PKMYT1	138	8	21.76	3.508e-3	3.430e-2
Estrogen signaling pathway	KEGG	2	ADCY9, KCNJ6	139	8	21.60	3.558e-3	3.470e-2
Apelin signaling pathway	KEGG	2	PRKAG2, ADCY9	140	8	21.45	3.608e-3	3.504e-2
AMPK inhibits chREBP transcriptional activation activity	Reactome	1	PRKAG2	6	8	250.21	3.991e-3	3.767e-2