

GeDiPNet Cluster 233 -- 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 13:53:49

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Hedgehog signaling pathway	KEGG	5	EVC, EVC2, GLI1, PRKACA, PRKACB	56	12	89.36	1.418e-9	1.512e-7
Hedgehog 'off' state	Reactome	4	GLI1, PRKACA, PRKACB, WDR35	56	12	71.49	2.041e-7	1.217e-5
Vasopressin-regulated water reabsorption	KEGG	3	DYNC2LI1, PRKACA, PRKACB	44	12	68.24	9.864e-6	3.317e-4
Intraflagellar transport	Reactome	3	DYNC2LI1, TRAF3IP1, WDR35	54	12	55.60	1.837e-5	5.586e-4
CREB1 phosphorylation through the activation of Adenylate Cyclase	Reactome	2	PRKACA, PRKACB	7	12	285.95	1.917e-5	5.784e-4
HDL assembly	Reactome	2	PRKACA, PRKACB	8	12	250.21	2.554e-5	7.280e-4
Hedgehog 'on' state	Reactome	3	EVC, EVC2, GLI1	70	12	42.89	4.018e-5	1.070e-3
Rap1 signalling	Reactome	2	PRKACA, PRKACB	16	12	125.10	1.090e-4	2.406e-3
Regulation of insulin secretion	Reactome	2	PRKACA, PRKACB	16	12	125.10	1.090e-4	2.406e-3
Melanogenesis	KEGG	3	PRKACA, PRKACB, CTNNB1	101	12	29.73	1.202e-4	2.598e-3
PKA activation in glucagon signalling	Reactome	2	PRKACA, PRKACB	17	12	117.75	1.234e-4	2.656e-3
Activation of SMO	Reactome	2	EVC, EVC2	18	12	111.20	1.388e-4	2.920e-3
DARPP-32 events	Reactome	2	PRKACA, PRKACB	19	12	105.35	1.550e-4	3.191e-3
PKA activation	Reactome	2	PRKACA, PRKACB	19	12	105.35	1.550e-4	3.191e-3
CD209 (DC-SIGN) signaling	Reactome	2	PRKACA, PRKACB	21	12	95.32	1.902e-4	3.764e-3