

GeDiPNet Cluster 530 -- 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: 2026-10-19 23:22:16

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Glycogen storage disease type IV (GBE1)	Reactome	1	GBE1	3	22	181.97	5.486e-3	3.872e-2
Gap junction	KEGG	2	HTR2A, PRKACG	89	22	12.27	1.139e-2	6.163e-2
CREB1 phosphorylation through the activation of Adenylate Cyclase	Reactome	1	PRKACG	7	22	77.99	1.276e-2	6.573e-2
Inflammatory mediator regulation of TRP channels	KEGG	2	HTR2A, PRKACG	99	22	11.03	1.396e-2	6.958e-2
Melanogenesis	KEGG	2	WNT7A, PRKACG	101	22	10.81	1.450e-2	7.118e-2
HDL assembly	Reactome	1	PRKACG	8	22	68.24	1.457e-2	7.132e-2
Dilated cardiomyopathy	KEGG	2	CACNG4, PRKACG	105	22	10.40	1.561e-2	7.438e-2
WNT mediated activation of DVL	Reactome	1	PIP5K1B	9	22	60.66	1.637e-2	7.625e-2
Serotonergic synapse	KEGG	2	HTR2A, PRKACG	115	22	9.49	1.853e-2	8.210e-2
cGMP effects	Reactome	1	PDE9A	11	22	49.63	1.997e-2	8.554e-2
Presynaptic depolarization and calcium channel opening	Reactome	1	CACNG4	12	22	45.49	2.177e-2	9.002e-2
Serotonin receptors	Reactome	1	HTR2A	12	22	45.49	2.177e-2	9.002e-2
LGI-ADAM interactions	Reactome	1	CACNG4	14	22	38.99	2.536e-2	9.816e-2
Rap1 signalling	Reactome	1	PRKACG	16	22	34.12	2.893e-2	1.058e-1
Regulation of insulin secretion	Reactome	1	PRKACG	16	22	34.12	2.893e-2	1.058e-1