

GeDiPNet Cluster 547 -- 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 00:02:53

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Glycosaminoglycan biosynthesis - chondroitin sulfate / dermatan sulfate	KEGG	2	UST, CSGALNACT1	21	66	17.33	5.839e-3	4.041e-2
Activation of Na-permeable kainate receptors	Reactome	1	GRIK1	2	66	90.98	1.096e-2	6.011e-2
ABO blood group biosynthesis	Reactome	1	ABO	3	66	60.66	1.640e-2	7.632e-2
Axon guidance	KEGG	4	LRRC4C, NTNG1, SEMA3C, SEMA3E	183	66	3.98	1.806e-2	8.097e-2
Vasopressin regulates renal water homeostasis via Aquaporins	Reactome	2	ADCY6, RAB11FIP2	43	66	8.46	2.324e-2	9.349e-2
Glutamatergic synapse	KEGG	3	ADCY6, GRIK1, GRM4	116	66	4.71	2.587e-2	9.954e-2
Biosynthesis of maresin-like SPMs	Reactome	1	CYP2C8	6	66	30.33	3.253e-2	1.133e-1
Vascular smooth muscle contraction	KEGG	3	ADCY6, CALCB, KCNMA1	134	66	4.07	3.735e-2	1.225e-1
RUNX3 regulates CDKN1A transcription	Reactome	1	ZFHX3	7	66	26.00	3.785e-2	1.235e-1
G alpha (s) signalling events	Reactome	3	ADCY6, CALCB, PDE7B	140	66	3.90	4.166e-2	1.304e-1
Synthesis of epoxy (EET) and dihydroxyeicosatrienoic acids (DHET)	Reactome	1	CYP2C8	8	66	22.75	4.314e-2	1.331e-1
G alpha (i) signalling events	Reactome	4	CXCR5, RGS4, GRM4, RGS7	249	66	2.92	4.788e-2	1.413e-1
Ca2+ activated K+ channels	Reactome	1	KCNMA1	9	66	20.22	4.840e-2	1.421e-1
Synthesis of (16-20)-hydroxyeicosatetraenoic acids (HETE)	Reactome	1	CYP2C8	9	66	20.22	4.840e-2	1.421e-1
Post-translational modification: synthesis of GPI-anchored proteins	Reactome	2	NTM, NTNG1	66	66	5.51	5.095e-2	1.464e-1