

GeDiPNet Cluster 167 -- 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: 2026-10-10 03:30:08. · Rows: 15 · Generated: 2026-10-09 23:23:18

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Folate biosynthesis	KEGG	3	GCH1, TH, SPR	28	44	29.25	1.410e-4	3.041e-3
Efferocytosis	KEGG	5	ANO3, PLA2G6, SLC2A1, VPS16, VPS11	157	44	8.69	2.578e-4	4.886e-3
Tetrahydrobiopterin (BH4) synthesis, recycling, salvage and regulation	Reactome	2	GCH1, SPR	11	44	49.63	7.065e-4	1.080e-2
Inhibition of PKR	Reactome	1	EIF2AK2	1	44	272.95	3.664e-3	3.639e-2
Defective SLC2A1 causes GLUT1 deficiency syndrome 1 (GLUT1DS1)	Reactome	1	SLC2A1	1	44	272.95	3.664e-3	3.639e-2
Insulin secretion	KEGG	3	ATP1A3, SLC2A1, KCNN2	86	44	9.52	3.799e-3	3.737e-2
Bile secretion	KEGG	3	ATP1A3, SLC2A1, KCNN2	90	44	9.10	4.317e-3	4.100e-2
RHO GTPases activate IQGAPs	Reactome	2	ACTB, TUBB4A	32	44	17.06	6.068e-3	5.162e-2
Degradation of GABA	Reactome	1	ALDH5A1	2	44	136.48	7.314e-3	5.810e-2
Serotonergic synapse	KEGG	3	CYP2D6, CACNA1B, KCNN2	115	44	7.12	8.516e-3	6.394e-2
Recycling pathway of L1	Reactome	2	ACTB, TUBB4A	40	44	13.65	9.367e-3	6.814e-2
Nicotine addiction	KEGG	2	CHRNA4, CACNA1B	41	44	13.31	9.825e-3	7.020e-2
Thyroid hormone signaling pathway	KEGG	3	ACTB, ATP1A3, SLC2A1	122	44	6.71	1.000e-2	7.077e-2
Cytoskeleton in muscle cells	KEGG	4	ACTB, ATP1A3, COL6A3, SGCE	232	44	4.71	1.006e-2	7.108e-2
Lactose synthesis	Reactome	1	SLC2A1	3	44	90.98	1.095e-2	7.498e-2