

GeDiPNet Cluster 518 -- 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 23:22:13

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Folate biosynthesis	KEGG	5	GCH1, TH, SPR, QDPR, PTS	28	80	26.81	1.007e-6	4.190e-5
Tetrahydrobiopterin (BH4) synthesis, recycling, salvage and regulation	Reactome	3	GCH1, SPR, PTS	11	80	40.94	4.519e-5	1.009e-3
Catecholamine biosynthesis	Reactome	2	TH, DDC	4	80	75.06	2.606e-4	4.043e-3
Ion transport by P-type ATPases	Reactome	4	ATP1A3, ATP13A2, ATP7B, ATP1A2	56	80	10.72	5.154e-4	6.822e-3
Efferocytosis	KEGG	6	ANO3, PLA2G6, SLC2A1, VPS16, VPS11, VPS41	157	80	5.74	6.142e-4	7.834e-3
Thyroid hormone signaling pathway	KEGG	5	ACTB, ATP1A3, SLC2A1, MED27, ATP1A2	122	80	6.15	1.304e-3	1.388e-2
Metal ion SLC transporters	Reactome	2	SLC30A10, CP	9	80	33.36	1.530e-3	1.563e-2
Insulin secretion	KEGG	4	ATP1A3, SLC2A1, KCNN2, ATP1A2	86	80	6.98	2.563e-3	2.277e-2
Presynaptic depolarization and calcium channel opening	Reactome	2	CACNA1B, CACNA1E	12	80	25.02	2.770e-3	2.406e-2
Bile secretion	KEGG	4	ATP1A3, SLC2A1, KCNN2, ATP1A2	90	80	6.67	3.023e-3	2.555e-2
Regulation of insulin secretion	Reactome	2	SLC2A1, CACNA1E	16	80	18.77	4.949e-3	3.635e-2
Inhibition of PKR	Reactome	1	EIF2AK2	1	80	150.13	6.661e-3	4.397e-2
Defective SLC2A1 causes GLUT1 deficiency syndrome 1 (GLUT1DS1)	Reactome	1	SLC2A1	1	80	150.13	6.661e-3	4.397e-2
Defective SLC20A2 causes idiopathic basal ganglia calcification 1 (IBGC1)	Reactome	1	SLC20A2	1	80	150.13	6.661e-3	4.397e-2
Serotonergic synapse	KEGG	4	CYP2D6, CACNA1B, KCNN2, DDC	115	80	5.22	7.217e-3	4.639e-2