

GeDiPNet Cluster 516 -- 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](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 23:21:20

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Tetrahydrobiopterin (BH4) synthesis, recycling, salvage and regulation	Reactome	2	GCH1, SPR	11	6	363.94	1.142e-5	3.246e-4
Folate biosynthesis	KEGG	2	GCH1, SPR	28	6	142.98	7.817e-5	1.558e-3
Signaling by Insulin receptor	Reactome	1	INS	2	6	1000.83	9.990e-4	1.132e-2
Biosynthesis of cofactors	KEGG	2	GCH1, SPR	154	6	26.00	2.369e-3	2.156e-2
IRS activation	Reactome	1	INS	5	6	400.33	2.496e-3	2.231e-2
Insulin receptor signalling cascade	Reactome	1	INS	6	6	333.61	2.994e-3	2.538e-2
FOXO-mediated transcription of oxidative stress, metabolic and neuronal genes	Reactome	1	INS	10	6	200.17	4.986e-3	3.635e-2
Signal attenuation	Reactome	1	INS	10	6	200.17	4.986e-3	3.635e-2
Purine ribonucleoside monophosphate biosynthesis	Reactome	1	IMPDH2	12	6	166.81	5.981e-3	4.097e-2
Pregnenolone biosynthesis	Reactome	1	TSPOAP1	12	6	166.81	5.981e-3	4.097e-2
eNOS activation	Reactome	1	SPR	13	6	153.97	6.478e-3	4.320e-2
Insulin processing	Reactome	1	INS	14	6	142.98	6.975e-3	4.528e-2
Acetylcholine Neurotransmitter Release Cycle	Reactome	1	TSPOAP1	17	6	117.75	8.465e-3	5.129e-2
Serotonin Neurotransmitter Release Cycle	Reactome	1	TSPOAP1	18	6	111.20	8.961e-3	5.313e-2
Norepinephrine Neurotransmitter Release Cycle	Reactome	1	TSPOAP1	18	6	111.20	8.961e-3	5.313e-2