

GeDiPNet Cluster 112 -- 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: 2026-10-10 06:09:23

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	14	155.97	6.899e-5	1.730e-3
Folate biosynthesis	KEGG	2	GCH1, SPR	28	14	61.28	4.688e-4	7.887e-3
Defective CYP17A1 causes Adrenal hyperplasia 5 (AH5)	Reactome	1	CYP17A1	1	14	857.86	1.166e-3	1.579e-2
Ovarian steroidogenesis	KEGG	2	INS, CYP17A1	52	14	32.99	1.618e-3	2.032e-2
Signaling by Insulin receptor	Reactome	1	INS	2	14	428.93	2.330e-3	2.646e-2
Prolactin signaling pathway	KEGG	2	INS, CYP17A1	71	14	24.16	2.995e-3	3.147e-2
Insulin secretion	KEGG	2	INS, CHRM3	86	14	19.95	4.361e-3	4.127e-2
Muscarinic acetylcholine receptors	Reactome	1	CHRM3	5	14	171.57	5.816e-3	5.013e-2
IRS activation	Reactome	1	INS	5	14	171.57	5.816e-3	5.013e-2
Insulin receptor signalling cascade	Reactome	1	INS	6	14	142.98	6.975e-3	5.637e-2
Glucocorticoid biosynthesis	Reactome	1	CYP17A1	10	14	85.79	1.160e-2	7.769e-2
FOXO-mediated transcription of oxidative stress, metabolic and neuronal genes	Reactome	1	INS	10	14	85.79	1.160e-2	7.769e-2
Signal attenuation	Reactome	1	INS	10	14	85.79	1.160e-2	7.769e-2
Androgen biosynthesis	Reactome	1	CYP17A1	11	14	77.99	1.275e-2	8.224e-2
Biosynthesis of cofactors	KEGG	2	GCH1, SPR	154	14	11.14	1.344e-2	8.463e-2