

GeDiPNet Cluster 348 -- 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: 2026-10-08 03:30:07. · Rows: 15 · Generated: 2026-10-07 22:02:24

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
ECM-receptor interaction	KEGG	3	FRAS1, FREM1, FREM2	89	22	18.40	5.471e-4	8.717e-3
Regulation of lipid metabolism by PPARalpha	Reactome	2	SIN3A, SIN3B	20	22	54.59	5.966e-4	9.322e-3
Transcriptional misregulation in cancer	KEGG	3	SIN3A, MET, PAX3	198	22	8.27	5.395e-3	4.700e-2
Loss of MECP2 binding ability to 5mC-DNA	Reactome	1	SIN3A	3	22	181.97	5.486e-3	4.749e-2
GLI proteins bind promoters of Hh responsive genes to promote transcription	Reactome	1	GLI3	3	22	181.97	5.486e-3	4.749e-2
MET activates STAT3	Reactome	1	MET	3	22	181.97	5.486e-3	4.749e-2
MECP2 regulates neuronal receptors and channels	Reactome	1	MET	4	22	136.48	7.308e-3	5.740e-2
MET activates PTPN11	Reactome	1	MET	5	22	109.18	9.127e-3	6.615e-2
MET interacts with TNS proteins	Reactome	1	MET	5	22	109.18	9.127e-3	6.615e-2
MET Receptor Activation	Reactome	1	MET	6	22	90.98	1.094e-2	7.412e-2
MET activates PI3K/AKT signaling	Reactome	1	MET	6	22	90.98	1.094e-2	7.412e-2
Regulation of MECP2 expression and activity	Reactome	1	SIN3A	6	22	90.98	1.094e-2	7.412e-2
InlB-mediated entry of Listeria monocytogenes into host cell	Reactome	1	MET	7	22	77.99	1.276e-2	8.117e-2
RUNX1 regulates genes involved in megakaryocyte differentiation and platelet function	Reactome	2	SIN3A, SIN3B	97	22	11.26	1.343e-2	8.373e-2
Factors involved in megakaryocyte development and platelet production	Reactome	2	GATA6, ZFPM2	99	22	11.03	1.396e-2	8.561e-2