GeDiPNet Cluster 656 -- 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: 2026-10-21 12:16:30. · Rows: 15 · Generated: 2026-10-21 08:35:36

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
MASTL Facilitates Mitotic Progression	Reactome	1	MASTL	3	5	800.67	1.249e-3	1.278e-2
Signaling by membrane-tethered fusions of PDGFRA or PDGFRB	Reactome	1	ETV6	5	5	480.40	2.080e-3	1.872e-2
Release of apoptotic factors from the mitochondria	Reactome	1	CYCS	5	5	480.40	2.080e-3	1.872e-2
Formation of apoptosome	Reactome	1	CYCS	6	5	400.33	2.496e-3	2.143e-2
Activation of caspases through apoptosome-mediated cleavage	Reactome	1	CYCS	6	5	400.33	2.496e-3	2.143e-2
Regulation of the apoptosome activity	Reactome	1	CYCS	10	5	240.20	4.157e-3	3.079e-2
Apoptosis - multiple species	KEGG	1	CYCS	32	5	75.06	1.325e-2	6.523e-2
Detoxification of Reactive Oxygen Species	Reactome	1	CYCS	34	5	70.65	1.408e-2	6.775e-2
Transcriptional activation of mitochondrial biogenesis	Reactome	1	CYCS	51	5	47.10	2.106e-2	8.600e-2
Legionellosis	KEGG	1	CYCS	56	5	42.89	2.310e-2	9.096e-2
Viral myocarditis	KEGG	1	CYCS	70	5	34.31	2.881e-2	1.037e-1
Platinum drug resistance	KEGG	1	CYCS	75	5	32.03	3.084e-2	1.080e-1
p53 signaling pathway	KEGG	1	CYCS	75	5	32.03	3.084e-2	1.080e-1
Respiratory electron transport	Reactome	1	CYCS	83	5	28.94	3.409e-2	1.145e-1
TP53 Regulates Metabolic Genes	Reactome	1	CYCS	86	5	27.93	3.530e-2	1.168e-1