

GeDiPNet Cluster 656 -- Enriched GO Terms (Biological Process)

GO term enrichment: Biological Process terms (gene2go, human/tax_id=9606 only), upper-tail hypergeometric test, fold enrichment = (overlap / cluster gene count) / (term gene count / universe size), Benjamini-Hochberg FDR-corrected. Top 15 terms per cluster by q-value. See scripts/build_cluster_go_enrichment.php on gedipnet.bicnirrh.res.in. Data as of: 2026-10-21 12:39:04. · Rows: 15 · Generated: 2026-10-21 08:33:18

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
female meiosis II	GO:0007147	1	MASTL	2	5	1868.70	5.351e-4	9.696e-3
vitellogenesis	GO:0007296	1	ETV6	4	5	934.35	1.070e-3	1.490e-2
mesenchymal cell apoptotic process	GO:0097152	1	ETV6	10	5	373.74	2.673e-3	2.427e-2
mitochondrial electron transport, ubiquinol to cytochrome c	GO:0006122	1	CYCS	14	5	266.96	3.741e-3	2.862e-2
mitochondrial electron transport, cytochrome c to oxygen	GO:0006123	1	CYCS	23	5	162.50	6.140e-3	3.654e-2
hematopoietic stem cell proliferation	GO:0071425	1	ETV6	25	5	149.50	6.672e-3	3.806e-2
execution phase of apoptosis	GO:0097194	1	CYCS	25	5	149.50	6.672e-3	3.806e-2
cellular respiration	GO:0045333	1	CYCS	41	5	91.16	1.092e-2	4.811e-2
intrinsic apoptotic signaling pathway	GO:0097193	1	CYCS	45	5	83.05	1.198e-2	4.984e-2
G2/M transition of mitotic cell cycle	GO:0000086	1	MASTL	53	5	70.52	1.410e-2	5.419e-2
negative regulation of fat cell differentiation	GO:0045599	1	ANKRD26	57	5	65.57	1.516e-2	5.640e-2
regulation of mitotic cell cycle	GO:0007346	1	MASTL	77	5	48.54	2.044e-2	6.532e-2
apoptotic signaling pathway	GO:0097190	1	CYCS	84	5	44.49	2.228e-2	6.796e-2
negative regulation of transcription by RNA polymerase II	GO:0000122	2	ETV6, IKZF5	1002	5	7.46	2.577e-2	7.338e-2
neurogenesis	GO:0022008	1	ETV6	102	5	36.64	2.700e-2	7.551e-2