

GeDiPNet Cluster 507 -- 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: 2026-10-20 03:23:14. · Rows: 15 · Generated: 2026-10-19 23:18:41

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
somatic stem cell division	GO:0048103	2	CDKN2A, WNT7A	10	5	747.48	2.575e-6	1.855e-4
rRNA transcription	GO:0009303	2	CDKN2A, TP53	15	5	498.32	6.006e-6	3.667e-4
replicative senescence	GO:0090399	2	CDKN2A, TP53	16	5	467.18	6.863e-6	4.055e-4
cellular senescence	GO:0090398	2	CDKN2A, TP53	57	5	131.14	9.088e-5	2.883e-3
somatic stem cell population maintenance	GO:0035019	2	CDKN2A, WNT7A	64	5	116.79	1.147e-4	3.416e-3
Ras protein signal transduction	GO:0007265	2	CDKN2A, TP53	79	5	94.62	1.750e-4	4.615e-3
positive regulation of gene expression	GO:0010628	3	CDKN2A, TP53, WNT7A	504	5	22.25	1.873e-4	4.862e-3
apoptotic signaling pathway	GO:0097190	2	CDKN2A, TP53	84	5	88.99	1.979e-4	5.044e-3
negative regulation of helicase activity	GO:0051097	1	TP53	1	5	3737.40	2.676e-4	6.245e-3
regulation of intrinsic apoptotic signaling pathway by p53 class mediator	GO:1902253	1	TP53	1	5	3737.40	2.676e-4	6.245e-3
negative regulation of G1 to G0 transition	GO:1903451	1	TP53	1	5	3737.40	2.676e-4	6.245e-3
asymmetric protein localization involved in cell fate determination	GO:0045167	1	WNT7A	1	5	3737.40	2.676e-4	6.245e-3
multicellular organism growth	GO:0035264	2	WDR11, TP53	115	5	65.00	3.709e-4	7.804e-3
negative regulation of cell growth	GO:0030308	2	CDKN2A, TP53	115	5	65.00	3.709e-4	7.804e-3
regulation of thymocyte apoptotic process	GO:0070243	1	TP53	2	5	1868.70	5.351e-4	9.880e-3