

GeDiPNet Cluster 319 -- 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: 2026-10-07 03:23:06. · Rows: 15 · Generated: 2026-10-07 09:59:12

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
SRP-dependent cotranslational protein targeting to membrane	GO:0006614	4	SRP72, SRP54, SRPRA, SRP19	10	15	498.32	5.628e-11	1.717e-8
cytosolic ribosome assembly	GO:0042256	3	EFL1, EIF6, SBDS	5	15	747.48	4.180e-9	7.951e-7
SRP-dependent cotranslational protein targeting to membrane, signal sequence recognition	GO:0006617	3	SRP54, SRPRA, SRP19	14	15	266.96	1.515e-7	1.718e-5
ribosome biogenesis	GO:0042254	4	NPM1, EFL1, EIF6, SBDS	122	15	40.85	2.233e-6	1.574e-4
regulation of DNA damage response, signal transduction by p53 class mediator	GO:0043516	2	NPM1, TP53	7	15	355.94	1.260e-5	6.253e-4
regulation of cell population proliferation	GO:0042127	4	CSF2, NPM1, TP53, MDM4	201	15	24.79	1.616e-5	7.621e-4
bone marrow development	GO:0048539	2	TP53, SBDS	9	15	276.84	2.158e-5	9.541e-4
cotranslational protein targeting to membrane	GO:0006613	2	SRPRA, SRP19	10	15	249.16	2.696e-5	1.127e-3
regulation of glycolytic process	GO:0006110	2	GCK, EIF6	13	15	191.66	4.667e-5	1.706e-3
protein targeting to ER	GO:0045047	2	SRP54, SRPRA	15	15	166.11	6.277e-5	2.133e-3
macrophage differentiation	GO:0030225	2	CSF2, NPM1	37	15	67.34	3.941e-4	8.112e-3
ribosomal large subunit biogenesis	GO:0042273	2	NPM1, EIF6	39	15	63.89	4.381e-4	8.716e-3
DNA damage response, signal transduction by p53 class mediator	GO:0030330	2	TP53, MDM4	48	15	51.91	6.641e-4	1.154e-2
negative regulation of helicase activity	GO:0051097	1	TP53	1	15	1245.80	8.027e-4	1.302e-2
regulation of intrinsic apoptotic signaling pathway by p53 class mediator	GO:1902253	1	TP53	1	15	1245.80	8.027e-4	1.302e-2