

GeDiPNet Cluster 240 -- 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 02:15:00

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
cytoplasmic translation	GO:0002181	24	RPL11, RPL15, RPL18, RPL26, RPL35, RPL35A, RPL5, RPL8, RPS10, RPS15A, RPS17, RPS19	126	52	68.45	2.802e-39	2.800e-35
translation	GO:0006412	25	RPL11, RPL15, RPL18, RPL26, RPL35, RPL35A, RPL5, RPL8, RPS10, RPS15A, RPS17, RPS19	310	52	28.98	3.769e-31	2.161e-27
rRNA processing	GO:0006364	13	RPL11, RPL26, RPL35A, RPL5, RPS17, RPS19, RPS24, RPS28, RPS7, TSR2, RPL27, RPS15	162	52	28.84	4.546e-16	3.803e-13
ribosomal small subunit biogenesis	GO:0042274	8	RPS15A, RPS17, RPS19, RPS24, RPS28, RPS7, RPS15, RPS27	75	52	38.33	2.996e-11	9.711e-9
ribosomal small subunit assembly	GO:0000028	4	RPS19, RPS28, RPS15, RPS27	13	52	110.57	3.741e-8	5.291e-6
ribosomal large subunit biogenesis	GO:0042273	5	HEATR3, RPL11, RPL26, RPL35A, RPL5	39	52	46.07	7.341e-8	9.301e-6
negative regulation of ubiquitin protein ligase activity	GO:1904667	3	RPL11, RPL5, RPS7	9	52	119.79	1.687e-6	1.259e-4
positive regulation of signal transduction by p53 class mediator	GO:1901798	3	RPL11, RPS20, RPS15	13	52	82.93	5.699e-6	3.328e-4
erythrocyte differentiation	GO:0030218	4	GATA1, RPS19, EPO, IKZF1	65	52	22.11	3.183e-5	1.279e-3
negative regulation of ubiquitin-dependent protein catabolic process	GO:2000059	3	RPL11, RPL5, RPS7	25	52	43.12	4.476e-5	1.658e-3
metanephric S-shaped body morphogenesis	GO:0072284	2	PAX8, PKD2	4	52	179.68	4.541e-5	1.675e-3
negative regulation of protein neddylation	GO:2000435	2	RPL11, RPL5	5	52	143.75	7.554e-5	2.459e-3
mesonephric tubule development	GO:0072164	2	PAX8, PKD2	7	52	102.68	1.581e-4	4.264e-3
embryonic organ development	GO:0048568	3	TP53, FGFR2, PKD2	42	52	25.67	2.161e-4	5.322e-3
response to salt stress	GO:0009651	2	TP53, EPO	9	52	79.86	2.700e-4	6.236e-3