

GeDiPNet Cluster 600 -- 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: 2026-10-20 00:01:11

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
melanosome transport	GO:0032402	3	MYO5A, RAB27A, MLPH	22	3	849.41	1.416e-9	3.165e-7
multivesicular body organization	GO:0036257	1	RAB27A	1	3	6229.00	1.605e-4	4.340e-3
cytotoxic T cell degranulation	GO:0043316	1	RAB27A	1	3	6229.00	1.605e-4	4.340e-3
positive regulation of constitutive secretory pathway	GO:1903435	1	RAB27A	1	3	6229.00	1.605e-4	4.340e-3
pigment granule localization	GO:0051875	1	RAB27A	2	3	3114.50	3.211e-4	7.044e-3
pigment granule transport	GO:0051904	1	RAB27A	2	3	3114.50	3.211e-4	7.044e-3
complement-dependent cytotoxicity	GO:0097278	1	RAB27A	3	3	2076.33	4.816e-4	9.241e-3
exosomal secretion	GO:1990182	1	RAB27A	4	3	1557.25	6.421e-4	1.113e-2
positive regulation of regulated secretory pathway	GO:1903307	1	RAB27A	5	3	1245.80	8.025e-4	1.283e-2
melanosome localization	GO:0032400	1	RAB27A	5	3	1245.80	8.025e-4	1.283e-2
vesicle-mediated transport	GO:0016192	2	MYO5A, RAB27A	326	3	38.21	8.997e-4	1.379e-2
vesicle transport along actin filament	GO:0030050	1	MYO5A	6	3	1038.17	9.630e-4	1.423e-2
natural killer cell degranulation	GO:0043320	1	RAB27A	8	3	778.63	1.284e-3	1.669e-2
regulation of Golgi organization	GO:1903358	1	MYO5A	13	3	479.15	2.086e-3	2.170e-2
post-Golgi vesicle-mediated transport	GO:0006892	1	MYO5A	16	3	389.31	2.567e-3	2.402e-2