

GeDiPNet Cluster 614 -- 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 00:01:25

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
phosphatidylinositol phosphate biosynthetic process	GO:0046854	2	PI4KA, TTC7A	43	4	217.29	3.094e-5	1.280e-3
reorganization of cellular membranes to establish viral sites of replication	GO:0140754	1	PI4KA	1	4	4671.75	2.141e-4	5.314e-3
positive regulation of organelle organization	GO:0010638	1	LMAN1	4	4	1167.94	8.560e-4	1.331e-2
gene expression	GO:0010467	2	LMAN1, MCFD2	269	4	34.73	1.215e-3	1.626e-2
negative regulation of protein targeting to mitochondrion	GO:1903215	1	LMAN1	6	4	778.63	1.284e-3	1.669e-2
host-mediated perturbation of viral process	GO:0044788	1	PI4KA	8	4	583.97	1.711e-3	1.958e-2
vesicle-mediated transport	GO:0016192	2	LMAN1, MCFD2	326	4	28.66	1.779e-3	2.001e-2
protein exit from endoplasmic reticulum	GO:0032527	1	LMAN1	14	4	333.70	2.994e-3	2.594e-2
early endosome to Golgi transport	GO:0034498	1	LMAN1	17	4	274.81	3.634e-3	2.863e-2
phosphatidylinositol-mediated signaling	GO:0048015	1	PI4KA	24	4	194.66	5.128e-3	3.369e-2
protein transport	GO:0015031	2	LMAN1, MCFD2	667	4	14.01	7.276e-3	3.994e-2
phosphatidylinositol biosynthetic process	GO:0006661	1	PI4KA	44	4	106.18	9.386e-3	4.504e-2
endoplasmic reticulum organization	GO:0007029	1	LMAN1	46	4	101.56	9.811e-3	4.606e-2
intracellular iron ion homeostasis	GO:0006879	1	TTC7A	71	4	65.80	1.511e-2	5.678e-2
hemopoiesis	GO:0030097	1	TTC7A	89	4	52.49	1.892e-2	6.335e-2