

GeDiPNet Cluster 510 -- 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 23:18:57

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Golgi to plasma membrane transport	GO:0006893	2	CCDC22, VPS35L	33	4	283.14	1.810e-5	8.586e-4
endocytic recycling	GO:0032456	2	CCDC22, VPS35L	65	4	143.75	7.116e-5	2.399e-3
protein transport	GO:0015031	3	CCDC22, VPS35L, WASHC5	667	4	21.01	1.763e-4	4.643e-3
regulation of actin nucleation	GO:0051125	1	WASHC5	2	4	2335.88	4.281e-4	8.531e-3
meiotic spindle assembly	GO:0090306	1	WASHC5	3	4	1557.25	6.421e-4	1.113e-2
endosome fission	GO:0140285	1	WASHC5	3	4	1557.25	6.421e-4	1.113e-2
polar body extrusion after meiotic divisions	GO:0040038	1	WASHC5	5	4	934.35	1.070e-3	1.514e-2
pyrimidine nucleobase catabolic process	GO:0006208	1	DPYSL5	7	4	667.39	1.498e-3	1.821e-2
regulation of vesicle size	GO:0097494	1	WASHC5	7	4	667.39	1.498e-3	1.821e-2
protein-containing complex organization	GO:0043933	1	WASHC5	8	4	583.97	1.711e-3	1.958e-2
negative regulation of dendrite morphogenesis	GO:0050774	1	DPYSL5	9	4	519.08	1.925e-3	2.069e-2
intracellular copper ion homeostasis	GO:0006878	1	CCDC22	18	4	259.54	3.848e-3	2.937e-2
regulation of Arp2/3 complex-mediated actin nucleation	GO:0034315	1	WASHC5	18	4	259.54	3.848e-3	2.937e-2
protein-containing complex localization	GO:0031503	1	WASHC5	20	4	233.59	4.275e-3	3.094e-2
oocyte maturation	GO:0001556	1	WASHC5	27	4	173.03	5.767e-3	3.561e-2