

GeDiPNet Cluster 630 -- 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 23:19:04

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
protein lipoylation	GO:0009249	2	LIPT2, LIPT1	5	4	1868.70	3.436e-7	3.561e-5
positive regulation of oxygen metabolic process	GO:2000376	1	LIPT2	2	4	2335.88	4.281e-4	8.531e-3
positive regulation of protein localization to kinetochore	GO:1905342	1	TRAPPC12	2	4	2335.88	4.281e-4	8.531e-3
regulation of kinetochore assembly	GO:0090234	1	TRAPPC12	3	4	1557.25	6.421e-4	1.113e-2
metaphase chromosome alignment	GO:0051310	1	TRAPPC12	16	4	291.98	3.421e-3	2.781e-2
vesicle tethering	GO:0099022	1	TRAPPC12	16	4	291.98	3.421e-3	2.781e-2
viral budding via host ESCRT complex	GO:0039702	1	MITD1	23	4	203.12	4.915e-3	3.307e-2
COPII vesicle coating	GO:0048208	1	TRAPPC12	23	4	203.12	4.915e-3	3.307e-2
midbody abscission	GO:0061952	1	MITD1	24	4	194.66	5.128e-3	3.369e-2
multivesicular body sorting pathway	GO:0071985	1	MITD1	24	4	194.66	5.128e-3	3.369e-2
negative regulation of protein binding	GO:0032091	1	MITD1	26	4	179.68	5.554e-3	3.509e-2
mitotic cytokinesis	GO:0000281	1	MITD1	68	4	68.70	1.448e-2	5.549e-2
protein modification process	GO:0036211	1	LIPT1	84	4	55.62	1.786e-2	6.127e-2
Golgi organization	GO:0007030	1	TRAPPC12	128	4	36.50	2.712e-2	7.682e-2
endoplasmic reticulum to Golgi vesicle-mediated transport	GO:0006888	1	TRAPPC12	133	4	35.13	2.817e-2	7.829e-2