

GeDiPNet Cluster 434 -- 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 15:02:22

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
central nervous system myelination	GO:0022010	2	MAL, PLP1	16	7	333.70	1.440e-5	6.943e-4
myelination	GO:0042552	2	MAL, PLP1	73	7	73.14	3.121e-4	6.916e-3
isotype switching to IgG isotypes	GO:0048291	1	HSPD1	1	7	2669.57	3.746e-4	7.813e-3
protein insertion into plasma membrane	GO:0098737	1	MAL	1	7	2669.57	3.746e-4	7.813e-3
positive regulation of glucagon secretion	GO:0070094	1	AIMP1	2	7	1334.79	7.491e-4	1.251e-2
mitochondrial unfolded protein response	GO:0034514	1	HSPD1	2	7	1334.79	7.491e-4	1.251e-2
mitotic spindle disassembly	GO:0051228	1	SPAST	3	7	889.86	1.123e-3	1.623e-2
cytokinetic process	GO:0032506	1	SPAST	3	7	889.86	1.123e-3	1.623e-2
membrane raft polarization	GO:0001766	1	MAL	3	7	889.86	1.123e-3	1.623e-2
'de novo' protein folding	GO:0006458	1	HSPD1	3	7	889.86	1.123e-3	1.623e-2
protein import into mitochondrial intermembrane space	GO:0045041	1	HSPD1	3	7	889.86	1.123e-3	1.623e-2
adhesion of symbiont to host	GO:0044406	1	HSPD1	4	7	667.39	1.498e-3	1.912e-2
protein localization to paranode region of axon	GO:0002175	1	MAL	4	7	667.39	1.498e-3	1.912e-2
positive regulation of microtubule depolymerization	GO:0031117	1	SPAST	5	7	533.91	1.872e-3	2.187e-2
biological process involved in interaction with symbiont	GO:0051702	1	HSPD1	6	7	444.93	2.246e-3	2.412e-2