

GeDiPNet Cluster 219 -- 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: 2026-10-10 03:23:27. · Rows: 15 · Generated: 2026-10-10 08:59:46

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
protein import into peroxisome matrix, receptor recycling	GO:0016562	3	PEX6, PEX1, PEX26	10	7	800.87	3.858e-9	7.375e-7
protein unfolding	GO:0043335	3	PEX6, PEX1, PEX26	12	7	667.39	7.071e-9	1.253e-6
protein import into peroxisome matrix	GO:0016558	3	PEX6, PEX1, PEX26	14	7	572.05	1.170e-8	1.953e-6
protein targeting to peroxisome	GO:0006625	2	PEX6, PEX1	10	7	533.91	5.405e-6	3.306e-4
peroxisome organization	GO:0007031	2	PEX6, PEX1	23	7	232.14	3.032e-5	1.271e-3
mitochondrial asparaginyl-tRNA aminoacylation	GO:0070145	1	DARS2	1	7	2669.57	3.746e-4	8.083e-3
regulation of aldosterone biosynthetic process	GO:0032347	1	CLCN2	1	7	2669.57	3.746e-4	8.083e-3
aspartyl-tRNA aminoacylation	GO:0006422	1	DARS2	2	7	1334.79	7.491e-4	1.295e-2
cell differentiation involved in salivary gland development	GO:0060689	1	CLCN2	2	7	1334.79	7.491e-4	1.295e-2
regulation of response to osmotic stress	GO:0047484	1	MLC1	2	7	1334.79	7.491e-4	1.295e-2
regulation of membrane depolarization during action potential	GO:0098902	1	CLCN2	2	7	1334.79	7.491e-4	1.295e-2
microtubule-based peroxisome localization	GO:0060152	1	PEX1	2	7	1334.79	7.491e-4	1.295e-2
stabilization of membrane potential	GO:0030322	1	CLCN2	3	7	889.86	1.123e-3	1.680e-2
protein transport	GO:0015031	3	MLC1, PEX1, PEX26	667	7	12.01	1.423e-3	1.928e-2
protein import into peroxisome matrix, translocation	GO:0016561	1	PEX6	4	7	667.39	1.498e-3	1.985e-2