

GeDiPNet Cluster 92 -- 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 16:21:38

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
proton transmembrane transport	GO:1902600	14	COX3, ATP6, ATP6V0A1, ATP8, COX1, COX2, ND1, ND2, ND3, ND4L, SLC36A1, SURF1	181	227	6.37	4.723e-8	6.475e-6
proton motive force-driven mitochondrial ATP synthesis	GO:0042776	9	ATP6, ATP8, ND1, ND2, ND3, ND4, ND4L, ND5, ATP5F1B	64	227	11.58	7.579e-8	9.533e-6
aerobic respiration	GO:0009060	9	COX1, MFN2, ND1, ND2, ND3, ND4, ND4L, ND5, SURF1	68	227	10.90	1.300e-7	1.503e-5
ATP synthesis coupled electron transport	GO:0042773	4	COX2, ND4, ND4L, ND5	7	227	47.04	7.213e-7	6.384e-5
monoatomic ion transmembrane transport	GO:0034220	18	ANO10, CACNA1A, CACNA1G, GRID2, TRPC3, ITPR1, CLCN2, KCNA6, KCNJ10, KCNN2, SCN8A, ATP2B3	404	227	3.67	2.357e-6	1.642e-4
respiratory chain complex IV assembly	GO:0008535	4	COX3, SURF1, SLC25A46, COA7	9	227	36.59	2.547e-6	1.744e-4
mitochondrion organization	GO:0007005	10	AFG3L2, LRRK2, VPS13D, OPA1, PRDX3, MFN2, WDR81, SLC25A46, SPG7, PNPT1	130	227	6.33	4.288e-6	2.652e-4
monoatomic ion transport	GO:0006811	23	CACNA1A, CACNA1G, GRID2, TRPC3, ITPR1, ATP6, ATP6V0A1, ATP8, CLCN2, KCNA6, KCNJ10, KCNN2	667	227	2.84	7.103e-6	3.973e-4
glycosphingolipid catabolic process	GO:0046479	4	GBA2, GALC, GLB1, SUMF1	12	227	27.44	9.724e-6	5.105e-4
regulation of SNARE complex assembly	GO:0035542	4	LRRK2, VPS41, STXBP1, VPS39	12	227	27.44	9.724e-6	5.105e-4
mitochondrial electron transport, NADH to ubiquinone	GO:0006120	6	ND1, ND2, ND3, ND4, ND4L, ND5	47	227	10.51	2.130e-5	9.451e-4
protein catabolic process	GO:0030163	8	AFG3L2, MME, TPP1, CLN6, PPT1, SPG11, HSPA8, NQO1	97	227	6.79	2.393e-5	1.029e-3
regulation of autophagy	GO:0010506	7	LRRK2, EP300, ITPR1, MTCL1, ERCC4, WDR24, ATM	73	227	7.89	2.935e-5	1.202e-3
action potential	GO:0001508	6	CACNA1G, KCNA6, SCN8A, SCN2A, KCNC3, KCND3	53	227	9.32	4.286e-5	1.605e-3
chaperone-mediated autophagy	GO:0061684	3	STUB1, HSPA8, ATG5	7	227	35.28	5.973e-5	2.049e-3