

GeDiPNet Cluster 191 -- 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 04:01:24

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
lysosome organization	GO:0007040	8	PPT1, CLN5, CLN8, GRN, TPP1, CLN3, CLN6, MFSD8	65	54	42.59	1.259e-11	4.538e-9
negative regulation of neuron apoptotic process	GO:0043524	9	DNAJC5, PPARGC1A, PPT1, SIRT1, CLN8, GRN, CLN3, MFSD8, SOD2	160	54	19.47	7.545e-10	1.743e-7
lysosomal lumen acidification	GO:0007042	5	PPT1, CLN5, GRN, CLN3, CLN6	25	54	69.21	8.474e-9	1.485e-6
tRNA-type intron splice site recognition and cleavage	GO:0000379	3	TSEN2, TSEN34, TSEN54	3	54	346.06	2.281e-8	3.495e-6
macromolecule catabolic process	GO:0009057	3	PPT1, CLN8, CLN6	3	54	346.06	2.281e-8	3.495e-6
mitochondrion organization	GO:0007005	7	FIS1, MFN1, PARP1, PPARGC1A, GSK3B, MFSD8, SOD2	130	54	18.63	9.044e-8	1.108e-5
lysosomal protein catabolic process	GO:1905146	4	GRN, TPP1, CLN3, MFSD8	16	54	86.51	1.104e-7	1.313e-5
insulin receptor signaling pathway	GO:0008286	5	RPS6KB1, GSK3B, MAPK1, MAPK3, INS	80	54	21.63	3.400e-6	2.208e-4
Bergmann glial cell differentiation	GO:0060020	3	GFAP, MAPK1, MAPK3	11	54	94.38	3.702e-6	2.362e-4
tRNA splicing, via endonucleolytic cleavage and ligation	GO:0006388	3	TSEN2, TSEN34, TSEN54	13	54	79.86	6.391e-6	3.649e-4
protein catabolic process	GO:0030163	5	PPT1, CLN5, CLN8, TPP1, CLN6	97	54	17.84	8.782e-6	4.718e-4
cellular response to oxygen-containing compound	GO:1901701	3	PARP1, GSK3B, INS	16	54	64.89	1.244e-5	6.191e-4
neuromuscular process controlling balance	GO:0050885	4	CLN8, TPP1, CLN3, MYH10	53	54	26.12	1.642e-5	7.699e-4
cellular response to oxidative stress	GO:0034599	5	ATP2A2, PARP1, PPARGC1A, ATP13A2, SOD2	111	54	15.59	1.694e-5	7.889e-4
negative regulation of oxidative stress-induced intrinsic apoptotic signaling pathway	GO:1902176	3	SIRT1, SOD2, INS	18	54	57.68	1.805e-5	8.277e-4