

GeDiPNet Cluster 157 -- 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 11:57:32

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
sensory perception of sound	GO:0007605	9	OTOF, DIAPH3, MYO7A, SLC52A3, WFS1, DIAPH1, SLC17A8, ALDH7A1, SLC26A4	162	37	28.06	2.235e-11	7.489e-9
riboflavin metabolic process	GO:0006771	2	SLC52A3, SLC52A2	5	37	202.02	3.800e-5	1.462e-3
riboflavin transport	GO:0032218	2	SLC52A3, SLC52A2	6	37	168.35	5.693e-5	1.980e-3
inner ear receptor cell differentiation	GO:0060113	2	DIAPH3, MYO7A	9	37	112.23	1.361e-4	3.805e-3
mitochondrial DNA replication	GO:0006264	2	TWINK, POLG	11	37	91.83	2.075e-4	5.183e-3
axonal transport of mitochondrion	GO:0019896	2	NEFL, OPA1	12	37	84.18	2.486e-4	5.900e-3
central nervous system myelination	GO:0022010	2	PLP1, KCNJ10	16	37	63.13	4.498e-4	8.903e-3
Rab protein signal transduction	GO:0032482	2	RAB33A, RAB9B	17	37	59.42	5.092e-4	9.680e-3
negative regulation of endoplasmic reticulum stress-induced intrinsic apoptotic signaling pathway	GO:1902236	2	OPA1, WFS1	20	37	50.51	7.087e-4	1.208e-2
mitochondrial fusion	GO:0008053	2	MFN2, OPA1	21	37	48.10	7.823e-4	1.287e-2
visual perception	GO:0007601	4	MYO7A, OPA1, WFS1, KCNJ10	215	37	9.40	8.357e-4	1.342e-2
microtubule polymerization	GO:0046785	2	DIAPH3, TRPV4	25	37	40.40	1.112e-3	1.615e-2
calcium ion import across plasma membrane	GO:0098703	2	CACNA1A, TRPV4	28	37	36.08	1.396e-3	1.841e-2
protein targeting to mitochondrion	GO:0006626	2	MFN2, TIMM8A	29	37	34.83	1.497e-3	1.912e-2
ectoderm and mesoderm interaction	GO:0007499	1	TP63	1	37	505.05	1.980e-3	2.242e-2