

GeDiPNet Cluster 243 -- 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 08:19:30

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
myelination	GO:0042552	4	EGR2, MPZ, PMP22, CNTNAP1	73	10	102.39	4.421e-8	6.110e-6
peripheral nervous system development	GO:0007422	2	EGR2, PMP22	26	10	143.75	8.319e-5	2.635e-3
rhombomere 3 structural organization	GO:0021659	1	EGR2	1	10	1868.70	5.351e-4	9.981e-3
rhombomere 3 formation	GO:0021660	1	EGR2	1	10	1868.70	5.351e-4	9.981e-3
rhombomere 5 structural organization	GO:0021665	1	EGR2	1	10	1868.70	5.351e-4	9.981e-3
rhombomere 5 formation	GO:0021666	1	EGR2	1	10	1868.70	5.351e-4	9.981e-3
neuromuscular junction development, skeletal muscle fiber	GO:0098529	1	CNTNAP1	1	10	1868.70	5.351e-4	9.981e-3
rhythmic behavior	GO:0007622	1	EGR2	2	10	934.35	1.070e-3	1.569e-2
postsynaptic density organization	GO:0097106	1	CNTNAP1	2	10	934.35	1.070e-3	1.569e-2
paranodal junction maintenance	GO:1990227	1	CNTNAP1	2	10	934.35	1.070e-3	1.569e-2
rod bipolar cell differentiation	GO:1904389	1	RHO	2	10	934.35	1.070e-3	1.569e-2
cell aggregation	GO:0098743	1	MPZ	2	10	934.35	1.070e-3	1.569e-2
thermotaxis	GO:0043052	1	RHO	2	10	934.35	1.070e-3	1.569e-2
positive regulation of Schwann cell differentiation	GO:0014040	1	EGR2	3	10	622.90	1.605e-3	1.983e-2
rhombomere 3 development	GO:0021569	1	EGR2	3	10	622.90	1.605e-3	1.983e-2