

GeDiPNet Cluster 295 -- 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 09:10:58

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
visual perception	GO:0007601	6	ATF6, CNGA3, CNGB3, GNAT2, PDE6C, PDE6H	215	7	74.50	1.500e-11	5.289e-9
retinal cone cell development	GO:0046549	2	GNAT2, PDE6C	11	7	485.38	6.605e-6	3.740e-4
signal transduction	GO:0007165	6	ATF6, CNGA3, CNGB3, GNAT2, NDRG4, PDE6C	2125	7	7.54	1.358e-5	6.621e-4
monoatomic cation transmembrane transport	GO:0098655	2	CNGA3, CNGB3	61	7	87.53	2.178e-4	5.354e-3
monoatomic cation transport	GO:0006812	2	CNGA3, CNGB3	61	7	87.53	2.178e-4	5.354e-3
positive regulation of ATF6-mediated unfolded protein response	GO:1903893	1	ATF6	1	7	2669.57	3.746e-4	7.813e-3
inorganic cation import across plasma membrane	GO:0098659	1	CNGA3	2	7	1334.79	7.491e-4	1.251e-2
background adaptation	GO:0120302	1	GNAT2	2	7	1334.79	7.491e-4	1.251e-2
cell migration involved in heart development	GO:0060973	1	NDRG4	2	7	1334.79	7.491e-4	1.251e-2
regulation of ATF6-mediated unfolded protein response	GO:1903891	1	ATF6	3	7	889.86	1.123e-3	1.623e-2
homeostasis of number of retina cells	GO:0048877	1	GNAT2	3	7	889.86	1.123e-3	1.623e-2
neural tissue regeneration	GO:0097719	1	GNAT2	3	7	889.86	1.123e-3	1.623e-2
retinal cone cell differentiation	GO:0042670	1	GNAT2	4	7	667.39	1.498e-3	1.912e-2
cone retinal bipolar cell differentiation	GO:1904390	1	GNAT2	4	7	667.39	1.498e-3	1.912e-2
detection of light stimulus	GO:0009583	1	GNAT2	5	7	533.91	1.872e-3	2.187e-2