

GeDiPNet Cluster 607 -- 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: 2026-10-20 03:23:14. · Rows: 15 · Generated: 2026-10-20 00:01:09

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
cell fate determination	GO:0001709	2	PAX6, PTCH2	18	6	346.06	1.311e-5	6.706e-4
negative regulation of microtubule depolymerization	GO:0007026	2	SPECC1L, MID1	32	6	194.66	4.243e-5	1.628e-3
eye development	GO:0001654	2	PAX6, SALL2	49	6	127.12	1.004e-4	3.103e-3
camera-type eye development	GO:0043010	2	PAX6, MITF	74	6	84.18	2.297e-4	5.603e-3
cell fate commitment	GO:0045165	2	PAX6, MITF	75	6	83.05	2.359e-4	5.698e-3
pancreatic A cell development	GO:0003322	1	PAX6	1	6	3114.50	3.211e-4	7.044e-3
forebrain-midbrain boundary formation	GO:0021905	1	PAX6	1	6	3114.50	3.211e-4	7.044e-3
neural crest cell delamination	GO:0036032	1	SPECC1L	1	6	3114.50	3.211e-4	7.044e-3
melanocyte apoptotic process	GO:1902362	1	MITF	2	6	1557.25	6.421e-4	1.113e-2
oligodendrocyte cell fate specification	GO:0021778	1	PAX6	2	6	1557.25	6.421e-4	1.113e-2
pallium development	GO:0021543	1	PAX6	3	6	1038.17	9.630e-4	1.423e-2
habenula development	GO:0021986	1	PAX6	3	6	1038.17	9.630e-4	1.423e-2
regulation of RNA biosynthetic process	GO:2001141	1	MITF	3	6	1038.17	9.630e-4	1.423e-2
anterior neural tube closure	GO:0061713	1	SPECC1L	4	6	778.63	1.284e-3	1.669e-2
regionalization	GO:0003002	1	PAX6	4	6	778.63	1.284e-3	1.669e-2