

GeDiPNet Cluster 51 -- 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 08:25:07

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
lens development in camera-type eye	GO:0002088	22	CRYAA, CRYAB, CRYBB1, CRYBB3, CRYGC, CRYGD, CRYGS, FOXE3, GJA8, LIM2, MIP, PAX6	48	223	38.41	3.546e-30	1.908e-26
visual perception	GO:0007601	22	BFSP2, COL18A1, COL2A1, CRYAA, CRYBB1, CRYBB3, CRYGC, CRYGD, CRYGS, MIP, PAX6, RHO	215	223	8.57	1.376e-14	8.733e-12
camera-type eye development	GO:0043010	14	BMP4, CRYAA, CRYAB, FOXE3, GJA8, JAG1, LIM2, MITF, PAX6, PITX2, CRYBA4, CRYBB2	74	223	15.85	1.911e-13	1.005e-10
lens fiber cell differentiation	GO:0070306	5	CRYGD, HSF4, PITX3, TDRD7, MAF	15	223	27.93	6.304e-7	5.687e-5
eye development	GO:0001654	7	CPAMD8, FOXE3, PAX6, CRYGB, SIPA1L3, CRYGA, SIX6	49	223	11.97	1.760e-6	1.302e-4
lens fiber cell development	GO:0070307	4	BFSP2, VIM, BFSP1, CRYGB	9	223	37.24	2.373e-6	1.650e-4
lens morphogenesis in camera-type eye	GO:0002089	4	CRYAA, PITX3, TDRD7, NECTIN3	15	223	22.35	2.430e-5	1.041e-3
gap junction-mediated intercellular transport	GO:1990349	3	GJA8, MIP, GJA3	6	223	41.90	3.266e-5	1.304e-3
axon ensheathment	GO:0008366	3	PPARD, QKI, PRX	7	223	35.91	5.665e-5	1.973e-3
maintenance of lens transparency	GO:0036438	3	MIP, GCNT2, CHMP4B	8	223	31.42	8.984e-5	2.794e-3
lens fiber cell morphogenesis	GO:0070309	3	CRYAA, EPHA2, CRYGB	8	223	31.42	8.984e-5	2.794e-3
iris morphogenesis	GO:0061072	3	FOXE3, PAX6, PITX2	9	223	27.93	1.336e-4	3.758e-3
embryonic eye morphogenesis	GO:0048048	3	MFAP5, RARB, FBN1	11	223	22.85	2.578e-4	6.043e-3
protein refolding	GO:0042026	4	CRYAA, CRYAB, HSPA1A, HSPA1L	27	223	12.41	2.792e-4	6.381e-3
cell population proliferation	GO:0008283	11	BMP4, CDKN2C, CNTNAP2, FGF18, FGFR3, HMGA2, OCA2, PAX6, PPARD, RARB, TYR	263	223	3.50	3.338e-4	7.224e-3