

GeDiPNet Cluster 189 -- 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: 2026-10-08 03:23:04. · Rows: 15 · Generated: 2026-10-08 07:25:14

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	26	ABCA4, HMCN1, AIPL1, RDH5, TRPM1, EYS, CDH3, BBS10, BEST1, CNGA3, FSCN2, PRPH2	215	209	10.81	1.377e-19	2.011e-16
complement activation	GO:0006956	10	CFHR1, CFI, C2, C3, C9, CFB, CFH, CFHR4, CFHR5, CFHR3	35	209	25.55	3.551e-12	1.443e-9
complement activation, alternative pathway	GO:0006957	5	C3, C9, CFB, CFH, CFHR5	16	209	27.94	6.592e-7	5.951e-5
retina development in camera-type eye	GO:0060041	8	BBS10, CNGA3, PRPH2, CRB1, NDP, RHO, RD3, RP1	85	209	8.42	4.926e-6	3.021e-4
detection of light stimulus involved in visual perception	GO:0050908	5	EYS, BEST1, PRPH2, CRB1, RPE65	24	209	18.63	5.963e-6	3.524e-4
phototransduction, visible light	GO:0007603	4	ABCA4, AIPL1, RHO, RP1	13	209	27.51	1.004e-5	5.325e-4
photoreceptor cell maintenance	GO:0045494	6	ABCA4, BBS10, ERCC6, CRB1, RHO, RP1	45	209	11.92	1.031e-5	5.431e-4
glutathione metabolic process	GO:0006749	6	SOD2, GSTM1, GSTP1, GSTT1, GSR, NDP	49	209	10.95	1.706e-5	8.036e-4
retina homeostasis	GO:0001895	4	AIPL1, ARMS2, CDH3, RPE65	15	209	23.84	1.884e-5	8.689e-4
photoreceptor cell outer segment organization	GO:0035845	4	PRPH2, TOPORS, CRB1, RP1	15	209	23.84	1.884e-5	8.689e-4
positive regulation of apoptotic process	GO:0043065	14	ALDH1A2, BARD1, MMP9, TGFB1, HTRA1, MMP2, SQSTM1, TNFRSF10A, AIFM1, APAF1, CASP3, CASP9	326	209	3.84	1.923e-5	8.837e-4
cellular response to light stimulus	GO:0071482	4	TRPM1, CRB1, RHO, RP1	16	209	22.35	2.490e-5	1.073e-3
response to hypoxia	GO:0001666	10	SOD2, MTHFR, VEGFA, ERCC2, MMP2, ND4, APAF1, CASP3, CASP9, NDP	176	209	5.08	2.986e-5	1.231e-3
reverse cholesterol transport	GO:0043691	4	ABCA1, APOE, CETP, LIPC	17	209	21.04	3.228e-5	1.309e-3
extracellular matrix organization	GO:0030198	9	MMP9, ELN, ERCC2, MMP2, FBLN5, DNAJB6, COL4A2, TNR, TNXB	145	209	5.55	3.761e-5	1.479e-3