

GeDiPNet Cluster 410 -- 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 12:18:34

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
vitamin A metabolic process	GO:0006776	3	LRAT, RLBP1, RPE65	7	128	62.57	1.077e-5	5.617e-4
visual perception	GO:0007601	8	EFEMP1, GJD2, RDH5, RGR, TYR, LRAT, RLBP1, RPE65	215	128	5.43	1.182e-4	3.493e-3
retinoid metabolic process	GO:0001523	4	RDH5, LRAT, LRP2, RPE65	38	128	15.37	1.294e-4	3.745e-3
negative regulation of defense response	GO:0031348	2	MICA, PPARG	3	128	97.33	1.390e-4	3.946e-3
camera-type eye development	GO:0043010	5	BMP4, EFEMP1, PRSS56, RPGRIP1L, RPE65	74	128	9.86	1.539e-4	4.261e-3
regulation of hormone metabolic process	GO:0032350	2	GNB3, TCF7L2	4	128	73.00	2.768e-4	6.452e-3
antigen processing and presentation	GO:0019882	4	HLA-C, HLA-DQA1, HLA-DQB1, HLA-B	48	128	12.17	3.236e-4	7.226e-3
monocyte differentiation	GO:0030224	3	BMP4, RXRA, PPARG	20	128	21.90	3.286e-4	7.296e-3
positive regulation of neuron differentiation	GO:0045666	5	NGF, BMP4, GPD5, PCP4, TCF4	87	128	8.39	3.288e-4	7.298e-3
response to bacterium	GO:0009617	6	CFB, TAB3, LRAT, CCL2, NAALADL2, SERPINE1	140	128	6.26	4.074e-4	8.498e-3
positive regulation of lipoprotein transport	GO:0140077	2	RXRA, PPARG	5	128	58.40	4.593e-4	9.231e-3
cellular response to low-density lipoprotein particle stimulus	GO:0071404	3	ABCA1, RXRA, PPARG	23	128	19.04	5.029e-4	9.797e-3
negative regulation of chondrocyte differentiation	GO:0032331	3	BMP4, EFEMP1, RARB	23	128	19.04	5.029e-4	9.797e-3
kidney development	GO:0001822	6	SERPINF1, BICC1, BMP4, PTCD2, RPGRIP1L, LRP2	146	128	6.00	5.092e-4	9.854e-3
retinoic acid receptor signaling pathway	GO:0048384	3	RARB, RXRA, PPARG	24	128	18.25	5.719e-4	1.071e-2