

GeDiPNet Cluster 54 -- 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: 2026-10-09 03:23:08. · Rows: 15 · Generated: 2026-10-09 06:29:01

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
camera-type eye development	GO:0043010	16	STRA6, BMP4, CRYBA4, HESX1, PAX2, PAX6, PITX2, RAX, SIX3, VAX1, VSX2, ARHGAP35	74	76	53.16	5.818e-24	1.696e-20
eye development	GO:0001654	9	SIX6, SOX2, PAX6, SIX3, RBP4, SMOC1, GDF3, MAB21L2, FZD5	49	76	45.16	3.365e-13	1.662e-10
visual perception	GO:0007601	13	SIX6, CRYBA4, PAX2, PAX6, RAX, SIX3, VSX2, RBP4, MFRP, CRYBB3, MIP, BEST1	215	76	14.87	3.472e-12	1.415e-9
lens development in camera-type eye	GO:0002088	8	CRYBA4, NHS, PAX6, PITX3, SIX3, CRYBB3, GJA8, MIP	48	76	40.98	1.697e-11	5.978e-9
pituitary gland development	GO:0021983	6	SOX2, BMP4, HESX1, PAX6, PITX2, SIX3	30	76	49.18	2.033e-9	4.181e-7
telencephalon regionalization	GO:0021978	4	BMP4, PAX6, SIX3, SHH	7	76	140.50	8.759e-9	1.503e-6
forebrain development	GO:0030900	7	SOX2, BMP4, HESX1, OTX2, PAX6, ARHGAP35, SHH	76	76	22.65	2.424e-8	3.631e-6
metanephric collecting duct development	GO:0072205	4	WNT7B, PAX2, PTCH1, SHH	9	76	109.28	3.134e-8	4.492e-6
negative regulation of transcription by RNA polymerase II	GO:0000122	18	RARB, SOX2, BMP4, DACH1, HESX1, PAX6, PITX2, PTCH1, TFAP2A, VAX1, VSX2, TBX18	1002	76	4.42	7.526e-8	9.407e-6
embryonic hindlimb morphogenesis	GO:0035116	5	RARB, BMP4, PITX2, SHH, FGF8	29	76	42.39	1.071e-7	1.271e-5
positive regulation of transcription by RNA polymerase II	GO:0045944	19	RARB, SOX2, BMP4, IKBKG, OTX2, PAX2, PAX6, PITX2, PITX3, RAX, SIX3, TFAP2A	1208	76	3.87	2.429e-7	2.545e-5
lung development	GO:0030324	7	STRA6, WNT7B, BMP4, PITX2, RBP4, SHH, FGF8	108	76	15.94	2.787e-7	2.860e-5
odontogenesis	GO:0042476	5	BMP4, PITX2, SHH, BCOR, FGF8	36	76	34.15	3.326e-7	3.318e-5
smooth muscle tissue development	GO:0048745	4	STRA6, BMP4, PTCH1, SHH	16	76	61.47	4.430e-7	4.213e-5
positive regulation of DNA-templated transcription	GO:0045893	15	SOX2, BMP4, OTX2, PAX2, PAX6, PITX2, PITX3, PTCH1, TFAP2A, TBX18, GDF6, SHH	778	76	4.74	4.544e-7	4.295e-5