

GeDiPNet Cluster 283 -- 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 06:28:51

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
thyroid gland development	GO:0030878	6	BRAF, FOXE1, NKX2-1, PAX8, TG, SMAD3	30	105	35.59	1.450e-8	2.345e-6
cell surface receptor protein tyrosine kinase signaling pathway	GO:0007169	7	ALK, NRG1, NTRK1, NTRK3, RET, GAB2, INSR	120	105	10.38	5.109e-6	3.080e-4
positive regulation of gene expression	GO:0010628	12	BRAF, HRAS, KRAS, MBIP, NKX2-1, NTRK3, PPARG, RET, TRIM24, SMAD3, TGFB2, BMP7	504	105	4.24	2.608e-5	1.104e-3
positive regulation of extrinsic apoptotic signaling pathway in absence of ligand	GO:2001241	3	RET, WWOX, TGFB2	11	105	48.54	2.753e-5	1.152e-3
positive regulation of DNA-templated transcription	GO:0045893	15	FOXE1, NCOA4, NFIA, NKX2-1, PAX8, PPARG, RET, SKAP1, TRIM24, TRIM27, FGF7, INSR	778	105	3.43	2.902e-5	1.198e-3
substantia propria of cornea development	GO:1903701	2	KCNQ3, TGFB2	2	105	177.97	3.127e-5	1.265e-3
telomere capping	GO:0016233	3	STN1, POT1, TINF2	12	105	44.49	3.655e-5	1.428e-3
neuron development	GO:0048666	5	ALK, NTRK1, TENM4, TGFB2, SOD2	77	105	11.56	7.293e-5	2.395e-3
telomere assembly	GO:0032202	2	POT1, TINF2	3	105	118.65	9.347e-5	2.882e-3
cellular response to estrogen stimulus	GO:0071391	3	NCOA4, TRIM24, BCAS3	19	105	28.10	1.564e-4	4.242e-3
MAPK cascade	GO:0000165	6	BRAF, HRAS, KRAS, NRAS, RET, SMAD3	147	105	7.26	1.816e-4	4.727e-3
regulation of transforming growth factor beta2 production	GO:0032909	2	SMAD3, TGFB2	4	105	88.99	1.863e-4	4.814e-3
response to isolation stress	GO:0035900	2	KRAS, SOD2	4	105	88.99	1.863e-4	4.814e-3
positive regulation of phosphatidylinositol 3-kinase/protein kinase B signal transduction	GO:0051897	7	NTRK1, NTRK3, RET, VAV3, INSR, TGFB2, TMEM100	217	105	5.74	2.246e-4	5.465e-3
negative regulation of telomere maintenance via telomerase	GO:0032211	3	STN1, POT1, TINF2	22	105	24.27	2.456e-4	5.843e-3