

GeDiPNet Cluster 290 -- 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 14:34:01

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
positive regulation of phosphatidylinositol 3-kinase/protein kinase B signal transduction	GO:0051897	34	ADRA2A, FGFR1, HGF, NTRK2, NTS, PDGFD, PTPN11, AKR1C2, AKR1C3, EGFR, EPHA8, ERBB4	217	990	2.96	1.284e-8	2.090e-6
axon guidance	GO:0007411	31	CNTN1, CNTN5, CRPPA, DSCAM, EPHA4, EPHB1, ETV1, FEZ1, NOTCH1, NOTCH2, UNC5C, CDH4	192	990	3.05	2.741e-8	4.052e-6
cell population proliferation	GO:0008283	37	ALKBH3, CDK5RAP3, ESRRB, FGFR1, HPSE2, KRAS, MTA3, NF1, NOTCH1, NOTCH2, RAP1B, RARB	263	990	2.66	5.540e-8	7.379e-6
cell migration	GO:0016477	39	CDH22, CTNNA2, CTNNA3, DOCK1, DOCK2, EPHB1, FGFR1, FMNL2, GPC6, MMP9, NF1, PTPRK	303	990	2.43	2.685e-7	2.807e-5
positive regulation of miRNA transcription	GO:1902895	14	AR, HIF1A, NOTCH2, TEAD1, EGFR, SMARCA4, TERT, TP53, MYC, NOTCH3, WT1, FGF2	56	990	4.72	9.009e-7	7.671e-5
positive regulation of endothelial cell chemotaxis	GO:2001028	7	FGFR1, HSPB1, MET, PRKD1, SEMA5A, VEGFA, FGF2	13	990	10.16	1.485e-6	1.155e-4
negative regulation of apoptotic process	GO:0043066	54	BRAF, CEACAM5, HGF, HIF1A, HSPB1, MMP9, NOTCH2, PLK2, RARB, AAMDC, AKT3, ANXA4	524	990	1.95	2.257e-6	1.616e-4
embryonic digestive tract development	GO:0048566	8	PCSK5, PKDCC, RARB, STRA6, CXCL8, FOXF2, MYB, TNF	19	990	7.95	2.701e-6	1.870e-4
regulation of cell population proliferation	GO:0042127	28	BCL6B, BMP6, BRAF, HIF1A, MEAK7, NF1, NOTCH1, SAV1, TIAL1, ALK, BIRC6, CCND3	201	990	2.63	2.736e-6	1.891e-4
intracellular glucose homeostasis	GO:0001678	9	HIF1A, KLF15, PPARGC1A, CARTPT, HK2, NR1D1, PIK3R1, STXBP3, RAF1	27	990	6.29	6.248e-6	3.657e-4
cell adhesion	GO:0007155	62	CADM2, CCR3, CDH22, CEACAM5, CEACAM6, CLSTN2, CNTN1, CNTN5, CTNNA2, CTNNA3, DAB1, DSCAM	665	990	1.76	1.075e-5	5.607e-4
Ras protein signal transduction	GO:0007265	15	ADRA2A, G3BP1, KRAS, NF1, PLK2, RASGRF1, IGF1, KSR2, NTN1, RASGEF1B, RSU1, TP53	79	990	3.58	1.453e-5	7.102e-4
pulmonary valve morphogenesis	GO:0003184	7	HEY1, HEY2, NOTCH1, NOTCH2, ADAMTS5, STRA6, JAG1	18	990	7.34	2.179e-5	9.740e-4
positive regulation of MAPK cascade	GO:0043410	28	ADRA2A, AR, FGFR1, HGF, LRRK2, NTRK2, RASGRF1, CARTPT, DAB2IP, EDN1, EGFR, EPHA8	224	990	2.36	2.189e-5	9.768e-4
intracellular signal transduction	GO:0035556	47	AKAP11, ASB1, HSPB1, HUNK, ITK, LATS2, LRRK2, MAP4K5, MAST4, MYZAP, NOTCH2, NRG2	471	990	1.88	2.339e-5	1.023e-3