

GeDiPNet Cluster 377 -- 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 05:53:03

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
cardiac muscle contraction	GO:0060048	29	ACTC1, CASQ2, CSRP3, DMD, GRK2, MYBPC3, MYH6, MYH7, MYL2, MYL3, MYL4, MYLK2	43	539	23.38	5.613e-35	4.082e-31
regulation of heart rate by cardiac conduction	GO:0086091	24	ANK2, CACNA1C, DSC2, DSG2, DSP, HCN4, JUP, KCNE1, PKP2, SCN1B, SCN5A, TRPM4	43	539	19.35	3.189e-26	1.125e-22
sarcomere organization	GO:0045214	24	ANKRD1, ACTN2, CSRP3, FHOD3, FLNC, ITGB1, LDB3, MYBPC3, MYH6, MYOM1, MYOZ2, MYPN	43	539	19.35	3.189e-26	1.125e-22
heart development	GO:0007507	47	ABCC9, ALPK3, CACNA1C, CSRP3, DNAAF3, EDN1, GRK2, LDB3, MAPK1, MYL2, PKP2, PPARD	273	539	5.97	2.684e-23	6.791e-20
ventricular cardiac muscle cell action potential	GO:0086005	13	ANK2, CAV3, KCNE1, PKP2, RYR2, SCN5A, GPD1L, KCNE2, NEDD4L, KCNH2, SNTA1, GJA5	17	539	26.51	1.777e-17	1.874e-14
muscle contraction	GO:0006936	22	CACNA1C, CRYAB, DMD, EMD, HCN4, MYH6, MYH7, MYL3, MYL4, MYOT, OXTR, TRIM63	85	539	8.97	2.018e-15	1.447e-12
regulation of ventricular cardiac muscle cell membrane repolarization	GO:0060307	12	ANK2, CAV3, KCNE1, SCN1B, SCN5A, AKAP9, KCNE2, SCN4B, KCNH2, SNTA1, GJA5, KCNQ1	21	539	19.81	6.818e-14	3.773e-11
positive regulation of gene expression	GO:0010628	49	ACTC1, ADCYAP1, AKT1, ANK2, APP, ATF3, AVP, AVPR2, HFE, IL1A, IL1B, IL4	504	539	3.37	9.424e-14	5.093e-11
regulation of ventricular cardiac muscle cell action potential	GO:0098911	9	CACNA1C, DSC2, DSG2, DSP, JUP, PKP2, RYR2, TRPM4, CTNNA3	11	539	28.37	6.761e-13	3.122e-10
regulation of heart rate	GO:0002027	14	ANK2, CASQ2, CAV3, DMD, HCN4, MYH6, MYH7, RYR2, SCN5A, GPD1L, TNNI3K, CALM3	39	539	12.45	1.815e-12	7.738e-10
vasodilation	GO:0042311	15	ABCC9, ADORA2A, BDKRB2, NOS3, NPPB, PPARD, SOD2, TNF, APOE, GPX1, NPPA, INS	50	539	10.40	5.825e-12	2.245e-9
cardiac myofibril assembly	GO:0055003	9	ACTC1, CSRP3, FHOD3, MYL2, SRF, TCAP, TTN, MYLK3, ADPRHL1	13	539	24.00	8.346e-12	3.103e-9
ventricular cardiac muscle tissue morphogenesis	GO:0055010	11	MYBPC3, MYH6, MYH7, MYL2, MYL3, PKP2, TNNC1, TNNI3, TNNT2, TPM1, ISL1	24	539	15.89	1.847e-11	6.358e-9
regulation of the force of heart contraction	GO:0002026	10	CSRP3, GRK2, MYH6, MYH7, MYL2, MYL3, MYL4, PLN, GAA, SLC9A1	19	539	18.25	2.684e-11	8.806e-9
cardiac muscle cell development	GO:0055013	11	ACTN2, ALPK3, CAV3, MYH6, SGCB, SGCD, TCAP, TTN, LRRC10, NKX2-5, PLEC	25	539	15.25	3.212e-11	1.036e-8