

GeDiPNet Cluster 3 -- 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 00:10:47

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
regulation of heart rate by cardiac conduction	GO:0086091	34	ACE, CACNA1C, KCNH2, KCNJ2, KCNQ1, PKP2, SCN5A, CTNNA3, DSC2, DSG2, DSP, JUP	43	415	35.60	7.306e-49	1.500e-44
cardiac muscle contraction	GO:0060048	31	CASQ2, KCNH2, KCNQ1, RYR2, SCN5A, MYBPC3, MYH7, MYL3, TTN, ACTC1, DMD, MYH6	43	415	32.46	2.160e-42	2.662e-38
ventricular cardiac muscle cell action potential	GO:0086005	15	KCNH2, KCNQ1, PKP2, RYR2, SCN5A, ANK2, KCNE1, GJA5, CAV3, GPD1L, KCNE3, KCNE5	17	415	39.73	1.603e-23	4.207e-20
regulation of heart rate	GO:0002027	20	CALM1, CALM2, CALM3, CASQ2, KCNQ1, RYR2, SCN5A, MYH7, ANK2, DMD, HCN4, MYH6	39	415	23.09	2.529e-23	6.445e-20
regulation of ventricular cardiac muscle cell membrane repolarization	GO:0060307	16	KCNH2, KCNQ1, SCN5A, ANK2, KCNE1, GJA5, AKAP9, CACNA2D1, CAV3, KCNE3, KCNE5, SCN1B	21	415	34.31	4.833e-23	1.197e-19
muscle contraction	GO:0006936	24	CACNA1C, TRDN, DES, MYH7, MYL3, TTN, DMD, HCN4, MYH6, RYR1, TACR2, KCND3	85	415	12.71	2.762e-20	4.592e-17
membrane repolarization during ventricular cardiac muscle cell action potential	GO:0098915	12	KCNH2, KCNQ1, KCNE1, KCNJ5, DLG1, KCND3, KCNE3, KCNE5, KCNJ8, SCN2B, KCNE2, KCNJ3	13	415	41.57	1.567e-19	2.252e-16
sarcomere organization	GO:0045214	18	ACTN2, FLNC, LDB3, MYBPC3, TTN, MYH6, MYOM1, TNNT2, TPM1, PLEC, PRKAR1A, OBSCN	43	415	18.85	4.380e-19	5.997e-16
regulation of ventricular cardiac muscle cell action potential	GO:0098911	11	CACNA1C, PKP2, RYR2, CTNNA3, DSC2, DSG2, DSP, JUP, TRPM4, CAV1, DLG1	11	415	45.03	5.686e-19	7.711e-16
heart development	GO:0007507	37	CACNA1C, EDN1, GJA1, KCNQ1, PKP2, LDB3, TGFB3, ABCC9, MYL2, TNNI3, PRKAR1A, CDKN1A	273	415	6.10	9.020e-19	1.179e-15
regulation of cardiac muscle contraction	GO:0055117	14	CALM1, CALM2, CALM3, RYR2, SCN5A, ANK2, HCN4, TNNI3K, GJA5, NKX2-5, SCN10A, CAV3	24	415	26.27	9.153e-18	1.028e-14
cardiac muscle cell action potential involved in contraction	GO:0086002	14	CACNA1C, KCNJ2, PKP2, SCN5A, KCNE1, SCN10A, CACNA2D1, SCN1B, SCN2B, SCN3B, KCNE2, CACNA1D	24	415	26.27	9.153e-18	1.028e-14
striated muscle contraction	GO:0006941	12	CASQ2, RYR2, MYH7, TTN, MYH6, RYR1, TNNI3, TNNT2, DTNA, GAA, MYLK2, CACNA1S	24	415	22.51	2.613e-14	1.538e-11
cardiac muscle cell development	GO:0055013	12	ACTN2, TTN, MYH6, PLEC, LRRC10, NKX2-5, CAV3, MYO18B, MTOR, MYH11, ALPK3, TCAP	25	415	21.61	4.925e-14	2.800e-11
regulation of cardiac muscle contraction by regulation of the release of sequestered calcium ion	GO:0010881	12	CACNA1C, CALM1, CALM2, CALM3, CASQ2, PLN, RYR2, TRDN, ANK2, DMD, CAMK2D, HRC	25	415	21.61	4.925e-14	2.800e-11