

Full name:	Cardiomyopathy (genepanel) - UZA
Abbreviation:	CMP
Description:	https://labogidsmedgen.uza.be/analyses/cardiomyopathie-cmp
Version number:	V5
Laboratory:	Centrum Medische Genetica - UZ Antwerpen
Created:	04 Jul 2019 - 13:22
Changed:	27 Nov 2023 - 09:06

Related Diseases

- [Familial isolated arrhythmogenic ventricular dysplasia, biventricular form](#)
- [Familial isolated arrhythmogenic ventricular dysplasia, left dominant form](#)
- [Familial isolated arrhythmogenic ventricular dysplasia, right dominant form](#)
- [Familial isolated dilated cardiomyopathy](#)
- [Familial isolated restrictive cardiomyopathy](#)

Related Analytes

GENE	% OF CODING SEQUENCE SUFFICIENTLY COVERED TO DETECT HETEROZYGOUS MUTATIONS	COPY NUMBER VARIATION	COMMENTS
ABCC9	100.00	0	
ACTC1	100.00	0	
ACTN2	100.00	0	
ALPK3	100.00	0	
ANKRD1	100.00	0	
BAG3	100.00	0	

GENE	% OF CODING SEQUENCE SUFFICIENTLY COVERED TO DETECT HETEROZYGOUS MUTATIONS	COPY NUMBER VARIATION	COMMENTS
<u>CALR3</u>	100.00	0	
<u>CALR3</u>	100.00	0	
<u>CAV3</u>	100.00	0	
<u>CDH2</u>	100.00	0	
<u>CRYAB</u>	100.00	0	
<u>CSRP3</u>	100.00	0	
<u>CTNNA3</u>	100.00	0	
<u>DES</u>	100.00	0	
<u>DOLK</u>	100.00	0	
<u>DSC2</u>	100.00	0	
<u>DSG2</u>	100.00	0	
<u>DSP</u>	100.00	0	
<u>EMD</u>	100.00	0	
<u>FHL1</u>	100.00	0	
<u>FHL2</u>	100.00	0	
<u>FLNC</u>	100.00	0	
<u>GLA</u>	100.00	0	
<u>JPH2</u>	100.00	0	
<u>JPH2</u>	100.00	0	
<u>JUP</u>	100.00	0	

GENE	% OF CODING SEQUENCE SUFFICIENTLY COVERED TO DETECT HETEROZYGOUS MUTATIONS	COPY NUMBER VARIATION	COMMENTS
<u>LAMA4</u>	100.00	0	
<u>LAMP2</u>	100.00	0	
<u>LDB3</u>	100.00	0	
<u>LMNA</u>	100.00	0	
<u>MIB1</u>	100.00	0	
<u>MYBPC3</u>	100.00	0	
<u>MYH6</u>	98.00	0	
<u>MYH7</u>	100.00	0	
<u>MYL2</u>	100.00	0	
<u>MYL3</u>	100.00	0	
<u>MYL3</u>	100.00	0	
<u>MYLK3</u>	100.00	0	
<u>MYOZ2</u>	100.00	0	
<u>MYOZ2</u>	100.00	0	
<u>MYPN</u>	100.00	0	
<u>NEBL</u>	100.00	0	
<u>NEXN</u>	100.00	0	
<u>NRAP</u>	100.00	0	
<u>PKP2</u>	100.00	0	
<u>PLN</u>	100.00	0	

GENE	% OF CODING SEQUENCE SUFFICIENTLY COVERED TO DETECT HETEROZYGOUS MUTATIONS	COPY NUMBER VARIATION	COMMENTS
<u>PPA2</u>	100.00	0	
<u>PRDM16</u>	100.00	0	
<u>PRKAG2</u>	100.00	0	
<u>RAF1</u>	100.00	0	
<u>RBM20</u>	100.00	0	
<u>RPL3L</u>	100.00	0	
<u>RYR2</u>	100.00	0	
<u>SCN5A</u>	100.00	0	
<u>SDHA</u>	100.00	0	
<u>SGCD</u>	99.00	0	
<u>SYNE1</u>	100.00	0	
<u>TAFAZZIN</u>	100.00	0	
<u>TCAP</u>	100.00	0	
<u>TGFB3</u>	100.00	0	
<u>TMEM43</u>	100.00	0	
<u>TNNC1</u>	100.00	0	
<u>TNNI3</u>	100.00	0	
<u>TNNI3K</u>	100.00	0	
<u>TNNT2</u>	100.00	0	
<u>TPM1</u>	100.00	0	

GENE	% OF CODING SEQUENCE SUFFICIENTLY COVERED TO DETECT HETEROZYGOUS MUTATIONS	COPY NUMBER VARIATION	COMMENTS
<u>TTN</u>	100.00	0	
<u>TTR</u>	100.00	0	
<u>VCL</u>	100.00	0	