

Genepanel PDF

Full name:	Primary Electrical disorders/Brugada syndrome (genepanel) - UZA
Description:	https://labogidsmedgen.uza.be/analyses/primaire-elektrische-aandoeningen
Version number:	V4
Laboratory:	Centrum Medische Genetica - UZ Antwerpen
Created:	09 Jul 2019 - 11:54
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Related Diseases

- [Catecholaminergic polymorphic ventricular tachycardia](#)
- [Familial atrial fibrillation](#)
- [Familial isolated arrhythmogenic ventricular dysplasia, left dominant form](#)
- [Familial isolated arrhythmogenic ventricular dysplasia, right dominant form](#)
- [Familial isolated dilated cardiomyopathy](#)
- [Familial progressive cardiac conduction defect](#)
- [Familial short QT syndrome](#)
- [Familial sick sinus syndrome](#)
- [Idiopathic ventricular fibrillation, non Brugada type](#)

Related Analytes

GENE	% OF CODING SEQUENCE SUFFICIENTLY COVERED TO DETECT HETEROZYGOUS MUTATIONS	COPY NUMBER VARIATION	COMMENTS
ABCB4	100.00	0	
ABCC9	100.00	0	
ACTN2	100.00	0	
AKAP9	100.00	0	
ANK2	100.00	0	

GENE	% OF CODING SEQUENCE SUFFICIENTLY COVERED TO DETECT HETEROZYGOUS MUTATIONS	COPY NUMBER VARIATION	COMMENTS
<u>CACNA1C</u>	100.00	0	
<u>CACNA2D1</u>	100.00	0	
<u>CACNB2</u>	100.00	0	
<u>CALM1</u>	100.00	0	
<u>CALM2</u>	100.00	0	
<u>CALM3</u>	100.00	0	
<u>CASQ2</u>	100.00	0	
<u>CAV3</u>	100.00	0	
<u>CDH2</u>	100.00	0	
<u>CLCA2</u>	100.00	0	
<u>CTNNA3</u>	100.00	0	
<u>DES</u>	100.00	0	
<u>DPP6</u>	100.00	0	
<u>DSC2</u>	100.00	0	
<u>DSG2</u>	100.00	0	
<u>DSP</u>	100.00	0	
<u>FLNC</u>	100.00	0	
<u>GJA1</u>	100.00	0	
<u>GJA5</u>	100.00	0	
<u>GNB2</u>	100.00	0	

GENE	% OF CODING SEQUENCE SUFFICIENTLY COVERED TO DETECT HETEROZYGOUS MUTATIONS	COPY NUMBER VARIATION	COMMENTS
<u>GNB5</u>	100.00	0	
<u>GPD1L</u>	100.00	0	
<u>HCN4</u>	100.00	0	
<u>JUP</u>	100.00	0	
<u>KCNA5</u>	100.00	0	
<u>KCND3</u>	100.00	0	
<u>KCNE1</u>	100.00	0	
<u>KCNE2</u>	100.00	0	
<u>KCNE3</u>	100.00	0	
<u>KCNE5</u>	100.00	0	
<u>KCNH2</u>	100.00	0	
<u>KCNJ2</u>	100.00	0	
<u>KCNJ5</u>	100.00	0	
<u>KCNJ8</u>	100.00	0	
<u>KCNK17</u>	100.00	0	
<u>KCNQ1</u>	100.00	0	
<u>LMNA</u>	100.00	0	
<u>MYL3</u>	100.00	0	
<u>MYL4</u>	100.00	0	
<u>NKX2-5</u>	100.00	0	

GENE	% OF CODING SEQUENCE SUFFICIENTLY COVERED TO DETECT HETEROZYGOUS MUTATIONS	COPY NUMBER VARIATION	COMMENTS
<u>NOS1AP</u>	100.00	0	
<u>NPPA</u>	100.00	0	
<u>PKP2</u>	100.00	0	
<u>PLN</u>	100.00	0	
<u>PPA2</u>	100.00	0	
<u>PRKAG2</u>	100.00	0	
<u>RANGRF</u>	100.00	0	
<u>RBM20</u>	100.00	0	
<u>RNF207</u>	100.00	0	
<u>RRAD</u>	100.00	0	
<u>RYR2</u>	100.00	0	
<u>SCN10A</u>	100.00	0	
<u>SCN1B</u>	100.00	0	
<u>SCN2B</u>	100.00	0	
<u>SCN3B</u>	100.00	0	
<u>SCN4B</u>	100.00	0	
<u>SCN5A</u>	100.00	0	
<u>SLC4A3</u>	100.00	0	
<u>SLMAP</u>	100.00	0	
<u>SNTA1</u>	100.00	0	

GENE	% OF CODING SEQUENCE SUFFICIENTLY COVERED TO DETECT HETEROZYGOUS MUTATIONS	COPY NUMBER VARIATION	COMMENTS
<u>TANGO2</u>	100.00	0	
<u>TECRL</u>	100.00	0	
<u>TGFB3</u>	100.00	0	
<u>TMEM43</u>	100.00	0	
<u>TNNI3K</u>	100.00	0	
<u>TRDN</u>	100.00	0	
<u>TRPM4</u>	100.00	0	
<u>TTN</u>	100.00	0	