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Full name:	Primary cardiac arrhythmias (113 genes) - VUB
Abbreviation:	PCA
Description:	http://www.brightcore.be/pca
Type of panel:	<u>Custom panel</u>
Provider:	home made
Version number:	V11
Laboratory:	<u>Centrum Medische Genetica - UZ Brussel VUB</u>
Created:	17 Jul 2019 - 09:45
Changed:	31 Aug 2022 - 16:01

Related Diseases

- Andersen-Tawil syndrome
- Brugada syndrome
- Catecholaminergic polymorphic ventricular tachycardia
- Familial atrial fibrillation
- Familial progressive cardiac conduction defect
- Familial short QT syndrome
- Familial sick sinus syndrome
- Hypokalemic periodic paralysis
- Idiopathic ventricular fibrillation, non Brugada type
- Jervell and Lange-Nielsen syndrome
- Romano-Ward syndrome

Related Analytes

GENE	% OF CODING SEQUENCE SUFFICIENTLY COVERED TO DETECT HETEROZYGOUS MUTATIONS	COPY NUMBER VARIATION	COMMENTS
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GENE	% OF CODING SEQUENCE SUFFICIENTLY COVERED TO DETECT HETEROZYGOUS MUTATIONS	COPY NUMBER VARIATION	COMMENTS
<u>ABCC9</u>	100.00	0	No comment
<u>ACTN2</u>	100.00	0	No comment
<u>ADRB1</u>	78.34	0	No comment
<u>ADRB2</u>	100.00	0	No comment
<u>AGTR1</u>	100.00	0	No comment
<u>AGXT2</u>	100.00	0	No comment
<u>AKAP9</u>	100.00	0	No comment
<u>ALG10B</u>	100.00	0	No comment
<u>ANK2</u>	100.00	0	No comment
<u>BAG3</u>	100.00	0	No comment
<u>CACNA1C</u>	100.00	0	No comment
<u>CACNA2D1</u>	100.00	0	No comment
<u>CACNA2D4</u>	99.99	0	No comment
<u>CACNB2</u>	100.00	0	No comment
<u>CALM1</u>	100.00	0	No comment
<u>CALM2</u>	100.00	0	No comment
<u>CALM3</u>	99.99	0	No comment
<u>CASQ2</u>	100.00	0	No comment
<u>CAV3</u>	100.00	0	No comment
<u>CIT</u>	100.00	0	No comment

GENE	% OF CODING SEQUENCE SUFFICIENTLY COVERED TO DETECT HETEROZYGOUS MUTATIONS	COPY NUMBER VARIATION	COMMENTS
<u>CKMT2</u>	100.00	0	No comment
<u>CRP</u>	100.00	0	No comment
<u>CSRP3</u>	100.00	0	No comment
<u>CTNNA3</u>	100.00	0	No comment
<u>DDR2</u>	97.72	0	No comment
<u>DEPDC5</u>	99.62	0	No comment
<u>DPP6</u>	96.95	0	No comment
<u>DSC3</u>	98.44	0	No comment
<u>DSG2</u>	99.61	0	No comment
<u>DSP</u>	100.00	0	No comment
<u>EMD</u>	99.84	0	No comment
<u>FGF12</u>	100.00	0	No comment
<u>GATA4</u>	80.69	0	No comment
<u>GATA5</u>	97.28	0	No comment
<u>GATA6</u>	81.11	0	No comment
<u>GJA5</u>	100.00	0	No comment
<u>GPD1L</u>	100.00	0	No comment
<u>HCN4</u>	92.35	0	No comment
<u>HSPA1L</u>	100.00	0	No comment
<u>JPH2</u>	95.10	0	No comment

GENE	% OF CODING SEQUENCE SUFFICIENTLY COVERED TO DETECT HETEROZYGOUS MUTATIONS	COPY NUMBER VARIATION	COMMENTS
<u>JUP</u>	100.00	0	No comment
<u>KCNA5</u>	100.00	0	No comment
<u>KCNAB2</u>	100.00	0	No comment
<u>KCNB2</u>	100.00	0	No comment
<u>KCND3</u>	100.00	0	No comment
<u>KCNE1</u>	100.00	0	No comment
<u>KCNE2</u>	100.00	0	No comment
<u>KCNE3</u>	100.00	0	No comment
<u>KCNE4</u>	100.00	0	No comment
<u>KCNE5</u>	94.02	0	No comment
<u>KCNH2</u>	94.44	0	No comment
<u>KCNJ16</u>	100.00	0	No comment
<u>KCNJ2</u>	100.00	0	No comment
<u>KCNJ5</u>	100.00	0	No comment
<u>KCNJ8</u>	100.00	0	No comment
<u>KCNK17</u>	100.00	0	No comment
<u>KCNK3</u>	95.81	0	No comment
<u>KCNQ1</u>	91.07	0	No comment
<u>KCNT1</u>	99.74	0	No comment
<u>KIF21B</u>	100.00	0	No comment

GENE	% OF CODING SEQUENCE SUFFICIENTLY COVERED TO DETECT HETEROZYGOUS MUTATIONS	COPY NUMBER VARIATION	COMMENTS
<u>LMNA</u>	99.93	0	No comment
<u>MYBPC3</u>	100.00	0	No comment
<u>MYH6</u>	100.00	0	No comment
<u>MYH7</u>	100.00	0	No comment
<u>MYL4</u>	100.00	0	No comment
<u>NAA10</u>	96.03	0	No comment
<u>NKX2-5</u>	100.00	0	No comment
<u>NKX2-6</u>	100.00	0	No comment
<u>NOS1AP</u>	100.00	0	No comment
<u>NPPA</u>	100.00	0	No comment
<u>NUP155</u>	100.00	0	No comment
<u>NUP37</u>	100.00	0	No comment
<u>PI4KA</u>	99.44	0	No comment
<u>PIK3CG</u>	100.00	0	No comment
<u>PITX2</u>	100.00	0	No comment
<u>PKP2</u>	99.87	0	No comment
<u>PLN</u>	100.00	0	No comment
<u>PRRX1</u>	100.00	0	No comment
<u>RANGRF</u>	100.00	0	No comment
<u>RBM20</u>	99.82	0	No comment

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<u>REM2</u>	100.00	0	No comment
<u>RIMS1</u>	99.79	0	No comment
<u>RNF207</u>	99.91	0	No comment
<u>RYR1</u>	98.38	0	No comment
<u>RYR2</u>	100.00	0	No comment
<u>SCN10A</u>	100.00	0	No comment
<u>SCN1B</u>	94.12	0	No comment
<u>SCN2B</u>	100.00	0	No comment
<u>SCN3B</u>	100.00	0	No comment
<u>SCN4A</u>	100.00	0	No comment
<u>SCN4B</u>	100.00	0	No comment
<u>SCN5A</u>	100.00	0	No comment
<u>SCNN1A</u>	100.00	0	No comment
<u>SDHAF3</u>	100.00	0	No comment
<u>SEMA3A</u>	100.00	0	No comment
<u>SHOX2</u>	99.15	0	No comment
<u>SIRT6</u>	100.00	0	No comment
<u>SLC2A5</u>	99.60	0	No comment
<u>SLC4A3</u>	100.00	0	No comment
<u>SLMAP</u>	100.00	0	No comment

GENE	% OF CODING SEQUENCE SUFFICIENTLY COVERED TO DETECT HETEROZYGOUS MUTATIONS	COPY NUMBER VARIATION	COMMENTS
<u>SNTA1</u>	84.25	0	No comment
<u>TBX5</u>	100.00	0	No comment
<u>TGFB2</u>	100.00	0	No comment
<u>TNNI3</u>	100.00	0	No comment
<u>TPM1</u>	99.98	0	No comment
<u>TRDN</u>	100.00	0	No comment
<u>TRPM4</u>	100.00	0	No comment
<u>TTN</u>	100.00	0	No comment
<u>UBR4</u>	99.99	0	No comment
<u>UBR5</u>	100.00	0	No comment
<u>WDR26</u>	100.00	0	No comment
<u>XIRP1</u>	100.00	0	No comment
<u>ZC3HC1</u>	100.00	0	No comment