

GenepanelDF

Full name:	Myopathy (genepanel) - UZA
Description:	<a href="https://labogidsmedgen.uza.be/analyses/myopathie-mu">https://labogidsmedgen.uza.be/analyses/myopathie-mu</a>
Version number:	MU_versie 3
Laboratory:	<u>Centrum Medische Genetica - UZ Antwerpen</u>
Created:	11 Dec 2020 - 08:57
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## Related Analytes

GENE	% OF CODING SEQUENCE SUFFICIENTLY COVERED TO DETECT HETEROZYGOUS MUTATIONS	COPY NUMBER VARIATION	COMMENTS
<u>ABHD5</u>	99.64	1	
<u>ACAD9</u>	99.97	1	
<u>ACADM</u>	99.64	1	
<u>ACADS</u>	100.00	1	
<u>ACADVL</u>	99.94	1	
<u>ACTA1</u>	99.99	1	
<u>ACTN2</u>	99.96	1	
<u>ADSS1</u>	99.99	1	
<u>AGK</u>	99.98	1	
<u>AGL</u>	99.92	1	
<u>AGRN</u>	99.83	1	
<u>ALDOA</u>	100.00	1	

GENE	% OF CODING SEQUENCE SUFFICIENTLY COVERED TO DETECT HETEROZYGOUS MUTATIONS	COPY NUMBER VARIATION	COMMENTS
<u>ALG14</u>	99.97	1	
<u>ALG2</u>	99.95	1	
<u>ANO5</u>	99.96	1	
<u>ANXA11</u>	99.88	1	
<u>ASCC1</u>	91.38	1	
<u>ATP1A2</u>	99.96	1	
<u>ATP2A1</u>	99.97	1	
<u>B3GALNT2</u>	94.03	1	
<u>B4GAT1</u>	99.95	1	
<u>BAG3</u>	100.00	1	
<u>BIN1</u>	100.00	1	
<u>BVES</u>	99.97	1	
<u>CACNA1S</u>	99.92	1	
<u>CAP2</u>	99.97	1	
<u>CAPN3</u>	99.98	1	
<u>CASQ1</u>	99.91	1	
<u>CAV3</u>	99.85	1	
<u>CAVIN1</u>	99.99	1	
<u>CFL2</u>	99.81	1	
<u>CHAT</u>	99.77	1	

GENE	% OF CODING SEQUENCE SUFFICIENTLY COVERED TO DETECT HETEROZYGOUS MUTATIONS	COPY NUMBER VARIATION	COMMENTS
<u>CHD7</u>	99.96	1	
<u>CHKB</u>	99.89	1	
<u>CHRNA1</u>	99.96	1	
<u>CHRNB1</u>	99.99	1	
<u>CHRND</u>	100.00	1	
<u>CHRNE</u>	99.95	1	
<u>CHRNG</u>	99.87	1	
<u>CLCN1</u>	99.97	1	
<u>CNBP</u>	99.97	1	
<u>COL12A1</u>	99.95	1	
<u>COL13A1</u>	99.56	1	
<u>COL25A1</u>	99.96	1	
<u>COL6A1</u>	100.00	1	
<u>COL6A2</u>	99.96	1	
<u>COL6A3</u>	99.99	1	
<u>COLQ</u>	99.97	1	
<u>COX6A2</u>	98.51	1	
<u>CPT2</u>	99.99	1	
<u>CRPPA</u>	99.59	1	
<u>CRYAB</u>	99.98	1	

GENE	% OF CODING SEQUENCE SUFFICIENTLY COVERED TO DETECT HETEROZYGOUS MUTATIONS	COPY NUMBER VARIATION	COMMENTS
<u>DAG1</u>	100.00	1	
<u>DCST2</u>	99.92	1	
<u>DES</u>	100.00	1	
<u>DGUOK</u>	99.76	1	
<u>DMD</u>	99.41	1	
<u>DMPK</u>	99.98	1	
<u>DNAJB6</u>	99.91	1	
<u>DNM2</u>	99.96	1	
<u>DNMT3B</u>	99.98	1	
<u>DOK7</u>	99.73	1	
<u>DPAGT1</u>	99.96	1	
<u>DPM2</u>	100.00	1	
<u>DPM3</u>	100.00	1	
<u>DYSF</u>	99.99	1	
<u>EMD</u>	97.92	1	
<u>ENO3</u>	99.98	1	
<u>ETFA</u>	99.84	1	
<u>ETFDH</u>	99.76	1	
<u>FAM111B</u>	99.99	1	
<u>FDX2</u>	99.94	1	

GENE	% OF CODING SEQUENCE SUFFICIENTLY COVERED TO DETECT HETEROZYGOUS MUTATIONS	COPY NUMBER VARIATION	COMMENTS
<u>FHL1</u>	99.92	1	
<u>FKRP</u>	99.99	1	
<u>FKTN</u>	99.91	1	
<u>FLAD1</u>	100.00	1	
<u>FLNC</u>	99.99	1	
<u>FXR1</u>	99.81	1	
<u>GAA</u>	99.99	1	
<u>GBE1</u>	99.84	1	
<u>GFER</u>	99.96	1	
<u>GFPT1</u>	99.90	1	
<u>GGPS1</u>	99.89	1	
<u>GMPPB</u>	99.95	1	
<u>GNE</u>	99.98	1	
<u>GYG1</u>	99.97	1	
<u>GYS1</u>	99.98	1	
<u>HACD1</u>	99.78	1	
<u>HADH</u>	99.97	1	
<u>HADHA</u>	99.96	1	
<u>HADHB</u>	99.97	1	
<u>HNRNPA1</u>	100.00	1	

GENE	% OF CODING SEQUENCE SUFFICIENTLY COVERED TO DETECT HETEROZYGOUS MUTATIONS	COPY NUMBER VARIATION	COMMENTS
<u>HNRNPA2B1</u>	99.95	1	
<u>HNRNPDL</u>	99.92	1	
<u>INPP5K</u>	99.99	1	
<u>ISCU</u>	99.94	1	
<u>ITGA7</u>	99.98	1	
<u>ITGA9</u>	99.80	1	
<u>JAG2</u>	98.50	1	
<u>KBTBD13</u>	100.00	1	
<u>KCNJ2</u>	100.00	1	
<u>KIF21A</u>	99.80	1	
<u>KLHL40</u>	100.00	1	
<u>KLHL41</u>	99.96	1	
<u>KLHL9</u>	100.00	1	
<u>KY</u>	98.80	1	
<u>LAMA2</u>	99.97	1	
<u>LAMB2</u>	99.99	1	
<u>LAMP2</u>	98.98	1	
<u>LARGE1</u>	99.99	1	
<u>LDB3</u>	98.02	1	
<u>LDHA</u>	99.77	1	

GENE	% OF CODING SEQUENCE SUFFICIENTLY COVERED TO DETECT HETEROZYGOUS MUTATIONS	COPY NUMBER VARIATION	COMMENTS
<u>LIMS2</u>	99.65	1	
<u>LMNA</u>	99.98	1	
<u>LMOD3</u>	99.96	1	
<u>LPIN1</u>	99.97	1	
<u>LRP4</u>	99.98	1	
<u>MAP3K20</u>	99.92	1	
<u>MATR3</u>	99.87	1	
<u>MB</u>	99.99	1	
<u>MEGF10</u>	99.90	1	
<u>MICU1</u>	99.98	1	
<u>MLIP</u>	99.94	1	
<u>MSTO1</u>	98.87	1	
<u>MTM1</u>	99.36	1	
<u>MUSK</u>	99.97	1	
<u>MYBPC1</u>	99.90	1	
<u>MYBPC3</u>	99.98	1	
<u>MYH14</u>	99.79	1	
<u>MYH2</u>	99.97	1	
<u>MYH3</u>	99.96	1	
<u>MYH7</u>	100.00	1	

GENE	% OF CODING SEQUENCE SUFFICIENTLY COVERED TO DETECT HETEROZYGOUS MUTATIONS	COPY NUMBER VARIATION	COMMENTS
<u>MYL1</u>	99.93	1	
<u>MYL2</u>	99.98	1	
<u>MYMX</u>	100.00	1	
<u>MYO18B</u>	99.98	1	
<u>MYO9A</u>	99.91	1	
<u>MYOD1</u>	99.82	1	
<u>MYOT</u>	99.98	1	
<u>MYPN</u>	99.97	1	
<u>NEB</u>	99.77	1	
<u>NPL</u>	99.95	1	
<u>OPA1</u>	99.87	1	
<u>ORAI1</u>	97.73	1	
<u>PABPN1</u>	99.67	1	
<u>PAX7</u>	99.96	1	
<u>PFKM</u>	99.82	1	
<u>PGAM2</u>	100.00	1	
<u>PGK1</u>	99.71	1	
<u>PGM1</u>	99.89	1	
<u>PHKA1</u>	99.57	1	
<u>PHKB</u>	99.79	1	

GENE	% OF CODING SEQUENCE SUFFICIENTLY COVERED TO DETECT HETEROZYGOUS MUTATIONS	COPY NUMBER VARIATION	COMMENTS
<u>PHOX2A</u>	96.75	1	
<u>PLEC</u>	99.98	1	
<u>PNPLA2</u>	99.99	1	
<u>PNPLA8</u>	99.81	1	
<u>POGLUT1</u>	99.91	1	
<u>POLG</u>	99.98	1	
<u>POLG2</u>	99.68	1	
<u>POMGNT1</u>	99.98	1	
<u>POMGNT2</u>	100.00	1	
<u>POMK</u>	99.98	1	
<u>POMT1</u>	99.91	1	
<u>POMT2</u>	99.93	1	
<u>POPDC3</u>	99.93	1	
<u>PREPL</u>	99.96	1	
<u>PRKAG2</u>	99.92	1	
<u>PYGM</u>	99.98	1	
<u>PYROXD1</u>	99.83	1	
<u>RAPSN</u>	99.99	1	
<u>RBCK1</u>	99.99	1	
<u>RXYLT1</u>	99.53	1	

GENE	% OF CODING SEQUENCE SUFFICIENTLY COVERED TO DETECT HETEROZYGOUS MUTATIONS	COPY NUMBER VARIATION	COMMENTS
<u>RYR1</u>	99.92	1	
<u>SCN4A</u>	99.77	1	
<u>SELENON</u>	95.81	1	
<u>SGCA</u>	99.99	1	
<u>SGCB</u>	99.62	1	
<u>SGCD</u>	99.94	1	
<u>SGCG</u>	99.87	1	
<u>SIL1</u>	99.99	1	
<u>SLC18A3</u>	100.00	1	
<u>SLC22A5</u>	99.99	1	
<u>SLC25A20</u>	99.90	1	
<u>SLC25A4</u>	99.96	1	
<u>SLC5A7</u>	99.97	1	
<u>SMCHD1</u>	99.82	1	
<u>SMPX</u>	99.37	1	
<u>SPEG</u>	99.97	1	
<u>SQSTM1</u>	100.00	1	
<u>STAC3</u>	99.94	1	
<u>STIM1</u>	99.97	1	
<u>SVIL</u>	99.94	1	

GENE	% OF CODING SEQUENCE SUFFICIENTLY COVERED TO DETECT HETEROZYGOUS MUTATIONS	COPY NUMBER VARIATION	COMMENTS
<u>SYNE1</u>	99.96	1	
<u>SYNE2</u>	99.85	1	
<u>SYT2</u>	99.89	1	
<u>TCAP</u>	100.00	1	
<u>TIA1</u>	99.56	1	
<u>TK2</u>	99.99	1	
<u>TMEM126B</u>	99.68	1	
<u>TMEM43</u>	99.98	1	
<u>TNNC2</u>	99.95	1	
<u>TNNI2</u>	100.00	1	
<u>TNNT1</u>	99.82	1	
<u>TNNT3</u>	100.00	1	
<u>TNPO3</u>	99.95	1	
<u>TNXB</u>	99.95	1	
<u>TOP3A</u>	99.95	1	
<u>TOR1AIP1</u>	99.84	1	
<u>TPI1</u>	99.95	1	
<u>TPM2</u>	99.93	1	
<u>TPM3</u>	99.95	1	
<u>TRAPP C11</u>	99.59	1	

GENE	% OF CODING SEQUENCE SUFFICIENTLY COVERED TO DETECT HETEROZYGOUS MUTATIONS	COPY NUMBER VARIATION	COMMENTS
<u>TRDN</u>	99.03	1	
<u>TRIM32</u>	100.00	1	
<u>TRIP4</u>	99.91	1	
<u>TRMT5</u>	99.83	1	
<u>TTN</u>	99.96	1	
<u>TUBB3</u>	100.00	1	
<u>TWNK</u>	100.00	1	
<u>UNC45B</u>	99.93	1	
<u>VAMP1</u>	99.70	1	
<u>VCP</u>	99.92	1	
<u>VMA21</u>	97.04	1	
<u>VWA1</u>	91.35	1	