

Full name:	Cerebral palsy (212 genes) - UZA
Description:	update: July 2021
Version number:	CP_versie2
Created:	04 Jul 2019 - 13:23
Changed:	14 Jul 2021 - 11:37

Related Analytes

GENE	% OF CODING SEQUENCE SUFFICIENTLY COVERED TO DETECT HETEROZYGOUS MUTATIONS	COPY NUMBER VARIATION	COMMENTS
<u>ACOX1</u>			
<u>ACTA2</u>			
<u>ADA2</u>			
<u>ADCY5</u>			
<u>ADD3</u>			
<u>AFG3L2</u>			
<u>AHI1</u>			
<u>AIMP1</u>			
<u>AKT3</u>			
<u>ALDH3A2</u>			
<u>ALDH5A1</u>			
<u>ALS2</u>			
<u>AMPD2</u>			

GENE	% OF CODING SEQUENCE SUFFICIENTLY COVERED TO DETECT HETEROZYGOUS MUTATIONS	COPY NUMBER VARIATION	COMMENTS
<u>AMT</u>			
<u>AP4B1</u>			
<u>AP4E1</u>			
<u>AP4M1</u>			
<u>AP4S1</u>			
<u>ARG1</u>			
<u>ARSA</u>			
<u>ARX</u>			
<u>ASPA</u>			
<u>ATAD3A</u>			
<u>ATL1</u>			
<u>ATM</u>			
<u>ATP7B</u>			
<u>AUTS2</u>			
<u>BCKDHA</u>			
<u>BCKDHB</u>			
<u>BSCL2</u>			
<u>BTD</u>			
<u>CACNA1A</u>			
<u>CDKL5</u>			

GENE	% OF CODING SEQUENCE SUFFICIENTLY COVERED TO DETECT HETEROZYGOUS MUTATIONS	COPY NUMBER VARIATION	COMMENTS
<u>CEP290</u>			
<u>CLN3</u>			
<u>COL4A1</u>			
<u>COL4A2</u>			
<u>COQ8A</u>			
<u>CTNNB1</u>			
<u>CYP2U1</u>			
<u>CYP7B1</u>			
<u>DARS1</u>			
<u>DBT</u>			
<u>DDC</u>			
<u>DDHD1</u>			
<u>DDHD2</u>			
<u>DGUOK</u>			
<u>DLD</u>			
<u>DYRK1A</u>			
<u>EIF2B1</u>			
<u>EIF2B2</u>			
<u>EIF2B3</u>			
<u>EIF2B4</u>			

GENE	% OF CODING SEQUENCE SUFFICIENTLY COVERED TO DETECT HETEROZYGOUS MUTATIONS	COPY NUMBER VARIATION	COMMENTS
<u>EIF2B5</u>			
<u>ELP2</u>			
<u>EPHB4</u>			
<u>ERLIN2</u>			
<u>F10</u>			
<u>FBXO31</u>			
<u>FH</u>			
<u>FLVCR2</u>			
<u>FOXC1</u>			
<u>FOXG1</u>			
<u>GAD1</u>			
<u>GALC</u>			
<u>GALT</u>			
<u>GAMT</u>			
<u>GBA1</u>			
<u>GCH1</u>			
<u>GCSH</u>			
<u>GFAP</u>			
<u>GJC2</u>			
<u>GLB1</u>			

GENE	% OF CODING SEQUENCE SUFFICIENTLY COVERED TO DETECT HETEROZYGOUS MUTATIONS	COPY NUMBER VARIATION	COMMENTS
<u>GLDC</u>			
<u>GLRA1</u>			
<u>GM2A</u>			
<u>GNAO1</u>			
<u>GNB1</u>			
<u>GPHN</u>			
<u>GRID2</u>			
<u>GRIN1</u>			
<u>GRIN2B</u>			
<u>HESX1</u>			
<u>HEXA</u>			
<u>HIKESHI</u>			
<u>HPRT1</u>			
<u>HSPD1</u>			
<u>HYCC1</u>			
<u>IFIH1</u>			
<u>ISG15</u>			
<u>ITPR1</u>			
<u>JAM3</u>			
<u>KANK1</u>			

GENE	% OF CODING SEQUENCE SUFFICIENTLY COVERED TO DETECT HETEROZYGOUS MUTATIONS	COPY NUMBER VARIATION	COMMENTS
<u>KCNC3</u>			
<u>KCNQ2</u>			
<u>KDM5C</u>			
<u>KIDINS220</u>			
<u>KIF1A</u>			
<u>KIF1C</u>			
<u>KIF5A</u>			
<u>L1CAM</u>			
<u>L2HGDH</u>			
<u>LAMA2</u>			
<u>MARS2</u>			
<u>MCPH1</u>			
<u>MECP2</u>			
<u>MMUT</u>			
<u>MOCS1</u>			
<u>MOCS2</u>			
<u>MTHFR</u>			
<u>MTOR</u>			
<u>MTPAP</u>			
<u>MTRFR</u>			

GENE	% OF CODING SEQUENCE SUFFICIENTLY COVERED TO DETECT HETEROZYGOUS MUTATIONS	COPY NUMBER VARIATION	COMMENTS
<u>MTTP</u>			
<u>NIPA1</u>			
<u>NKX2-1</u>			
<u>NKX6-2</u>			
<u>NOTCH3</u>			
<u>NPC1</u>			
<u>NPC2</u>			
<u>NPHP1</u>			
<u>NT5C2</u>			
<u>PAFAH1B1</u>			
<u>PAK3</u>			
<u>PANK2</u>			
<u>PCCA</u>			
<u>PCCB</u>			
<u>PCYT2</u>			
<u>PDHA1</u>			
<u>PDHX</u>			
<u>PHYH</u>			
<u>PIK3CA</u>			
<u>PLA2G6</u>			

GENE	% OF CODING SEQUENCE SUFFICIENTLY COVERED TO DETECT HETEROZYGOUS MUTATIONS	COPY NUMBER VARIATION	COMMENTS
<u>PLAA</u>			
<u>PLP1</u>			
<u>PMM2</u>			
<u>PNP</u>			
<u>POLG</u>			
<u>POLR1C</u>			
<u>POLR3A</u>			
<u>POLR3B</u>			
<u>PPT1</u>			
<u>PYCR2</u>			
<u>QDPR</u>			
<u>RARS1</u>			
<u>RASA1</u>			
<u>REEP1</u>			
<u>RNASEH2A</u>			
<u>RNASEH2B</u>			
<u>RNASEH2C</u>			
<u>RNASET2</u>			
<u>RTN2</u>			
<u>SACS</u>			

GENE	% OF CODING SEQUENCE SUFFICIENTLY COVERED TO DETECT HETEROZYGOUS MUTATIONS	COPY NUMBER VARIATION	COMMENTS
<u>SAMHD1</u>			
<u>SCN8A</u>			
<u>SELENOI</u>			
<u>SEPSECS</u>			
<u>SHH</u>			
<u>SIX3</u>			
<u>SLC16A2</u>			
<u>SLC17A5</u>			
<u>SLC19A3</u>			
<u>SLC2A1</u>			
<u>SLC5A6</u>			
<u>SLC6A1</u>			
<u>SLC6A5</u>			
<u>SPAST</u>			
<u>SPG11</u>			
<u>SPG7</u>			
<u>SPR</u>			
<u>SPTBN2</u>			
<u>ST3GAL5</u>			
<u>STAT2</u>			

GENE	% OF CODING SEQUENCE SUFFICIENTLY COVERED TO DETECT HETEROZYGOUS MUTATIONS	COPY NUMBER VARIATION	COMMENTS
<u>STING1</u>			
<u>STXBP1</u>			
<u>SUOX</u>			
<u>SURF1</u>			
<u>TAF2</u>			
<u>TECPR2</u>			
<u>TGIF1</u>			
<u>TH</u>			
<u>TPP1</u>			
<u>TRAPPC12</u>			
<u>TREX1</u>			
<u>TSEN15</u>			
<u>TSEN2</u>			
<u>TSEN54</u>			
<u>TTPA</u>			
<u>TUBA1A</u>			
<u>TUBA8</u>			
<u>TUBB</u>			
<u>TUBB2A</u>			
<u>TUBB2B</u>			

GENE	% OF CODING SEQUENCE SUFFICIENTLY COVERED TO DETECT HETEROZYGOUS MUTATIONS	COPY NUMBER VARIATION	COMMENTS
<u>TUBB3</u>			
<u>TUBB4A</u>			
<u>TUBG1</u>			
<u>UBE3A</u>			
<u>USP18</u>			
<u>VPS11</u>			
<u>VPS37A</u>			
<u>VPS53</u>			
<u>YY1AP1</u>			
<u>ZBTB18</u>			
<u>ZC4H2</u>			
<u>ZFYVE26</u>			
<u>ZIC2</u>			