



SLC29A3 (NM_018344.6) - cDNA + Protein - 2026-07-11

AGTGGTCCTG GCCGTGCGCC GGAGGCAGCG GCGGCGTGGC GCAGCGGCCA -2
CATGGCCGTT GTCTCAGAGG ACGACTTTCA GCACAGTTCA AACCTCCACCT 49 [M1?](#) [V4D](#) [S13*](#) [S15Pfs*86](#)
MetAlaVal ValSerGluA spAspPheGl nHisSerSer AsnSerThrT 17

ACAAGAACCAC AAGCAGCAGT CTCCTGAGCTG ACCAGGAGGC ACTGCTTGAG 99 [R18G](#) [R25*](#)
yrArgThrTh rSerSerSer LeuArgAlaA spGlnGluAl aLeuLeuGlu 33

AAGCTGCTGG ACCGCCCGCC CCTTGGCCTG CAGAGGCCCG AGGACCGCTT 149 [P41Lfs*60](#) [E47Rfs*54](#)
LysLeuLeuA spArgProPr oProGlyLeu GlnArgProG luAspArgPh 50

CTGTGGCACA TACATCATCT TCTTCAGCCT GGGCATTGGC AGTCTACTGC 199 [G61Y](#)
eCysGlyThr TyrIleIleP hePheSerLe uGlyIleGly SerLeuLeuP 67

CATGGAACTT CTTTATCACT GCCAAGGAGT ACTGGATGTT CAAACTCCGC 249 [K81Nfs](#)
roTrpAsnPh ePheIleThr AlaLysGluT yrTrpMetPh eLysLeuArg 83

AACTCCTCCA GCCCAGCCAC CGGGGAGGAC CCTGAGGGCT CAGACATCCT 299
AsnSerSerS erProAlaTh rGlyGluAsp ProGluGlyS erAspIleLe 100

GAACTACTTT GAGAGCTACC TTGCCGTTGC CTCCACCGTG CCCTCCATGC 349 [c.302_303insCTACTTTGAGAGCTACC](#) [F103X](#) [V109I](#) [M116R](#)
uAsnTyrPhe GluSerTyrL euAlaValAl aSerThrVal ProSerMetL 117

TGTGCCTGGT GGCCAAC TTC CTGCTTGTC ACAGGGTTGC AGTCCACATC 399

euCysLeuVa lAlaAsnPhe LeuLeuValA snArgValAl aValHisIle 133

CGTGTCTGG CCTCACTGAC GGTCATCCTG GCCATCTTCA TGGTGATAAC 449 R133C R134H L139P

ArgValLeuA laSerLeuTh rValIleLeu AlaIlePheM etValIleTh 150

TGCACTGGTG AAGGTGGACA CTTCCCTCCTG GACCCGTGGC TTTTTTGCGG 499

rAlaLeuVal LysValAspT hrSerSerTr pThrArgGly PhePheAlaV 167

TCACCATTGT CTGCATGGTG ATCCTCAGCG GTGCCTCCAC TGTCTTCAGC 549 T180A

aThrIleVa lCysMetVal IleLeuSerG lyAlaSerTh rValPheSer 183

AGCAGCATCT ACGGCATGAC CGGCTCCTTT CCTATGAGGA ACTCCCAGGC 599 S184R

SerSerIleT yrGlyMetTh rGlySerPhe ProMetArgA snSerGlnAl 200

ACTGATATCA GGAGGAGCCA TGGGCGGGAC GGTCAGCGCC GTGGCCTCAT 649 S203P c.625G>A

aLeuIleSer GlyGlyAlaM etGlyGlyTh rValSerAla ValAlaSerL 217

TGGTGGACTT GGCTGCATCC AGTGATGTGA GGAACAGCGC CCTGGCCTTC 699 D225G A230T

euValAspLe uAlaAlaSer SerAspValA rgAsnSerAl aLeuAlaPhe 233

TTCTGACGG CCACTGTCTT CCTCGTGCTC TGCATGGGAC TCTACCTGCT 749 T236M T236T

PheLeuThrA laThrValPh eLeuValLeu CysMetGlyL euTyrLeuLe 250

GCTGTCCAGG CTGGAGTATG CCAGGTACTA CATGAGGCCT GTTCTTGCGG 799 R258T

uLeuSerArg LeuGluTyrA laArgTyrTy rMetArgPro ValLeuAlaA 267

CCCATGTGTT TTCTGGTGAA GAGGAGCTTC CCCAGGACTC CCTCAGTGCC 849

laHisValPh eSerGlyGlu GluGluLeuP roGlnAspSe rLeuSerAla 283

CCTTCGGTGG CCTCCAGATT CATTGATTCC CACACACCCC CTCTCCGCCC 899

ProSerValA laSerArgPh eIleAspSer HisThrProP roLeuArgPr 300

CATCCTGAAG AAGACGGCCA GCCTGGGCTT CTGTGTCACC TACGTCITCT 949 [C310X](#) [Y314Tfs](#) [F316V](#)

oIleLeuLys LysThrAlaS erLeuGlyPh eCysValThr TyrValPheP 317

TCATCACCAG CCTCATCTAC [CCCGCCATCT](#) GCACCAACAT CGAGTCCCTC 999 [P324S](#) [P324L](#) [I326V](#)

heIleThrSe rLeuIleTyr ProAlaIleC ysThrAsnIl eGluSerLeu 333

AACAAGGGTT CGGGCTCACT GTGGACCACC AAGTTTTTCA TCCCCCTCAC 1049 [c.1045delC](#)

AsnLysGlyS erGlySerLe uTrpThrThr LysPhePheI leProLeuTh 350

TACCTTCCTC CTGTACAAC T TGCTGACCT ATGTGGCCGG CAGCTCACC G 1099 [c.1087C>T](#) [R363Q](#) [A367T](#)

rThrPheLeu LeuTyrAsnP heAlaAspLe uCysGlyArg GlnLeuThrA 367

CCTGGATCCA GGTGCCAGGG CCCAATAGCA AGGCGCTCCC AGGGTTCGTG 1149

laTrpIleGl nValProGly ProAsnSerL ysAlaLeuPr oGlyPheVal 383

CTCCTCCGGA CCTGCCTCAT [CCCCTCTTC](#) GTGCTCTGTA ACTACCAGCC 1199 [R386W](#) [R386Q](#) [c.1172C>A](#)

LeuLeuArgT hrCysLeuIl eProLeuPhe ValLeuCysA snTyrGlnPr 400

CCGCGTCCAC CTGAAGACTG TGGTCTTCCA GTCCGATGTG TACCCCGCAC 1249 [D412N](#)

oArgValHis LeuLysThrV alValPheGl nSerAspVal TyrProAlaL 417

TCCTCAGCTC CCTGCTGGGG [CTCAGCAACG](#) GCTACCTCAG [CACCTGGCC](#) 1299 [c.1269](#) [1270delinsA](#) [G427S](#) [T431I](#)

euLeuSerSe rLeuLeuGly LeuSerAsnG lyTyrLeuSe rThrLeuAla 433

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LeuLeuTyrG lyProLysIl eValProArg GluLeuAlaG luAlaThrGl 450

AGTGGTGATG TCCTTTTATG TGTGCTTGGG CTTAACACTG GGCTCAGCCT 1399

yValValMet SerPheTyrV alCysLeuGl yLeuThrLeu GlySerAlaC 467

GCTCTACCCT CCTGGTGCAC CTCATCTAGA AGGGAGGACA CAAGGACATT *21

ysSerThrLe uLeuValHis LeuIleStop

GGTGCTTCAG AGCCTTTGAA GATGAGAAGA GAGTGCAGGA GGGCTGGGGG *71

CCATGGAGGA AAGGCCTAAA GTTTCACCTG GGGACAGAGA GCAGAGCACA *121

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TAACATTCCA CCTTCTTTCT AGCCCTTCAA AGATGCTGCC AGTGTTGCGC *321

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ACCTCCCAGC TGCCTCATT CCAGCTGACA GCGAGATGCA AGCAAATGCT *421 c.1893G>A

CAGCTCTCCT TACCCTGAAG GGGTCTCCCT GGAATGGAAG TCCCCTGGCA *471

TGGTCAGTCC TCAGGCCCAA GACTCAAGTG TGCACAGACC CCTGTGTTCT *521

GTGGGTGAAC AACTGCCAC TAACCAGACT GGAAAACCCA GAAAGATGGG *571

CCTTCCATGA ATGCTTCATT CCAGAGGGAC CAGAGGGCCT CCCTGTGCAA *621

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ACCTGGTGGT CTATGGCCTG GGTCAAGATG AGGGTCTTTC AGTGTTCTG *721

TTTACAACAT GTCAAAGCCA TTGGTTCAAG GGCCTAATAA ATACTTGCCT *771

ATTCAA

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