



SLC29A3 (NM_018344.6) - cDNA - 2025-04-19

AGTGGTCCTG GCCGTGCGCC GGAGGCAGCG GCGGCGTGGC GCAGCGGCCA -2
CATGGCCGTT GTCTCAGAGG ACGACTTTCA GCACAGTTCA AACTCCACCT 49 M1? V4D S13* S15Pfs*86
ACAGAACCAC AAGCAGCAGT CTCCGAGCTG ACCAGGAGGC ACTGCTTGAG 99 R18G
AAGCTGCTGG ACCGCCC GCCCTGGCCTG CAGAGGCCCG AGGACCGCTT 149 P41Lfs*60 E47Rfs*54
CTGTGGCACA TACATCATCT TCTTCAGCCT GGGCCATTGGC AGTCTACTGC 199 G61V
CATGGAACCT CTTTATCACT GCCAAGGAGT ACTGGATGTT CAAACTCCGC 249 K81Nfs
AACTCCTCCA GCCCAGCCAC CGGGGAGGAC CCTGAGGGCT CAGACATCCT 299
GAACTACTTT GAGAGCTACC TTGCCGTTGC CTCCACCGTG CCCTCCATGC 349 c.302_303insCTACTTTGAGAGCTACC F103X V109I M116R
TGTGCCTGGT GGCCAACCTC CTGCTTGTCA ACAGGGTTGC AGTCCACATC 399
CGTGTCCCTGG CCTCACTGAC GGTCATCCTG GCCATCTTCA TGGTGATAAC 449 R133C R134H L139P
TGCACCTGGT AAGGTGGACA CTTCTCCTG GACCCGTGGC TTTTTTGCGG 499
TCACCATTGT CTGCATGGTG ATCCTCAGCG GTGCCCTCCAC TGTCTTCAGC 549 T180A
AGCAGCATCT ACGGCATGAC CGGCTCCTTT CCTATGAGGA ACTCCCAGGC 599 S184R
ACTGATATCA GGAGGAGCCA TGGGCGGGAC GGTCAGCGCC GTGGCCTCAT 649 S203P c.625G>A
TGGTGGACTT GGCTGCATCC AGTGAATGTGA GGAACAGCGC CCTGGCCTTC 699 D225G A230T
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GCTGTCCAGG CTGGAGTATG CCAGGTACTA CATGAGGCCT GTTCTTGCGG 799 R258T
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CCTTCGGTGG CCTCCAGATT CATTGATTCC CACACACCCC CTCTCCGCCC 899
CATCTGAAG AAGACGGCCA GCCTGGGCTT CTGTGTCCACC TACGTCTTCT 949 C310X Y314Tfs F316V
TCATCACCAG CCTCATCTAC CCCGCCATCT GCACCAACAT CGAGTCCCTC 999 P324S P324L I326V
AACAAAGGGTT CGGGCTCACT GTGGACCACC AAGTTTTTCA TCCCCCTCAC 1049 c.1045delC

TACCTTCCTC CTGTACAAC T TGCTGACCT ATGTGGCCGG CAGCTCACCG 1099 c.1087C>T R363Q A367T
CCTGGATCCA GGTGCCAGGG CCCAATAGCA AGGCGCTCCC AGGGTTCGTG 1149
CTCCTCCGGA CCTGCCTCAT CCCCCTCTTC GTGCTCTGTA ACTACCAGCC 1199 R386W R386Q c.1172C>A
CCGCGTCCAC CTGAAGACTG TGGTCTTCCA GTCCGATGTG TACCCCGCAC 1249 D412N
TCCTCAGCTC CCTGCTGGGG CTCAGCAACG GCTACCTCAG CACCCTGGCC 1299 c.1269_1270delinsA G427S T431I
CTCCTCTACG GGCCTAAGAT TGTGCCCAGG GAGCTGGCTG AGGCCACGGG 1349 G437R E444X c.1339G>A T449R
AGTGGTGATG TCCTTTTATG TGTGCTTGGG CTTAACACTG GGCTCAGCCT 1399
GCTCTACCCT CCTGGTGCAC CTCATCTAGA AGGGAGGACA CAAGGACATT *21
GGTGTTCAG AGCCTTTGAA GATGAGAAGA GAGTGCAGGA GGGCTGGGGG *71
CCATGGAGGA AAGGCCATAA GTTTCAC TTG GGGACAGAGA GCAGAGCACA *121
CTCGGGCCTC ATCCCTCCCA AGATGCCAGT GAGCCACGTC CATGCCCATT *171
CCGTGCAAGG CAGATATTCC AGTCATATTA ACAGAACACT CCTGAGACAG *221
TTGAAGAAGA AATAGCACAA ATCAGGGGTA CTCCCTTCAC AGCTGATGGT *271
TAACATTCCA CCTTCTTTCT AGCCCTTCAA AGATGCTGCC AGTGTTCGCC *321
CTAGAGTTAT TACAAAGCCA GTGCCAAAAC CCAGCCATGG GCTCTTTGCA *371
ACCTCCCAGC TGCCTCAT T 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
GGGATCAAGC ATGCTTGCC TGGGTTTTCA AAAAAAGAGG GATCCTCATG *671
ACCTGGTGGT CTATGGCCTG GGTCAAGATG AGGGTCTTTC AGTGTTCCCTG *721
TTTACAACAT GTCAAAGCCA TTGGTTCAAG GGCCTAATAA ATACTTGCCT *771
ATTCAA

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