



LACC1 (NM_001128303.2) - cDNA - 2026-03-01

CCGGCCTCAC GCGACCCACC ATTCCCGCCG CCCCCTCAGG GTGCCC GCCG -542
TTCCCGCCGC CCGGCTTTCT AACCGGGCCC CTAGTTCCCC GCCCGTGCC -492
CTCTGGAGAC CTGCAGCTCC TGCCGCCCTG CGCCCGCTCC CAGGGCCCGT -442
CGTTCCGCCG CCCTATCCCT CCTCAAGGGG CCCCTAGCTG CCTCCTCGCG -392
ACCCTTTCCG GACTCGGCCT GCCACTCCT GCCCGCTAAC CCGCCTGGCT -342
CCCGGGCGAG AGCCCTCGCG CGGCTCTGGT TCCTGTTCCCT CTAACGCCGC -292
CGGGGCTGCG GGATGCCGAC TCCGCGGACC GCCCAGACCC GGAAGTCTGCT -242
AGGCAGCAGC GGGCTCGCGG CGCTTGGCTC ATCCCGGGAT TCCCAGCTC -192
TCGCGCTGGG CCCGCCCGT TCGCACCAAG CACGCCAGGC GGCCCTGGCC -142
TACCTCCCTC CCGCTCCCG GCAGCTGGCA CGAGGGAACC TGGCCGTCAG -92
GTTTCCCCTG GGATCCTGGG ACGGTATCAG GCGGGGAATC TGTGCGGCCG -42
CGGCGAGGTG ATTTATTTGG CATAAAAGTA TTCTTTCAAG **GATGGCAGAA** 9 *c.3G>A*
GCTGTTTTGA TTGATCTTTT TGGTTTGAAA TTGAACTCTC **AAAAAAACTG** 59 *c.56_57insA*
CCATCAGACA TTAAGTGAAGA CTTTGAATGC TGTCCAATAC CACCATGCTG 109
CCAAGGCCAA GTTTCTCT**GT** ATAATGTGTT GCAGTAACAT CAGCTATGAA 159 *C43fs*
AGGGATGGAG AACCAAGATAA TTGTGAAATA GAAACAAGCA ATGGATTATC 209
AGCTCTCTTG GAAGAATTTG AGATTGTTAG CTGTCCCAGC ATGGCTGCCA 259
CTTTGTATAC CATTAACAG AAAATTGATG AAAAAATCT GAGCAGCATT 309
AAGTAATTG TACCCAGGCA CAGGAAGACA TTAATGAAAG CTTTTATTGA 359
TCAACTCTTC **ACT**GATGTTT ACAATTTTGA ATTTGAAGAT TTGCAAGTGA 409 *c.372del*
CTTTTAGGGG AGGGCTTTTT AAACAGTCCA TTGAAATAAA CGTAATCACA 459
GCTCAAGAAC TAAGAGGAAT TCAGAATGAA ATAGAAACAT TTTTGAGAAG 509

TCTGCCAGCA CTGAGAGGAA AATTAACAT TATCACTTCT TCTTTGATCC 559
CAGATATTTT CATACATGGA TTTACTACAA GAACAGGTGG GATATCTTAT 609 T195I
ATACCAACTC TTAGCTCATT CAATCTCTTC AGTAGTTCCA AACGGAGAGA 659
TCCCAAGGTA GTGGTTCAAG AAAATCTGCG TAGGTTGGCG AATGCTGCAG 709
GATTTAATGT GGAGAAATTT TACCGAATAA AGACTCATCA TTCCAATGAC 759
ATCTGGATTA TGGGAAGAAA GGAGCCTGAC TCTTATGATG GAATAACCAC 809 I254V
AAATCAGAGA GGAGTCACAA TAGCAGCTCT TGGTGCAGAC TGTATACCGA 859 T276fs A278P C284R
TAGTTTTTGC AGATCCAGTC AAAAAAGCAT GTGGGGTTGC TCACGCTGGT 909
TGGAAAGGTA CTTTGTTTGGG TGTTCCTATG GCTACAGTGA ATGCTATGAT 959
AGCAGAATAT GGCTGCAGTT TGGAAGACAT TGTGTGTGTA CTTGGACCTT 1009 I330del
CAGTAGGACC TTGCTGTTTT ACTCTTCCAA GGGAATCAGC AGAGGCATTT 1059 p.Glu348Ter
CATAATCTTC ATCCTGCATG TGTACAACATA TTTGATTCAC CAAATCCCTG 1109 S366* C370Y
TATCGACATC CGTAAAGCCA CAAGGATTCT TCTAGAACAG GGAGGAATTC 1159
TTCCACAGAA TATTCAGGAC CAGAACCAAG ATCTCAACCT CTGTACATCT 1209
TGCCATCCTG ACAAGTTTTT CTCCCATGTC CGAGATGGCC TTAATTTTTGG 1259 R414X
TACACAGATT GGCTTCATAT CAATTAAGA ATGAGATACT TGACTGGATT *16
TTTGTATAAC TGCTTCCTGC CTCCTTCCAA ACTGACTGCA AGAGAGAAAT *66
TTAGCTGTTT GATTTACTTA AAACCAAATG GATTACAATG GATAATTCAT *116
CTTTTGGGTA TATTTTTACT ATTATTCAA GCCAAATGAT TTTCATTTAA *166
TTGTAATAAT AACTGACAAA AATCAGTATG TTGTAGCTAA TATGTTTTAT *216
GCATGAGAAT TATCTTAAA GTTTGTCTC CCTGTTTATT ACACAGATCA *266
GGAATAGATT TGTTCAATTC AGTATTTATT GGATACCCTC TATTGGTCAG *316
GCATTGTGTT AAGCATATGT GAATCAAAAT GAACACAAC TTTTCCTTTG *366
AGTCTGATAC AGTGAAGGAG ATAAACACTT CTACAACCTA AATTTAATTT *416
TAATAGCAGT AGAAGAGAAC ATAAGGAATA GAGGTTAATT TTACCCAGAA *466
GCAGGATAGA GAAAATATTA CAGAGAAAAT CACATATCAC ATGGGCTCGA *516
AAGATGTAGA GGTTTTTGAC AAATGAAGAA CAACCATAAC AGGTAGAGGG *566
AACACCATGA ACCAGGGCAT GAAACTGAAA GTGCATAACA TATTCTAGAG *616

AGAGAAGGGT GTGGGCATGA GTTAGGGCTG GAAAAACAGG TTGGAAACAG *666
ATAAGTAAGG GTCCTCAAATG CAATGTCAAA GAGCTTGCAG TTTATTTTCC *716
AGGCAATGAG TAGGCAGCCA AAAAAAAAAA AGTAAGGATG TTTTTTTTTT *766
TTTTCCCATG GCATCATATT TAAGAGGATG GATTTAAATT GTGTGAGACC *816
AAAGCATAGA GACTAGATAA GAGGCGATCA AAATATTTCA AAAAGAAATA *866
ATGAAGATCC AATGAAGGAA GTGGAAATTA AAATAGGGAA GAGAGTAGAT *916
GGATTAGAGA GACATTTAAG AGATGGAATC AATAGATCCT GTTACTAGAT *966
AATGGAAGTA AGAGGTGAGG AAGAGTGAA AAGTCATTAA TGACTCTAAG *1016
ATTTCTGCTT GGCTGCTTAC CAAGATTGGC AACAAAGGGA GGGAGAAGGT *1066
TTGGAAAAAG AGAGAAGGAT AATGAGTTTG ACTTTACATA GAATGAAGGG *1116
CATCCAGATA GAAATCTTTG GTTAATAATT AGAAATATAG ACCTAGAAAT *1166
TAGGAGGAAA CCTGAGACAG AGACAAATAT TTCAAAGCTT ACAATACAGA *1216
GATGATACCT GATTCATTG GAGCAGGTTT GATCATCTAG GCAGAAATTA *1266
GGATGAGAAA AAAGGAGATC CAATAATACA ACCTTATAGT CACAGAAGTA *1316
AGAAAAAAG GGTAGTTGTT TTGAAGAAGC CAGGATAGGT GTGGAAAGTA *1366
CTCAAAAAGA AATCTTCAGG GATAAAATAA AGTGATAATT TAAAAGAAAT *1416
CAATGGATTA AACATATTGA AACTGTTCTA TAGGCAGTGG TCATTGAGTC *1466
AGCTTTCAGT GCATTAGGAA GAAGATGCAT AGGTGTCAAC TCTTTTCTGA *1516
CAGCATTAC TAGAGAAGAG AAAAAGCTGG GGACTACATC TTCAAGGAAG *1566
GGACTTTTTT TGGATGAGCA GTTTTGAGTG TGTGTCAG TTAAAGAGAG *1616
GAATTAGGTT AGTTTTCATT TGGGAAAAAT TGTATATATA TTTAATGTAA *1666
GTTATCACAT TGCATCTTAA AAATATCTT ATTTAATACA TATATTTCCCT *1716
ACATGTATAT GTGGTAGCAT GATAGCAAAT AACATTTGTT TGGTATTTCC *1766
AAAGGACTTT CATGTACATT GCCTCATTTT ACCTTTACAG CTECTCTGAA *1816
ATACACAGGC ATTATCCCTT TTATTCAGCT GAGAAAACCTG AGCTTCATTG *1866
AGGTGGAGGT CAAAAATCAC AAAATTTGTG ATGAATTAAG ATTTGAACAT *1916
ATGTTTTGTG ACTCCAGTTT TCCTTTCAGA TTTTAAAATT AATTAAAGGG *1966
ATCTTCATTA TACTTTTATT GTTAACTTTT TGTTAACATA ATTTATTCAT *2016

ACATTCAGTG AAAATTTTGT TGAGGTACTG GGACAGGTTA AAAAATACAG *2066
TTGTAGCCCT CAGGATATTT AATATCCAGT GAAAAGTGAC AGTCAGTAAA *2116
CCAACAATCT CAATACTTTG ATATATGTTG TGAGGTTGTG ATAACCGATT *2166
CTTGTTTAGT TTAATTCTAT ATCTCCCTTA GACCAGTGTT AAATTTAAAT *2216
AAAACACCTC ATTTTTTCCA ATTCAGGGAA GGCACATAAC ATAAAGCATA *2266
GGATAGAAAT GTTGAACTCA TCCAAAATAT TATTTTGTTC AATGAAAATG *2316
ATGAAGATTA AGGAATACTT CCATGTATTG AGTAAGGTTG ATAATTTTCT *2366
AATCTTCAC TGTGCATTAT TTTGTTTGAA GTTGGTAAAT TTGGAGTATC *2416
CTGCAGACAC ATTTTGCTTT ATGTACTACA ACATTCTACA ACCAAATAAA *2466
AATTATTTG ATTATCTGA

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