



IL1RN (NM_173842.3) - cDNA + Protein - 2026-05-25

AGTCCACTGC CTTGCTGCAG TCACAGAATG GAAATCTGCA GAGGCCTCCG 23

Met GluIleCysA rgGlyLeuAr 8

CAGTCACCTA ATCACTCTCC TCCTCTTCCT GTTCCATTCA GAGACGATCT 73 [S21*](#)

gSerHisLeu IleThrLeuL euLeuPheLe uPheHisSer GluThrIleC 25

GCCGACCCTC TGGGAGAAAA TCCAGCAAGA TGCAAGCCTT CAGAATCTGG 123 [R26*](#)

ysArgProSe rGlyArgLys SerSerLysM etGlnAlaPh eArgIleTrp 41

GATGTTAACC AGAAGACCCTT CTATCTGAGG AACCAACCAAC TAGTTGCTGG 173 [Q45*](#) [T47Tfs*4](#) [N52KfsX25](#) [N18Kfs*4](#) [Q54X](#) [A60A](#)

AspValAsnG lnLysThrPh eTyrLeuArg AsnAsnGlnL euValAlaGl 58

ATACTTGCAA GGACCAAATG TCAATTTAGA AGAAAAGATA GATGTGGTAC 223 [p.Asp72_Ile76del](#)

yTyrLeuGln GlyProAsnV alAsnLeuGl uGluLysIle AspValValP 75

CCATTGAGCC TCATGCTCTG TTCTTGGGAA TCCATGGAGG GAAGATGTGC 273 [E77X](#) [C91F](#)

roIleGluPr oHisAlaLeu PheLeuGlyI leHisGlyGl yLysMetCys 91

CTGTCCTGTG TCAAGTCTGG TGATGAGACC AGACTCCAGC TGGAGGCAGT 323

LeuSerCysV alLysSerGl yAspGluThr ArgLeuGlnL euGluAlaVa 108

TAACATCACT GACCTGAGCG AGAACAGAAA GCAGGACAAG CGCTTCGCCT 373 [Q119X](#) [A124T](#)

lAsnIleThr AspLeuSerG luAsnArgLy sGlnAspLys ArgPheAlaP 125

TCATCCGCTC AGACAGTGGC CCACCACCA GTTTTGAGTC TGCCGCCTGC 423 S130S c.396delC A106T

heIleArgSe rAspSerGly ProThrThrS erPheGluSe rAlaAlaCys 141

CCCGTTGGT TCCTCTGCAC AGCGATGGAA GCTGACCAGC CCGTCAGCCT 473

ProGlyTrpP heLeuCysTh rAlaMetGlu AlaAspGlnP roValSerLe 158

CACCAATATG CCTGACGAAG GCGTCATGGT CACCAAATTC TACTTCCAGG 523

uThrAsnMet ProAspGluG lyValMetVa lThrLysPhe TyrPheGlnG 175

AGGACGAGTA GTACTGCCCA GGCCTGCCTG TTCCCATTCT TGCATGGCAA *39

luAspGluSt op

GGACTGCAGG GACTGCCAGT CCCCTGCC CAGGGCTCCC GGCTATGGGG *89

GCACTGAGGA CCAGCCATTG AGGGGTGGAC CCTCAGAAGG CGTCACAA~~CA~~ *139 c.*138C>G

ACCTGGTCAC AGGACTCTGC CT~~C~~CTCTTCA ACTGACCAGC CTCCATGCTG *189 c.*162C>T

CCTCCAGAAT GGTCTTTCTA ATGTGTGAAT CAGAGCACAG CAGCCCCTGC *239

ACAAAGCCCT TCCATGTCGC CTCTGCATTG AGGATCAAAC CCCGACCACC *289

TGCCCAACCT GCTCTCCTCT TGCCACTGCC TCTTCCCTCC TCATTCCACC *339

TTCCCATGCC CTGGATCCAT CAGGCCACTT GATGACCCCC AACCAAGTGG *389

CTCCCACACC CTGTTTTACA AAAAAGAAAA GACCAGTCCA TGAGGGAGGT *439

TTTTAAGGGT TTGTGGAAAA TGAAAATTAG GATTTTCATGA TTTTTTTTTT *489

TCAGTCCCCG TGAAGGAGAG CCCTTCATTT GGAGATTATG TTCTTTCGGG *539

GAGAGGCTGA GGACTTAAAA TATTCCTGCA TTTGTGAAAT GATGGTGAAA *589

GTAAGTGGTA GCTTTTCCCT TCTTTTTCTT CTTTTTTTGT GATGTCCCAA *639

CTTGTA AAAA TTA AAAGTTA TGGTACTATG TTAGCCCAT AATTTTTTTT *689

TTCTTTTAA AACACTTCCA TAATCTGGAC TCCTCTGTCC AGGCACTGCT *739

GCCCAGCCTC CAAGCTCCAT CTCCACTCCA GATTTTTTAC AGCTGCCTGC *789
AGTACTTTAC CTCCTATCAG AAGTTTCTCA GCTCCCAAGG CTCTGAGCAA *839
ATGTGGCTCC TGGGGGTTCT TTCTTCCTCT GCTGAAGGAA TAAATTGCTC *889
CTTGACATTG TAGAGCTTCT GGCACCTGGA GACTTGTATG AAAGATGGCT *939
GTGCCTCTGC CTGTCTCCCC CACCGGGCTG GGAGCTCTGC AGAGCAGGAA *989
ACATGACTCG TATATGTCTC AGGTCCCTGC AGGGCCAAGC ACCTAGCCTC *1039
GCTCTTGGCA GGTACTCAGC GAATGAATGC TGTATATGTT GGGTGCAAAG *1089
TTCCCTACTT CCTGTGACTT CAGCTCTGTT TTACAATAAA ATCTTGAAAA *1139
TGCC

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