



IL1R1 (NM_000877.4) - cDNA + Protein - 2026-04-29

```
AGTTCCCGGC CGCGAGGGCG GGC GCAGCTT GTGGCCGGCG GCCGGAGCCG -309
ACTCGGAGCG CGCGGC GCCG GCGGGAGGA GCCGGAGAGC GGCCGGGCCG -259
GGCGGTGGGG GCGCCGGCCT GCCCCGCGCG CCCCAGGGAG CGGCAGGAAT -209
GTGACAATCG CGCGCCCGCG CACCGAAGCA CTCCTCGCTC GGCTCCTAGG -159
GCTCTCGCCC CTCTGAGCTG AGCCGGGTTT CGCCCGGGGC TGGGATCCCA -109
TCACCCTCCA CGGCCGTCCG TCCAGGTAGA CGCACCCCTCT GAAGATGGTG -59
ACTCCCTCCT GAGAAGCTGG ACCCCTTGGT AAAAGACAAG GCCTTCTCCA -9
AGAAGAATAT GAAAGTGTTA CTCAGACTTA TTTGTTTCAT AGCTCTACTG 42
      Me tLysValLeu LeuArgLeuI leCysPheIl eAlaLeuLeu 14

ATTTCTTCTC TGGAGGCTGA TAAATGCAAG GAACGTGAAG AAAAAATAAT 92
IleSerSerL euGluAlaAs pLysCysLys GluArgGluG luLysIleIl 31

TTTAGTGTC A TCTGCAAATG AAATTGATGT TCGTCCCTGT CCTCTTAACC 142
eLeuValSer SerAlaAsnG luIleAspVa lArgProCys ProLeuAsnP 48

CAAATGAACA CAAAGGCACT ATAAC TTGGT ATAAAGATGA CAGCAAGACA 192
roAsnGluHi sLysGlyThr IleThrTrpT yrLysAspAs pSerLysThr 64

CCTGTATCTA CAGAACAAGC CTCCAGGATT CATCAACACA AAGAGAAACT 242
ProValSerT hrGluGlnAl aSerArgIle HisGlnHisL ysGluLysLe 81
```

TTGGTTTGT CCGCTAAGG TGGAGGATTC AGGACATTAC TATTGCGTGG 292
uTrpPheVal ProAlaLysV alGluAspSe rGlyHisTyr TyrCysValV 98

TAAGAAATTC ATCTTACTGC CTCAGAATTA AAATAAGTGC AAAATTTGTG 342
alArgAsnSe rSerTyrCys LeuArgIleL ysIleSerAl aLysPheVal 114

GAGAATGAGC CTAAC TTATG TTATAATGCA CAAGCCATAT TTAAGCAGAA 392 K131E
GluAsnGluP roAsnLeuCy sTyrAsnAla GlnAlaIleP heLysGlnLy 131

ACTACCCGTT GCAGGAGACG GAGGACTTGT GTGCCCTTAT ATGGAGTTTT 442
sLeuProVal AlaGlyAspG lyGlyLeuVa lCysProTyr MetGluPheP 148

TTAAAAATGA AAATAATGAG TTACCTAAAT TACAGTGGTA TAAGGATTGC 492
heLysAsnGl uAsnAsnGlu LeuProLysL euGlnTrpTy rLysAspCys 164

AAACCTCTAC TTCTTGACAA TATACACTTT AGTGGAGTCA AAGATAGGCT 542
LysProLeuL euLeuAspAs nIleHisPhe SerGlyValL ysAspArgLe 181

CATCGTGATG AATGTGGCTG AAAAGCATAG AGGGAECTAT ACTTGTCATG 592
uIleValMet AsnValAlaG luLysHisAr gGlyAsnTyr ThrCysHisA 198

CATCCTACAC ATACTTGGGC AAGCAATATC CTATTACCCG GGTAATAGAA 642
laSerTyrTh rTyrLeuGly LysGlnTyrP roIleThrAr gValIleGlu 214

TTTATTACTC TAGAGGAAA CAAACCCACA AGGCCTGTGA TTGTGAGCCC 692
PheIleThrL euGluGluAs nLysProThr ArgProValI leValSerPr 231

AGCTAATGAG ACAATGGAAG TAGACTTGGG ATCCCAGATA CAATTGATCT 742

oAlaAsnGlu ThrMetGluV alAspLeuGl ySerGlnIle GlnLeuIleC 248

GTAATGTCAC CGGCCAGTTG AGTGACATTG CTTACTGGAA GTGGAATGGG 792

ysAsnValTh rGlyGlnLeu SerAspIleA laTyrTrpLy sTrpAsnGly 264

TCAGTAATTG ATGAAGATGA CCCAGTGCTA GGGGAAGACT ATTACAGTGT 842

SerValIleA spGluAspAs pProValLeu GlyGluAspT yrTyrSerVa 281

GGAAAATCCT GCAAACAAAA GAAGGAGTAC CCTCATCACA GTGCTTAATA 892

lGluAsnPro AlaAsnLysA rgArgSerTh rLeuIleThr ValLeuAsnI 298

TATCGGAAAT TGAAAGTAGA TTTTATAAAC ATCCATTTAC CTGTTTTGCC 942

leSerGluIl eGluSerArg PheTyrLysH isProPheTh rCysPheAla 314

AAGAATACAC ATGGTATAGA TGCAGCATAT ATCCAGTTAA TATATCCAGT 992

LysAsnThrH isGlyIleAs pAlaAlaTyr IleGlnLeuI leTyrProVa 331

CACTAATTTT CAGAAGCACA TGATTGGTAT ATGTGTCACG TTGACAGTCA 1042

lThrAsnPhe GlnLysHisM etIleGlyIl eCysValThr LeuThrValI 348

TAATTGTGTG TTCTGTTTTT ATCTATAAAA TCTTCAAGAT TGACATTGTG 1092

leIleValCy sSerValPhe IleTyrLysI lePheLysIl eAspIleVal 364

CTTTGGTACA GGGATTCTTG CTATGATTTT CTCCCAATAA AAGCTTCAGA 1142

LeuTrpTyrA rgAspSerCy sTyrAspPhe LeuProIleL ysAlaSerAs 381

TGGAAAGACC TATGACGCAT ATATACTGTA TCCAAAGACT GTTGGGGAAG 1192

pGlyLysThr TyrAspAlaT yrIleLeuTy rProLysThr ValGlyGluG 398

GGTCTACCTC TGACTGTGAT ATTTTGTGT TTAAAGTCTT GCCTGAGGTC 1242
lySerThrSe rAspCysAsp IlePheValP heLysValLe uProGluVal 414

TTGGAAAAAC AGTGTGGATA TAAGCTGTTC ATTTATGGAA GGGATGACTA 1292
LeuGluLysG lnCysGlyTy rLysLeuPhe IleTyrGlyA rgAspAspTy 431

CGTTGGGGAA GACATTGTTG AGGTCATTAA TGAAAACGTA AAGAAAAGCA 1342
rValGlyGlu AspIleValG luValIleAs nGluAsnVal LysLysSerA 448

GAAGACTGAT TATCATTTTA GTCAGAGAAA CATCAGGCTT CAGCTGGCTG 1392
rgArgLeuIl eIleIleLeu ValArgGluT hrSerGlyPh eSerTrpLeu 464

GGTGGTTCAT CTGAAGAGCA AATAGCCATG TATAATGCTC TTGTTCAGGA 1442
GlyGlySerS erGluGluGlnIleAlaMet TyrAsnAlaL euValGlnAs 481

TGGAATTAAA GTTGTCTGCG TTTGAGCTGGA GAAAATCCAA GACTATGAGA 1492
pGlyIleLys ValValLeuL euGluLeuGln uLysIleGln AspTyrGluL 498

AAATGCCAGA ATCGATTAAA TTCATTAAGC AGAAACATGG GGCTATCCGC 1542
ysMetProGln uSerIleLys PheIleLysG lnLysHisGln yAlaIleArg 514

TGGTCAGGGG ACTTTACACA GGGACCACAG TCTGCAAAGA CAAGGTTCTG 1592
TrpSerGlyA spPheThrGln nGlyProGln SerAlaLysT hrArgPheTr 531

GAAGAATGTC AGGTACCACA TGCCAGTCCA GCGACGGTCA CCTTCATCTA 1642
pLysAsnVal ArgTyrHisM etProValGln nArgArgSer ProSerSerL 548

AACACCAGTT ACTGTCACCA GCCACTAAGG AGAAACTGCA AAGAGAGGCT 1692

ysHisGlnLe uLeuSerPro AlaThrLysG luLysLeuGl nArgGluAla 564

CACGTGCCTC TCGGGTAGCA TGGAGAAGTT GCCAAGAGTT CTTTAGGTGC *32

HisValProL euGlyStop

CTCCTGTCTT ATGGCGTTGC AGGCCAGGTT ATGCCTCATG CTGACTTGCA *82

GAGTTCATGG AATGTAAC TAATCATCCTT TATCCCTGAG GTCACCTGGA *132

ATCAGATTAT TAAGGGAATA AGCCATGACG TCAATAGCAG CCCAGGGCAC *182

TTCAGAGTAG AGGGCTTGGG AAGATCTTTT AAAAAGGCAG TAGGCCCGGT *232

GTGGTGGCTC ACGCCTATAA TCCCAGCACT TTGGGAGGCT GAAGTGGGTG *282

GATCACCAGA GGTCAGGAGT TCGAGACCAG CCCAGCCAAC ATGGCAAAAC *332

CCCATCTCTA CTA AAAAATAC AAAAATGAGC TAGGCATGGT GGCACACGCC *382

TGTAATCCCA GCTACACCTG AGGCTGAGGC AGGAGAATTG CTTGAACCGG *432

GGAGACGGAG GTTGCAGTGA GCCGAGTTTG GGCCACTGCA CTCTAGCCTG *482

GCAACAGAGC AAGACTCCGT CTCAAAAAA GGGCAATAAA TGCCCTCTCT *532

GAATGTTTGA ACTGCCAAGA AAAGGCATGG AGACAGCGAA CTAGAAGAAA *582

GGGCAAGAAG GAAATAGCCA CCGTCTACAG ATGGCTTAGT TAAGTCATCC *632

ACAGCCCAAG GCGGGGGCTA TGCCTTGTCT GGGGACCCTG TAGAGTCACT *682

GACCCTGGAG CGGCTCTCCT GAGAGGTGCT GCAGGCAAAG TGAGACTGAC *732

ACCTCACTGA GGAAGGGAGA CATATTCTTG GAGAACTTTC CATCTGCTTG *782

TATTTTCCAT ACACATCCCC AGCCAGAAGT TAGTGTCCGA AGACCGAATT *832

TTATTTTACA GAGCTTGAAA ACTCACTTCA ATGAACAAAG GGATTCTCCA *882

GGATTCCAAA GTTTTGAAGT CATCTTAGCT TTCCACAGGA GGGAGAGAAC *932

TTAAAAAAGC AACAGTAGCA GGGAATTGAT CCACTTCTTA ATGCTTTCCT *982

CCCTGGCATG ACCATCCTGT CTTTGTAT TATCCTGCAT TTTACGTCTT *1032

TGGAGGAACA GCTCCCTAGT GGCTTCCCTC GTCTGCAATG TCCCTTGAC *1082

AGCCACACA TGAACCATCC TTCCCATGAT GCCGCTCTC TGTCATCCCG *1132

CTCCTGCTGA AACACCTCCC AGGGGCTCCA CCTGTTTCAGG AGCTGAAGCC *1182
CATGCTTTCC CACCAGCATG TCAC'TCCCAG ACCACCTCCC TGCCCTGTCC *1232
TCCAGCTTCC CCTCGCTGTC CTGCTGTGTG AAT'TCCCAGG TTGGCCTGGT *1282
GGCCATGTGC CCTGCCCCCA GCACTCCTCT GTCTCTGCTC TTGCCTGCAC *1332
CCTTCCTCCT CCTTTGCCTA GGAGGCCTTC TCGCATTTTC TCTAGCTGAT *1382
CAGAA'TTTTA CCAAAATTCA GAACATCCTC CAATTCCACA GTCTCTGGGA *1432
GACTTTCCCT AAGAGGCGAC TTCTCTCCA GCCTTCTCTC TCTGGTCAGG *1482
CCCAC'TGCAG AGATGGTGGT GAGCACATCT GGGAGGCTGG TCTCCCTCCA *1532
GCTGGAATTG CTGCTCTCTG AGGGAGAGGC TGTGGTGGCT GTCTCTGTCC *1582
CTCACTGCCT TCCAGGAGCA ATTTGCACAT GTAACATAGA TTTATGTAAT *1632
GCTTTATGTT TAAAAACATT CCCC'AATTAT CTTATTTAAT TTTTGCAATT *1682
ATTCTAATTT TATATATAGA GAAAGTGACC TATTTTTTAA AAAAATCACA *1732
CTCTAAGTTC TATTGAACCT AGGACTTGAG CCTCCATTTT TGGCTTCTAG *1782
TCTGGTGTTC TGAGTACTTG ATTT'CAGTTC AATAACGGTC CCCCTCACT *1832
CCACACTGGC ACGTTTGTGA GAAGAAATGA CATTTTGCTA GGAAGTGACC *1882
GAGTCTAGGA ATGCTTTTAT TCAAGACACC AAATTCCAAA CT'TCTAAATG *1932
TTGGAATTTT CAAAAATTGT GTTTAGATTT TATGAAAAAC TCTTCTACTT *1982
TCATCTATTC TTTCCCTAGA GGCAAACATT TCTTAAAATG TTTCATTTTC *2032
ATTAAAAATG AAAGCCAAAT TTATATGCCA CCGATTGCAG GACACAAGCA *2082
CAGTTTTAAG AGTTGTATGA ACATGGAGAG GACTTTTGGT TTTTATATTT *2132
CTCGTATTTA ATATGGGTGA ACACCAACTT TTATTTGGAA TAATAATTTT *2182
CCTCCTAAAC AAAAACACAT TGAGTTTAAG TCTCTGACTC TTGCCTTTCC *2232
ACCTGCTTTC TCCTGGGCCC GCTTTGCCTG CTTGAAGGAA CAGTGTGTGT *2282
CTGGAGCTGC TGTTCACAAC GACAGGGCCT AGCTTTCATT TGACACACAG *2332
ACTACAGCCA GAAGCCCATG GAGCAGGGAT GTCACGTCTT GAAAAGCCTA *2382
TTAGATGTTT TACAAATTTA ATTTTGCAGA TTATTTTAGT CTGTCA'TCCA *2432
GAAAATGTGT CAGCATGCAT AGTGCTAAGA AAGCAAGCCA ATTTGGAAAC *2482
TTAGGTTAGT GACAAAATTG GCCAGAGAGT GGGGGTGATG ATGACCAAGA *2532

ATTACAAGTA GAATGGCAGC TGGAATTTAA GGAGGGACAA GAATCAATGG *2582
ATAAGCGTGG GTGGAGGAAG ATCCAAACAG AAAAGTGCAA AGTTATTCCC *2632
CATCTTCCAA GGGTTGAATT CTGGAGGAAG AAGACACATT CCTAGTTCCC *2682
CGTGAACTTC CTTTGACTTA TTGTCCCCAC TAAAACAAAA CAAAAAATT *2732
TTAATGCCTT CCACATTAAT TAGATTTTCT TGCAGTTTTT TTATGGCATT *2782
TTTTTAAAGA TGCCCTAAGT GTTGAAGAAG AGTTTGCAA TGCAACAAAA *2832
TATTTAATTA CCGGTTGTTA AAACGGTTT AGCACAATTT ATATTTTCCC *2882
TCTCTTGCCCT TTCTTATTTG CAATAAAAGG TATTGAGCCA TTTTTTAAAT *2932
GACATTTTTG ATAAATTATG TTTGTACTAG TTGATGAAGG AGTTTTTTTT *2982
AACCTGTTTA TATAATTTG CAGCAGAAGC CAAATTTTTT GTATATTAAA *3032
GCACCAAATT CATGTACAGC ATGCATCACG GATCAATAGA CTGTACTTAT *3082
TTTCCAATAA AATTTTCAA CTTTGTACTG TTA

IL1R1 (NM_000877.4) - cDNA + Protein - 2026-04-29

