

TLR7 (NM_016562.4) - cDNA + Protein - 2026-11-15

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ACTTCATCTC AGAAGACTCC AGATATAGGA TCACTCCATG CCATCAAGAA -101
AGTTGATGCT ATTGGGCCCA TCTCAAGCTG ATCTTGGCAC CTCTCATGCT -51
CTGCTCTCTT CAACCAGACC TCTACATTCC ATTTTGGAAG AAGACTAAAA -1
ATGGTGTTTC CAATGTGGAC ACTGAAGAGA CAAATTCTTA TCCTTTTTAA 50
MetValPheP roMetTrpTh rLeuLysArg GlnIleLeuI leLeuPheAs 17

CATAATCCTA ATTTCCAAAC TCCTTGGGGC TAGATGGTTT CCTAAAACTC 100  R28G
nIleIleLeu IleSerLysL euLeuGlyAl aArgTrpPhe ProLysThrL 34

TGCCCTGTGA TGTCACTCTG GATGTTCCAA AGAACCATGT GATCGTGGAC 150
euProCysAs pValThrLeu AspValProL ysAsnHisVa lIleValAsp 50

TGCACAGACA AGCATTTGAC AGAAATTCCT GGAGGTATTC CCACGAACAC 200
CysThrAspL ysHisLeuTh rGluIlePro GlyGlyIleP roThrAsnTh 67

CACGAACCTC ACCCTCACCA TTAACCACAT ACCAGACATC TCCCCAGCGT 250
rThrAsnLeu ThrLeuThrI leAsnHisIl eProAspIle SerProAlaS 84

CCTTTCACAG ACTGGACCAT CTGGTAGAGA TCGATTTCAG ATGCAACTGT 300
erPheHisAr gLeuAspHis LeuValGluI leAspPheAr gCysAsnCys 100

GTACCTATTC CACTGGGGTC AAAAAACAAC ATGTGCATCA AGAGGCTGCA 350
ValProIleP roLeuGlySe rLysAsnAsn MetCysIleL ysArgLeuGl 117

GATTAAACCC AGAAGCTTTA GTGGACTCAC TTATTTAAAA TCCCTTTACC 400
nIleLysPro ArgSerPheS erGlyLeuTh rTyrLeuLys SerLeuTyrL 134

TGGATGGAAA CCAGCTACTA GAGATACCGC AGGGCCTCCC GCCTAGCTTA 450
euAspGlyAs nGlnLeuLeu GluIleProG lnGlyLeuPr oProSerLeu 150

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GlnLeuLeuS erLeuGluAl aAsnAsnIle PheSerIleA rgLysGluAs 167

TCTAACAGAA CTGGCCAACA TAGAAATACT CTACCTGGGC CAAAACTGTT 550
nLeuThrGlu LeuAlaAsnI leGluIleLe uTyrLeuGly GlnAsnCysT 184

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CTAAACTTGA CAAAGTTAAA AGTGCTCTCC CTGAAAGATA ACAATGTCAC 650
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LeuAsnLeuT hrLysLeuLy sValLeuSer LeuLysAspA snAsnValTh 217

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rAlaValPro ThrValLeuP roSerThrLe uThrGluLeu TyrLeuTyrA 234

ACAACATGAT TGCAAAAATC CAAGAAGATG ATTTTAATAA CCTCAACCAA 750
snAsnMetIl eAlaLysIle GlnGluAspA spPheAsnAs nLeuAsnGln 250

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LeuGlnIleL euAspLeuSe rGlyAsnCys ProArgCysT yrAsnAlaPr 267

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oPheProCys AlaProCysL ysAsnAsnSe rProLeuGln IleProValA 284

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snAlaPheAs pAlaLeuThr GluLeuLysV alLeuArgLe uHisSerAsn 300

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SerLeuGlnH isValProPr oArgTrpPhe LysAsnIleA snLysLeuGl 317

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nGluLeuAsp LeuSerGlnA snPheLeuAl aLysGluIle GlyAspAlaL 334

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ysPheLeuHi sPheLeuPro SerLeuIleG lnLeuAspLe uSerPheAsn 350

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PheGluLeuG lnValTyrAr gAlaSerMet AsnLeuSerG lnAlaPheSe 367

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rSerLeuLys SerLeuLysI leLeuArgIl eArgGlyTyr ValPheLysG 384

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luLeuLysSe rPheAsnLeu SerProLeuH isAsnLeuGl nAsnLeuGlu 400

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ValLeuAspL euGlyThrAs nPheIleLys IleAlaAsnL euSerMetPh 417

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SerLysAsnS erIlePhePh eValLysSer SerAspPheG lnHisLeuSe 517

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CAAATCAATC TCTGGAATAA ATAGAGAGGT AATTAAATTG CTGGAGCCAA *1700
CTA
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