

Infervers - TNFAIP3 (NM_006290.4) - cDNA + Protein - 2020-07-05

| | | | | | | |
|------------|------------|-------------|-------------|-------------|------------|------------------------------|
| GCAGTCTGCA | GTCTTCGTGG | CGGGCCAAGC | GAGCTTGGAG | CCC CGGGGGG | -202 | |
| CGGAGCGGTG | AGAGCGGCCG | CCAAGAGAGA | TCACACCCCC | AGCCGACCCT | -152 | |
| GCCAGCGAGC | GAGCCCCACC | CCAGGCGTCC | ATGGAGCGTC | GCCTCCGCCC | -102 | |
| GGTCCCTGCC | CCGACCCCCG | CCTGCGGCGC | GCTCCTGCCT | TGACCAGGAC | -52 | |
| TTGGGACTTT | GCGAAAGGAT | CGCGGGGCCC | GGAGAGGTGT | TGGAGAGCAC | -2 | |
| AATG | GCTGAA | CAAGTCCTTC | CTCAGGCTTT | GTATTTGAGC | AATATGCGGA | 49 |
| MetAlaGlu | GlnValLeuP | roGlnAlaLe | uTyrLeuSer | AsnMetArgL | 17 | |
| | | | | | | |
| AAGCTGTGAA | GATACGGAG | AGA ACTCCAG | AAGACATTTT | TAAACCTACT | 99 | <u>R22Q</u> |
| ysAlaValLy | sIleArgGlu | ArgThrProG | luAspIlePh | eLysProThr | 33 | |
| | | | | | | |
| AATGGGATCA | TTCATCATTT | TAAAACCATG | CACCGATAACA | CACTGGAAAT | 149 | <u>R45X</u> |
| AsnGlyIleI | leHisHisPh | eLysThrMet | HisArgTyrT | hrLeuGluMe | 50 | |
| | | | | | | |
| GTTCAGAACT | TGCCAGTTTT | GTCCTCAGTT | TCGGGAGATC | ATCCACAAAG | 199 | |
| tPheArgThr | CysGlnPheC | ysProGlnPh | eArgGluIle | IleHisLysA | 67 | |
| | | | | | | |
| CCCTCATCGA | CAGAAACATC | CAGGCCACCC | TGGAAAGCCA | GAAGAAACTC | 249 | |
| laLeuIleAs | pArgAsnIle | GlnAlaThrL | euGluSerGl | nLysLysLeu | 83 | |
| | | | | | | |
| AACTGGTGT | C | GAGAAGTCCG | GAAGCTTGTG | GCGCTGAAAA | CGAACGGTGA | 299 |
| AsnTrpCysA | rgGluValAr | gLysLeuVal | AlaLeuLysT | hrAsnGlyAs | 100 | <u>p.W85GfsX11 R87X K91*</u> |
| | | | | | | |
| CGGCAATTGC | CTCATGCATG | CCACTTCTCA | GTACATGTGG | GGCGTTCAGG | 349 | |
| pGlyAsnCys | LeuMetHisA | laThrSerGl | nTyrMetTrp | GlyValGlnA | 117 | |
| | | | | | | |
| ACACAGACTT | GGTACTGAGG | AAGGCGCTGT | TCAGCACGCT | CAAGGAAACA | 399 | |
| spThrAspLe | uValLeuArg | LysAlaLeuP | heSerThrLe | uLysGluThr | 133 | |
| | | | | | | |
| GACACACGCA | ACTTTAAATT | CCGCTGGCAA | CTGGAGTCTC | TCAAATCTCA | 449 | <u>D134fs R141C</u> |
| AspThrArgA | snPheLysPh | eArgTrpGln | LeuGluSerL | euLysSerGl | 150 | |
| | | | | | | |
| GGAATTTGTT | GAAA | CGGGGC | TTTGCTATGA | TACTCGGAAC | TGGAATGATG | 499 |
| nGluPheVal | GluThrGlyL | euCysTyrAs | pThrArgAsn | TrpAsnAspG | 167 | <u>T155M</u> |
| | | | | | | |
| AATGGGACAA | TCTTATCAAA | ATGGCTTCCA | CAGACACACC | CATGGCCCGA | 549 | <u>R183*</u> |
| luTrpAspAs | nLeuIleLys | MetAlaSerT | hrAspThrPr | oMetAlaArg | 183 | |

AGTGGACTTC AGTACAACCTC ACTGGAAGAA ATACACATAT TTGTCCTTTG 599 [Q187X](#) [C596_598 del A](#)
 SerGlyLeuG lnTyrAsnSe rLeuGluGlu ileHisIleP heValLeuCy 200

CAACATCCTC AGAAGGCCAA TCATTGTCAT TTCAGACAAA ATGCTAAGAA 649
 sAsnIleLeu ArgArgProI leIleValIil eSerAspLys MetLeuArgS 217

GTTTGGAATC AGGTTCCAAT TTCGCCCTT TGAAAGTGGG TGGAAATTTAC 699 [p.F224Sfs*4](#) [p.L227*](#)
 erLeuGluSe rGlySerAsn PheAlaProL euLysValGl yGlyIleTyr 233

TTGCCTCTCC ACTGGCCTGC CCAGGAATGC TACAGATACC CCATTGTTCT 749 [C243Y](#)
 LeuProLeuH isTrpProAl aGlnGluCys TyrArgTyrP roIleValLe 250

CGGCTATGAC AGCCATCATT TTGTACCCTT GGTGACCCTG AAGGACAGTG 799 [D253 F257DEL](#)
 uGlyTyrAsp SerHisHisP heValProLe uValThrLeu LysAspSerG 267

GGCCTGAAAT CCGAGCTGTT CCACTTGTTA ACAGAGACCG GGAAGATTT 849 [p.P268Lfs*19](#) [p.R271*](#)
 lyProGluIil eArgAlaVal ProLeuValA snArgAspAr gGlyArgPhe 283

GAAGACTTAA AAGTTCACTT TTTGACAGAT CCTGAAAATG AGATGAAGGA 899 [T292P](#)
 GluAspLeuL ysValHisPh eLeuThrAsp ProGluAsnG luMetLysGl 300

GAAGCTCTTA AAAGAGTACT TAATGGTGAT AGAAATCCCC GTCCAAGGCT 949 [p.Y306*](#)
 uLysLeuLeu LysGluTyrL euMetValIil eGluIlePro ValGlnGlyT 317

GGGACCATGG CACAACCTCAT CTCATCAATG CCGCAAAGTT GGATGAAGCT 999
 rpAspHisGl yThrThrHis LeuIleAsnA laAlaLysLe uAspGluAla 333

AACTTACCAA AAGAAATCAA TCTGGTAGAT GATTACTTTG AACTTGTTCA 1049 [P336fs](#) [E338*](#)
 AsnLeuProL ysGluIleAs nLeuValAsp AspTyrPheG luLeuValGl 350

GCATGAGTAC AAGAAATGGC AGGAAAACAG CGAGCAGGGG AGGAGAGAGG 1099
 nHisGluTyr LysLysTrpG lnGluAsnSe rGluGlnGly ArgArgGluG 367

GGCACGCCCA GAATCCCATG GAACCTTCCG TGCCCCAGCT TTCTCTCATG 1149 [Q370Rfs*16](#)
 lyHisAlaGl nAsnProMet GluProSerV alProGlnLe uSerLeuMet 383

GATGTAAAAT GTGAAACGCC CAACTGCCCC TTCTTCATGT CTGTGAACAC 1199 [D384G](#)
 AspValLysC ysGluThrPr oAsnCysPro PhePheMetS erValAsnTh 400

CCAGCCTTTA TGCCATGAGT GCTCAGAGAG GCGGCAAAAG AATCAAAACA 1249 [Q415fs](#)
 rGlnProLeu CysHisGluC ysSerGluAr gArgGlnLys AsnGlnAsnL 417

AACTCCCAAA GCTGAACTCC AAGCCGGGCC CTGAGGGGCT CCCTGGCATG 1299
 ysLeuProLy sLeuAsnSer LysProGlyP roGluGlyLe uProGlyMet 433

GCGCTCGGGG CCTCTCGGGG AGAAGCCTAT GAGCCCTTGG CGTGGAACCC 1349 [W448C](#) [N449Tfs*28](#)
 AlaLeuGlyA laSerArgGl yGluAlaTyr GluProLeuA laTrpAsnPr 450

TGAGGAGTCC ACTGGGGGGC CTCATTGGC CCCACCGACA GCACCCAGCC 1399
 oGluGluSer ThrGlyGlyP roHisSerAl aProProThr AlaProSerP 467

CTTTTCTGTT CAGTGAGACC ACTGCCATGA AGTGCAGGAG CCCC GGCTGC 1449 [M476I](#) [C478*](#)
 roPheLeuPh eSerGluThr ThrAlaMetL ysCysArgSe rProGlyCys 483

CCCTTCACAC TGAATGTGCA GCACAACGGA TTTTGTGAAC GTTGCCACAA 1499 [V489Afs*7](#)
 ProPheThrL euAsnValGl nHisAsnGly PheCysGluA rgCysHisAs 500

CGCCCGCAA CTTACGCCA GCCACGCCCC AGACCACACA AGGCACTTGG 1549
 nAlaArgGln LeuHisAlaS erHisAlaPr oAspHisThr ArgHisLeuA 517

ATCCCGGAA GTGCCAAGCC TGCCTCCAGG ATGTTACCAG GACATTTAAT 1599
 spProGlyLy sCysGlnAla CysLeuGlnA spValThrAr gThrPheAsn 533

GGGATCTGCA GTACTTGCTT CAAAAGGACT ACAGCAGAGG CCTCCTCCAG 1649
 GlyIleCysS erThrCysPh eLysArgThr ThrAlaGluA laSerSerSe 550

CCTCAGCACC AGCCTCCCTC CTTCTGTCA CCAGCGTTCC AAGTCAGATC 1699
 rLeuSerThr SerLeuProP roSerCysHi sGlnArgSer LysSerAspP 567

CCTCGGGCT CGTCCGGAGC CCCTCCCCGC ATTCTTGCCA CAGAGCTGGA 1749
 roSerArgLe uValArgSer ProSerProH isSerCysHi sArgAlaGly 583

AACGACGCC CTGCTGGCTG CCTGTCTCAA GCTGCACGGA CTCCTGGGGA 1799 [A588Vfs*80](#)
 AsnAspAlaP roAlaGlyCy sLeuSerGln AlaAlaArgT hrProGlyAs 600

CAGGACGGGG ACGAGCAAGT GCAGAAAAGC CGGCTGCGTG TATTTTGGGA 1849 [p.T604Rfs*93](#)
 pArgThrGly ThrSerLysC ysArgLysAl aGlyCysVal TyrPheGlyT 617

CTCCAGAAAA CAAGGGCTTT TGCACACTGT GTTTCATCGA GTACAGAGAA 1899
 hrProGluAs nLysGlyPhe CysThrLeuC ysPheIleGl uTyrArgGlu 633

AACAAACATT TTGCTGCTGC CTCAGGGAAA GTCAGTCCCA CAGCGTCCAG 1949 [p.His636fsTer1](#) [T647P](#)
 AsnLysHisP heAlaAlaAl aSerGlyLys ValSerProT hrAlaSerAr 650

GTTCCAGAAC ACCATTCCGT GCCTGGGGAG GGAATGCGGC ACCCTTGAA 1999
 gPheGlnAsn ThrIleProC ysLeuGlyAr gGluCysGly ThrLeuGlyS 667

GCACCATGTT TGAAGGATAC TGCCAGAAGT GTTTCATTGA AGCTCAGAAT 2049 [I679T](#)
 erThrMetPh eGluGlyTyr CysGlnLysC ysPheIleGl uAlaGlnAsn 683

CAGAGATTTT ATGAGGCCAA AAGGACAGAA GAGCAACTGA GATCGAGCCA 2099
 GlnArgPheH isGluAlaLy sArgThrGlu GluGlnLeuA rgSerSerGl 700

GCGCAGAGAT GTGCCTCGAA CCACACAAAG CACCTCAAGG CCCAAGTGCG 2149
 nArgArgAsp ValProArgT hrThrGlnSe rThrSerArg ProLysCysA 717

CCCGGGCCTC CTGCAAGAAC ATCCTGGCCT GCCGCAGCGA GGAGCTCTGC 2199
 laArgAlaSe rCysLysAsn IleLeuAlaC ysArgSerGl uGluLeuCys 733

ATGGAGTGTC AGCATCCCAA CCAGAGGATG GGCCCTGGGG CCCACCGGGG 2249 [Q737Sfs*79](#)
 MetGluCysG lnHisProAs nGlnArgMet GlyProGlyA laHisArgGl 750

TGAGCCTGCC CCCGAAGACC CCCCCAAGCA GCGTTGCCGG GCCCCCGCCT 2299
 yGluProAla ProGluAspP roProLysGl nArgCysArg AlaProAlaC 767

GTGATCATT TGGCAATGCC AAGTGCAACG GCTACTGCAA CGAATGCTTT 2349
 ysAspHisPh eGlyAsnAla LysCysAsnG lyTyrCysAs nGluCysPhe 783

CAGTTCAAGC AGATGTATGG **CTA**ACCGGAA ACAGGTGGGT CACCTCCTGC *26
 GlnPheLysG lnMetTyrGl yStop

AAGAAGTGGG GCCTCGAGCT GTCAGTCATC ATGGTGCTAT CCTCTGAACC *76
 CCTCAGCTGC CACTGCAACA GTGGGCTTAA GGGTGTCTGA GCAGGAGAGG *126
 AAAGATAAGC TCTTCGTGGT GCCCACGATG CTCAGGTTTG GTAACCCGGG *176
 AGTGTTCCTCA GGTGGCCTTA GAAAGCAAAG CTTGTAACTG GCAAGGGATG *226
 ATGTCAGATT CAGCCCCAAGG TTCTCTCTCT CCTACCAAGC AGGAGGCCAG *276
 GAACTTCTTT GGACTTGAA GGTGTGCGGG GACTGGCCGA GGCCCCTGCA *326

CCCTGCGCAT CAGGACTGCT TCATCGTCTT GGCTGAGAAA GGGAAAAGAC *376
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 CTGCAAGAAG CTCGAAGGAA CTCAGGGAAA ATGGACGTAT TCAGAGAGTG *526
 TTTGTAGTTC ATGGTTTTTC CCTACCTGCC CGGTTCTTTT CCTGAGGACC *576
 CGGCAGAAAT GCAGAACCAT CCATGGACTG TGATTCTGAG GCTGCTGAGA *626
 CTGAACATGT TCACATTGAC AGAAAAACAA GCTGCTCTTT ATAATATGCA *676
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