Volume 15 Number 9 1987 Nucleic Acids Research

The murine tumor necrosis factor-beta (lymphotoxin) gene sequence

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Submitted February 4, 1987; Reformatted April 23, 1987 Accession no. Y00137

The Tumor Necrosis Factor-Beta (Lymphotoxin) gene of the mouse was isolated with a human lymphotoxin cDNA probe (1) and completely sequenced. The positions of the TATA (Goldberg-Hogness) box (overlined in figure), start of transcription (question mark), and splice junctions of the first intron (arrows) are inferred by homology with the human gene sequence (2). The polyadenylation recognition sequence (overlined) and site of poly-A addition (star) are also shown.

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   1 TGAAAGCTCCCTCTGTACAGAGCATTGGAAGCCTGGGGTGTACATTTGGGGTTACATGATCTTGGGGTTCTAAGAGAATACCCCCAAATCATCTTCCAGA
 101 CCTGGAACATTCTAGGACAGGGTTCTCAACCTTCCTAACTCCATGACCCTTTAATACAGTTCCTCATGTTGTGGTGACCCCAACCATACAATTATTTCG
 201 TTGCTATTTCATAACTGTAATTTCGCTGCTATTATGAACATAATGTAAATATTTGTTTTAAATAGAGGTTTGCCAAAGAGACCTTGCCACAGGTTGAGAC
 301 TGCCGCTCCAGAGAGTAAGGGACACATTAAAATTGTTACACACCAGATCCCCCAAATTTGGGGAGAGGGCACTGTAATGGAACTTCTTGACATTAAACTG
 401 GCAGATAAACTGGCAGAAAAAAAAAAAAAAAAAGCTGGGCAGTGGTGGCACACACCTTTAATCCCAGCACTTGGAGGCAGAGGCAGGCGGATTTCTGAGT
 501 TCTAGGCCAGCCTGGTCGACAGAGTGAGTTTCAGGACAGCCAGGGCTACACAGAGAAACCCTGTCTCGAAAAAAGCAAAAAAAAAAAAAAAAAACTGGCA
 601 GATGACCAGAAAATACAGATATATTGGAATAACTGTGACTTGAACCCCCAAAGACAAGAGAGGAAATAGGCCTGAAGGGGCGGCAGGCATGTCAAGCATC
 701 CAGAGCCCTGGGTTCGAACCTGAAAAAACAAAGGTGCCGCTAACCACATGTGGCTTCGGAGCCCTCCAGACATGACCATGATCGACAGAGAGGGAAATGT
 801 GCAGAGAAGCCTGTGAGCAGTCAAGGGTGCAGAAGTGATATAAACCATCACTCTTCAGGGAACCAGGCTTCCAGTCACAGCCCAGCTGTACCCTCTCCAC
 901 GAATTGCTCGGCCGTTCACTGGAACTCCTGGGCCTGACCCAGCTCCCTGCTAGTCCCTGCGGCCCACAGTTCCCCGGACCCGACTCCCTTTCCCAGAACG
1001 CAGTAGTCTAAGCCCTTAGCCTGCGGTTCTCTCCTAGGCCCCAGCCTTTCCTGCCTTCGACTGAAACAGCAGCATCTTCTAAGCCTGGGGCTTCCCCAAG
                                                          ______                   ?
1101 CCCCAGCCCCGACCTAGAACCCGCCCGCTGCCTGCCACACTGCCGCTTCCTCTATAAAGGGACCCGACGCCAGCGCCCAGGACCCCGCACAGCAGGTGAG
                                                                                          ↓
1201 CCTCTCCTACCCTGTCTCCTTGGGCTTACCCTGGTATCAGGCATCCCTCAGGATCCCCAGCCTTAATGGGTCTGGTCCTCCTGTCGTGGCTTTGATTTTT
1301 GGTCTGTTCCTGTGGCGGCCTTATCAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTTTCTCT
1401 CTCTCTGCCTCTGTTAGCCATTGTCTGTTTCTATGGTGGAGCTTTCCTCTTCCCCTCTGTCTCTCCTTATCCCTGCTCACTTCAGGGTTCCCCTGCCTGT
1501 CCCCTTTTCTGTCTGTCGCCCTGTCTCTCAGGGTGGCTGTCTCAGCTGGGAGGTAAGGTCTGTCTTCCTCTGTGTGCCCCGCCTCCGCTACACACACACA
                                                -30                                     -20
                           ↓         met thr leu leu gly arg leu his leu leu arg val leu gly thr pro pro
1601 CTCTCTCTCTCTCTCTCAGCAGGTTCTCCAC ATG ACA CTG CTC GGC CGT CTC CAC CTC TTG AGG GTG CTT GGC ACC CCT CCT
                            -10
     val phe leu leu gly leu leu leu ala leu pro leu gly ala gln
1683 GTC TTC CTC CTG GGG CTG CTG CTG GCC CTG CCT CTA GGG GCC CAG GTGAGGCAGCAAGAGATTGGGGTGCTGGGGTGGCCTAGC
                                                      1                                  10
                                                 gly Leu Ser Gly Val Arg Phe Ser Ala Ala Arg Thr Ala His
1768 TAACTCAGAGTCCTAGAGTCCTCTCCACTCTCTTCTGTCCCAG GGA CTC TCT GGT GTC CGC TTC TCC GCT GCC AGG ACA GCC CAT

                             20                                  30
     Pro Leu Pro Gln Lys His Leu Thr His Gly Ile Leu Lys Pro Ala Ala His Leu Val G
1853 CCA CTC CCT CAG AAG CAC TTG ACC CAT GGC ATC CTG AAA CCT GCT GCT CAC CTT GTT G GTAAACTTCTGCCTCCAGAGGA
1933 GAGGTCCAGTCCCTGCCTTTTGTCCTACTTGCCCAGGGGCCCAGGCGATCTTCCCATCTCCCCACACCAACTTTTCTTACCCTAAGGGCAGGCACCCCAC
2033 TCCCAATCTCCCTACCAACCATCCCACTTGTCCAGTGCCTGCTCCTCAGGGATGGGGACCTCTGATCTTGATAGCCCCCCAATGTCTTGTGCCTCTTCCC
                                     40                                      50
          ly Tyr Pro Ser Lys Gln Asn Ser Leu Leu Trp Arg Ala Ser Thr Asp Arg Ala Phe Leu Arg His Gly Phe
2133 AG   GG TAC CCC AGC AAG CAG AAC TCA CTG CTC TGG AGA GCA AGC ACG GAT CGT GCC TTT CTC CGA CAT GGC TTC

                 60                                      70                                      80
     Ser Leu Ser Asn Asn Ser Leu Leu Ile Pro Thr Ser Gly Leu Tyr Phe Val Tyr Ser Gln Val Val Phe Ser Gly
2206 TCT TTG AGC AAC AAC TCC CTC CTG ATC CCC ACC AGT GGC CTC TAC TTT GTC TAC TCC CAG GTG GTT TTC TCT GGA

                                     90                                      100
     Glu Ser Cys Ser Pro Arg Ala Ile Pro Thr Pro Ile Tyr Leu Ala His Glu Val Gln Leu Phe Ser Ser Gln Tyr
2281 GAA AGC TGC TCC CCC AGG GCC ATT CCC ACT CCC ATC TAC CTG GCA CAC GAG GTC CAG CTC TTT TCC TCC CAA TAC

                 110                                     120                                     130
     Pro Phe His Val Pro Leu Leu Ser Ala Gln Lys Ser Val Tyr Pro Gly Leu Gln Gly Pro Trp Val Arg Ser Met
2356 CCC TTC CAT GTG CCT CTC CTC AGT GCG CAG AAG TCT GTG TAT CCG GGA CTT CAA GGA CCG TGG GTG CGC TCA ATG

                                     140                                     150
     Tyr Gln Gly Ala Val Phe Leu Leu Ser Lys Gly Asp Gln Leu Ser Thr His Thr Asp Gly Ile Ser His Leu His
2431 TAC CAG GGG GCT GTG TTC CTG CTC AGT AAG GGA GAC CAG CTG TCC ACC CAC ACC GAC GGC ATC TCC CAT CTA CAC

                 160                                 169
     Phe Ser Pro Ser Ser Val Phe Phe Gly Ala Phe Ala Leu
2506 TTC AGC CCC AGC AGT GTA TTC TTT GGA GCC TTT GCA CTG TAG ATTCTAAAGAAACCCAAGAATTGGATTCCAGGCCTCCATCCTGA
2592 CCGTTGTTTCAAGGGTCACATCCCCACAGTCTCCAGCCTTCCCCACTAAAATAACCTGGAGCTCTCACGGGAGTCTGAGACACTTCAGGGGACTACATCT
2692 TCCCCAGGGCCACTCCAGATGCTCAGGGGACGACTCAAGCCTACCTAGAAGTTCCTGCACAGAGCAGGGTTTTTGTGGGTCTAGGTCGGACAGAGACCTG
2792 GACATGAAGGAGGGACAGACATGGGAGAGGTGGCTGGGAACAGGGGAAGGTTGACTATTTATGGAGAGAAAAGTTAAGTTATTTATTTATAGAGAATAGA
2892 AAGAGGGGAAAAATAGAAAGCCGTCAGATGACAACTAGGTCCCAGACACAAAGGTGTCTCACCTCAGACAGGACCCATCTAAGAGAGAGATGGCGAGAGA
2992 ATTAGATGTGGGTGACCAAGGGGTTCTAGAAGAAAGCACGAAGCTCTAAAAGCCAGCCACTGCTTGGCTAGACATCCACAGGGACCCCCTGCACCATCTG
                                  *
             ______
3092 TGAAACCCAATAAACCTCTTTTCTCTGAGATTCTGTCTGCTTGTGTCTGTCTTGCGTTGGGGGAGAAACTTCCTGGTCTCTTTAAGGAGTGGAGCAGGGG
3192 ACAGAGGCCTCAGTTGGCCATGGATCC
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1. Gray, P.W., et al. (1984) Nature 312, 721-724.
2. Nedwin, G.E., et al. (1985) Nucleic Acids Res. 13, 6361-6373.