

# Sequence of a cDNA encoding the platelet aggregation inhibitor trigramin

Michael P.Neeper and Marlene A.Jacobson\*

Department of Pharmacology, Merck Sharp and Dohme Research Laboratories, West Point, PA 19486, USA

Submitted June 13, 1990

EMBL accession no. X51530

The cDNA for trigramin was cloned from a  $\lambda$ ZAP library prepared from polyA<sup>+</sup> or total mRNA extracted from the venom glands of *Trimeresurus gramineus*. The 2017 nucleotide (nt) insert has an open reading frame of 1053 nucleotides (nt) containing the coding region for the 72 aa mature trigramin determined from venom purified protein (1). The sequence contains seven additional amino-terminal residues which share homology with the platelet aggregation inhibitor, bitistatin isolated from the venom of *Bitis arietans* (2). An additional C-terminal alanine residue was identified in the cDNA clone which is not observed in venom purified trigramin. The putative signal

sequence (underlined) is 1146 nucleotides upstream from the mature coding region and suggests that trigramin may be translated as a precursor protein which is processed post-translationally. The 3' untranslated region contains a polyadenylation signal (AATAAA) 16 nucleotides upstream from the poly-A region.

## REFERENCES

- Huang, T.-F. *et al.* (1989) *Biochemistry* **28**, 661–666.
- Shebuski, R.J. *et al.* (1989) *J. Biol. Chem.* **264**, 21550–21556.

```

1  CGCTCAGGTTGGCTTGAAGCAGGAAAGAGATTGCTGTCTTCCAGCCAAATCCAGTCTCC 60
61  AAAATGATCCAAGTCTTTTGATAACCATATGCTTAGCAGTTTTTCCTTATCAAGGGAGC 120
    M I Q V L L I T I C L A V F P Y Q G
121  TCCATAATCCTGGAATCTGGGAATCTTAATGATTATGAAGTAGTGTATCCAGAAAAAGTC 180
181  ACTGCATTGCCCAAAGGAGCTGTTTCAGCAAAAGTATGAAGACGCCATGCAATATGAATTT 240
241  AAGGTGAATGGAGAGCCAGTGGTCCTTCCCTGGAAAAAATAAAGGACTTTTTTCAGAA 300
301  GATTACAGCGAGATTCAATTTCCCTGATGGCAGAGAAATTACAGCATACCCCTCGGTT 360
361  GAGGATCACTGCTATTATCATGGACGCATCGAGAATGATGCTGACTCAACTGCAAGCATC 420
421  AGTGCATGTGATGGTTTGAAGGACATTTCAAGCTTCAAGGGGAGATGTACCTTATTGAA 480
481  CCCTTGGAGCTTTCGACAGTGAAGCCCATGCACTTCAAAATATGAAAATGTAGAAAAA 540
541  GAGGACGAGCCCCCAAAATGTGTGGAGTAACCCAGAATTGGGAATCATATGAGTCCACC 600
601  AAAAAGGCCTCTCAGTTAAATGTTACTCCTGAACAACAAGATTCCCCCAAGATACATT 660
661  AAGCTTGGTATATTTGTGGACCCGGAATGTACACAAAATACAGTGGCAATTTCTGAAAG 720
721  ATAACAAAAGGTTACATCAAATGATCAACAATATAAATATGATGTGCAGAGCTCTGAAT 780
781  ATGTGTACAACACTGAGTGTCTAGAAATTTGGTCCGAAAAAGATTGATTACGGTGCAG 840
841  GCATCAGCGCCTACTACTTTGACCTTATTTGGAGCCTGGAGAGAGACAGTCTTGCTGAAT 900
901  CGCACCAATCATGATCATGCTCAGTTACTCAGGCCCACTATCTTCAATGGAAACGTTATA 960
961  GGAAGGGCTCCCGTGGCGGTATGTGTGACCCGAAGCGTTCTGTAGCAATTTGTCGGGAT 1020
1021  CATAACGCAATAGTTTTTGTGGTTCAGTTACAATGACCCATGAGATGGGTCTAAATCTG 1080
1081  GGCATGCATCATGATGAAGATAAATGTAATTGTAACACATGCATTATGTCTAAAGTGTTA 1140
1141  AGCCGCAACCTTCCAATATTTTCAGCGAATGTAGTAAGGATTATTATCAGACATTTCTT 1200
1201  ACTAATCATAACCCACAATGCATTCTCAATGCACCCCTTGAGAACAGATACTGTTTCACT 1260
1261  CCAGTTTCTGGAATGAACCTTTGGAGGGCGGAGAAGATTGTGACTGTGGCTCTCCTGCA 1320
    V S G N E L L E A G E D C D C G S P A
1321  AATCCGTGCTGCGATGCTGCAACCTGTAACCTGATACCCGGGGCCAGTGTGGAGAAGGA 1380
    N P C C D A A T C K L I P G A Q C G E G
1381  CTGTGTTGTGACCAGTGCAGCTTTATAGAAGAAGAACAGTATGCCGATAGCAAGGGGT 1440
    L C C D Q C S F I E E G T V C R I A R G
1441  GATGACCTGGATGATTACTGCAATGGCAGATCTGCTGGCTGTCCAGAAATCCCTTCCAT 1500
    D D L D D Y C N G R S A G C P R N P F H
1501  GCCTAACCAACAATGGAGCTGGAATGGTCTGCAACAGCAACAGGCAGTGTGCTGATGTGA 1560
    A *
1561  ATACAGCCTACTAATCAACCTCTGGCTTCTCTCAGATTTGATTTTGGAGATCCTCCTCG 1620
1621  AGAAGTTTGGCTTCCCTGTAGTCCAAAGAGACCCATCTGCCTGCATCCTACTAGTAAAT 1680
1681  CACTCTTAGCTTTCATATGGAATCTAAATCTGCAATATTTCTTCCATATTTAATCTG 1740
1741  TTTACCTCTTGTGTAATCAAGCCTTTTTCCACCACAAAGCTCCATGGATATGTACAAC 1800
1801  ACCAAGGGCTTATTTGCTGTCAAGAAAAAATAAGCCATTTTACCGTTTCCCAATTTCCA 1860
1861  GAGCACATTTAATGCAACAGGTTCTGCCTTTAGAGCTGGTGTATTCAAAGTCAATGTTTC 1920
1921  CTCTCCCTCTCCAAAAATTTTCATGCTGGCTTTCCAAGATGTAATTGCTTCCATCAATAA 1980
1981  CTCACTATTCTCATTCAAAAAAAAAAAAAAAAAAAAAA 2017

```

\* To whom correspondence should be addressed