

Complete nucleotide sequence of the *Pvu* II restriction enzyme gene from *Proteus vulgaris*

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The gene coding for the *Pvu* II restriction enzyme was isolated by screening pools of pBR322 for the presence of enzyme activity. We present its complete nucleotide sequence which contains an open reading frame of 157 amino acids. The approximate molecular weight of 18kDa is in good agreement with SDS-PAGE determined molecular weight of the protein. The location of the open reading frame is consistent with deletion analysis data (1). Computer-predicted promoter sequences are underlined, the Shine-Dalgarno signal is doubly underlined. The presented sequence overlaps partially with the methylase gene recently published (2). The region upstream of the *Pvu* II-R gene contains also the promoter elements for the methylase gene which is transcribed in the opposite direction (1). No homology between the *Pvu* II-R gene sequence and other known restriction enzyme sequences was found.

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REFERENCES

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1  ACTAGTTGTGTAGGCAGGTTTTTTTCCAAATTCACATATCATTGCTACTCATAGTCTGTAGATTCAAAGTCATCATA
81  CATCATTATCCCGTCTATGAGCAGAATAACAATCCTTTATCAGCCGATTAACCCCTTGCAAGAAGTGAATAAAAAATGC
161  GAGGCGAGCTAGGTCTATCCCAAGAAAGCTTAGCTGATCTAGTGGGAATCCATAGAACCTACATTGGTTCAATTGAACGA
241  GCGGAAGGAATATATCGATAGACAACAATTGAGCGAATAGCAATGCCITAAATGTTTCTATATCAATACTAATGATGGA
      M S H P D L N K L L E L W P H I Q E Y Q D L A L
321  ACACGAAATGAGTCACCCAGATCTAATAAATTATTAGAGCTTTGGCCGCATATACAGGAATATCAAGACTTAGCATT
      K H G I N D I F Q D N G G K L L Q U L L I T G L T U L
401  AAACATGGAATAAATGATATTTTTCAAGATAATGGTGGAAAGTTGCTTCAAGTCCTTCTAATTACAGGATTAACAGTACT
      P G R E G N D A U D N A G Q E Y E L K S I N I D L T
481  ACCAGGACGAGAAGGTAAATGATGCTGTAGATAACGCAGGACAGAATACGAGTTAAATCAATAACATAGACCTCACTA
      K G F S T H H H M N P U I I A K Y R Q U P W I F A I Y
561  AAGTTTTTCAACTCACCACCACATGAATCCTGTAATTATTGCAAAATATAGACAAGTACCTTGGATTTTTGCCATATAC
      R G I A I E A I Y R L E P K D L E F Y Y D K W E R K W
641  CGTGGTATCGCAATAGAAGCTATATACAGATTAGAGCCAAAGATCTAGAATTTTACTATGATAAATGGGAAGGAATG
      Y S D G H K D I N N P K I P U K Y U M E H G T K I Y
721  GTATTCAGATGGGCATAAAGATATTAACAACCCCTAAATACCTGTAATAATATGTAATGGAACATGGGACAAAGATTTACT
      *
801  AAATTGGAGCTACATTCATGGTCCGATAAGACCCCAATTATGTTAAACGGGCGAGTTTACACCTTAAACCGCCCGTCAG
881  TCACCATCAGAACGCATCAGCAGATTTTAAAGCACCACACCCCATACACCCCAATCCATCCTGAAAGTTTATAAC
961  GGTTCGTGTGACGTTTGAGGGCTGTTACATCCGTTTTTCGTCCGACTTTGATCGCCTAAACCGATGAAAGTCGCAAACT
1041  TGTGTGGCTGAAAGCGTTTTATCCTGTTAAACCGGACTGAAACCCCGACTACGACTCTGCTCCTGTGCTGGA
1121  TCTGCTGTGCAGCGTTCTGATACCTGTTCAAGCAGTCCGGTTAAGTCCGCTACTGTTGACTGATTTCCCTGTATTGCAT
1201  GGCTAACTGACTGTTCTGTGTCTCGAGTTCCCCGACACGCTGAGATAAATTGCTGCATAACGGTCTCTTGTGTTGTA
1281  CAAGGTGTTCAAGGCGTTCTCTAAGAGTTGTTCTGTCTCGGTCA

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