

Thursday, January 20, 2011 2:18 PM

BmTdp2-v5

The figure displays a sequence alignment diagram for the **BmTdp2** gene. The sequence is shown in three horizontal rows, each representing a different reading frame. Vertical tick marks indicate positions along the sequence. Green boxes highlight specific regions: **BmTdp2 (STOP codon removed)**, **V5 epitope tag**, and **V5 ...ag**. The alignment shows the presence of several domains and a V5 epitope tag.

**Sequence Regions:**

- BmTdp2 (STOP codon removed):** Indicated by green boxes spanning the sequence from position 5 to approximately 560. The first instance covers positions 5-160, the second 160-240, the third 240-320, the fourth 320-400, and the fifth 400-560.
- V5 epitope tag:** Indicated by an orange box spanning the sequence from approximately 560 to 657.
- V5 ...ag:** Indicated by an orange box spanning the sequence from 657 to 680.

**Sequence Data:**

```

5' ATGAAATCGTACGCCTGGCCGGTCAAAGACGTAAACCTGCCCAAGGAGCTGCACACGCCAAGGAATAACTCTGCCGTC
      +-----+
      M N R T H W A V K D V N L P K E L H T A K G I T L P S
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
      +-----+
      GTGGACGCGACAGGCAGGCCGTGCCGTCGATATCACTCAGCACGATTGACGTCGGTCTCTCTTTCCCGTGAGGCAC
      +-----+
      W T R Q A S R A V D I T Q H D F D V G L S F P G E A
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
      +-----+
      GCGGGCTGGTCGAGCAAGTGGCCCGCGAACCTCGAGGCACCGCGTCGGTCAAACGCCTATTTTACGACAACAATTATGTT
      +-----+
      R G L V E Q V A R E L E A R V G P N A Y F Y D N N Y V
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
      +-----+
      TCCCAGCTTCCCCGACCGTCGCTCGACACCCTACTTCAGGACATCTACCGAACCGCTGCAAACGTGATCGTAGTCTTCGT
      +-----+
      S Q L A R P S L D T L L Q D I Y R N R C K L I V V F V
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
      +-----+
      CGGCGACGACTATCAGCGAAAAGACCGGTGC GGCGTCGAGTTCCCGCGATT CGCGAAATCATCATGGCACGGCCGAAC
      +-----+
      G D D Y Q R K D R C G V E F R A I R E I I M A R A E
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
      +-----+
      AACGGATCATGTTCGTGC GTGTGGACGATGGCGCTGTCGATGGCGTGTTCGCACGGACGGCTACGTGGATGCGAGACGG
      +-----+
      Q R I M F V R V D D G A V D G V F R T D G Y V D A R R
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
      +-----+
      TTCAATCCTTCTGAGATGCCAGTTCATGCCAGCGCGTCGCCCTCATCACTTAACGGTGGCGCGCCGACCCAGC
      +-----+
      F N P S E I A Q F I A E R V A L I T F K G R A D P A
      | | | | | | | | | | | | | | | | | | | | | | | | | | |
      +-----+
      TTTCTTGTACAAAGTGGTTGATCTAGAGGGCCCGCGGTTCGAAGGTAAGCCTATCCCTAACCTCTCGGTCTCGATT
      +-----+
      F L Y K V V D L E G P R F E G K P I P N P L L G L D
      | | | | | | | | | | | | | | | | | | | | | | | | | | |
      +-----+
      CTACGCGTACCGGTTAG
      +-----+
      S T R T G .
  
```