

## IDENTIFICATION

**Species:** *Setaria italica*

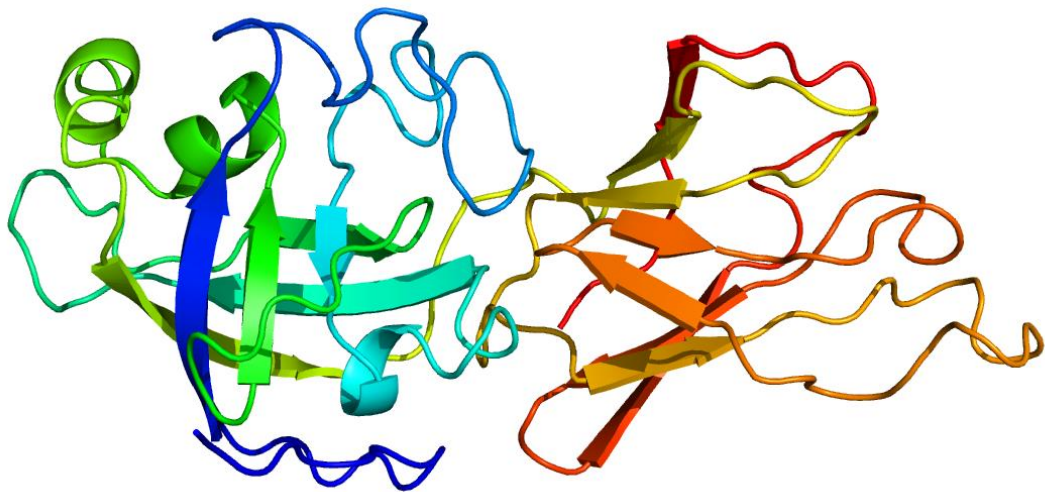
**Locus:** Seita.9G325900

**Gene Model:** Seita.9G325900.1.p

**Description:** SitEXPB-20

**Family:** Beta Expansin

**3D structure:**



## GENOME DATABASES

Phytozome: [https://phytozome-next.jgi.doe.gov/info/Sitalica\\_v2\\_2](https://phytozome-next.jgi.doe.gov/info/Sitalica_v2_2)

KEGG: <https://www.genome.jp/entry/gn:T02818>

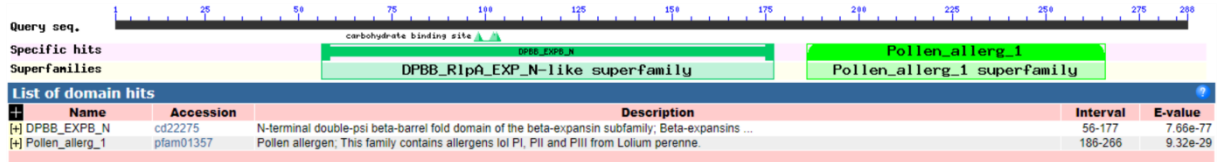
## EXTERNAL RESOURCES

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## GENE STRUCTURE



## DOMAIN ARCHITECTURE



## SEQUENCES

### Peptide

>SitEXPB-20

MGVPSLPSAAAAALVLLALLAGGHCREAQLDTGDLDAAGTENYNASDAAVYWGP  
WQKARATWYQGPNAGPDDNNGGACGFKHTNQYPFMSMGSCGNQPLFKDGGKCGS  
CYKIRCTKDKSCSGKAETVIITDMNYYPVSKYHFDLSGTAFGRLAKPGLNDKLRHSGI  
IDIEFTRVPCEFPGLKIGFHVVEYSNPVYFAVLVEYEDGDGDVQVVDLMESKTAHGPP  
TGRWTPMRESWGNVWRMDTNHRMQAPFSIRIRNESGKTLVAHNVIPANWRPNTFY  
RSFVQYS\*

### CDS (coding sequence)

>SitEXPB-20

ATGGGAGTCCCCTCCTCCCTCCCCTCCGCCGCCGCGGGCGGCGCTCGTGCTCCTGGC  
CCTCCTCGCCGGCGGGCACTGCCGCGAGGCCAGCTCGACACCGGGCGACCTCGAC  
GCGGCCGGCACCGAGAACTACAACGCCAGCGACGCCGCGGTGTACTGGGGCCCC  
TGGCAGAAGGCCCGGGCCACCTGGTACGGTCAGCCCAACGGCGCAGGCCCCGAC  
GACAACGGTGGTGCCTGCGGCTTCAAGCACACCAACCAGTACCCGTTTCATGTCTA  
TGGGCTCCTGCGGCAACCAGCCATTGTTCAAGGACGGCAAGGGCTGCGGCTCCTG  
CTACAAGATTCGTTGCACCAAGGACAAGTCTGCTCCGGCAAGGCGGAAACGGT  
GATCATCACCGACATGAACTACTACCCGGTGTCCAAGTACCACTTCGACCTCAGC  
GGCACGGCGTTCGGCAGGCTCGCCAAGCCCGGCCTCAACGACAAGCTCCGCCACT  
CCGGCATCATCGACATCGAGTTCACCAGGGTGCCGTGCGAGTTCCTCGGGCCTCAA  
GATCGGGTTCACGTGGAGGAGTACTCGAACCCCGTCTACTTCGCGGTACTCGTC  
GAATACGAGGACGGCGACGGCGACGTGGTGCAGGTGGACCTCATGGAGTCGAAG  
ACGGCGCACGGCCCGCCGACGGGGCGGTGGACGCCGATGCGCGAGTCCTGGGGC  
AACGTCTGGCGCATGGACACCAACCACCGCATGCAGGCGCCCTTCTCGATCCGCA  
TCCGCAACGAGTCCGGCAAGACGCTCGTCCGCCACAACGTCATCCCGGCCAACTG  
GAGGCCAACACCTTCTACCGCTCCTTCGTCCAGTACAGCTGA

### Nucleotide

>SitEXPB-20

TTGCTCGCACTCTTCACTCACTGCCGCCACTGCCTAACTAGCTAGAGGAAGCCG  
AAAGGGGAAACGGCCAAGGCAGCCATGGGAGTCCCCTCCTCCCTCCCCTCCGCCG

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CCAGCTCGACACCGGCGACCTCGACGCGGGCCGGCACCGAGA ACTACAACGCCAG  
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AGCAAGAGCTGCGGGTGGGGCCCACTTGCATGTGCGCGTCCCTACTCGATCTCCG  
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TGA ACTACTACCCGGTGTCCAAGTACCACTTCGACCTCAGCGGCACGGCGTTCCG  
CAGGCTCGCCAAGCCCGGCCTCAACGACAAGCTCCGCCACTCCGGCATCATCGAC  
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GCCAACTGGAGGCCAACACCTTCTACCGCTCCTTCGTCCAGTACAGCTGAGCTG  
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