

## IDENTIFICATION

**Species:** *Setaria italica*

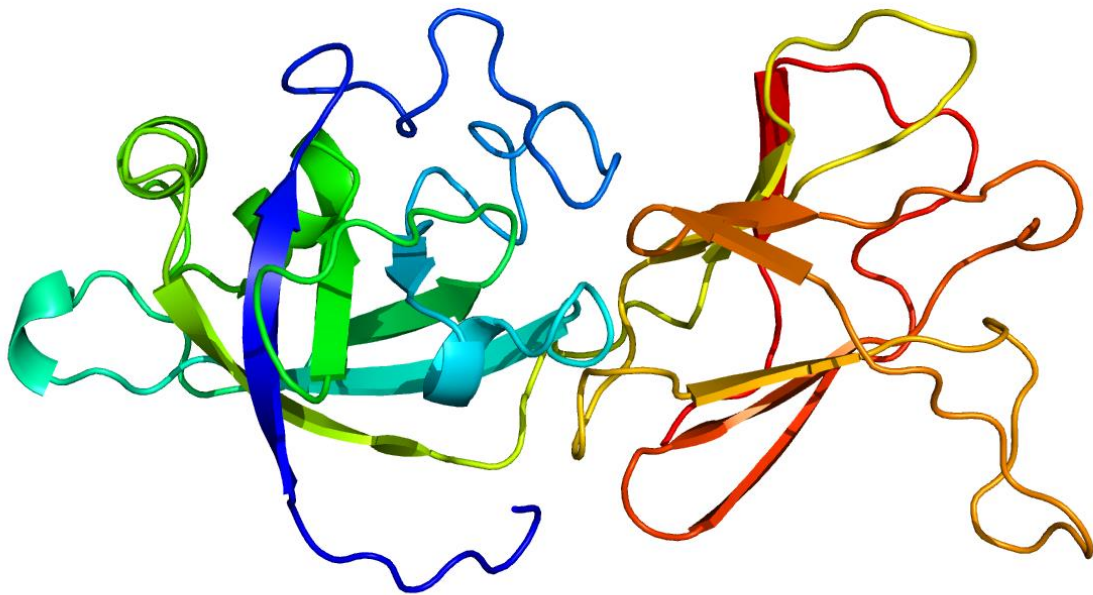
**Locus:** Seita.9G326900

**Gene Model:** Seita.9G326900.1.p

**Description:** SitEXPB-25

**Family:** Beta Expansin

**3D structure:**



## GENOME DATABASES

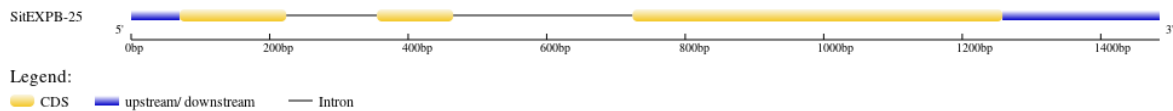
Phytozome: [https://phytozome-next.jgi.doe.gov/info/Sitalica\\_v2\\_2](https://phytozome-next.jgi.doe.gov/info/Sitalica_v2_2)

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

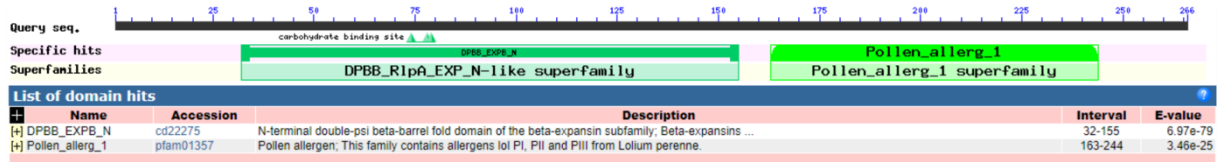
## EXTERNAL RESOURCES

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## GENE STRUCTURE



## DOMAIN ARCHITECTURE



## SEQUENCES

### Peptide

>SitEXPB-25

MAAAVISSAKVAAALVAVFAVLATYAEAGGWLPKATWYGAPNGAGPDDNGGA  
CGFKHTNQYPYMSMTSCGNEPLFKDGGKGCACYQIRCLNSTHDACSGRAKRVIITD  
MNYYPVSKYHFDLSGTAFGAMAKTGLNDKLRHAGILEIQFRRVPCNYKGLNVNFRV  
QVGSNPNYFAVLVQYAGKDGA VVQVDLMETDSTTGKPTGVWTPMRVSWGAVWRL  
DTRPTQAPFLRIRSDSGKTLVASNVIPADWKPMTDYPSNVQFP\*

### CDS (coding sequence)

>SitEXPB-25

ATGGCCGCCGCGTGATCATCTCCTCCGCCAAGGTGGCTGCTGCACTCGTCGCAG  
TGTTTCGCCGTGCTTGCCACGTACGCCGAAGCTGGCGGCTGGCTCCCGGCCAAGGC  
CACCTGGTACGGCGCGCCCAACGGCGCCGGTCCCGACGACAACGGTGGCGCGTG  
CGGGTTCAAGCACACCAACCAGTACCCGTACATGTCCATGACGTCGTGCGGGAAC  
GAGCCCCTGTTCAAGGACGGCAAGGGCTGTGGCGCATGCTACCAGATACGGTGC  
CTGAACAGCACCCACGACGCCTGCTCCGGCAGGGCGAAGCGTGTGATCATCACG  
GACATGAACTACTACCCGGTGTCCAAGTACCCTTCGACCTGAGCGGCACGGCGT  
TCGGCGCCATGGCCAAGACGGGGCTCAACGACAAGCTCCGGCACGCCGGCATT  
TCGAGATCCAGTTCGGGAGGGTGCCCTGCAACTACAAGGGCCTGAACGTCAACT  
CCGCGTCCAGGTGGGCTCCAACCCCAACTACTTCGCCGTGCTGGTGCAGTACGCC  
GGCAAGGACGGCGCCGTGGTGCAGGTGGACCTCATGGAGACCGACAGCACCACG  
GGCAAGCCGACGGGGGTGTGGACGCCGATGCGCGTGTCTGTGGGGCGCCGTCTGG  
AGGCTGGACACCGACCGCCCCACGCAGGCGCCCTTCTCGCTGCGCATCCGCAGCG  
ACTCCGGCAAGACGCTGGTGGCCAGCAACGTCATCCCGGCAGACTGGAAGCCCA  
TGACCGACTACCCCTCCAACGTGCAGTTCCTTAA

### Nucleotide

>SitEXPB-25

AAGTACACAACACATATACGAACACTAATCCCGGGGATCTCTGGTAAGCTGGTAC  
TAGGATCGAGCTGAGATGGCCGCCCGGTGATCATCTCCTCCGCCAAGGTGGCTG  
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GCTCCCGGCCAAGGCCACCTGGTACGGCGCGCCCAACGGCGCCGGTCCCGACGA  
CAACGGTATGCACGAGCAGAGCGTGGCCGCGCCCCGGCCGTCGCGAACACGATG  
CGTGTGGCGTGCTATCTTTCGCCGTCCCAACAATGCTGTGTGTGTGACTCTCTGT  
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AAAAACAGATACGGTGCCTGAACAGCACCCACGACGCCTGCTCCGGCAGGGCG  
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TCGTGGGGCGCCGTCTGGAGGCTGGACACCGACCGCCCCACGCAGGCGCCCTTCT  
CGCTGCGCATCCGCAGCGACTCCGGCAAGACGCTGGTGGCCAGCAACGTCATCCC  
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AATGTAATACAGTACTACGTATCAAGTTGT CAGTTCAAGAAAATATATTCAAGTT  
TGT