

## IDENTIFICATION

**Species:** *Setaria italica*

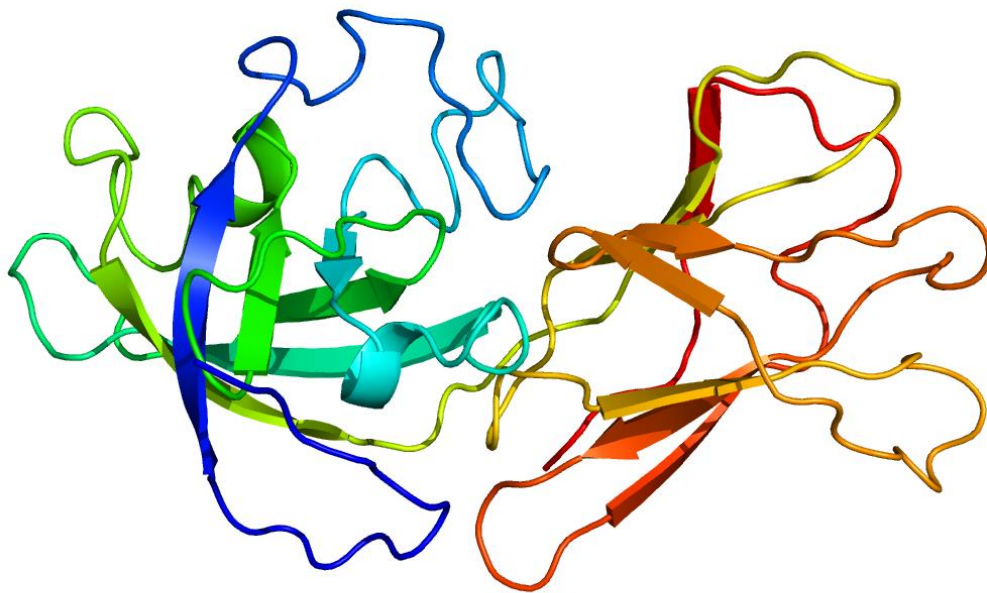
**Locus:** Seita.4G006000

**Gene Model:** Seita.4G006000.1.p

**Description:** SitEXPA-10

**Family:** Alpha Expansin

**3D structure:**



## GENOME DATABASES

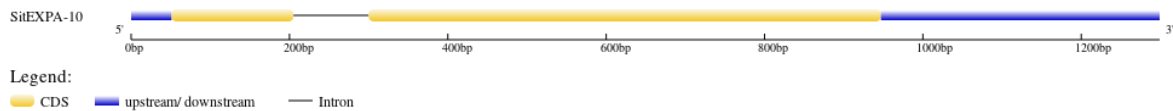
Phytozome: [https://phytozome-next.jgi.doe.gov/info/Sitalica\\_v2\\_2](https://phytozome-next.jgi.doe.gov/info/Sitalica_v2_2)

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

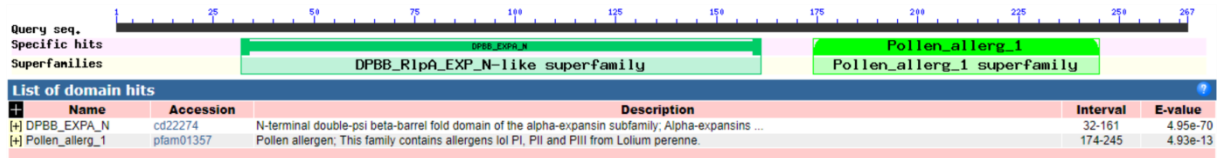
## EXTERNAL RESOURCES

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## GENE STRUCTURE



## DOMAIN ARCHITECTURE



## SEQUENCES

### Peptide

>SitEXPA-10

MATTPAIMVALIVAAAQVASAYYQQPFKTSWQDAHATFYGEDSGLGADFGGAC  
GFGANDIVSLYSTYTAALSTPLFADGNGCGQCYEIRCENSRWCNPGSPTVTLTATNL  
CPPNVYLPNDNGGWCNPPRQHFDMAPPSFYRLAQRVAGIIPVQFRRVPCQRRGGVRL  
CLQGNYYWLLVYVMNVAGGGDVSSLA VKRAGEPDCNYKHASHNWGITYQVFGTL  
GNVQGLVVRMTSYSSPQQTIVVSDAIPAGWITGLCYQGSNNFY\*

### CDS (coding sequence)

>SitEXPA-10

ATGGCGACA ACTCCAGCGATCATGGTGGCATTGATCGTGGCAGCGGCGGCAG  
GTGGCGAGCGGTACTACCAGCAGCCCTTCAAGACGTCCGACTGGCAGGACGCC  
CACGCCACCTTCTACGGCGAAGACTCCGGCCTCGGAGCAGACTTCGGCGGCGCGT  
GCGGGTTCGGCGCCAACGACATCGTGTCTCTCTACTCGACGTACACGGCGGCGCT  
GAGCACGCCGCTGTTCCGCCGACGGCAACGGGTGCGGGCAGTGCTACGAGATCCG  
GTGCGTCAACTCCCGGTGGTGCAACCCCGGCTCGCCGACGGTGACCCTCACC GCC  
ACCAACCTCTGCCCCGCCAACGTGTACCTCCCCAACGACAACGGCGGGTGGTGCA  
ACCCGCCGCGGCAGCACTTCGACATGGCGCCGCCCTCCTTCTACCGCCTCGCCA  
GCGGGTCGCCGGCATCATCCCCGTCCAGTTCGCCCGCGTGCCCTGCCAGAGGCCGA  
GGCGGGGTCAGGCTCTGCCTCAGGGCAACTACTACTGGTCTCCTCGTCTACGTCA  
TGAACGTCGCCGGCGGAGGGCAGCTCTCCTCCCTGGCCGTCAAGAGGGGCCGGCG  
AGCCAGACTGCAACTACAAGCACGCAAGCCACA ACTGGGGGATCACGTACCAGG  
TCTTCGGCACGCTCGGCAACGTGCAGGGGCTCGTTCGTCAGGATGACCAGCTACAG  
CTCGCCG CAGCAGACCATCGTTCGTCAGCGACGCCATCCCCGCCGGATGGATCACC  
GGACTCTGCTACCAGGGATCCAACA ACTTCTACTGA

### Nucleotide

>SitEXPA-10

ACATCGCCGTTATCCATCCATCGATCAAGACCTAGCCGTTGTCGTCGAGCCATGG  
CGACA ACTCCAGCGATCATGGTGGCATTGATCGTGGCAGCGGCGGCGCAGGTGG  
CGAGCGCGTACTACCAGCAGCCCTTCAAGACGTCCGACTGGCAGGACGCCACG

CCACCTTCTACGGCGAAGACTCCGGCCTCGGAGCAGACTTCGGTATGTATTGTTG  
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ATCAATGCTGCCAATGCAACTTACAGGCGGCGCGTGCGGGTTCGGCGCCAACGAC  
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CACGCAAGCCACAACCTGGGGGATCACGTACCAGGTCTTCGGCACGCTCGGCAAC  
GTGCAGGGGCTCGTCGTCAGGATGACCAGCTACAGCTCGCCGCAGCAGACCATC  
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CCAACAACCTTCTACTGATTAATCAATTGCCTGACGAGCTGATGATGATCCAGGGG  
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TTCAATTATTATTATGTATATTATTTGTCCCTGCGTTTCTTGGATCGATATTATGCT  
CCCTTTATTTGGGTTCAATTTTCGTAGGATGGCAGTGCTAATCGATCGATCTTCTCC  
GGGTAAAGTGTGTGCGTATGTGTTTCTTTTTTTATATATAAAAAGGATTCTTTTGT  
CAAATGTACCTTAACTATGTGATGTACTIONACCGG