

IDENTIFICATION

Species: *Setaria italica*

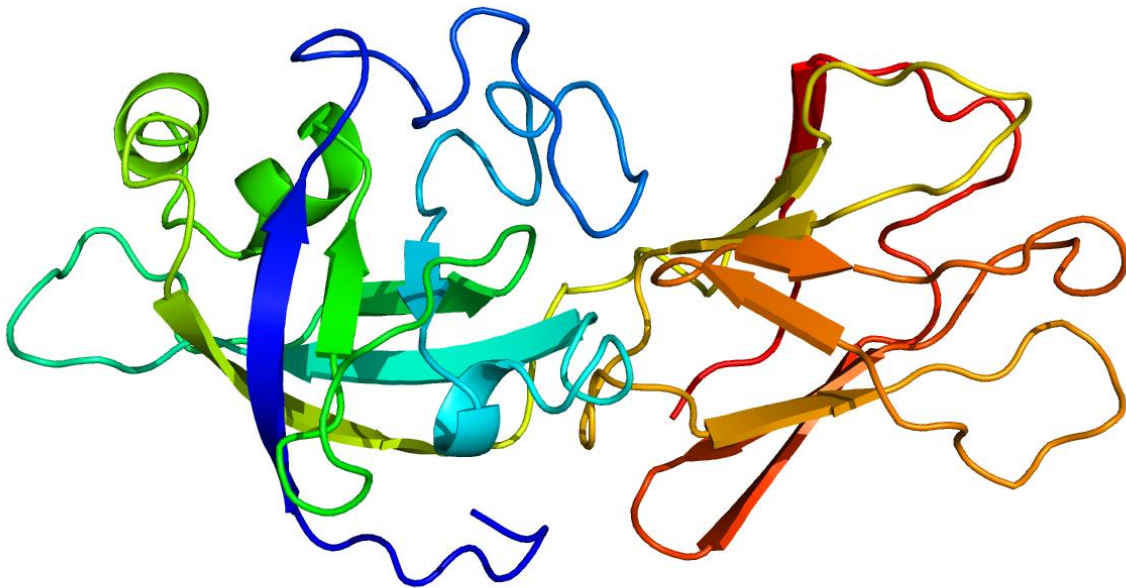
Locus: Seita.9G327000

Gene Model: Seita.9G327000.1.p

Description: SitEXPB-26

Family: Beta Expansin

3D structure:



GENOME DATABASES

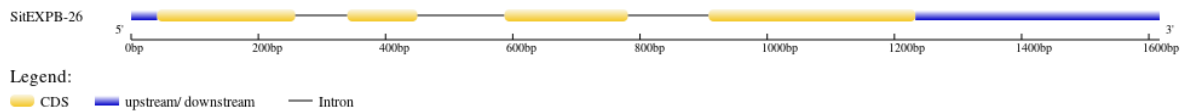
Phytozome: https://phytozome-next.jgi.doe.gov/info/Sitalica_v2_2

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

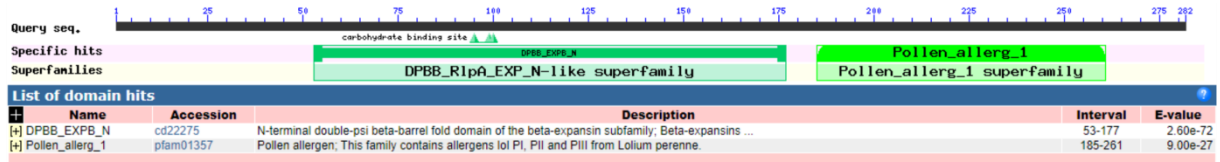
EXTERNAL RESOURCES

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GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>SitEXPB-26

MAAVMISFKAIALVAALLSVVATYSAHAEPNYNETTARRELYYSVGGSTPSTTWRRPAR
ATWYGRHNGAGPDNNGGGCGYSNTNLYPFNSMTTCGNQPLFLDGGKGGCACYQIKC
TSKNNPACSGEPKQVIITDVNYDTKIAPYHFDLSGTAFGAMAKPGYNDKLRKAGIID
MEFRRVPCNYKGLPVRFHVMGGCNPFFYFAVIVYYAGSDGAVVQVDLKEANSNTWR
PLYESWGAVWRIDPGHPLKAPLSLRVRSDSGKILVANNVIPLNWRGNADYRTIAQFR
*

CDS (coding sequence)

>SitEXPB-26

ATGGCCGCCGTGATGATCTCCTTCAAGGCTATTGCACTGGTTGCAGCACTCCTCTC
CGTGGTGGCCACGTACAGCGCTCACGCCGAACCGAACTACAACGAGACCACCGC
CCGCAGAGAATTGTACTACTCCGTCGGCTCCACCCCAGCACCACCTGGCGGCCT
GCCAGGGCCACCTGGTACGGCCGGCACAACGGCGCCCGGCCCTGACAACAACGGT
GGCGGGTGTGGGTACAGCAACACGAACCTGTACCCGTTCAATTCATGACGACCT
GCGGCAACCAGCCCCTGTTCTTGGACGGCAAGGGCTGCGGGCGCATGCTACCAGAT
AAAGTGCACCAGTAAGAACAACCCTGCCTGCTCCGGCGAGCCAAGCAGGTGAT
CATCACCAGCTAAACTACGACACCAAGATCGCCCCCTACCACTTCGACCTCAGC
GGCACGGCGTTCGGCGCCATGGCCAAGCCCGGCTATAACGACAAGCTCCGCAAG
GCCGAATCATCGACATGGAGTTCAGGAGGGTGGCCCTGCAACTACAAGGGCCTG
CCGGTGAGGTTCCACGTGATGGGCGGCTGCAACCCGTTCTACTTCGCGGTGATCG
TGTACTIONCGCCGGCAGTGACGGCGCCGTGGTGCAGGTGGACCTCAAGGAGGCCA
ACTCCAACACGTGGAGGCCGCTCTACGAGTCGTGGGGCGCCGTTTGGAGGATCGA
CCCCGGCCACCCGCTGAAGGCGCCCCCTCTCGCTGCGCGTGCGCAGCGACTCCGGC
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ACCGCACCATCGCCCAGTTCGCTGA

Nucleotide

>SitEXPB-26

AAATCGAGCCGAAAGCAGTAGGGTCAAGCTGAGATCGATCGATGGCCGCCGTGA
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ACGACACCAAGATCGCCCCCTACCACTTCGACCTCAGCGGCACGGCGTTCGGCGC
CATGGCCAAGCCCGGCTATAACGACAAGCTCCGCAAGGCCGGAATCATCGACAT
GGAGTTCAGGAGGTCAGTGTAGTGTACTAGTGTGTACCATTTAGAGTAGCACATT
TCTCACGATCGTCGTGAGTTGGTTAATAATCGTTCCTTTGTAACCTGAAGATGTGAT
CTCATATATATGCGGGCGTGCCACGCAGGGTGCCCTGCAACTACAAGGGCCTGCC
GGTGAGGTTCCACGTGATGGGCGGCTGCAACCCGTTCTACTTCGCGGTGATCGTG
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GGAAATAGCTTTTGTGTTATTACAGTCTTTTTGCGAGGTTTCAAATTGTTAGT
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AAGCAAGCAGTTACAAGTA