

IDENTIFICATION

Species: *Setaria italica*

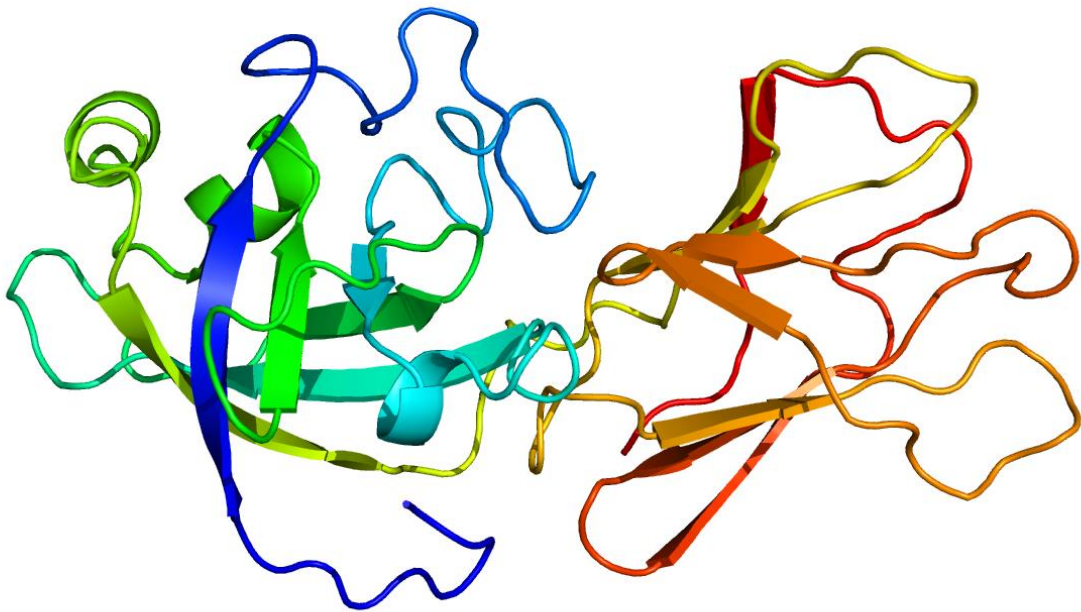
Locus: Seita.9G326300

Gene Model: Seita.9G326300.1.p

Description: SitEXPB-22

Family: Beta Expansin

3D structure:



GENOME DATABASES

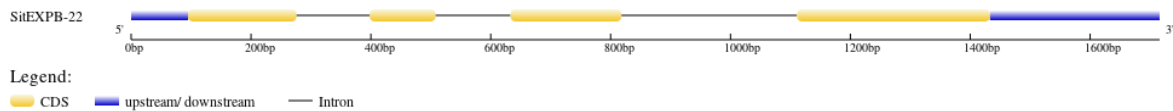
Phytozome: https://phytozome-next.jgi.doe.gov/info/Sitalica_v2_2

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

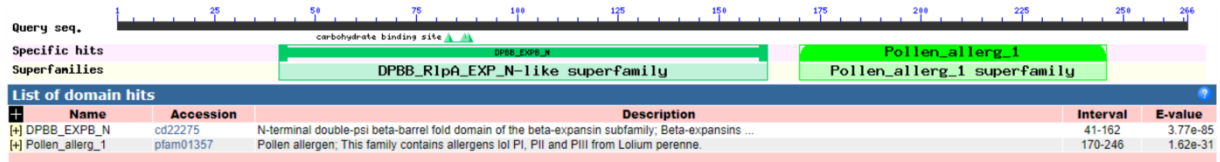
EXTERNAL RESOURCES

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GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>SitEXPB-22

MASSSKAAAFALLFSLLVITYGSCTRPVNFNESDFTADPNWEAARATWYGAPTGAG
PDDDDGGACGFKVNLPPFSAMTSCGNEPLFKDGKGCSCYQIRCTNHAACSGNPETV
IITDMNYYPVAKYHFDLSGTAFGAMAKPGRNDEL RHAGIIDIQFKRVPCNYPGQKVT
FHVEEGSNAVYLA VLVEFEDGDGDVVQVDLMEANSGSWTPMRESWGSIWRLDSNH
RLQAPFSVRITNESGRMLVANQVIPANWV PNTYYRSIIQY*

CDS (coding sequence)

>SitEXPB-22

ATGGCCTCCTCTTCCAAGGCTGCAGCATTGCTGCACTGCTCTTCTCCCTCCTTGT
CACGTATGGCTCGTGCCTCGGCCGGTGAACCTTAACGAGTCGGACTTCACCGCC
GACCCCAACTGGGAGGCCGCCAGGGCCACCTGGTATGGGGCACCCACCGGCC
GGTCCTGACGACGACGGTGGCGCCTGCGGGTTCAAGAACGTGAACCTGCCACCGT
TCTCGGCGATGACGTCCTGCGGCAACGAGCCACTGTTCAAGGACGGCAAGGGCT
GCGGCTCCTGCTACCAGATACGATGCACCAACCACGCTGCGTGCTCCGGCAACCC
GGAGACGGTGATAATCACCGACATGAACTACTACCCCGTCGCCAAGTACCACTTC
GACCTCAGCGGCACGGCCTTCGGCGCCATGGCCAAGCCAGGCCGCAACGATGAG
CTCCGCCATGCCGGCATCATCGACATCCAATTCAAGAGGGTGCCCTGCAACTACC
CCGGCCAGAAGGTGACGTTCCACGTCGAGGAGGGCTCGAACGCCGTCTACTTGGC
GGTGCTCGTCGAGTTCGAAGACGGCGACGGCGATGTGGTGCAGGTGGACCTCAT
GGAAGCCAACTCCGGGTCATGGACTCCGATGCGCGAGTCCTGGGGATCCATCTGG
AGGCTGGACTCCAACCACCGGCTGCAGGCGCCCTTCTCAGTGCGCATACCAACG
AGTCCGGCAGGATGCTGGTGGCCAACCAGGTCATCCCGGCCAACTGGGTGCCCA
ACACCTATTACCGCTCCATCATCCAGTACTAG

Nucleotide

>SitEXPB-22

ACCGAATCTTAGTGTCTGCTCGGTA TAGCAGTAGCTATACCTTCAGTAGATCTTA
AGCTTGGAGTAGAATTTGTGTTTGCTGCACTGAGCTAAGATGGCCTCCTCTTCCAA
GGCTGCAGCATTGCTGCACTGCTCTTCTCCCTCCTTGTCACGTATGGCTCGTGCA

CTCGGCCGGTGAAC TTTAACGAGTCGGACTTCACCGCCGACCCCAACTGGGAGGC
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TACGTAATTCTCGGTCATGGCTACGTATGGGTATTGGCGTATTGCTGAATGCCGC
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CCTGCTACCAGGTACGTAGACTTTTCCGTCTCTGCCGTGTCGTGGAAAACAGGAA
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ACGATGAGCTCCGCCATGCCGGCATCATCGACATCCAATTCAAGAGGTGGGTACC
ATGCATTGCTGCTCGTTGCACAGAGCCGCAGAACAAGAATCATTAGCTCGACCGTC
TAGCTTACCTGTTCTGTGGAGCCCTTGTACTTTTGCTCAACCGATTTTGACGACAC
GACAGCCAGTTTTAAATGGGGGGCTGGGGCCCACGTAGATTTCGCAGAAATATTTA
GTACCAGTACTTCCAATTCCTCCGAATTTGGAGTCTGCATGCACTGTGGATCGA
CAAAGGTTGCTTAATTTGAAGCCTAATCCATGTCCAAACGCACCACATGGCTTGT
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CCTTCTCAGTGCGCATCACCAACGAGTCCGGCAGGATGCTGGTGGCCAACCAGGT
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ACTGTCTATGAATGTAATGGTGTGATCAAGGTTTTAAATTATAAACACTGTTTTGT
GCACC