

IDENTIFICATION

Species: *Brachypodium stacei*

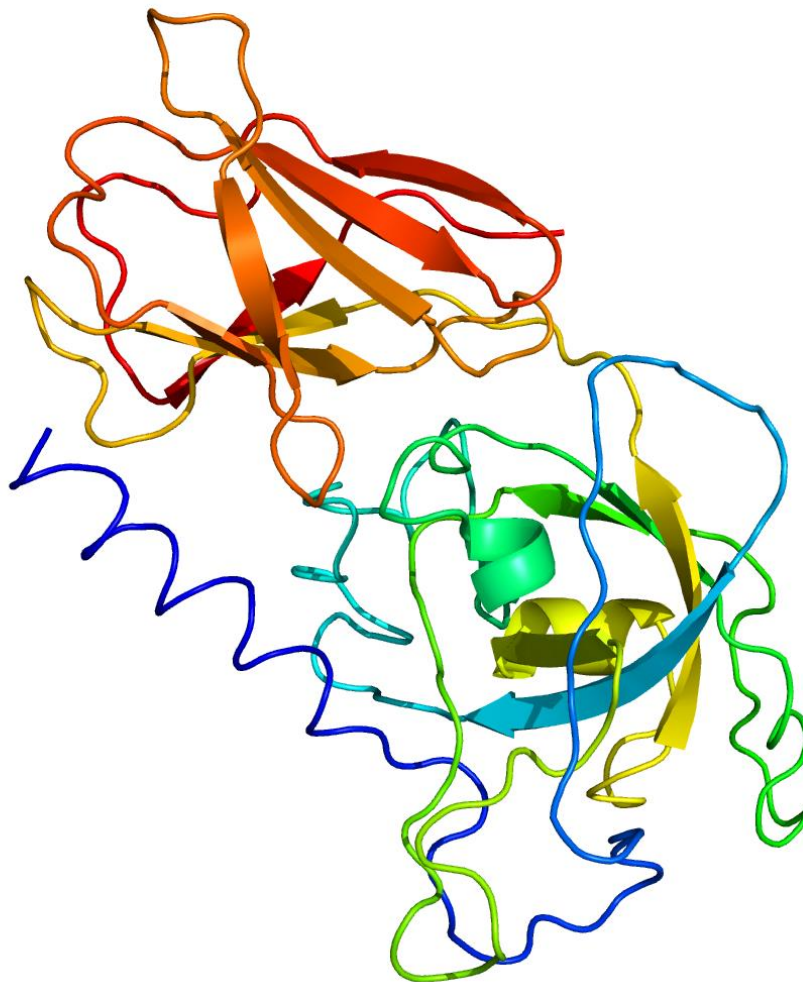
Locus: Brast04G015800

Gene Model: Brast04G015800.1.p

Description: BstEXPA-18

Family: Alpha Expansin

3D structure:



GENOME DATABASES

Phytozome: https://phytozome-next.jgi.doe.gov/info/Bstacei_v1_1

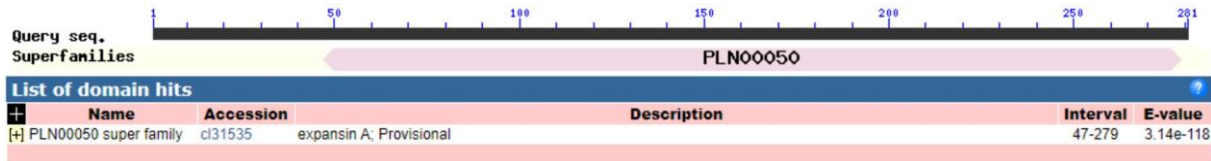
EXTERNAL RESOURCES

<https://brachypodium.org/>

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>BstEXPA-18

MAPVLRALLLAFLVAAPSAVARGPHLPGHHGLVHRHGSVHAHAAPLGGGAWSSAHA
TFYGGGDASGTMGGACGYGNLYSTGYGANTAALSTALYNDGLSCGACFEVRCDDPA
GTEAGTTHACLGTSSVVITATNLCPPNNALPSDDGGWCNPPRAHFDMSQPVFQRIALY
KAGIVPVSYRRVACQKKGGIRFTINGHSYFNLVLVSNVGGPGDVHAVAVKSERSPSW
QALSRNWGQNWQSNALLDRQCLSFRVTAGDRSVVSSNAVPRGWAFGQTFSGAQF
T*

CDS (coding sequence)

>BstEXPA-18

ATGGCGCCCGTCCTCCGAGCCCTGCTCCTCGCCTTCCTCGTGGCCGCGCCGTCCGC
GGTAGCACGAGGGCCGCATTTACCCGGCCACCACGGCCTGGTCCACCGCCACGG
GAGCGTCCACGCGCACGCGCCGCTGGGCGGCGGCGCGTGGTTCCTCGGCGCACGC
GACGTTCTACGGCGGCGGCGACGCGTCGGGCACCATGGGCGGGGCGTGCGGGTA
CGGGAACCTCTACAGCACGGGCTACGGCGCCAACACGGCGGCGCTGAGCACGGC
GCTCTACAACGACGGGCTGAGCTGCGGCGCCTGCTTCGAGGTCCGCTGCGACCCG
GCCGGCACAGAAGCAGGCACAACCCACGCGTGCCTGGGAACCTCCGTCGTCATC
ACGGCCACCAACCTCTGCCCCGCCAACAACGCGCTCCCCTCCGACGACGGCGGCT
GGTGCAACCCTCCCCGCGCCCACTTCGACATGTCCCAGCCCGTCTTCCAGCGCAT
CGCCCTCTACAAGCCGGCATTGTCCCCGTCTCCTACCGCAGGGTGGCGTGCCAG
AAGAAGGGGGGAATCAGGTTACGATCAACGGCCACTCCTACTTCAACCTGGTGC
TCGTCTCCAACGTCGGCGGGCCCCGGGACGTGCACGCGGTGGCCGTGAAGTCCG
AGCGCTCCCCTTCTGGCAGGCCCTGTCGCGCAACTGGGGACAGAACTGGCAGAG
CAACGCGCTGCTCGACCGCCAGTGCTTCTCCTTCCGCGTCACGGCAGGGGACGGC
CGCTCCGTCGTCTCAGCAACGCCGTCCCCCGCGGCTGGGCATTCGGCCAGACCT
TCAGCGGCGCCAGTTCACCTGA

Nucleotide

>BstEXPA-18

GCCATGCCGCGTGCTCACTTGCTCCGCCCCGGCGGCTCCCTCTATTTATCCCCGT
CCCAACCGGGAACCACAAACGCCTCACCCAGCATTCCACTTCTCCCCGTAGCCCG

TAGCCGCGCCCTAGCTTCTCCCGTGGCCATGGCGCCCGTCCTCCGAGCCCTGCTCC
TCGCCCTTCTCGTGGCCGCGCCGTCCGCGGTAGCACGAGGGCCGCATTTACCCGG
CCACCACGGCCTGGTCCACCGCCACGGGAGCGTCCACGCGCACGCGCCGCTGGG
CGGCGGGCGCGTGGTCCTCGGCCGACGCGACGTTCTACGGCGGGCGGGCGACGCGTC
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CGCCTGCTTCGAGGTCCGCTGCGACCCGGCCGGCACAGAAGCAGGCACAACCCA
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AACGCGCTCCCCTCCGACGACGGCGGGTGGTGCAACCCTCCCCGCGCCCACTTCG
ACATGTCCCAGCCCGTCTTCCAGCGCATCGCCCTCTACAAGGCCGGCATTGTCCC
CGTCTCCTACCGCAGGTATGTCAATTCCCCCCTAGTAATTCCCCTGATTTCTCTCT
CTGTTCTGTGGTCTCTGGATCTGGAGTGACACCTGACTGACAGTGGCGTGCTTCTT
CTTGAATCTTCTGCAGGGTGGCGTGCCAGAAGAAGGGGGGAATCAGGTTTCACGA
TCAACGGCCACTCCTACTTCAACCTGGTGCTCGTCTCCAACGTCGGCGGGGCCCGG
GGACGTGCACGCGGTGGCCGTGAAGTCCGAGCGCTCCCCTTCCTGGCAGGCCCTG
TCGCGCAACTGGGGACAGAACTGGCAGAGCAACGCGCTGCTCGACCGCCAGTGC
CTCTCCTTCCGCGTCACGGCAGGGGACGGCCGCTCCGTCGTCTCCAGCAACGCCG
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AAGTCGCCCTTCGTTCTAAGTACTATCTAGTTTTACCCCGAGATTCTGCCGTAGTA
GTGAGTAGTACTACTTCGATTGGAGCGTGCTGGGATGAGCCATGGTTTTATGGGT
GGTTCTTCCCTCAAGCATTACGTTCTTTTGAAGAAGCAGTCAGTAGTAGTAGCAGG
TTAGTTAGGCCTGGTATTAGCATGGGCTTTTAATTGTCCTGGTGTGAGTGTAGCA
AGAGTGAAGTGGTGGTTTGGAGCGAGCTTTTGGCTAGGATGGCAGCGGTGGTAAA
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CTCTTGGATGATGGCCTTGTCTCGACGGTAATCTCTGTGCGGCTTGTACTGTTCCCTC
ATTCTGGGGTTCAACTAATGCATTTGTGGCTTAAGCCTGTTCCCTTTCTTTAACT