

IDENTIFICATION

Species: *Brachypodium stacei*

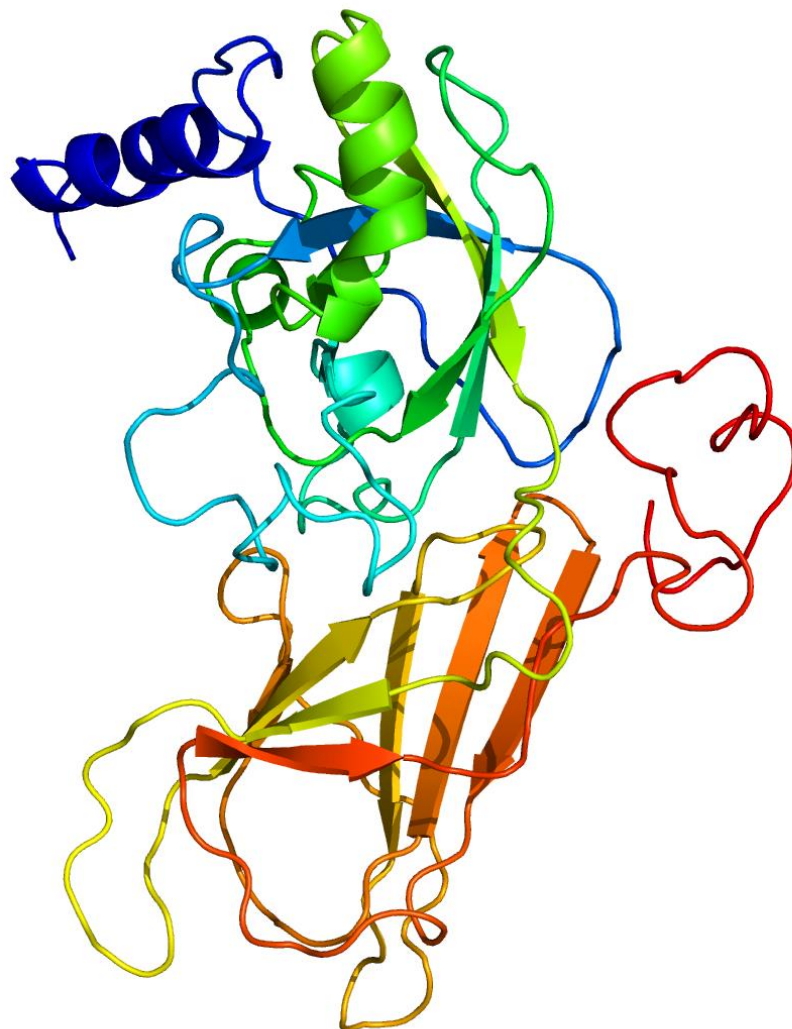
Locus: Brast07G236800

Gene Model: Brast07G236800.1.p

Description: BstEXPA-27

Family: Alpha Expansin

3D structure:



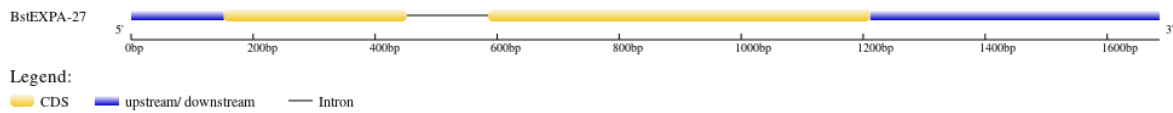
GENOME DATABASES

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

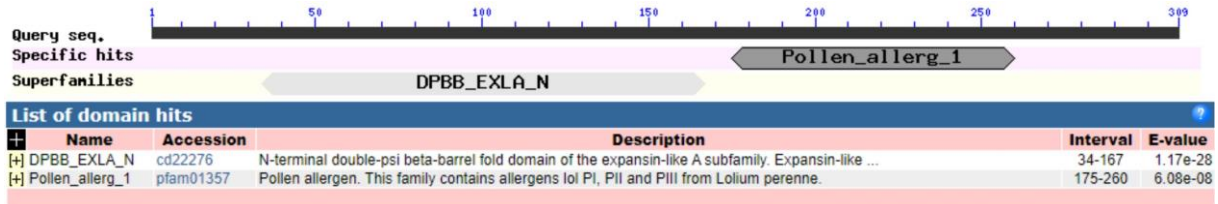
EXTERNAL RESOURCES

<https://brachypodium.org/>

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>BstEXPA-27

MAAAQLLLLLLLVLTLLCLTVAAASASSSAASSYRCGWCRSRRSSVATASILPPDAAS
TGAAACGYGTPAAAASTGGFYLAASAEFFRHGQAACGSCYQLRCRDGASCRKGG
VKVVVTGEIGTNRTASGGGGGRFMLPREAFAAMAAVHGDLQQQEVDFFRIPCELH
KGRSLAVKVEETSSRNNKSGGRLALRFLFLGGQTDIAAVEVAPASSSSSSFSWRYLTR
KQGVWSTARAPAGPLRLRVVVTAGSGGKWL RADGEVIPAEWVPRVYDTGLRVSE
FAMGTCSCSAGDEDEDEEGQGEFFR*

CDS (coding sequence)

>BstEXPA-27

ATGGCCGCCGCCAGCTGCTTCTTCTTCTTCTTCTAGTTCTAACCCTCCTCTGCCTC
ACGGTGGCCGCCGCGAGCGCCTCTTCATCCGCTGCCTCCTCGTACCGCTGCGGCT
GGTGCCGCAGCCGCCGCTCTAGTGTTGCTACCGCCTCCATCCTCCCTCCTGACGCC
GCCAGCACCGGCCGCCGCCGCTGCGGCTACGGGACGCCGGCAGCCGCAGCCAGC
ACCGGCGGCTTCTACTTGGCCGCCGCGCCAGCGCCGAGTTCTTCCGCCATGGCCAAG
CTGCCTGCGGCTCATGCTACCAGCTGAGGTGCAGAGACGGGGCCTCGTGCAGAA
AGGGCGGCGTCAAGGTCGTCGTCACCGGCGAGATCGGGACCAACAGGACGGCAT
CCGGCGGCGGCGGAGGGAGGTTTCATGCTTCCCAGGGAGGCCTTCGCCGCCATGG
CTGCCGCCGTCATGGCGACCTGCAGCAGCAGGAGGTGGATTTTCAGGAGGATCCC
CTGCGAGCTGCACAAGGGCAGGAGCCTGGCCGTGAAGGTGGAGGAGACGTCGAG
CAGGAACAACAAGAGCGGCGGCCGCTCGCGCTCCGCTTCTTCTTCTTCTTCTTT
TCATGGCGGTACCTGACGCGGAAGCAGGGAGTGTGGAGCACGGCGCGGGCGCCG
GCGGGGCGGCTGCGGCTGCGGGTGGTGGTACGGCGGGGTCCGGCGGCAAGTGG
CTGCGGGCCGACGGGGAAGTGATCCCCGCCGAGTGGGTTCCCGGCCGGGTCTAC
GATACCGGGCTCAGGGTGTCCGAATTCGCCATGGGCACTTGCTCCTGCTCCGCCG
GAGACGAAGACGAAGACGAAGAAGGCCAGGGGGAAGAGGAATTCAGATGA

Nucleotide

>BstEXPA-27

TCCACAGCCTTAGCACTCCTATATATATATCCAGCTTCTAGCTAGTTCATGGCCCCGCA
CGTCCCCTGACATGCCCTTAAGCTCACACGCTAGCTAGCTCACCAGATCAACCCA
TCGACGACGTACTTGGGTA CTTGGGTA CTTGGTTTGACGCCATGGCCGCCGCCA
GCTGCTTCTTCTTCTTCTTCTAGTTCTAACCCTCCTCTGCCTCACGGTGGCCGCCG
GAGCGCCTTTCATCCGCTGCCTCCTCGTACCGCTGCGGGCTGGTGCCGCAGCCGC
CGCTCTAGTGTTGCTACCGCCTCCATCCTCCCTCCTGACGCCGCCAGCACCGGCG
CGCCGCCTGCGGGTACGGGACGCCGGCAGCCGCAGCCAGCACCGGCGGGCTTCTA
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TGCTACCAGGTGCGCATCATAATTCATATCTCGACATTCGACAAGCGCTCTGTTG
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TAACTCAACTTGTTTCGACGTTGCTGCTGCAGCTGAGGTGCAGAGACGGGGCCTCG
TGCAGAAAGGGCGGCGTCAAGGTCGTCGTCACCGGCGAGATCGGGACCAACAGG
ACGGCATCCGGCGGCGGCGGAGGGAGGTTTCATGCTTCCCAGGGAGGCCTTCGCC
GCCATGGCTGCCGCCGTCATGGCGACCTGCAGCAGCAGGAGGTGGATTTTCAGG
AGGATCCCCTGCGAGCTGCACAAGGGCAGGAGCCTGGCCGTGAAGGTGGAGGAG
ACGTCGAGCAGGAACAACAAGAGCGGCGGCCCTCGCGCTCCGCTTCTTCTTCC
TCGGCGGCCAGACCGACATCGCCGCCGTCGAGGTGCGGCCTGCTTCTTCTTCTT
TCTTCTTTTTTCATGGCGGTACCTGACGCGGAAGCAGGGAGTGTGGAGCACGGCGC
GGGCGCCGGCGGGGCCGCTGCGGGTGC GGTTGGTGGTACGGCGGGGTCCGGCG
GCAAGTGGCTGCGGGCCGACGGGGAAGTGATCCCCGCCGAGTGGGTTCCCGGCC
GGGTCTACGATACCGGGCTCAGGGTGTCCGAATTCGCCATGGGCACTTGCTCCTG
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GATGATCGATCCACTGCACCGCGGAGCTAGCTATACCTACAAAGATATAACGATC
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GAGGACGTGAGATTTGGTTAGGACAACAACAAGAGCAAAACCTGTCTGCATGCC
CTGTCAATCGAACGGTGCATGTCTGGCCGTAAACCGGGGAGATTGGCTTGTAGCG
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GTTTTGGTCTTGGGATCACATGACAATGTTACTGTTTTTGC