IDENTIFICATION

Species: *Boechera stricta*

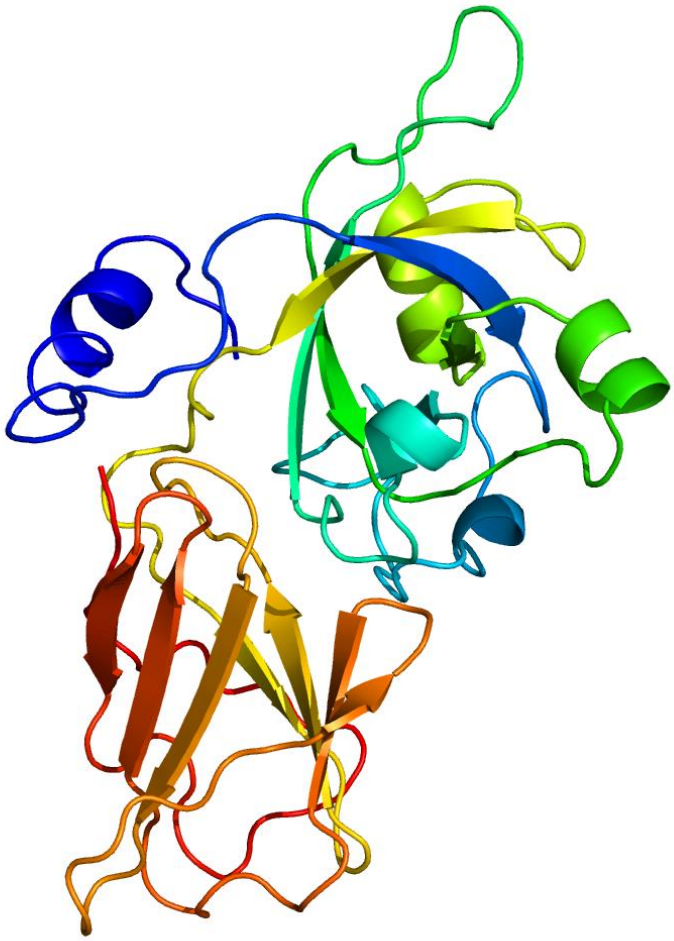
Locus: Bostr.28625s0163

Gene Model: Bostr.28625s0163.1.p

Description: BosEXPB-24

Family: Beta Expansin

3D structure:



GENOME DATABASES

Phytozome: https://phytozome-next.jgi.doe.gov/info/Bstricta_v1_2

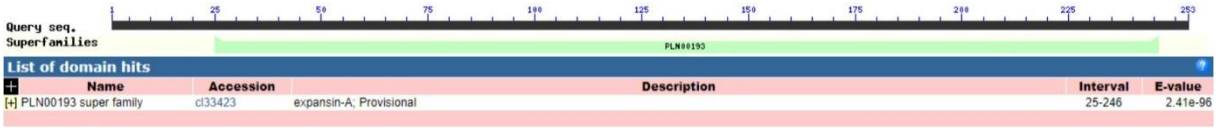
KEGG:-

EXTERNAL RESOURCES

-

GENE STRUCTURE

DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>BosEXPA-24

MDMKGKYLVTVILLVGTLSVGMCSNGWIRAHATYYGVNDSPASLGGACGYDNPYH
AGFGAHTAALSGALFRSGESCGGCYQVRCDFPADPKWCLRGAAVTVTATNFCPSNN
NNGWCNLPRHHFDMSSPAFFRIARRGNEGIVPVFYRRVGCKRRGGVRFTMRGQGNF
NMVMISNVGGGGSVRAVAVRGSKGKTWLQMTRNWGANWQSSGDLRGQRLSFRVT
LVDRKTLTFLNVVPSSWWFGQTFSSRGRQFV*

CDS (coding sequence)

>BosEXPA-24

ATGGATATGAAGGGAAAATATTTGGTAACGGTTATTCTCTTGGTTGGTACGTTAA
GTGTGGGGATGTGTTCTAACGGTTGGATAAGAGCTCATGCAACGTATTATGGTGT
TAATGATAGCCCTGCTTCACTTGGCGGAGCGTGTGGGTATGACAATCCGTACCAC
GCCGGATTCGGAGCCCACACGGCGGCGCTAAGCGGTGCGCTATTTAGAAGCGGC
GAGTCATGCGGTGGGTGCTACCAGGTGAGGTGCGACTTTCCGGCGGATCCTAAGT
GGTGTCTCCGAGGAGCCGCGGTGACGGTGACGGCTACAAACTTTTGTCCGTCGAA
CAACAATAATGGTTGGTGCAATCTCCCTCGCCATCACTTTGACATGTCCTCGCCCG
CTTTCTTCCGCATTGCCCGTCGCGGCAATGAAGGCATTGTTCCCGTCTTCTATCGC
CGGGTGGGATGCAAAAGAAGAGGAGGCGTGAGGTTTACGATGAGAGGGCAAGG
GAACTTCAATATGGTAATGATCTCAAACGTTGGCGGCGGCGGCTCAGTGAGAGCT
GTAGCGGTGAGAGGCTCAAAGGGAAAGACTTGGCTTCAGATGACCCGTAATTGG
GGTGCCAACTGGCAGAGCTCCGGCGATCTCCGGGGACAAAGACTCTCCTTCAGAG
TAACTCTTGTTGATCGCAAAACGCTGACGTTTTTGAACGTTGTCCCTTCTTCTTGG
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Nucleotide

>BosEXPA-24

ATGGATATGAAGGGAAAATATTTGGTAACGGTTATTCTCTTGGTTGGTACGTTAA
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TAATGATAGCCCTGCTTCACTTGGTAAAATGTCCATTAAACTATAAGTTTATTATA
CTTTTATTTGTTACTTTAGTTTTTGTATAGTAAATATAAAATTTTAAAACAATTTTA
TAGGCGGAGCGTGTGGGTATGACAATCCGTACCACGCCGGATTCGGAGCCCACA
CGGCGGCGCTAAGCGGTGCGCTATTTAGAAGCGGCGAGTCATGCGGTGGGTGCT

ACCAGGTGAGGTGCGACTTTCCGGCGGATCCTAAGTGGTGTCTCCGAGGAGCCGC
GGTGACGGTGACGGCTACAAACTTTTGTCCGTCGAACAACAATAATGGTTGGTGC
AATCTCCCTCGCCATCACTTTGACATGTCCTCGCCCGCTTTCTTCCGCATTGCCCG
TCGCGGCAATGAAGGCATTGTTCCCGTCTTCTATCGCCGGTAACGTATTCAAATTT
TCAATGCTATATATAAGAGTTACAATGCAGTGTTTATATTTAAATGTCAAAATAG
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TAAACTTTATAGGGTGGGATGCAAAAGAAGAGGAGGCGTGAGGTTTACGATGAG
AGGGCAAGGGAACTTCAATATGGTAATGATCTCAAACGTTGGCGGCGGCGGCTC
AGTGAGAGCTGTAGCGGTGAGAGGCTCAAAGGGAAAGACTTGGCTTCAGATGAC
CCGTAATTGGGGTGCCAACTGGCAGAGCTCCGGCGATCTCCGGGGACAAAGACT
CTCCTTCAGAGTAACTCTTGTTGATCGCAAAACGCTGACGTTTTTGAACGTTGTCC
CTTCTTCTTGGTGGTTTGGCCAAACCTTCTCTTCTCGAGGACGCCAATTTGTCTGA