

IDENTIFICATION

Species: *Boechera stricta*

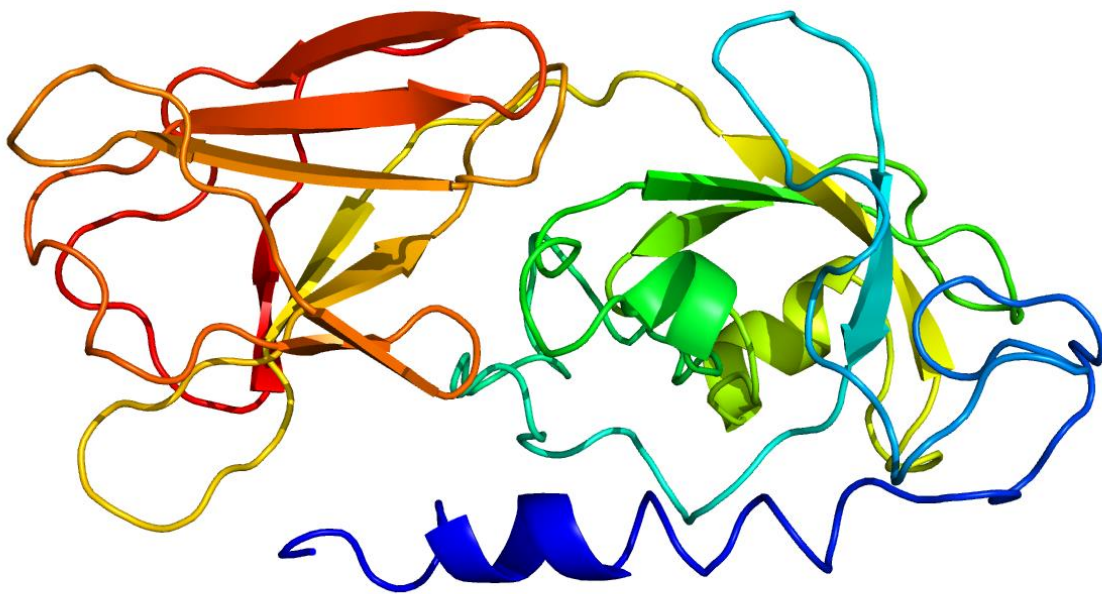
Locus: Bostr.25849s0013

Gene Model: Bostr.25849s0013.1.p

Description: BosEXPA-20

Family: Alpha Expansin

3D structure:



GENOME DATABASES

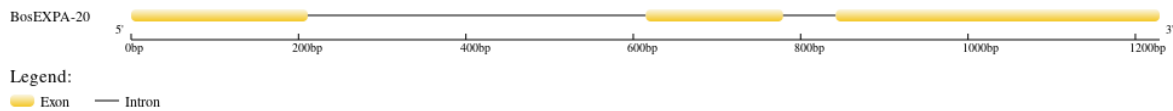
Phytozome: https://phytozome-next.jgi.doe.gov/info/Bstricta_v1_2

KEGG:-

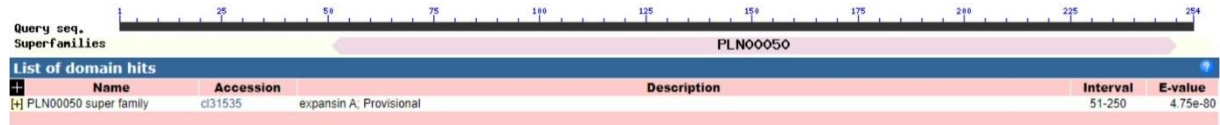
EXTERNAL RESOURCES

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GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>BosEXPA-20

MKLLNLIYVEFFMIIMAIWVVPISYGHGADVAEAPIGDAAEAPEISDPTRAFDTAWY
DARATFYGDIHGEGACGYGNLFRQGYGLATAALSTALFNDGYTCGACFEIMCTRDP
QWCLPGSIMITKHFDLSLAMFLKIAKYKAGVVPVRYRRIPCRKTGGVKFETKGNQYF
LMILPYNVGGAGDIKYMQVKGNKTGWITMKNWGWQHWTGVSALTGQGLSFRVTT
DGITKDFMNVMPKNWGFQTFNGRINF*

CDS (coding sequence)

>BosEXPA-20

ATGAAACTTTTAGAAAATTTGATATATGTAGAATTTTTATGATAATAATGGCGAT
ATGGGTCGTGCCAATAAGTTATGGTCATGGTGCCGATGTAGCCGAGGCACCCATT
GGTGATGCAGCTGAAGCACCCGAGATTAGTGACCCAACCAGGGCATTTCGACACT
GCTTGGTATGACGCACGAGCCACATTTTACGGTGACATCCATGGTGAGGGAGCTT
GTGGATACGGTAATCTATTCAGACAAGGCTATGGTCTTGCCACAGCAGCGTTAAG
CACGGCACTCTTCAACGACGGGTACACATGCGGGGCTTGTTTTGAGATCATGTGC
ACGCGTGATCCACAATGGTGTGGCCGGATCCATCATGATCACCAAACATTTTG
ATCTCTCCCTAGCAATGTTCCCTCAAGATCGCCAAGTACAAAGCTGGGGTTGTCCC
GGTTAGATACAGACGTATTCCTTGTAGGAAAACCGGTGGTGTAAAGTTTGAAACC
AAAGGCAACCAATATTTCTTAATGATCTTGCCATAACAATGTAGGAGGAGCTGGAG
ATATTAAGTACATGCAAGTTAAGGGAAACAAGACAGGGTGGATAACAATGAAAA
AGAATTGGGGACAACATTGGACCACTGGTGTTCATTGACTGGCCAAGGTTTATC
GTTCAGGGTTACGACGAGTGATGGGATTACAAAAGATTTTATGAATGTGATGCCA
AAGAACTGGGGATTTGGACAGACTTTTAATGGAAGGATTAACCTTTTAG

Nucleotide

>BosEXPA-20

ATGAAACTTTTAGAAAATTTGATATATGTAGAATTTTTATGATAATAATGGCGAT
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GGTGATGCAGCTGAAGCACCCGAGATTAGTGACCCAACCAGGGCATTTCGACACT
GCTTGGTATGACGCACGAGCCACATTTTACGGTGACATCCATGGTGGTATTATAT
GGTCTTGGTTAAAACGAATCTAATTAATTATTGAATTGAATGTTTTAAATGCTAA
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ACATTTTCATAAAATATATTTACAAAGTATAATGCAAATTGCCAGCTAGTCTTCTC
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CCAAAAAATAAAGATAACATGTAAACATAAAACCAACAGATATGTAAACAAAC
AATCAAAGTCTTAATTACTTTTGAATAATTATTACATACTTTTTTTTATTTTACTTTC
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ACAGCAGCGTTAAGCACGGCACTCTTCAACGACGGGTACACATGCGGGGCTTGT
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CACCGCTACAAATTTCTGTCCATCAAATTACACCAAACCAAAGACATTTGGTGC
AACCACCATAGAAACATTTTGATCTCTCCCTAGCAATGTTCCCTCAAGATCGCCA
AGTACAAAGCTGGGGTTGTCCCGGTTAGATACAGACGTATTCCTTGTAGGAAAAC
CGGTGGTGTTAAGTTTGAAACCAAAGGCAACCAATATTTCTTAATGATCTTGCCA
TACAATGTAGGAGGAGCTGGAGATATTAAGTACATGCAAGTTAAGGGAAACAAG
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