

## IDENTIFICATION

**Species:** *Boechera stricta*

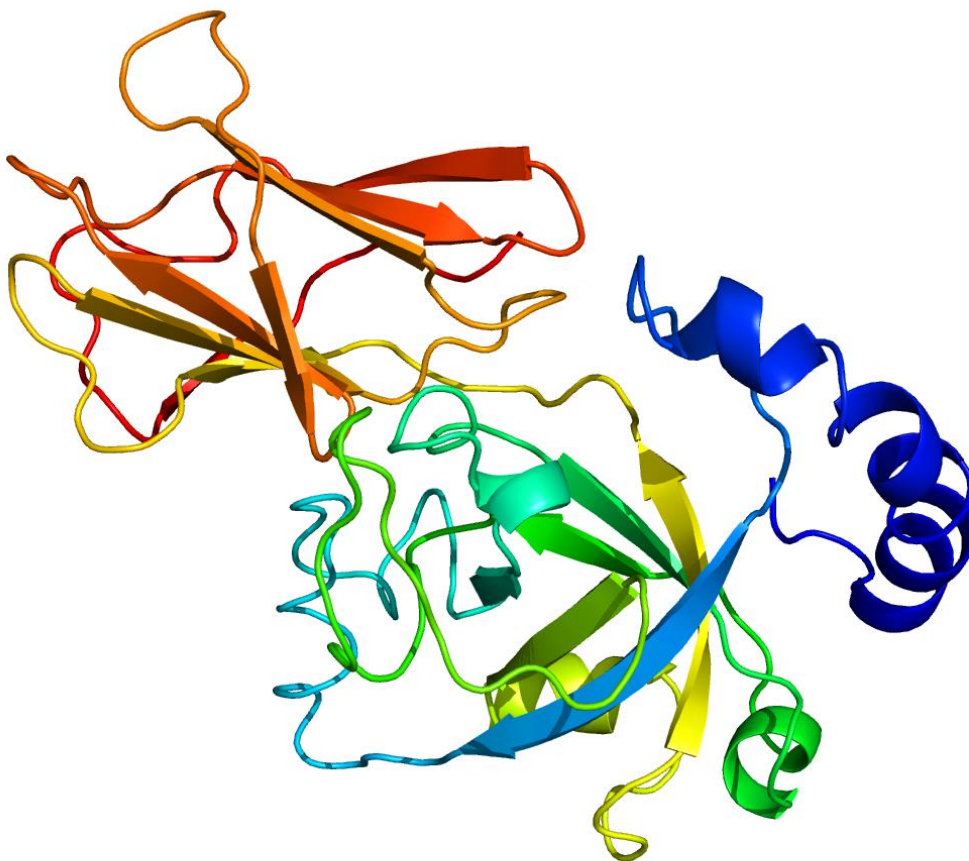
**Locus:** Bostr.13671s0203

**Gene Model:** Bostr.13671s0203.1.p

**Description:** BosEXPA-13

**Family:** Alpha Expansin

**3D structure:**



## GENOME DATABASES

Phytozome: [https://phytozome-next.jgi.doe.gov/info/Bstricta\\_v1\\_2](https://phytozome-next.jgi.doe.gov/info/Bstricta_v1_2)

KEGG:-

## EXTERNAL RESOURCES

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## GENE STRUCTURE



## DOMAIN ARCHITECTURE



## SEQUENCES

### Peptide

>BosEXPA-13

MGPISSWSFNKFFAIVFVVFAISGEFVAGYYRPGPWRYAHATFYGDETGSETMGGACGYGNLFSNGYGVSTAALSTTLFKDGYGCGQCFQITCMKSPHCYYGNPSTVVTATNL CPPNWYQDSNNGGWCNPPRTHFDMAKPAFMKLANWKAGIIPVTYRRVPCQRSGGM RFQFQGNAYWLLIFVMNVGGAGDIKSMVKGSRTNWISMShNWGASYQAFSSLYG QLSFRVTSYTTGQTIYAWNVAPANWSAGKTYKSLANFR\*

### CDS (coding sequence)

>BosEXPA-13

ATGGGTCCAATCTCAAGTTCTTGGAGTTTCAACAAATTCTTCGCAATAGTTTTTGT  
CGTTTTCGCCATCTCCGGTGAGTTCGTCGCTGGATACTATCGACCAGGCCCATGG  
AGATATGCTCACGCCACTTTCTACGGCGACGAGACCGGTAGTGAAACTATGGGTG  
GTGCATGTGGGTACGGAAACCTTTTTAACAGTGGTTACGGTGTGTCCACGGCAGC  
GCTAAGCACGACGCTGTTCAAAGACGGTTACGGATGCGGCCAATGTTTTCAAATA  
ACGTGTATGAAGTCGCCGATTGTTATTATGGAAACCCATCAACGGTGGTCACAG  
CAACCAACCTTTGCCCTCCTAATTGGTACCAAGACTCCAACAATGGTGGTTGGTG  
CAATCCTCCTAGAACCCATTTGATATGGCTAAACCGGCTTTCATGAAACTCGCT  
AATTGGAAGGCCGGTATCATCCAGTTACATACCGGAGAGTGCCATGCCAAAGG  
AGTGGAGGTATGAGGTTTCAATTCCAAGGCAATGCTTATTGGCTTCTCATATTCGT  
CATGAACGTCGGTGGCGCCGGAGACATCAAGAGCATGGCCGTGAAAGGTAGCCG  
GACGAATTGGATAAGCATGAGCCACAATTGGGGAGCGTCTTACCAAGCTTTTTTCG  
TCTCTACGGTCAATCTCTATCTTTCCGGGTCATTCTTACACCACAGGTCAAAC  
CATCTATGCTTGGAACGTTGCTCCGGCTAACTGGAGCGCCGGTAAGACTTACAAG  
AGCCTTGCCAATTTCCGTTGA

### Nucleotide

>BosEXPA-13

ATGGGTCCAATCTCAAGTTCTTGGAGTTTCAACAAATTCTTCGCAATAGTTTTTGT  
CGTTTTCGCCATCTCCGGTGAGTTCGTCGCTGGATACTATCGACCAGGCCCATGG  
AGATATGCTCACGCCACTTTCTACGGCGACGAGACCGGTAGTGAAACTATGGGTA  
CGTTAACAATTTCAATTTCACTTCGCTTGCATTTACCATGCATGAAATCTGTCCAAC

ATTTTTGGATATCTCCGCACGATTAACAAAACCTTAATGTAGTAAAAATTTATAAA  
AGGATGTCCAAATTTTTTCTACTGGATCCGTAGTCCAAACCAGTTATTTCAATTG  
CATGTTCTCTGAACCGAACCTAATAATCACAATATTTACACATAGGACCAATGG  
CATAATAACTTTATGTATATATGCAGGTGGTGCATGTGGGTACGGAAACCTTTTT  
AACAGTGGTTACGGTGTGTCCACGGCAGCGCTAAGCACGACGCTGTTCAAAGAC  
GGTTACGGATGCGGCCAATGTTTTCAAATAACGTGTATGAAGTCGCCGCATTGTT  
ATTATGGAAACCCATCAACGGTGGTCACAGCAACCAACCTTTGCCCTCCTAATTG  
GTACCAAGACTCCAACAATGGTGGTTGGTGCAATCCTCCTAGAACCCATTTTCGAT  
ATGGCTAAACCGGCTTTCATGAAACTCGCTAATTGGAAGGCCGGTATCATCCCAG  
TTACATACCGGAGGTATTTATAGTATACGACCTTAGTTATTCAACTCCAGAACTAT  
ATAATTAACTAATATATGTTATAATGTGATTGACGTATAGAGTGCCATGCCAAAG  
GAGTGGAGGTATGAGGTTTCAATTCCAAGGCAATGCTTATTGGCTTCTCATATTC  
GTCATGAACGTCGGTGGCGCCGGAGACATCAAGAGCATGGCCGTGAAAGGTAGC  
CGGACGAATTGGATAAGCATGAGCCACAATTGGGGAGCGTCTTACCAAGCTTTTT  
CGTCTCTCTACGGTCAATCTCTATCTTTCCGGGTCACTTCTTACACCACAGGTCAA  
ACCATCTATGCTTGGAACGTTGCTCCGGCTAACTGGAGCGCCGGTAAGACTTACA  
AGAGCCTTGCCAATTTCCGTTGA