

## IDENTIFICATION

**Species:** *Boechera stricta*

**Locus:** Bostr.4824s0001

**Gene Model:** Bostr.4824s0001.1.p

**Description:** BosEXPA-05

**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

Query seq. MDHATFYGGSAASGTMALSTALFNDGKSCGGCYQMVCDATKVPQWCLKGKWITI  
Superfamilies PLN00193

Name	Accession	Description	Interval	E-value
PLN00193 super family	cl33423	expansin-A, Provisional	2-208	9.17e-109

## SEQUENCES

### Peptide

>BosEXPA-05

MQAHATFYGGSAASGTMALSTALFNDGKSCGGCYQMVCDATKVPQWCLKGKWITI  
TATNFCPPNYALPNDNGGWCNPPRPHFDMAQPAFETIAKYRAGIVPVLRYR VGCRRS  
GGTRFTMNGRDYFELVLISNVGGAGEISQVWIKGSKSNKWETMSRNWGSNWQSLTY  
LNGQSLSFKIQT SNGKIKTGLNVVPSNWQFGQSFKSNLNF\*

### CDS (coding sequence)

>BosEXPA-05

ATGCAAGCTCATGCAACCTTCTATGGCGGAAGTGCTGCTTCTGGTACAATGGCGT  
TAAGCACTGCATTGTTCAACGACGGCAAATCTTGTGGCGGTTGTTACCAAATGGT  
CTGTGATGCGACCAAAGTGCCACAATGGTGTCTTAAAGGCAAATGGATAACAATC  
ACAGCTACAACTTCTGTCCTCCAAATTATGCTTTACCAAATGATAATGGTGGTTG  
GTGTAACCCTCCGAGGCCTCATTTCGACATGGCTCAGCCTGCGTTTGAGACCATT  
GCTAAGTACAGAGCCGGAATAGTCCCGGTTCTCTATAGAAGGGTTCGGATGTAGA  
AGAAGCGGAGGTACGAGATTCACAATGAATGGTAGAGATTACTTCGAGCTTGTG  
CTCATCTCAAATGTAGGAGGTGCAGGTGAAATCTCCCAAGTATGGATCAAAGGCT  
CTAAAAGCAACAATGGGAAACAATGTCAAGAACTGGGGATCTAATTGGCAA  
GCCTTACTTACCTTAATGGCCAAAGTCTCTCATTCAAATCCAAACCAGTAATGG  
CAAATCAAGACAGGACTCAATGTCGTTCTTTCGAATTGGCAGTTTGGTCAGAGC  
TTCAAGAGCAACTTAACTTCTAA

### Nucleotide

>BosEXPA-05

ATGCAAGCTCATGCAACCTTCTATGGCGGAAGTGCTGCTTCTGGTACAATGGGTA  
AGTGGTTTTCTTGGGCTTAGGGTTTCTTCTCTTCCCAAGAAACCCCTCAAAG  
ATCCAAGTTCTTTAATTACAAGAAATCAATTACCCCTCAATGGTTTTGGTTCGA  
ATTCAGTTATTCGGTTAGATTAATAATGCAACCAGTCGTATAGTACATAACCTCTA  
ATATCCTTTTTTCCCGGTCTGAATTCAGGTGGAGCATGTGGTTACGGCAACCTCT  
AGACCGATGGTTACGGGACAAACACGGCAGCGTTAAGCACTGCATTGTTCAACG  
ACGGCAAATCTTGTGGCGGTTGTTACCAAATGGTCTGTGATGCGACCAAAGTGCC  
ACAATGGTGTCTTAAAGGCAAATGGATAACAATCACAGCTACAACTTCTGTCCT

CCAAATTATGCTTTACCAAATGATAATGGTGGTTGGTGTAAACCCTCCGAGGCCTC  
ATTTTCGACATGGCTCAGCCTGCGTTTGAGACCATTGCTAAGTACAGAGCCGGAAT  
AGTCCCGGTTCTCTATAGAAGGTAAAAAATAACAACCTAACTTAGATTTTATTG  
AATTTATCCGGCGTAAACTAACAAAACCGATCAAATTTTCAGTTTGGTTTCTATA  
ACCACACCGTAAATTACTTTCTAATAAGCTAGAGACTTGTCTAAGCAATATATG  
CATGTGTGCGCTAATATAAGGGTTCGTTGGGGATGATTATCCTGTAGGGTCGGAT  
GTAGAAGAAGCGGAGGTACGAGATTCACAATGAATGGTAGAGATTACTTCGAGC  
TTGTGCTCATCTCAAATGTAGGAGGTGCAGGTGAAATCTCCAAGTATGGATCAA  
AGGCTCTAAAAGCAACAAATGGGAAACAATGTCAAGAACTGGGGATCTAATTG  
GCAAAGCCTTACTTACCTTAATGGCCAAAGTCTCTCATTCAAATCCAAACCAGT  
AATGGCAAATCAAGACAGGACTCAATGTCGTTCCCTTCGAATTGGCAGTTTGGTC  
AGAGCTTCAAGAGCAACTTAACTTCTAA