

## IDENTIFICATION

**Species:** *Boechera stricta*

**Locus:** Bostr.7867s0661

**Gene Model:** Bostr.7867s0661.1.p

**Description:** BosEXPB-01

**Family:** Beta Expansin

**3D structure:**



## GENOME DATABASES

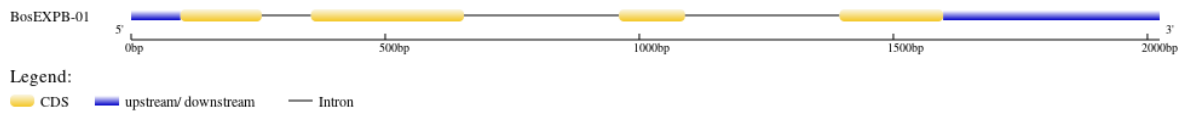
Phytozome: [https://phytozome-next.jgi.doe.gov/info/Bstricta\\_v1\\_2](https://phytozome-next.jgi.doe.gov/info/Bstricta_v1_2)

KEGG:-

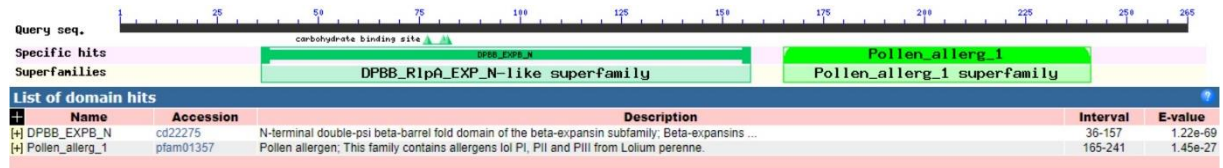
## EXTERNAL RESOURCES

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## GENE STRUCTURE



## DOMAIN ARCHITECTURE



## SEQUENCES

### Peptide

>BosEXPB-01

MLQSPVMFATIIYIVLQLLTGSYALATTHRHVSNHWLPAVATWYGSPDGDGSDGGA  
CGYGTLDVVKPLHARVGA VNPILFKNGEGCGACYKVRCLDKSICSRRAVTVIITDECP  
GCKSTSTHFDLSGAVFGRLAIAGESGPLNRGLIPVIYRRTACKYRGKNIAFHVNEGS  
TDFWLSLLVEFEDGEGDIGSMHIRQAGARDWLEMKHVWGANWCIVGGPLKGPFSIK  
LTTL SAGKTL SATDVVPRNWAPKATYTSRLNFSPVL\*

### CDS (coding sequence)

>BosEXPB-01

ATGCAGCTCTCTCCGGTCATGTTTGCTACAATCTACATTGTCCTGCAGCTTCTTAC  
CGGCTCGTACGCTTTGGCTACAACCCATCGCCACGTGTCAAACCTCTCACTGGCTTC  
CCGCAGTCGCTACATGGTACGGAAGCCCCGACGGCGACGGCAGTGATGGAGGAG  
CGTGTGGGTACGGTACGTTGGTGGATGTGAAGCCGTTACATGCGAGGGTTGGAGC  
GGTGAATCCTATTCTCTTCAAAAACGGTGAAGGCTGCGGCGCTTGTTACAAGGTT  
CGATGTTTGGACAAGAGCATTGTTCCAGGAGAGCCGTTACCGTCATAATCACCG  
ATGAGTGTCCGGGCTGCTCTAAAACCAGCACTCACTTCGACCTCAGTGGTGCCGT  
CTTCGGCCGCTTGCTATTGCCGGAGAGTCTGGCCCTCTCCGTAACCGCGGACTC  
ATCCCCGTCATTTACCGCCGGACGGCATGCAAATATCGAGGGAAGAACATAGCGT  
TCCATGTGAACGAAGGATCAACTGATTTTTGGCTATCTCTGTTGGTCGAGTTTGAA  
GACGGAGAAGGAGACATTGGCTCCATGCACATTCGCCAAGCAGGAGCGAGGGAT  
TGGTTAGAGATGAAGCACGTATGGGGAGCCAACTGGTGCATCGTTGGAGGACCA  
CTCAAGGGACCATTCTCCATCAAGCTCACCACTTTGTCCGCTGGTAAAACACTCTC  
TGCCACTGACGTCGTCCCTAGAAACTGGGCTCCCAAAGCAACTTACACTTCCCGC  
CTCAACTTCTCCCCCGTCCTCTGA

### Nucleotide

>BosEXPB-01

TAACTCACTCACTCAATCTCTCTCTCACTGTCGGTAAACTAACTCCTTTACTTTT  
CCGGCTCCGATTCTGCTCCGGAAAACAACCTCCGGCAGAAAATGCAGCTCTCTCCG  
GTCATGTTTGCTACAATCTACATTGTCCTGCAGCTTCTTACCGGCTCGTACGCTTT

GGCTACAACCCATCGCCACGTGTCAAACCTCTCACTGGCTTCCCGCAGTCGCTACA  
TGGTACGGAAGCCCCGACGGCGACGGCAGTGATGGTAATTAAGACACATAATTA  
AAACTCAACTCACACTCTAGTGATATAAACTATAAGCTAATATTAATTTGTATAC  
CGGAATTGCGTATAAAATGTAGGAGGAGCGTGTGGGTACGGTACGTTGGTGGAT  
GTGAAGCCGTTACATGCGAGGGTGGAGCGGTGAATCCTATTCTCTTCAAAAACG  
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ATTTTTGACCATTGACCATTGATCTGTATCTATCTTTTTTTCTCATAGATTTTTTT  
TTTTGCATAATAAAAAAGGACGGCATGCAAATATCGAGGGAAGAACATAGCGTT  
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TCTGTACACTACTTCATAGAGCATTGAAATTC