

IDENTIFICATION

Species: *Boechera stricta*

Locus: Bostr.23794s0099

Gene Model: Bostr.23794s0099.1.p

Description: BosEXPA-16

Family: Alpha Expansin

3D structure:



GENOME DATABASES

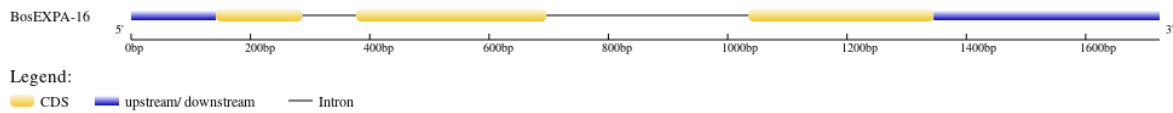
Phytozome: https://phytozome-next.jgi.doe.gov/info/Bstricta_v1_2

KEGG:-

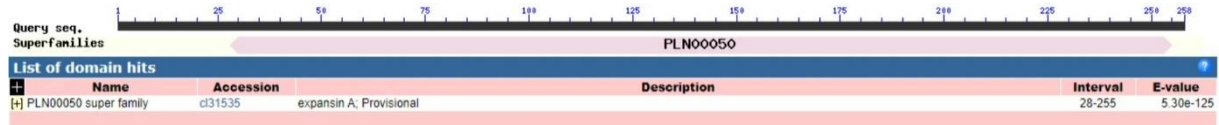
EXTERNAL RESOURCES

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GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>BosEXPA-16

MAIKLAILFTTFVLFSLADARIPGVYSGGGWQNAHATFYGGSDASGTMGGACGYGN
LYSQYGTNTAALSTALFNNGMSCGACFELKCANDPQWCHSGSPSILITATNFCPPNL
AQPSDNGGWCNPPREHFDLAMPVFLKIAQYRAGIVPVS YRRVPCRKRGGIRFTINGH
RYFNLVLITNVAGAGDIVRGSVKGSRTGWMSLSRNWQNWQSNVAVLVGQSLFRV
TGSDRRTSTSWNIVPSNWQFGQTFVGKNFRV*

CDS (coding sequence)

>BosEXPA-16

ATGGCTATTA AACTAGCAATTTTATTTACCACATTTGTCCTTTTTAGCCTCGCCGA
CGCTAGAATCCCCGGCGTTTACTCCGGTGGCGGGTGGCAAATGCACACGCCACT
TTTTACGGTGGCAGCGACGCGTCCGGCACTATGGGAGGAGCTTGTGGTTACGGTA
ACCTATACAGCCAAGGGTACGGGACCAACACGGCAGCTTTGAGCACGGCGCTGT
TTAACAACGGTATGAGTTGTGGAGCCTGCTTTGAGCTAAAATGCGCCAACGACCC
TCAATGGTGCCACTCAGGTAGTCCTTCGATCCTCATCACCGCAACCAATTTCTGCC
CACCAA AACTTGGCTCAGCCCAGCGACAACGGAGGATGGTGCAACCCACCACGTG
AACACTTTGACCTAGCCATGCCTGTCTTCCCTCAAGATCGCTCAATATCGCGCCGGC
ATTGTCCCCGTCTCATAACCGCAGGGTGCCTGTAGAAAGAGAGGTGGAATAAGGT
TCACGATCAACGGTCACCGTTACTTCAACTTGGTTCTGATCACAAACGTGGCTGG
AGCAGGAGACATCGTGAGGGGAAGCGTGAAAGGTTACGGACTGGTTGGATGAG
TTT GAGCAGGA ACTGGGGTCAA AACTGGCAATCTAACGCTGTTTTGGTTGGTCAG
TCACTTTCCCTTCCGTGTGACAGGCAGTGACCGTAGAACATCTACTTCATGGAACA
TCGTTCCCTTCTAACTGGCAGTTTGGTCAAACCTTTGTCGGGAAGAATTCAGGGTT
TAA

Nucleotide

>BosEXPA-16

TAACAAACCTTACTCTTTCTCTAAACAAGAGCGCAAGCTCGCAAAGCGCTCTTGT
TCTTTCTTCATTTTCTCCTTTAACTCTTTTATTGCTCACCTCTCATAGTAATTTAG
AACCTTTTCTAATAATTTACACACAAAATGGCTATTA AACTAGCAATTTTATT
TACCACATTTGTCTTTT TAGCCTCGCCGACGCTAGAATCCCCGGCGTTTACTCCG
GTGGCGGGTGGCAA AATGCACACGCCACTTTTTACGGTGGCAGCGACGCGTCCGG

CACTATGGGTCAGTCCATAAAAAACAGAGCATATATACTTCAAAAGAGTACTTTC
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GGCGCTGTTTAACAACGGTATGAGTTGTGGAGCCTGCTTTGAGCTAAAATGCGCC
AACGACCCTCAATGGTGCCACTCAGGTAGTCCTTCGATCCTCATCACCGCAACCA
ATTTCTGCCCACCAAACCTGGCTCAGCCCAGCGACAACGGAGGATGGTGCAACCC
ACCACGTGAACACTTTGACCTAGCCATGCCTGTCTTCCTCAAGATCGCTCAATATC
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CAACAGTTGAACCACAAATAATTTAGAAGCATTTTTTTGTGTTTGTGTGTATTATGT
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CATG