

IDENTIFICATION

Species: *Boechera stricta*

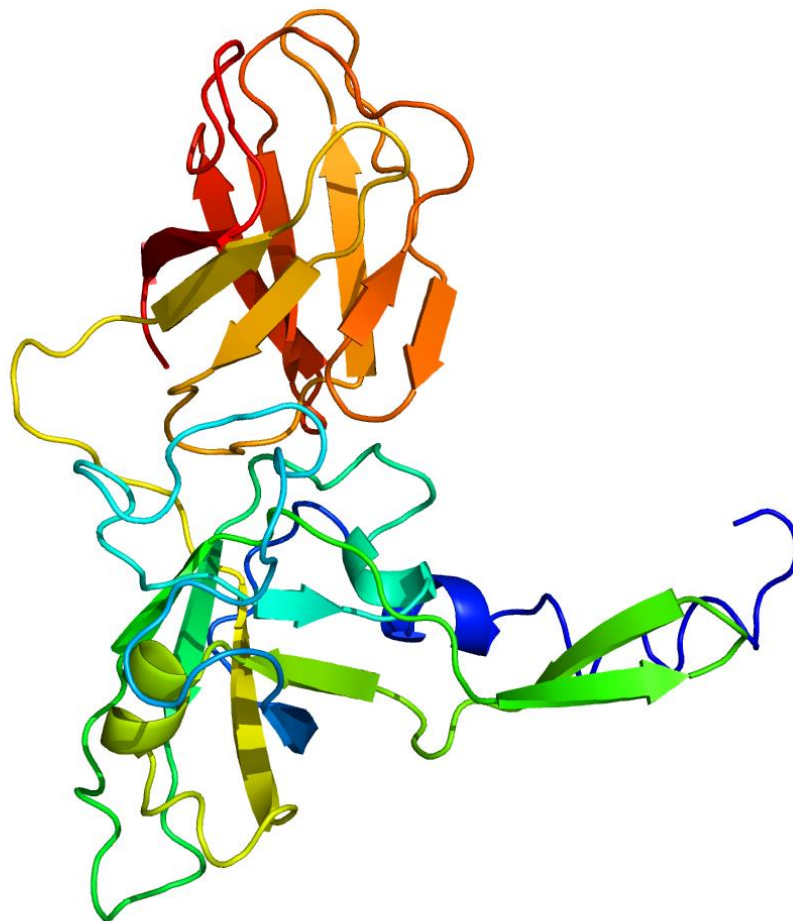
Locus: Bostr.13129s0435

Gene Model: Bostr.13129s0435.1.p

Description: BosEXPA-12

Family: Alpha Expansin

3D structure:



GENOME DATABASES

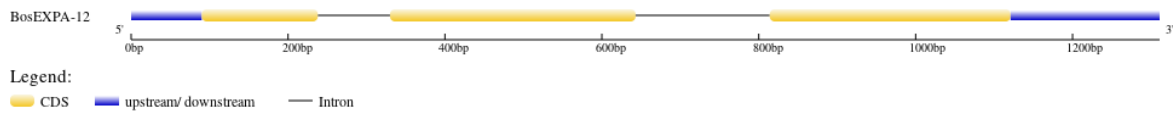
Phytozome: https://phytozome-next.jgi.doe.gov/info/Bstricta_v1_2

KEGG:-

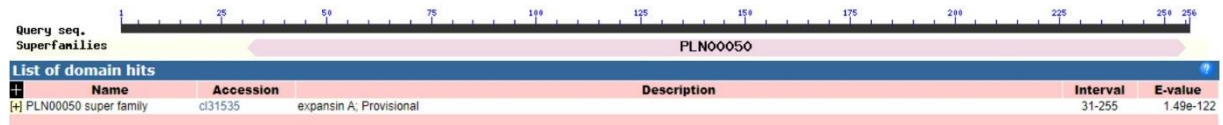
EXTERNAL RESOURCES

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GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>BosEXPA-12

MNLIEYSQILFVSLCTLNFFFYVINSDDNNGGWERGHATFYGGADASGTMGGACGYG
NLYSQGYGLQTAALSTALFNSGQRCGACFELQCEDDPEWCIPGSIIVSATNFCPPNFA
LANDNNGWCNPPLKHFDLAEP AFLQIAQYRAGIVPVAFRRVPCEKGGGIRFTINGNSY
FDLVLITN VGGAGDIRAVSLKGSKTNQWQSMSRNWQNWQSNTYIGGQTL SFQVTG
SDGQAVVSYDVVPHDWQFGQTFEGGQF*

CDS (coding sequence)

>BosEXPA-12

ATGAATCTTATAGAATATTCCCAGATTTTATTTGTTTCACTTTGTACCCTCAACTTC
TTTTTCTACGTTATAAACTCCGACGACAACGGAGGCTGGGAGAGAGGCCATGCTA
CCTTCTACGGCGGAGCTGATGCATCCGGCACAATGGGTGGTGCATGTGGGTACGG
TAACTTGTACAGCCAAGGCTATGGGCTACAAACCGCGGCTCTGAGCACGGCTTTG
TTCAATAGCGGACAGAGATGTGGGGCTTGCTTTGAGCTACAGTGTGAGGATGATC
CTGAGTGGTGCATCCCTGGTTCATCATCGTCTCAGCTACAACTTCTGTCCACCA
AACTTTGCCTTAGCCAATGATAATGGTGGTGGTGAATCCTCCCCTCAAGCACTT
TGACTTAGCCGAGCCTGCCTTCCTCCAAATTGCTCAGTACCGAGCTGGGATCGTTC
CTGTGCGATTTAGAAGGGTTCCATGTGAGAAAGGTGGAGGTATAAGGTTCCACAAT
AAACGGGAATTCGTATTTTCGACCTGGTGGTGCATCACAACGTGGGTGGTGGTGGG
GATATAAGGGCCGTCTCTTTGAAAGGCTCAAAGACTAATCAGTGGCAATCCATGT
CAAGAACTGGGGACAGAATTGGCAAAGCAACACTTACATCGGAGGTCAAACCC
TCTCTTTTCAAGTCACTGGTAGTGATGGTCAGGCTGTTGTGAGCTACGATGTTGTG
CCTCATGATTGGCAGTTCGGTCAAACCTTTTGAAGGCGGACAATTCTAG

Nucleotide

>BosEXPA-12

ATGCAGTAGTGAACCTCCCTAAACCCTATATAAGTGAAGTCTTCAACGAATTACCA
ACCTCACTCATCTCCGAATTATCCCATCAGAATCATGAATCTTATAGAATATTCC
CAGATTTTATTTGTTTCACTTTGTACCCTCAACTTCTTTTTTCTACGTTATAAACTCC
GACGACAACGGAGGCTGGGAGAGAGGCCATGCTACCTTCTACGGCGGAGCTGAT
GCATCCGGCACAATGGGTACTTATAACATACTTTTTCCATGAGCTCACAATCAT
CACAATTTGATATTTAACATATTTAGCCGCTGAAGTGTGAGGTTTTTTGTAGGTG

GTGCATGTGGGTACGGTAACTTGTACAGCCAAGGCTATGGGCTACAAACCGCGGC
TCTGAGCACGGCTTTGTTCAATAGCGGACAGAGATGTGGGGCTTGCTTTGAGCTA
CAGTGTGAGGATGATCCTGAGTGGTGCATCCCTGGTTCATCATCGTCTCAGCTA
CAAACCTTCTGTCCACCAAACCTTTGCCTTAGCCAATGATAATGGTGGTTGGTGCAA
TCCTCCCCTCAAGCACTTTGACTTAGCCGAGCCTGCCTTCCTCCAAATTGCTCAGT
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AAAACCTGTACGTACCACTTATGTCCTCTTTAATGACAGGGTTCATGTGAGAAA
GGTGGAGGTATAAGGTTTACAATAAACGGGAATTCGTATTTTCGACCTGGTGCTGA
TCACAAACGTGGGTGGTGCTGGAGATATAAGGGCCGTCTCTTTGAAAGGCTCAA
GACTAATCAGTGGCAATCCATGTCAAGAACTGGGGACAGAATTGGCAAAGCAA
CACTTACATCGGAGGTCAAACCCTCTCTTTTCAAGTCACTGGTAGTGATGGTCAG
GCTGTTGTGAGCTACGATGTTGTGCCTCATGATTGGCAGTTCGGTCAAACCTTTGA
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AAGAGTCAATGATTGTGTTAAGACAAGACTCTGCTTCTCATGGATCATATCCAC
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AGGGCACTTTGTATTCGTTTAGCACACAAGACCTATCCCCA