

IDENTIFICATION

Species: *Brachypodium sylvaticum*

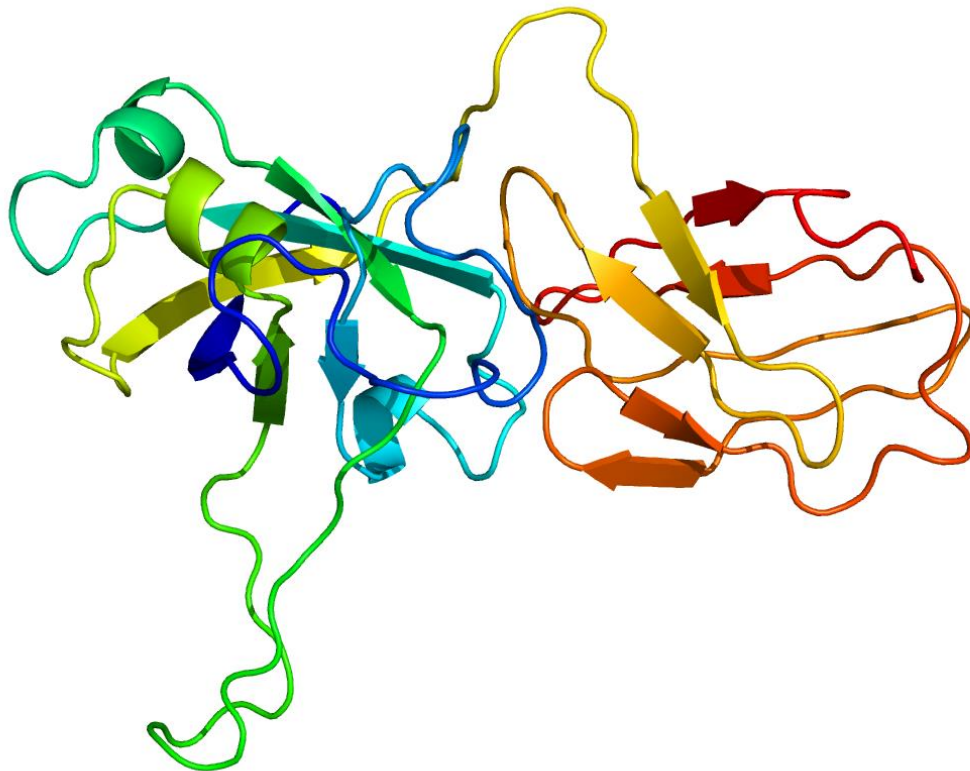
Locus: Brasy2G068000

Gene Model: Brasy2G068000.1.p

Description: BsyEXPA-07

Family: Alpha Expansin

3D structure:



GENOME DATABASES

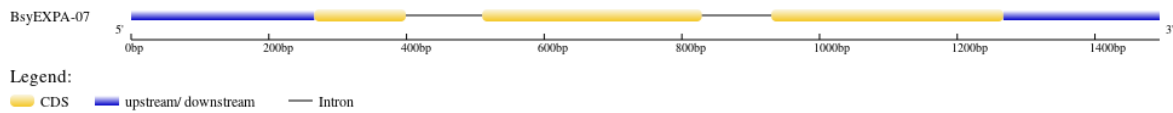
Phytozome: https://phytozome-next.jgi.doe.gov/info/Bsylvaticum_v1_1

KEGG:-

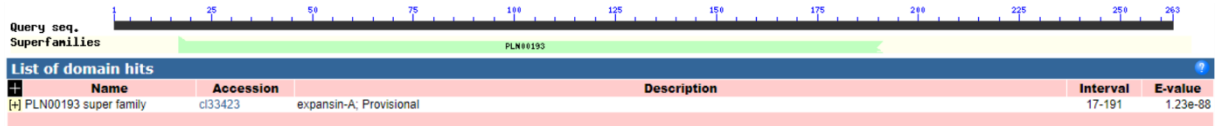
EXTERNAL RESOURCES

<http://jaiswallab.cgrb.oregonstate.edu/genomics/brasy>

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>BsyEXPA-07

MTAQRSMHLFAAVVAVVLCFAPAKSDWLPATATFYGEPDASGTMGGACGYGNLYD
QGYGVSNAALSTALFNDGASCGQCYLIICDTSKSGWCKPGTSATVSATNFCPPNWAL
PNDNGGWCNPPRVHFDMSQPSWETIAIYRAGIVPPLYQQVKCWRYGGVRFIAGFN
YFELVLVTNVLGGSGSVKSMVVKGLARGGSRRCRGTGARTGSAWPGWRSSRSASRSP
PAGSTSSSRTPCPPGGSSDRPSAPTASSTTRSRTDLN*

CDS (coding sequence)

>BsyEXPA-07

ATGACGGCGCAACGTTCCATGCATCTGTTTCGCCGCTGTTGTTGCAGTAGTACTGTG
CTTTGCGCCGGCCAAGTCCGACTGGCTGCCGGCCACCGCCACGTTCTACGGCGAA
CCCGACGCCTCCGGCACAATGGGTGGTGCCTGTGGGTACGGGAACCTGTACGACC
AGGGGTACGGGGTGAGCAACGCGGCGCTGAGCACGGCGCTGTTCAACGACGGCG
CGTCGTGCGGGCAGTGCTACCTGATCATCTGCGACACGAGCAAGTCCGGGTGGTG
CAAGCCCGGCACGTCCGCCACGGTGTCCGCCACCAACTTCTGCCCGCCAACTGG
GCGCTCCCCAACGACAACGGCGGCTGGTGCAACCCTCCCCGCGTCCACTTCGACA
TGTCCCAGCCTTCTGGGAGACCATCGCCATCTACCGCGCCGGCATCGTCCCCGT
CCTTACCAACAGGTGAAGTGTGGAGGTACGGAGGGGTGAGGTTACCATTGCC
GGGTTCACTACTTCGAGCTGGTGCTGGTGACCAACGTCGGGGGGAGCGGGTCCG
TGAAGAGCATGGCCGTGAAGGGACTGGCACGGGGTGGATCCAGATGTCGAGGAA
CTGGGGCGCGAACTGGCAGTGCTTGGCCGGGCTGGAGAAGCAGCCGCTCAGCTT
CGCGCTCACCTCCACCGGCGGGCAGTACCTCGTCTTCCAGGACGCCGTGCCCGCC
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AGAACGAGAGATTAAATTGA

Nucleotide

>BsyEXPA-07

TAAGAAGGCGCAAGTCAATCCGCGGACGTTGCAGAGCCATGTGCACTCATAACGA
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CCATGCCGGCCTTAATCCATCCTGTGTTTCTATTTAAGCAGCAGCAATGTCGCAAT
CATTCTCACCTCCAAATCCAGTCGCCACAATATCCAAGCTAGCTGCGAGGCCGT

GCTATCTTGAGCAGAACACTGTCAGCTGAAGAGATTTTCAGGAGAAGATGACGGC
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ATGCATGCATGTA AAAATGTGAAAATTTTAAGATGTGATCTGATTTCTGAATAATG
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CCAACGACAACGGCGGCTGGTGAACCCTCCCCGCGTCCACTTCGACATGTCCCA
GCCTTCCTGGGAGACCATCGCCATCTACCGCGCCGGCATCGTCCCCGTCCTCTACC
AACAGTACGCAA ACTAAAGCTCGCGTCCATCAATCAAAAATATGCAGTTCAGGACC
CGATGGATGAACTTACTAATGACGATATCTTGTGGATTTGCATTGTTTCAGGGTGA
AGTGCTGGAGGTACGGAGGGGTGAGGTTACCATTGCCGGGTTCAACTACTTCGA
GCTGGTGCTGGTGACCAACGTCGGGGGGAGCGGGTCCGTGAAGAGCATGGCCGT
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CAGTGCTTGGCCGGGCTGGAGAAGCAGCCGCTCAGCTTCGCGCTCACCTCCACCG
GCGGGCAGTACCTCGTCTTCCAGGACGCCGTGCCCGCCGGGTGGCAGTTCGGACA
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TGTTTAC