

IDENTIFICATION

Species: *Phaseolus vulgaris*

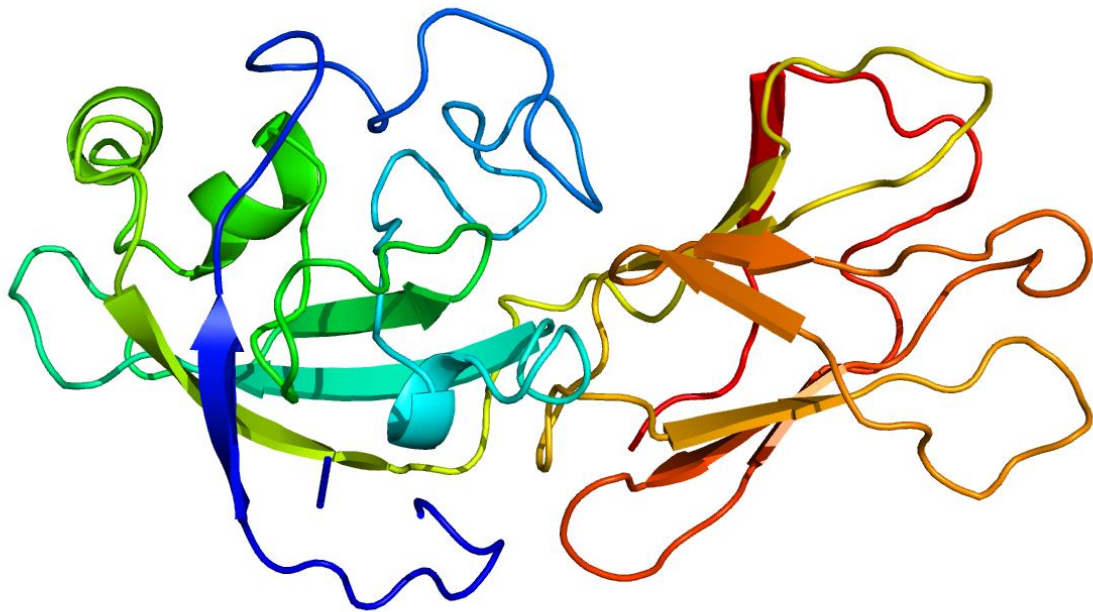
Locus: Phvul.007G235300

Gene Model: Phvul.007G235300.1.p

Description: PvEXPA-13

Family: Alpha Expansin

3D structure:



GENOME DATABASES

Phytozome: https://phytozome-next.jgi.doe.gov/info/Pvulgaris_v2_1

KEGG: <https://www.genome.jp/entry/gn:T03093>

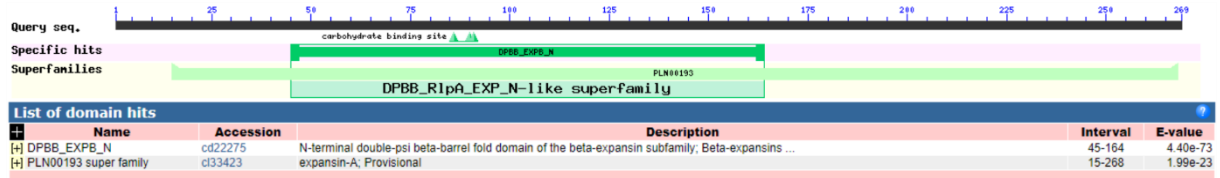
EXTERNAL RESOURCES

<https://www.pulsedb.org/organism/636>

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>PvEXPA-13

MSPTHKPAFSLNLLASLSILLVVPSSCFNPKKIANASIDSSNWSPGVATWYGPANG
DGSEGGACGYGSTVGVPPFSSMIAAGSPPLFESGKGCSCYQVKCRGNEACSGKPVR
VVITDLCPECEAAHFDLSGAAFGAMAVPGQGNQLRNAGKIVIEYSKVECEYRGMSIA
FRVDSGSNQEYFAVMVEYEEGDGELDKVELKEESAGSWIPMQKSWGAVWKFNKGS
PLRAPLSIKLTNFRSRKTVVASNVIPHGWTGHTYRSNVNF*

CDS (coding sequence)

>PvEXPA-13

ATGTCTCCTACACATAAACCTGCATTCTCTCATTCACTCAATCTTTTGGCTTCACTT
TCAATACTCCTAGTGGTCCCTTCTTGTTCACACCCCAAAAAAATTGCTAATGC
TTCCATTGATTCATCCAATTGGTCACCTGGTGTGGCTACTTGGTATGGACCTGCCA
ATGGGGATGGAAGTGAAGGTGGTGTGTTATGGCAGCACTGTTGGGGTGCC
TCCATTCTCATCAATGATAGCAGCAGGAAGCCCTCCATTGTTTGAATCAGGCAA
GGCTGTGGTTCTTGTACCAGGTGAAGTGCAGAGGGAATGAAGCGTGCTCAGGCA
AACCTGTGAGGGTAGTGATCACTGATCTGTGTCCTGAATGTGAAGCCGCACATTT
TGATTTGAGTGGTGTGCTTTTGGTGCAATGGCAGTTCCAGGGCAAGGCAATCAG
CTACGCAATGCTGGCAAATAGTCATTGAATACAGCAAGGTTGAATGCGAGTATC
GCGGCATGTCAATAGCTTTTCGTGTGGACTCTGGATCGAACCAAGAATATTTTGC
AGTGATGGTTGAATACGAGGAGGGAGATGGTGAACCTTGACAAGGTTGAACTGAA
GGAAGAATCTGCAGGATCATGGATTCCCATGCAAAAATCTTGGGGTGCAAGTTTGG
AAATTTAACAAAGGGTCACCACTGAGAGCACCATTATCTATCAAGCTAACCAACT
TTAGGTCTAGGAAGACTGTTGTGGCTAGCAATGTCATCCCTCATGGTTGGACACC
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Nucleotide

>PvEXPA-13

GCACCTAAGGGAAGTAACAGCATCCCAGTGATACTGTCATAACTAATATGTCTCC
TACACATAAACCTGCATTCTCTCATTCACTCAATCTTTTGGCTTCACTTTCAACT
CCTAGTGGTCCCTTCTTGTTCACACCCCAAAAAAATTGCTAATGCTTCCATTG

ATTCATCCAATTGGTCACCTGGTGTGGCTACTTGGTATGGACCTGCCAATGGGGA
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GGTTTGCATATTATGGGTGGTCCGATAACAGCCTAATAGTAGGTGGTCCGATAAG
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GTGGACTTTAACTACCTCAACCTCATGAAACCGACTCATGAGATTATGTTTGCAA
CCATTTATATACAATGAATTGTCCTCGTCTCTATGAAATCTCCAACGTTCTGTCTC
TGAAAATGGTACAAAAATTGGATTTACTCTAGAGAAAAATGATGAATTTGAATTT
TTGCAGGGTTGAATGCGAGTATCGCGGCATGTCAATAGCTTTTCGTGTGGACTCT
GGATCGAACCAAGAATATTTTGCAGTGATGGTTGAATACGAGGAGGGAGATGGT
GAACTTGACAAGGTTGAACTGAAGGAAGAATCTGCAGGATCATGGATTCCCATG
CAAAAATCTTGGGGTGCAGTTTGGAAATTTAACAAAGGGTCACCACTGAGAGCA
CCATTATCTATCAAGCTAACCAACTTTAGGTCTAGGAAGACTGTTGTGGCTAGCA
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