

IDENTIFICATION

Species: *Phaseolus vulgaris*

Locus: Phvul.008G034700

Gene Model: Phvul.008G034700.1.p

Description: PvEXPA-14

Family: Alpha Expansin

3D structure:



GENOME DATABASES

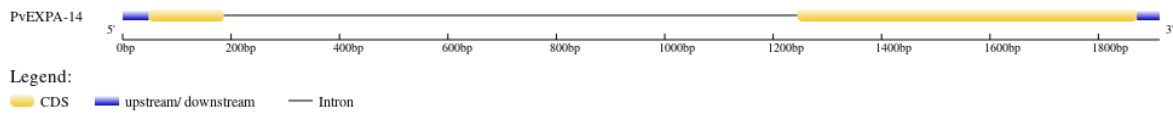
Phytozome: https://phytozome-next.jgi.doe.gov/info/Pvulgaris_v2_1

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

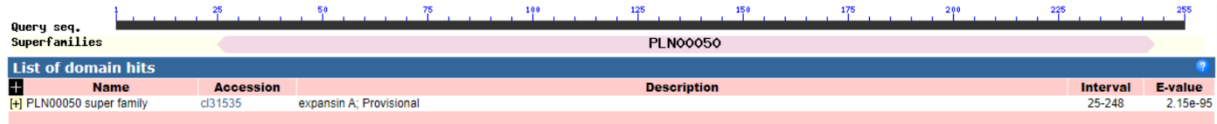
EXTERNAL RESOURCES

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

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>PvEXPA-14

MFMASSNSLLPLALLMVLCVPAFSYDSTWQSAHATFYGDMQGGETMQGACGYGNL
FQQGYGLETAALSTALFNGLSCGACFEIKCVDDPQWCIPNAGSIKVTATNFCPPNYS
SPNFDHWCNPPQKHFDLSMSMFTTIAEYKAGIIPVKYRRVPCSKSGGVKFKQTAGNPY
WLQVLLYNVGDGGDVSQVNIKGSNSNGWTSMSRVWGQNWVTGENLVGQSLSFQV
STSDGRVLEFDGAIPSNWQFGQSYEANTNF*

CDS (coding sequence)

>PvEXPA-14

ATGTTTCATGGCTTCGTCTAACAGTTTGCTTCCTTTGGCCCTTTTAATGGTTCTCTGT
GTACCAGCCTTCTCATATGACAGTACATGGCAGAGTGCCCATGCAACTTTCTATG
GTGACATGCAAGGTGGAGAAACCATGCAGGGAGCTTGTGGTTATGGTAATCTCTT
CCAGCAGGGTTACGGGCTTGAAACTGCAGCCCTAAGCACAGCACTATTCAACAAT
GGTCTGAGTTGTGGTGCATGTTTTGAGATAAAGTGTGTGGACGATCCTCAATGGT
GCATTCCAAATGCAGGCTCAATCAAAGTGACTGCAACAAATTTCTGTCCTCCCAA
TTACTCCTCACCAAATTTTGACCATTGGTGCAACCCTCCGCAGAAACACTTTGACT
TGCCATGAGTATGTTCCACCACCATGCCGAGTACAAAGCTGGGATCATCCCAGT
GAAGTATCGTCGTGTGCCATGCTCCAAATCTGGGGGTGTCAAGTTCCAAACTGCT
GGGAACCCTTATTGGCTTCAAGTTTTGCTGTACAACGTTGGCGATGGTGGTGATG
TTTCTCAGGTGAACATCAAAGGTTCCAACAGCAATGGGTGGACATCCATGTCTAG
GGTTTGGGGACAGAATTGGGTCACTGGAGAGAACTTGGTGGGGCAATCTTTGTCC
TTTCAGGTAAGTACCAGTGATGGAAGAGTGTGGAGTTTGATGGGGCTATACCTT
CCAATTGGCAATTTGGGCAGAGCTACGAGGCCAACACAAATTTTATAG

Nucleotide

>PvEXPA-14

CTTCCACTTCATCTTCTTCCTCATCTTCTTTCATCTTCTTCTCATCTCATGTTTCATGG
CTTCGTCTAACAGTTTGCTTCCTTTGGCCCTTTTAATGGTTCTCTGTGTACCAGCCT
TCTCATATGACAGTACATGGCAGAGTGCCCATGCAACTTTCTATGGTGACATGCA
AGGTGGAGAAACCATGCGTAAGTAAAACTCTCCCTCATAACTTTATATATGTAA
TATAAATTCAGTGTATCATTCTCAGTTTCTGCATATTTTTTCCATTTAATTAGTTT
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AGAGAGAGGAAGAAGAGGGGATGAAGAAGTGCATTAATTATTATTTAAAAATCA
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TAATTATAACAACAGAAGAAAAAATTATAACGACACGTAAATATATTTATAAA
CCAAGAAAACATAAAAAAGGCATAACAGATAACTTACCAAAAAATAGATTA AAAAG
TAGAAAAATGGAATATTTTTCTTAAGTATATAGAACATTCAACGTACGGAAAGAT
GCTATTTCTATTTTCATACATAAAACAATTTGGAACAACACATCTCTTTCTTCGAA
ACACAGGAAGAAGAAGATACAAAATTTGATCTGCAAATTTTCTGTCTCGAAAGA
GACAGAAAGGTAGTTTAGATATTTTTCTTTATCATTAAATTATTATTTACAAACTTT
TGTCCGTATTGCATTCAATTTTATAAATTAAGCAATATTCATTACCATACAAAAGA
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AAAACCTGCCTCCATTAATTAATTTGTATTTTTTCAAATTCTGATTACTGTTTTG
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GTTACGGGCTTGAAACTGCAGCCCTAAGCACAGCACTATTCAACAATGGTCTGAG
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GTTTCTGCTCATAAAGTTATAGGAGT