

IDENTIFICATION

Species: *Phaseolus vulgaris*

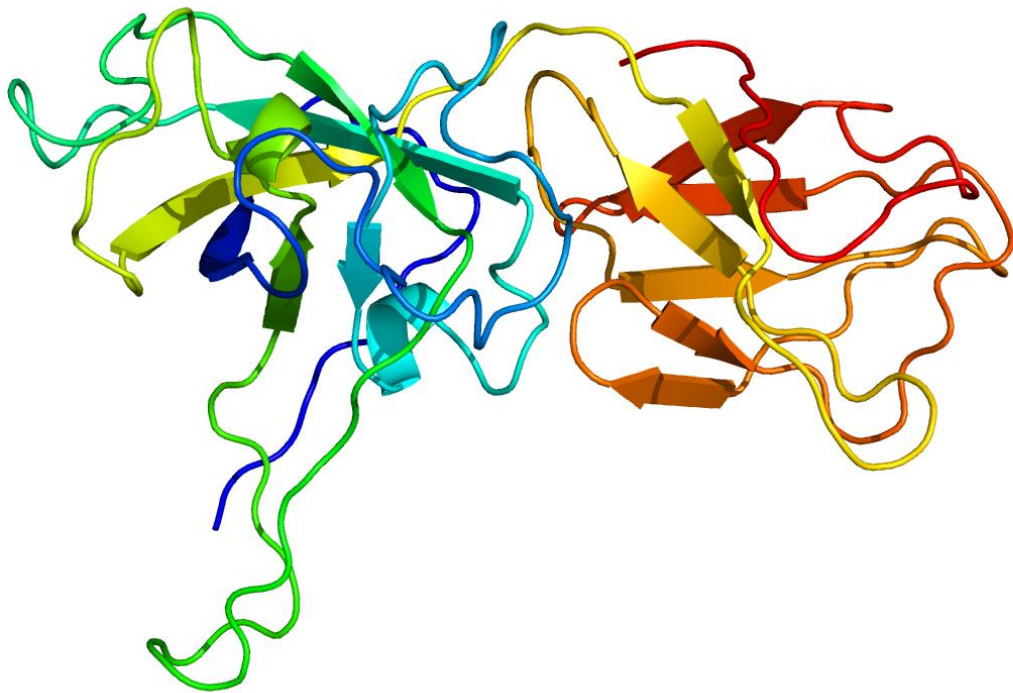
Locus: Phvul.001G232600

Gene Model: Phvul.001G232600.1.p

Description: PvEXPA-04

Family: Alpha Expansin

3D structure:



GENOME DATABASES

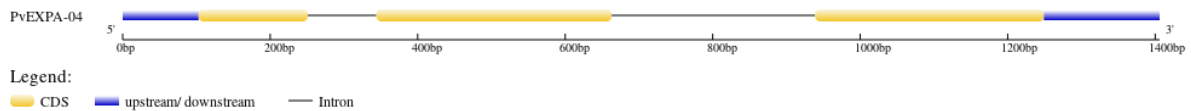
Phytozome: https://phytozome-next.jgi.doe.gov/info/Pvulgaris_v2_1

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

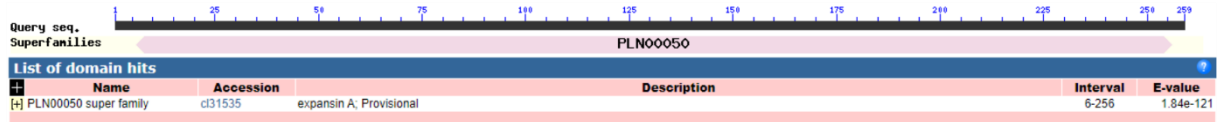
EXTERNAL RESOURCES

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

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>PvEXPA-04

MPMLNIFAIVSLLPFLTSPQAKIPGAFSGGPWQTAHATFYGGSDASGTMGGACGYGN
LYSQYGVNTAALSTALFNNGFSCGACFQIKCTHDPKWCLPGNPSIFVTATNFCPPNY
ALPSDNGGWCNPPRPHFDLAMPFLKIAQYRAGIVPVSYRRVGCRCRKEGGMRFTMNG
FRYFNLILITNVGGAGDIVRASLKGSRSGWMSMSRNWQNWQSNTVLVGQSLSFRV
TGSDDRSSTSWNIVPSNWQFGQTFGLGKNFRI*

CDS (coding sequence)

>PvEXPA-04

ATGCCGATGCTGAACATCTTTGCCATTGTCTCCCTCTTGCCCTTTCTCACTCCCTCC
CAAGCAAAAATTCCCAGCGCCTTTTCCGGTGGCCCATGGCAAACCGCTCATGCCA
CTTTCTACGGTGGCAGCGACGCCTCAGGCACTATGGGAGGGGCATGTGGGTATGG
GAACCTATACTCCCAAGGGTATGGTGTCAATACTGCGGCACTCAGCACTGCTCTG
TTCAACAATGGCTTCAGTTGTGGAGCGTGTTCCAAATTAATGCACCCATGACC
CAAATGGTGTCTTTCCCAGTAACCCTTCAATCTTCGTCACCGCCACAACTTCTGC
CCTCCTAACTACGCTCTCCCAGCGACAATGGCGGCTGGTGAACCCTCCCAGAC
CGCACTTCGACCTCGCCATGCCCATGTTCCCTTAAAAATCGCACAATATCGTGCCGG
CATCGTCCCTGTCTCTTACCGCCGGGTGGGTGCAGGAAAGAAGGAGGGATGAG
GTTACGATGAACGGATTCCGTTACTTCAACTTGATCTTGATCACCAACGTGGGA
GGTGCAGGGGATATCGTGAGGGCGAGCTTGAAAGGGTCGAGGAGCGGGTGGATG
AGCATGAGCCGCAACTGGGGGCAGAACTGGCAGTCAAACACGGTTCTGGTTGGT
CAGTCACTCTCCTTCAGGGTGACAGGCAGTGACCGACGCAGCTCCACCTCTTGA
ACATTGTCCCATCTAATTGGCAATTCGGCCAAACCTTCTTGGGCAAGAATTCAG
AATCTAG

Nucleotide

>PvEXPA-04

AGCCACTCTCCCTCCATAATAAATACATGCCAACCTTCCCTCCATTTCTCATCAC
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GATGTTTTGTAGGAGGGGCATGTGGGTATGGGAACCTATACTCCCAAGGGTATGG
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CTAATGTACTCTACTCCTTAAAATGGTAGAAAATAGTAACAATTATGGGAATAAA
ACCCACAACACGCTCACGTGAATATTAAGAGAAACAGTAATTTGAGTTAATTA
TACATGTCTAGAATGAATTATGGTTAAATGGTTGGAATTATATTAATGTATGAAA
GAATGAATAAATAATATGTGCATTGTGTGAATGATTGGGTGTGGTGGGATGCAGG
GTGGGTTGCAGGAAAGAAGGAGGGATGAGGTTACGATGAACGGATTCCGTTAC
TTCAACTTGATCTTGATCACCAACGTGGGAGGTGCAGGGGATATCGTGAGGGCGA
GCTTGAAAGGGTTCGAGGAGCGGGTGGATGAGCATGAGCCGCAACTGGGGGCAGA
ACTGGCAGTCAAACACGGTTCTGGTTGGTCAGTCACTCTCCTTCAGGGTGACAGG
CAGTGACCGACGCAGCTCCACCTCTTGGAACATTGTCCCATCTAATTGGCAATTC
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GTGTTTGGATCCTTTATGTTTTGTTTTACCATTTTTCTTTTTGGTTGCTTATTTACAC
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