

IDENTIFICATION

Species: *Phaseolus vulgaris*

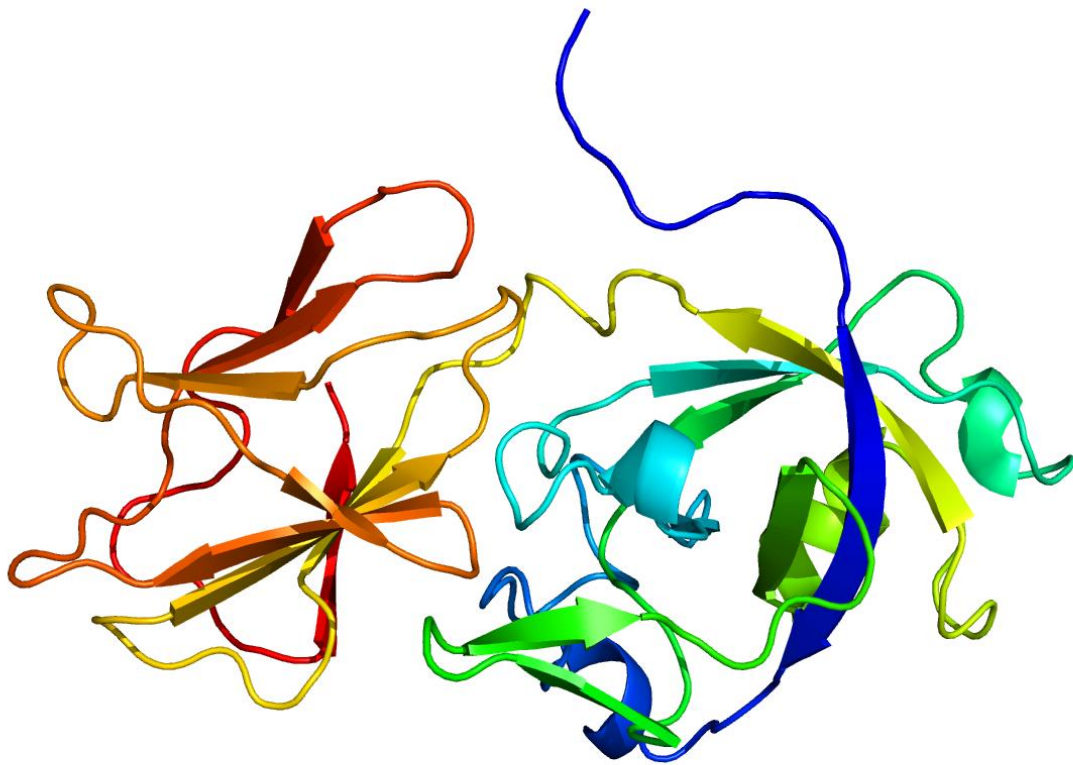
Locus: Phvul.011G117600

Gene Model: Phvul.011G117600.1.p

Description: PvEXPA-26

Family: Alpha Expansin

3D structure:



GENOME DATABASES

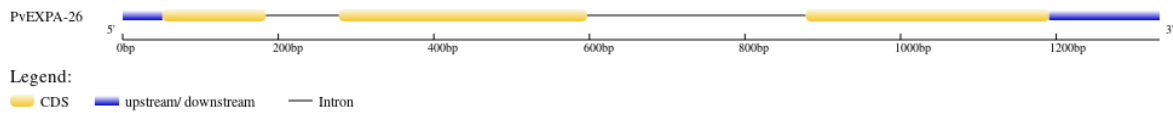
Phytozome: https://phytozome-next.jgi.doe.gov/info/Pvulgaris_v2_1

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

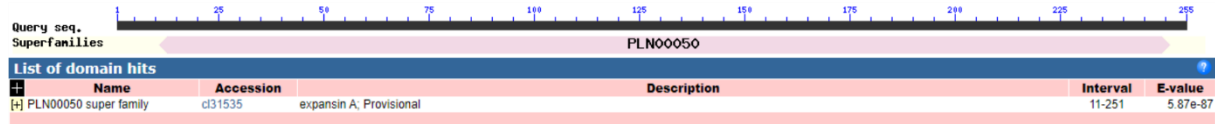
EXTERNAL RESOURCES

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

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>PvEXPA-26

MGALQSTLLYLILLHSCRIVAYSNQEWKKATATYAKDSEGLVTEGACGYGDLHKE
SYGKHSAGLSTMLFNRGSTCGACYEIRCVDHILWCVMGSPSVVVTVTDFCAPNYGLS
VDYGGWCNFPREHFEMSKTAF AEIAKNKADIVPVQYRRVKCERSGGVRFMSGGSH
FYQVLISNVGVDGEVIAVKVKGSRGTGWIPMARNWGNWHCNVNFQNPQLSFEVTIS
GGKTLTSYVAPAKWMLGQTFEGKQFQDE*

CDS (coding sequence)

>PvEXPA-26

ATGGGTGCTCTTCAGTCTACACTTCTCTACTTGATTTTACTACACTCATGCAGGAT
TGTTGCTTACAGTAACCAAGAGTGGAAGAAAGCCACTGCAACGTATGCCAAAGA
CTCAGAGGGGTCTCTTGTACCGAAGGAGCTTGTGGTTATGGAGATCTCCACAAG
GAAAGTTATGGGAAACACAGTGCTGGCTTAAGCACCATGTTGTTCAACAGAGGG
AGCACATGTGGTGCCTGCTATGAGATTAGATGTGTTGACCACATCTTGTGGTGTG
TGATGGGAAGCCCTTCTGTAGTTGTTACTGTTACAGATTTCTGTGCTCCAAATTAT
GGGCTTTCAGTTGATTATGGTGGCTGGTGCAATTTTCCAAGAGAACATTTTGAGA
TGTCAAAGACTGCATTTGCTGAAATTGCCAAGAATAAAGCTGATATAGTGCCGGT
TCAGTATAGAAGAGTAAAGTGTGAAAGAAGTGGTGGCGTGAGATTCACAATGAG
TGGGGGTTCTCACTTCTATCAAGTGCTGATTTCCAATGTTGGTGTGGATGGTGAAG
TGATTGCTGTGAAAGTGAAGGGGTCTAGAACAGGATGGATACCAATGGCAAGGA
ACTGGGGACAAAACACTGGCACTGCAATGTCAACTTTCAGAATCAGCCTTTGTCTT
TGAGGTAACAATCAGTGGTGGAAAAACACTCACATCTTACAATGTAGCACCCGCA
AAGTGGATGTTAGGACAGACATTTGAAGGAAAACAGTTTCAGGATGAGTAG

Nucleotide

>PvEXPA-26

AAAGAATTTCAATTTAAAGTATTAATCAGTTTCTAAGCTCTATTTTCTCAGATGGG
TGCTCTTTCAGTCTACACTTCTCTACTTGATTTTACTACACTCATGCAGGATTGTTGC
TTACAGTAACCAAGAGTGGAAGAAAGCCACTGCAACGTATGCCAAAGACTCAGA
GGGGTCTCTTGTACCGGTA CACTTCTCTGTCTCCTTGGTTCTTCTTAGATAGTCT
CAGGATGAAAACAACATCATGTTTTTGACAATGTGGTTGTACTATGTGTTGCAGA
AGGAGCTTGTGGTTATGGAGATCTCCACAAGGAAAGTTATGGGAAACACAGTGC

TGGCTTAAGCACCATGTTGTTCAACAGAGGGAGCACATGTGGTGCCTGCTATGAG
ATTAGATGTGTTGACCACATCTTGTGGTGTGTGATGGGAAGCCCTTCTGTAGTTGT
TACTGTTACAGATTTCTGTGCTCCAAATTATGGGCTTTCAGTTGATTATGGTGGCT
GGTGAATTTTCCAAGAGAACATTTTGAGATGTCAAAGACTGCATTTGCTGAAAT
TGCCAAGAATAAAGCTGATATAGTGCCGGTTCAGTATAGAAGGTAACCAAATA
AAAGTTTCAATGGTAAAGATTCATTACATTTAGGGTAAAATCTGTTTTAGGAGTT
CTATTTTCAGTCAAAATTGGTCTTGACCTTAAAAACATGATTTTTTTTTGTATTTCT
GATATTTTGAGAATTTTATCCTTCACCCCAACTGTTTTGGTAACTGTAAAAGAAC
GAAATTTAGCATGTAACATATAAGACCAAATATTTGGTAAAAGTGAAGAGACT
TAAAGCACATTTGAGTCTATTATGTTAATATTTAAGTTTGTGTTAGAGTAAAGTGT
GAAAGAAGTGGTGGCGTGAGATTCACAATGAGTGGGGGTTCTCACTTCTATCAAG
TGCTGATTTCCAATGTTGGTGTGGATGGTGAAGTGATTGCTGTGAAAGTGAAGGG
GTCTAGAACAGGATGGATACCAATGGCAAGGAAGTGGGGACAAAAGTGGCACTG
CAATGTCAACTTTCAGAATCAGCCTTTGTCCTTTGAGGTAACAATCAGTGGTGGGA
AAAACACTCACATCTTACAATGTAGCACCCGCAAAGTGGATGTTAGGACAGACAT
TTGAAGGAAAACAGTTTCAGGATGAGTAGATTCACAAGTCTAGATAGGATAAGTT
TTGGGGAGGCTTGAATTTTAACTTTATAAGCTGTAATTGTAAACCATGATTAGTG
AAATCACCTGTCAAAGAGCACAAGCTTAATTGTATATATATATATATTTGCTCATGA
TTCAT