

IDENTIFICATION

Species: *Phaseolus vulgaris*

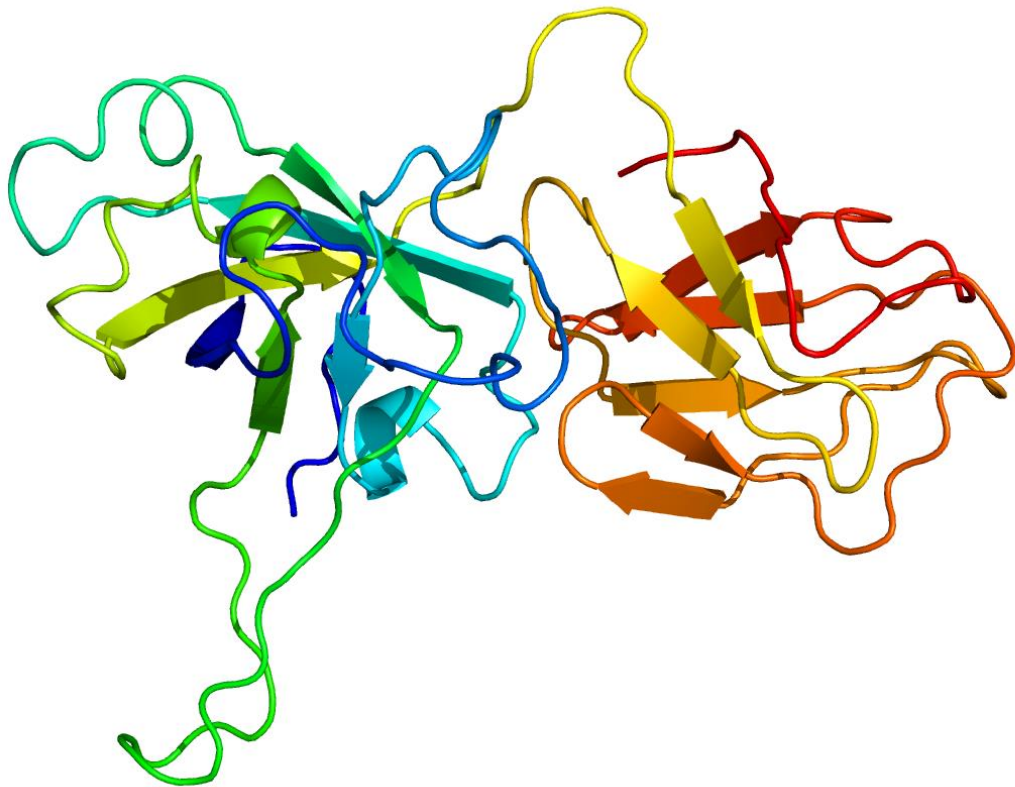
Locus: Phvul.L006043

Gene Model: Phvul.L006043.1.p

Description: PvEXPA-27

Family: Alpha Expansin

3D structure:



GENOME DATABASES

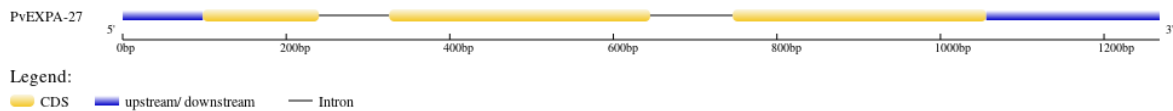
Phytozome: https://phytozome-next.jgi.doe.gov/info/Pvulgaris_v2_1

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

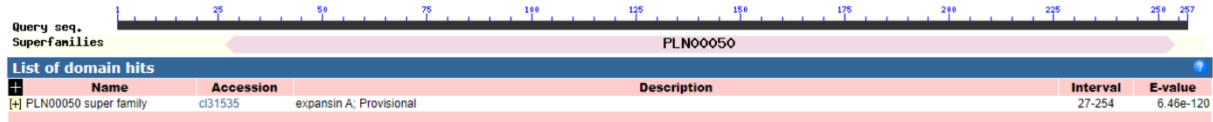
EXTERNAL RESOURCES

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

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>PvEXPA-27

MAVLGIALCFASIMWMVDARIPGVYTTGGAWQSAHATFYGGSDASGTMGGACGYGN
LYSQYGVNTAALSTALFNGLSCGACFEIKCANDKEWCHSGSPSIFITATNFCPPNY
ALPNDNGGWCNPPRPHFDLAMPMLKIAEYRAGIVPVA YRRVACMKHGGIRFTINGF
RYFNLVLISNVAGAGDLVHAYVKGTRSGWMPMSRNWQNWQSNVAVLVGQALSFR
VTASDRRSSTSWNIAPPHWQFGQTFTGKNFRV*

CDS (coding sequence)

>PvEXPA-27

ATGGCTGTGCTCGGTATAGCACTGTGCTTTGCATCCATAATGTGGATGGTGGACG
CTCGAATTCCAGGCGTTTATACCGGCGGCGCGTGGCAAAGTGCTCACGCCACCTT
CTACGGAGGATCCGATGCTTCCGGCACAATGGGGGGAGCTTGCGGGTACGGAAA
CCTGTACAGCCAAGGGTACGGAGTGAACACGGCGGCGTGTGAGCACAGCACTGTT
CAACAATGGGCTGAGCTGCGGAGCGTGTTTTGGAGATAAAATGCGCGAACGACAA
GGAGTGGTGTCACTCCGGAAGCCCTTCCATCTTCATCACTGCCACCAACTTCTGTC
CTCCGAACTACGCTCTTCCCAACGACAATGGCGGCTGGTGAACCCTCCTCGCCC
TCACTTCGACCTCGCCATGCCCATGTTCTCAAATCGCCGAATACCGCGCCGGC
ATCGTACCTGTGGCGTACCGCAGGGTGGCATGTATGAAGCATGGGGGAATAAGG
TTCACGATCAACGGTTTCCGTTACTTCAACTTGGTGTGCTGATCAGCAACGTGGCGG
GTGCAGGGGATCTGGTGCACGCATACGTTAAAGGGACGAGAAGCGGTTGGATGC
CGATGAGCCGGAACCTGGGGTCAAACCTGGCAGTCAAACGCCGTTTTGGTGGGAC
AGGCTTTGTCTTCAGAGTCACCGCCAGTGACCGTCGCTCTTCCACCTCTTGGAAC
ATTGCTCCGCCGCATTGGCAATTTGGTCAAACCTTCACTGGAAAAAACTTTTCGTGT
CTGA

Nucleotide

>PvEXPA-27

CCATAAGTACTCCACCCCTACTCGCTACCCACTCAATACTCATCTTCATTATCTCT
CTCTGCTCTGCTCTTCGCTTTCTCTTCACTTTCAACACAAAAATGGCTGTGCTCGG
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GTTTATACCGGCGGCGCGTGGCAAAGTGCTCACGCCACCTTCTACGGAGGATCCG
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CATGTGTTTTTAAACGTTTATCATTTTTCTCTAACAATGTGTGTGTTTCAGGGGGAGC
TTGCGGGTACGGAAACCTGTACAGCCAAGGGTACGGAGTGAACACGGCGGCGTT
GAGCACAGCACTGTTCAACAATGGGCTGAGCTGCGGAGCGTGTTTTGAGATAAA
ATGCGCGAACGACAAGGAGTGGTGTCACTCCGGAAGCCCTTCCATCTTCATCACT
GCCACCAACTTCTGTCTCCTCCGAACCTACGCTCTTCCCAACGACAATGGCGGCTGGT
GCAACCCTCCTCGCCCTCACTTCGACCTCGCCATGCCCATGTTCTCAAATCGCC
GAATACCGCGCCGGCATCGTACCTGTGGCGTACCGCAGGTACGCACATGTTTAAT
TCTCAAATGTTATTAATAAAGTTAGTTATAAAGTGGTTTTATTAGTTAGTTGGTGGT
GGTTAATGTGGTTTTGGTGTTTTTGTTTAGGGTGGCATGTATGAAGCATGGGGGAAT
AAGGTTACGATCAACGGTTTTCCGTTACTTCAACTTGGTGCTGATCAGCAACGTG
GCGGGTGCAGGGGATCTGGTGCACGCATACGTTAAAGGGACGAGAAGCGGTTGG
ATGCCGATGAGCCGGAACCTGGGGTCAAACTGGCAGTCAAACGCCGTTTTGGTG
GGACAGGCTTTGTCCTTCAGAGTCACCGCCAGTGACCGTCGCTCTTCCACCTCTTG
GAACATTGCTCCGCCGCATTGGCAATTTGGTCAAACCTTCACTGGAAAAAACTTT
CGTGTCTGACTCTCACACACACCTTTACTTTTTTTTTTTTTTTTTCTTTTTTTTTTTTT
TCTTAATATATATAAATATATATAAATAAAGTGAAAGTTCGTTTTCTTTTTGTTTCAGC
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ACTGCATGTTTCGGGAGACTGTGATGGAGTGCAAGGGGAAGTTGATTAGT