

IDENTIFICATION

Species: *Phaseolus vulgaris*

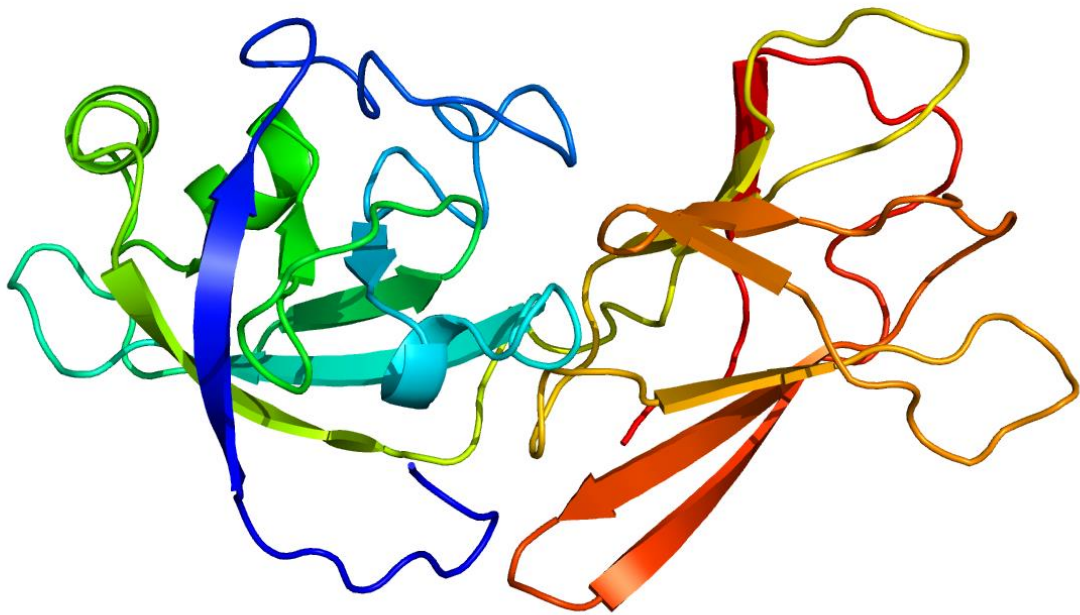
Locus: Phvul.011G024801

Gene Model: Phvul.011G024801.1.p

Description: PvEXLA-01

Family: Expansin Like Alpha

3D structure:



GENOME DATABASES

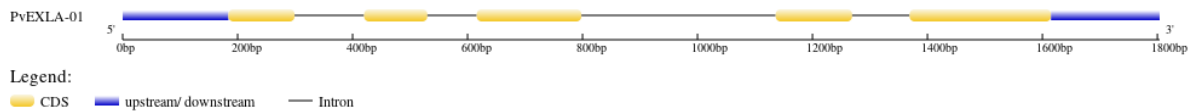
Phytozome: https://phytozome-next.jgi.doe.gov/info/Pvulgaris_v2_1

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

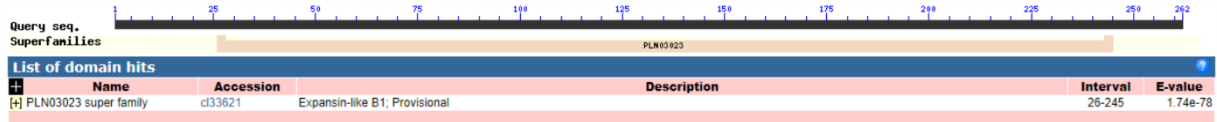
EXTERNAL RESOURCES

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

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>PvEXLA-01

MAFFLLFFLSLLASSATACDRCLHQSKASFYSRASVLSTGACGYGSLALDISGGHLAG
GVASLFFKNGAGCGACFEIRCKNPSFCSTEGTRVVLTDLSHNNETDFVLSKRAFSGM
AQKKGREILKLGIVDIEYKRVPCNYQNQLAVRVEESSKNPDYLAIKFLYQGGQTEI
VAVDVAQADSSNWSFMSRNNGAVWDTNRVPK GALQFRLVVTAGYDGKWIWAKN
VLPSDWKNGVIYDSGLQITDIAQEGCSPCDDSIWS*

CDS (coding sequence)

>PvEXLA-01

ATGGCTTTCTTTCTCCTCTTTTTCTCCTCCTTCTTGCTTCTTCTGCCACTGCTTGCG
ATCGCTGCCTGCACCAATCCAAGGCTTCTTTACTCCAGAGCTTCTGTTCTTTCA
ACTGGGGCATGTGGGTATGGCTCTTTGGCACTAGACATAAGTGGTGGACACCTTG
CAGGTGGTGTGGCCTCTCTCTCAAAAACGGAGCCGGTTGTGGTGCTTGCTTTGA
GATAAGATGCAAGAACCCGAGTTTTTGCAGCACAGAGGGTACTAGAGTGGTATT
GACTGATGATCTTAGTCACAACAATGAACTGACTTTGTGCTGAGCAAAAGAGCT
TTCTCAGGCATGGCTCAGAAGGGAAAGGGCCGAGAAATATTGAACTTGGCATT
GTTGACATTGAATACAAGAGAGTACCCTGCAACTACCAAAATCAGAATTTGGCTG
TCCGTGTAGAAGAATCAAGCAAGAATCCTGATTACTTAGCCATTAAATTTTTGTA
CCAAGGAGGTCAAACAGAGATAGTAGCCGTTGATGTGGCTCAGGCTGATTCTTCA
AACTGGAGCTTCATGAGCAGAAACAACGGGGCAGTGTGGGACACAAACAGGGTA
CCCAAAGGAGCATTGCAGTTTCGGTTAGTGGTAACAGCAGGGTATGATGGGAAG
TGGATTTGGGCAAAGAATGTCCTACCTTCTGATTGGAAAAATGGTGTCATATATG
ATTCTGGCCTTCAGATAACAGACATTGCACAAGAGGGTTGTTCCCTTGTGATGA
TTCCATCTGGTCATGA

Nucleotide

>PvEXLA-01

TTCTTTGTGCAGCCGCGTTAACTCAGTGCCTTTCCCTTTCATCCATTCTTATCTAT
TACCAAAGCTTTTTGGAAAATGCTGATCTGTCACCAATATATCAGTGTGTATATA
TATATACCTAGCTTCTTCTCCTTCTTTCTCAAACTCATCCTCAAAACAATTCAA
CATCATCCAACACACATGGCTTTCTTTCTCCTCTTTTTCTCCTTCTGCTTCTT
CTGCCACTGCTTGGGATCGCTGCCTGCACCAATCCAAGGCTTCTTTACTCCAGA

GCTTCTGTTCTTTCAAGTAACATCATTCATTCATTCATCATTTTCATTACTGTCATAA
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AGACATAAGTGGTGGACACCTTGCAGGTGGTGTGGCCTCTCTCTTCAAAAACGGA
GCCGGTTGTGGTGCTTGTCTTTGAGGTGTGTGTGCAAATCAGAAGGACCATGTACC
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CAGGCATGGCTCAGAAGGGAAAGGGCCGAGAAATATTGAAACTTGGCATTGTTG
ACATTGAATACAAGAGGTAGGCTTAAATCACTTCAGTTTTGGATAAAGTTTTATC
CTTTTCCTTTGGTTCTTCCTTTCTTTTCTTTGCTTTGCCACTGGTTTTGGCCTGAC
CCCCTCCCCACCTACCGGCCACCCACCACCTATACAGAACAATCATTGTGGAC
CAACCCTTTAATATTATGAATCCCTACCTCAATCATGTGCCACTTTAATGACAGT
AACGGTCTAATGCCTTTTATCTGCATAATAATATTTTCATGACCCTGTGTTAATCTT
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CGTGTAGAAGAATCAAGCAAGAATCCTGATTACTTAGCCATTAATTTTTGTACC
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