

## IDENTIFICATION

**Species:** *Phaseolus vulgaris*

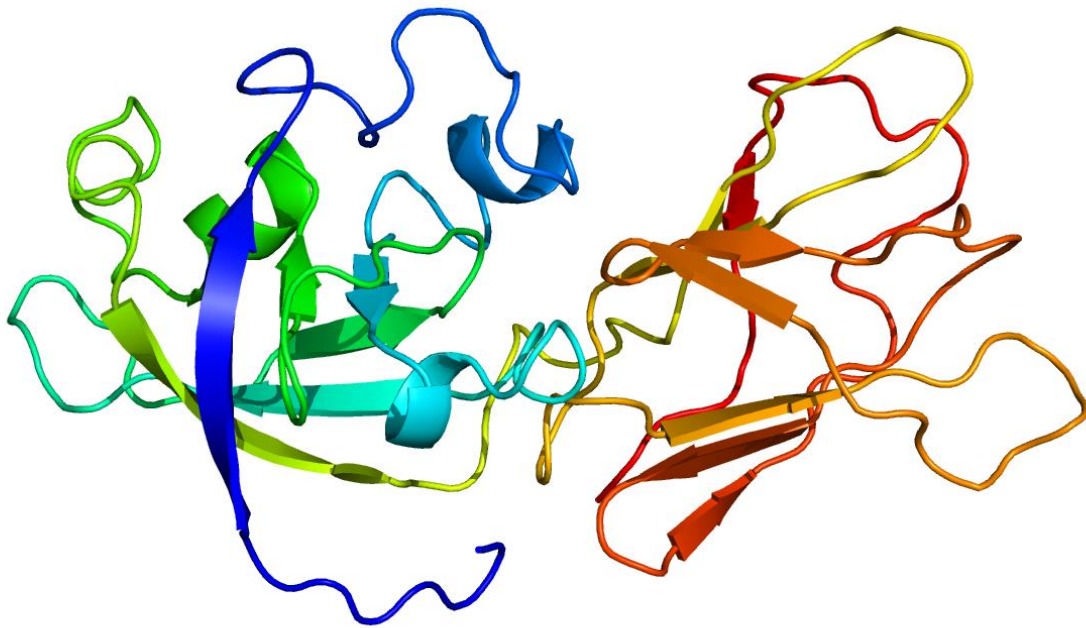
**Locus:** Phvul.003G224600

**Gene Model:** Phvul.003G224600.1.p

**Description:** PvEXLB-03

**Family:** Expansin Like Beta

**3D structure:**



## GENOME DATABASES

Phytozome: [https://phytozome-next.jgi.doe.gov/info/Pvulgaris\\_v2\\_1](https://phytozome-next.jgi.doe.gov/info/Pvulgaris_v2_1)

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

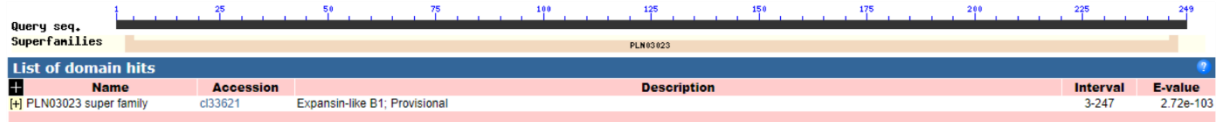
## EXTERNAL RESOURCES

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

## GENE STRUCTURE



## DOMAIN ARCHITECTURE



## SEQUENCES

### Peptide

>PvEXLB-03

MELGFKHQLGLVCVILLFPALCNCNEYFTNSRATYYGTSDGNGTPTGACGFGHEYGRK  
MNWYDGRVAGVSGLWRNGAGCGTCYQVKCKIAELCDVKGAYLVATDQGYGDRT  
DFVMSPNAFRLGGNKNASAEKLYGTVDIEYRRVPCTYIGNVLFHIKESSSNPGYLA  
VVILNVNGKYDVNAVEMWQKGERWEALRRVYGAVFDFANPPRGEILLRFQVGVK  
WMIPNIAIPANWKPGATYDTKLQLY\*

### CDS (coding sequence)

>PvEXLB-03

ATGGAAGTGGGTTTTAAGCACCAACTTGGCCTTGTTTGTGTCATACTGCTCTTCCC  
TGCCTGTGTAAGTGAATATTTACCAATTCAAGAGCAACCTATTATGGC  
ACCTCTGATGGCAACGGTACTCCAAGTGGAGCTTGTGGATTCGGGGAGTATGGAA  
GGAAGATGAATTGGTATGATGGAAGAGTCGCAGGGGTCTCTGGGCTATGGAGGA  
ATGGAGCTGGTTGTGGTACGTGTTATCAGGTAAGTGCAAAATAGCAGAACTGTG  
CGATGTGAAAGGAGCATACTGGTGGCAACAGACCAGGGTTATGGAGACAGAAC  
AGATTTCTGTGATGAGCCCAAACGCCTTCTCAAGATTGGGAGGCAATAAAAATGCA  
TCTGCAGAGCTTAAGAAATATGGTACAGTGGATATTGAATACAGGAGGGTTCCAT  
GTACCTACATCGGCAACGTCTTGTTCACATAAAGGAAAGTAGCAGCAACCCTGG  
TACTTGGCTGTTGTGATTCTGAATGTAAATGGAAAATACGATGTCAATGCTGTTG  
AAATGTGGCAGAAAGGGAAAGAACGATGGGAAGCCTTGCGCAGGGTCTATGGGG  
CAGTGTGTTGACTTTGCTAATCCACCAAGAGGTGAAATCCTATTGAGGTTTCAAGT  
GGGTGTTAAATGGATGATACCAAACATCGCTATCCCTGCTAATTGGAAGCCTGGA  
GCAACTTATGACACCAAACCTCAGCTTTACTAG

### Nucleotide

>PvEXLB-03

AATACAACCTCATGTATCTTCGCTTCCAATCTCATAAACGCTTCTCAAATCTTAT  
GCTTTGGTTTATAGCATTGGTCACAATCTCGTAATTAATTACTTCTGTATTTCTAT  
CCTATATATCTTTGCGCCTGATAGAGTTGAATTTGTCATGGAAGTGGGTTTTAAGC  
ACCAACTTGGCCTTGTGTTGTGTCATACTGCTTCCCTGCACTGTGTAAGTGAAT  
GAATATTTACCAATTCAAGAGCAACCTATTATGGCACCTCTGATGGCAACGGTA  
CTCCAAGTACGTGCTTGTCAATTTGTCTCTACCAGCCTTACACTCTTTGTTTTGCA

GCTTAGGACTCAACTACCATGCATGCCCATCTTTGAGACTAAAGATTCTCTTTTTTC  
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TACCTGGTGGCAACAGACCAGGGTTATGGAGACAGAACAGATTTTCGTGATGAGC  
CCAAACGCCTTCTCAAGATTGGGAGGCAATAAAAATGCATCTGCAGAGCTTAAG  
AAATATGGTACAGTGGATATTGAATACAGGAGGGTTCATGTACCTACATCGGCA  
ACGTCTTGTTTCACATAAAGGAAAGTAGCAGCAACCCTGGTTACTTGGCTGTTGT  
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ACAATTTGTAACTTATTGAGTAGTTTGTTAATTTTACGATGAAATTGGTTGTTGA  
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GCAGTGTTTGACTTTGCTAATCCACCAAGAGGTGAAATCCTATTGAGGTTTCAAG  
TGGGTGTTAAATGGATGATACCAAACATCGCTATCCCTGCTAATTGGAAGCCTGG  
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TGTAAGAGTGTACCCGGAATAAGAATAAGATCAAAGTTATTTTAGGCTGTC