

## IDENTIFICATION

**Species:** *Prunus persica*

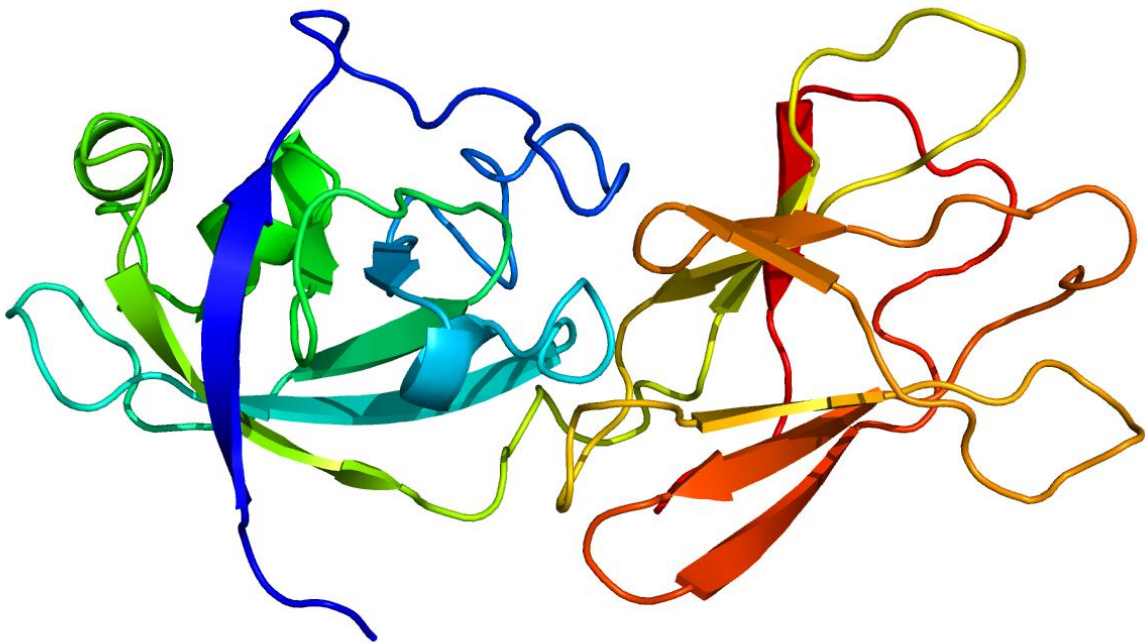
**Locus:** Prupe.8G174500

**Gene Model:** Prupe.8G174500.1.p

**Description:** PrpEXLA-01

**Family:** Expansin Like Alpha

**3D structure:**



## GENOME DATABASES

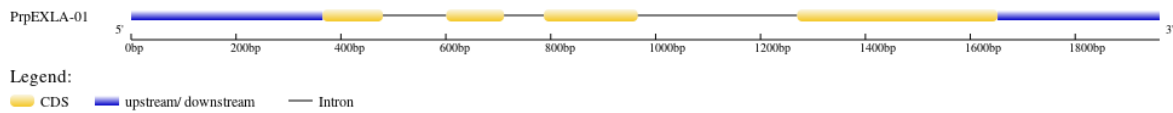
Phytozome: [https://phytozome-next.jgi.doe.gov/info/Ppersica\\_v2\\_1](https://phytozome-next.jgi.doe.gov/info/Ppersica_v2_1)

KEGG: <https://www.genome.jp/entry/gn:T03092>

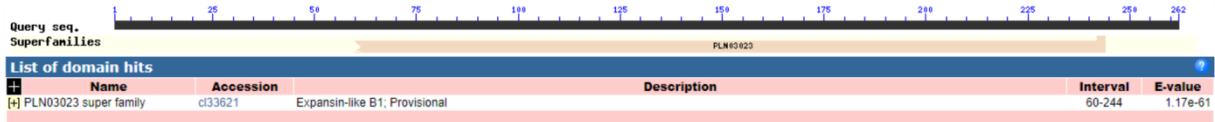
## EXTERNAL RESOURCES

[https://www.rosaceae.org/species/prunus\\_persica/genome\\_v2.0.a1](https://www.rosaceae.org/species/prunus_persica/genome_v2.0.a1)

## GENE STRUCTURE



## DOMAIN ARCHITECTURE



## SEQUENCES

### Peptide

>PrpEXLA-01

MALFLCFLFFFLISSASACDRCRHQSKAA YFSTASALSSGACGYGSLALGLGGGHLAA  
GVPSLYKDGAGCGACFQIRCKNTTLCTKQGTRVTLTDLNKSNTDFVLSSRAFMAM  
AQKGLGQDILRHGIVDVEYKRVPCYKQNLALRVEESSQKPHYLAIKILYQGGQTEI  
VAIDVAQVGSSNWGFLTRNNGAIWDTSRVPAGGLQFRFLVTAGYDGKTVWAQNVL  
PANWKPGMIYDTKVQISDIAKEGCSTTCDDGSWK\*

### CDS (coding sequence)

>PrpEXLA-01

ATGGCTTTGTTTCTTTGCTTCCTCTTCTTTCTCATCTCCTCTGCCTCTGCTTGTG  
ACCGCTGTAGGCACCAATCCAAGGCAGCCTATTTCTCCACAGCCTCTGCACTTTC  
ATCTGGGGCTTGTGGGTATGGTTCCTTGGCCTTGGGACTTGGTGGAGGACACCTT  
GCAGCTGGTGTGCCTTCCCTCTACAAAGATGGAGCTGGCTGTGGTGCATGCTTCC  
AGATAAGATGCAAGAACAACACTCTTTGCACAAAACAAGGGACCAGAGTTACTT  
TGACTGATCTCAATAAAAGTAATCAGACAGATTTTGTCTCAGCAGCAGAGCTTT  
CATGGCCATGGCTCAAAGGGTTTGGGCCAAGACATTTTGAGACACGGCATTGTC  
GATGTGGAATATAAGAGGGTACCATGTGAATACAAAACCAAATCTAGCCTTG  
CGTGTGGAAGAATCGAGCCAAAAGCCACATTACTTAGCAATCAAATTCTGTATC  
AAGGTGGTCAGACAGAAATAGTAGCCATTGATGTTGCTCAGGTTGGTTCTTCAA  
TTGGGGTTTCTGACTCGAAACAATGGGGCAATCTGGGACACGAGTAGGGTTCCG  
GCAGGGGGCCTACAGTTCCGGTTCTTGGTGACGGCCGGGTACGATGGGAAGACG  
GTTTGGGCACAGAATGTGCTCCCTGCTAACTGGAAACCTGGGATGATATATGACA  
CAAAGTTCAAATAAGTGACATTGCAAAGAGGGTTGCTCTACTACTTGTGATGA  
TGGGAGCTGGAAATGA

### Nucleotide

>PrpEXLA-01

CCAGTCTCATGTTTACACAGAGCCTTGAAAAAACTCAAAAAGAGTCGGTGACA  
GACAAAACCCATAATCTTCCACTTTTCTTTGTCCAGCATTTCAGCAATTGCCTGTC  
TCTTTCCTTCTTGTTATTATAGCTTTCCACAAATCCCCCATAATCACTTACAGCA  
AACAAACCAAACCCATACTAAATAAAAAATAAGTCCAAAGTTTTGTATTTTCAGC  
ACATGCTGACCTGTCTCCATAGTCCACAGTCCACCCTCCCTTTTCTCCAATCTTTT

GAACTATATATATAGCCACGGCTTTCTCTTCCTTTCACTATAACTTTCTGCAATC  
AATTCTGATCAGCAAATCAAACCTCCAAAATGGCTTTGTTTCTTTGCTTCCTCTT  
CTTCTTTCTCATCTCCTCTGCCTCTGCTTGTGACCGCTGTAGGCACCAATCCAAGG  
CAGCCTATTTCTCCACAGCCTCTGCACTTTCATGTAAGATCATCAGTTTCTTAATC  
TCCTTACCCTTGATGTAATTTCTCTGTTTGATTAACCCAGTTGATGATTTTGTG  
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TATGGTTCCTTGGCCTTGGGACTTGGTGGAGGACACCTTGCAGCTGGTGTGCCTTC  
CCTCTACAAAGATGGAGCTGGCTGTGGTGCATGCTTCCAGGTAATAATTTTCTTC  
TTAATTTGTTGGCTGAAATTTGTATGCCATACATTGTATTGATTTGATTTTGTGTTG  
CAGATAAGATGCAAGAACAACAACCTTTTGCACAAAACAAGGGACCAGAGTTACT  
TTGACTGATCTCAATAAAAGTAATCAGACAGATTTTGTTCAGCAGCAGAGCTT  
TCATGGCCATGGCTCAAAGGGTTTGGGCCAAGACATTTTGAGACACGGCATTGT  
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AAAGATTATTGGGCCTTATGTTTCGTTGTCAAACCACACCTCAATTGCTTTGAAGA  
GTCGTTTTATAGTGAAAG