

## IDENTIFICATION

**Species:** *Prunus persica*

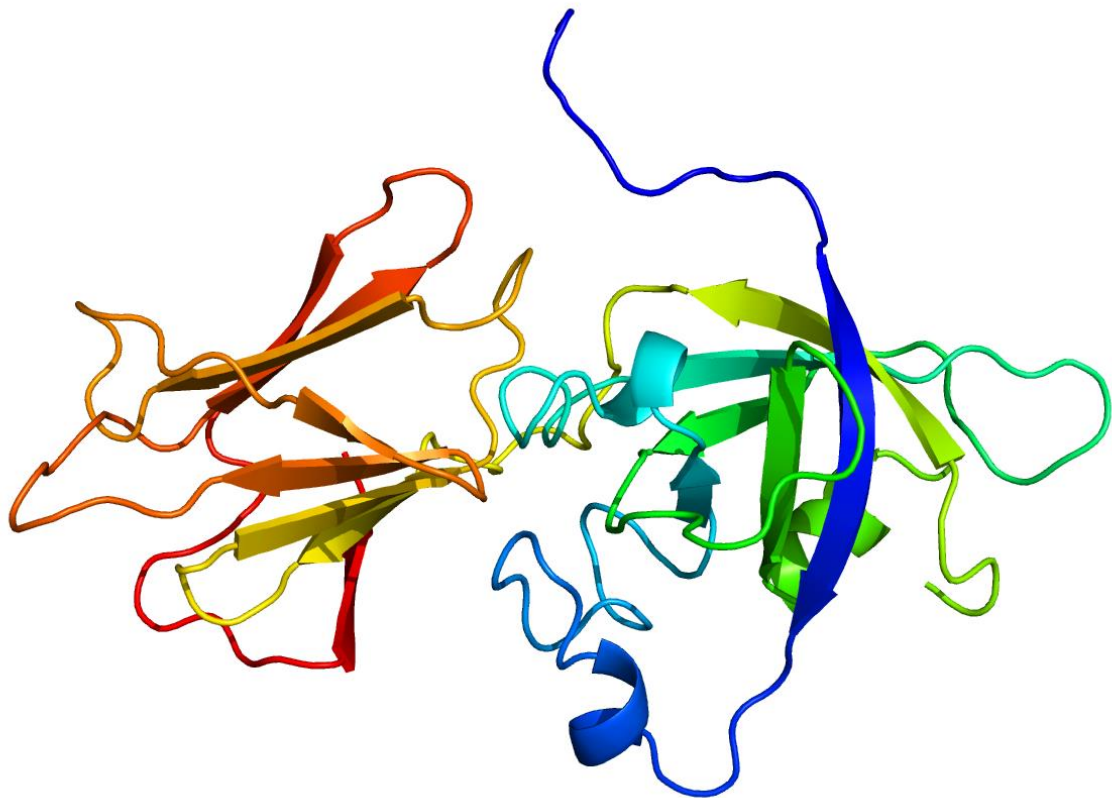
**Locus:** Prupe.5G195200

**Gene Model:** Prupe.5G195200.1.p

**Description:** PrpEXPA-14

**Family:** Alpha Expansin

**3D structure:**



## GENOME DATABASES

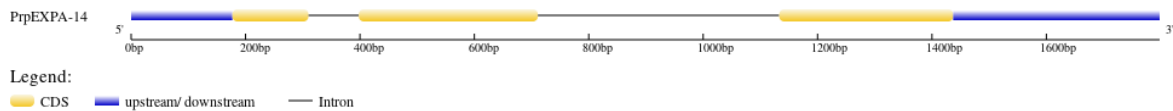
Phytozome: [https://phytozome-next.jgi.doe.gov/info/Ppersica\\_v2\\_1](https://phytozome-next.jgi.doe.gov/info/Ppersica_v2_1)

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

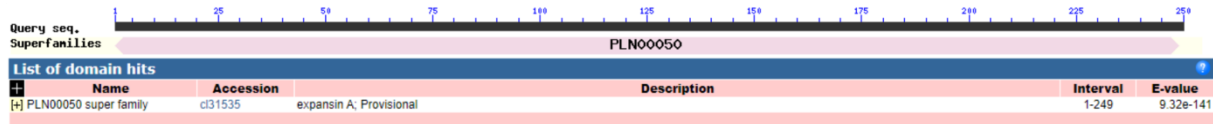
## EXTERNAL RESOURCES

[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

>PrpEXPA-14

MAVLGLALVGFLLSLSSSAYGSDGGWVNAHATFYGGGDASGTMGGACGYGNLYS  
QGYGTNTAALSTALFNGLSCGACFEIRCASDPKWCLPGSIFVTATNFCPPNNALPNN  
AGGWCNPPQQHFDLAQPVFQRIAQYRAGIVPVSYRRVPCIKKGGIRFTINGHSYFNLV  
LITNVGGAGDVHAVSIKGSKTGWQTLRSRWGQNWQSN SYLNGQSLSFKVTTSDGRT  
VVANNVAPAGWSFGQTFSGVQF\*

### CDS (coding sequence)

>PrpEXPA-14

ATGGCAGTTCTTGGGCTTGCCTTGGTTGGTTTTCTTCTTCTTTCTCTGAGCTCCTCT  
GCTTATGGCTCTGATGGGGGCTGGGTTAATGCGCATGCCACTTTCTATGGAGGAG  
GTGATGCCTCTGGCACAATGGGCGGGGCTTGTGGATATGGCAACCTGTATAGCCA  
AGGGTATGGAACCAACACAGCAGCTCTGAGCACAGCCCTGTTCAACAATGGGCT  
AAGCTGCGGGGCTTGTCTTGTAGATTAGGTGTGCGAGTGATCCAAAATGGTGTCTT  
CCAGGCTCAATTTTCGTACAGCCACCAACTTCTGCCCTCCAACAATGCCCTCCC  
CAACAATGCAGGCGGTTGGTGCAACCCTCCACAGCAACATTTTGATCTTGCCCAG  
CCAGTCTTCCAGCGGATTGCTCAATACAGAGCTGGGATTGTGCCTGTGTCTTACC  
GAAGGGTCCCATGCATAAAGAAGGGAGGCATAAGATTCACAATCAACGGCCACT  
CATACTTCAATCTGGTGCTGATCACAACGTTGGCGGTGCCGGAGATGTTTCATGC  
AGTTTCCATCAAAGGGTCAAAAACCTGGTTGGCAAACCTTGTCTAGGAACTGGGGG  
CAGAATTGGCAGAGCAACTCTTATCTGAATGGCCAGAGTCTCTCCTTCAAGGTCA  
CCACCAGCGACGGCCGCACCGTCGTCGCCAACAACGTCGCTCCTGCCGGCTGGTC  
ATTTGGCCAGACATTCAGTGGCGTACAATTCTGA

### Nucleotide

>PrpEXPA-14

CCTAAGCAAACAAAGCTCTGTTTCTCCTCCCCTCCTCCCACCATCTATTTATCCCC  
CCCACTCTCCTCCACTTCTCCTCACAACCTCACAGCCCTCCTCTGCTCCTCCTTCCCT  
TCTTTCTCTTTCTTCATTTGCTCTCTTTCTCACACTTCCAAAAGGTCTGCCTCTGCT  
TCAAAAACATGGCAGTTCTTGGGCTTGCCTTGGTTGGTTTTCTTCTTTCTCTGAG  
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CACAGCCACCAACTTCTGCCCTCCAAACAATGCCCTCCCCAACAATGCAGGCGGT  
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ATGTTTCCTTTCACACTCCACCCAAGTAACAGGGGTTTTTTTTGTAATTCAGTAAAA  
CAAATTTATAATTTCTAGTGGTTTTAGTTTCGCCACATTTAAATGGCAAGTTTTAA  
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ATCCATCTAAGTTCCATGTTTGATTTCGATCACCCCAACATATATCAGCTTTTTAAT  
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