

## IDENTIFICATION

**Species:** *Prunus persica*

**Locus:** Prupe.3G256600

**Gene Model:** Prupe.3G256600.1.p

**Description:** PrpEXPA-09

**Family:** Alpha Expansin

**3D structure:**



## GENOME DATABASES

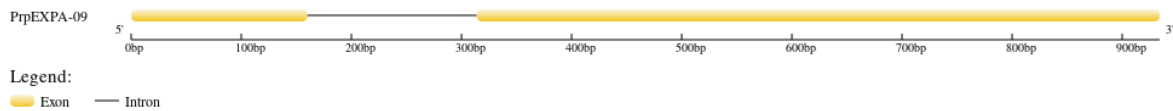
Phytozome: [https://phytozome-next.jgi.doe.gov/info/Ppersica\\_v2\\_1](https://phytozome-next.jgi.doe.gov/info/Ppersica_v2_1)

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

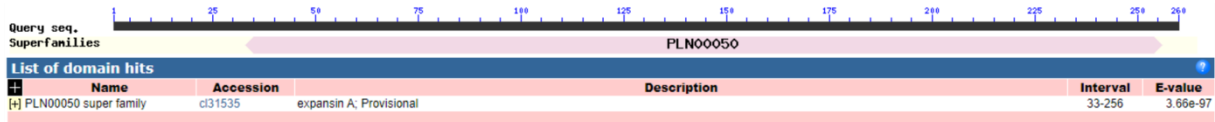
## EXTERNAL RESOURCES

[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-09

MAKFQNLFTWAVFITLLVQAMGDVIPLAKGRAGKIWHDAHATFYGDLNGGETMQG  
ACGYGDLFQQGYGLETAALSTKLFKDGHACGACFQIRCVKDPQWCIPNAGAITITAT  
NFCPPNWIPAPDHCNPPQRHFDLSMTMFTKLAQAKAGIIPVKYRRVPCQKSGGVKF  
ELKGNPYWLTALVFNVGGAGDVANVKIKGSSTDWLQMSRNWGQVWQTGSNIVGQ  
SLSFLVTTSDGKTLRFDDVAPTNWQFGQTYEGRINF\*

### CDS (coding sequence)

>PrpEXPA-09

ATGGCTAAGTTTCAGAACTTGTTTACATGGGCAGTGTTTCATCACTCTTCTGGTTCA  
AGCCATGGGCGATGTAATCCCTTTAGCTAAGGGACGCGCCGGCAAGATTTGGCAT  
GATGCACACGCAACGTTTTATGGTGACCTGAACGGAGGAGAAACCATGCAGGGG  
GCTTGTGGATATGGTGATCTCTTCCAACAAGGCTATGGCCTGGAGACAGCAGCAC  
TAAGCACAAAGCTGTTCAAGGACGGGCACGCTTGCGGTGCTTGTTTTCAGATCCG  
GTGTGTCAAGGATCCACAATGGTGCATCCCTAATGCCGGTGCAATCACAATCACT  
GCAACCAATTTTTGTCCTCCAAATTGGATTCCAGCTCCTGATCATTGGTGCAACCC  
GCCACAGAGACACTTCGATTTGTCCATGACGATGTTCAAAAACCTCGCACAAAGCG  
AAAGCCGGGATAATCCCGGTTAAATATCGCAGAGTCCCGTGCCAGAAAAGCGGA  
GGGGTTAAGTTTGAGCTTAAGGGAAACCCCTACTGGCTTACTGCATTGGTGTTC  
ACGTTGGCGGTGCCGGTGATGTTGCAAACGTTAAAATTAAGGCTCTAGCACTGA  
CTGGCTTCAAATGTCTCGCAATTGGGGCCAAGTTTGGCAGACGGGAAGCAACATA  
GTAGGGCAAAGCTTATCATTCTTGGTCACCACAAGTGATGGGAAAACACTTAGGT  
TTGATGATGTTGCACCAACAAATTGGCAATTTGGTCAGACCTATGAGGGGAGAAT  
AAATTTTGA

### Nucleotide

>PrpEXPA-09

ATGGCTAAGTTTCAGAACTTGTTTACATGGGCAGTGTTTCATCACTCTTCTGGTTCA  
AGCCATGGGCGATGTAATCCCTTTAGCTAAGGGACGCGCCGGCAAGATTTGGCAT  
GATGCACACGCAACGTTTTATGGTGACCTGAACGGAGGAGAAACCATGCGTAAG  
TGAAAGAGTTTTTGTGTTGCACCGGTTACATATAACCTCCTTCCCACGATAGCAAAC  
TCGTGTACTTAATATGAGAGGAATGTTATATATAACCGGCACATAACTATTTTTAT

TTTTATATCAAGTTTTAACTTTGTGATTCTTAAACAGAGGGGGCTTGTGGATATGG  
TGATCTCTTCCAACAAGGCTATGGCCTGGAGACAGCAGCACTAAGCACAAAGCTG  
TTCAAGGACGGGCACGCTTGCGGTGCTTGTTTTCAGATCCGGTGTGTCAAGGATC  
CACAATGGTGCATCCCTAATGCCGGTGCAATCACAATCACTGCAACCAATTTTTG  
TCCTCAAATTGGATTCCAGCTCCTGATCATTGGTGCAACCCGCCACAGAGACAC  
TTCGATTTGTCCATGACGATGTTACAAAACCTCGCACAAAGCGAAAGCCGGGATAA  
TCCCGTTAAATATCGCAGAGTCCCGTGCCAGAAAAGCGGAGGGGTAAAGTTTGA  
GCTTAAGGGAAACCCCTACTGGCTTACTGCATTGGTGTTC AACGTTGGCGGTGCC  
GGTGATGTTGCAAACGTTAAAATTAAGGCTCTAGCACTGACTGGCTTCAAATGT  
CTCGCAATTGGGGCCAAGTTTGGCAGACGGGAAGCAACATAGTAGGGCAAAGCT  
TATCATTCTTGGTCACCACAAGTGATGGGAAAACACTTAGGTTTGATGATGTTGC  
ACCAACAAATTGGCAATTTGGTCAGACCTATGAGGGGAGAATAAATTTTTGA