

## IDENTIFICATION

**Species:** *Prunus persica*

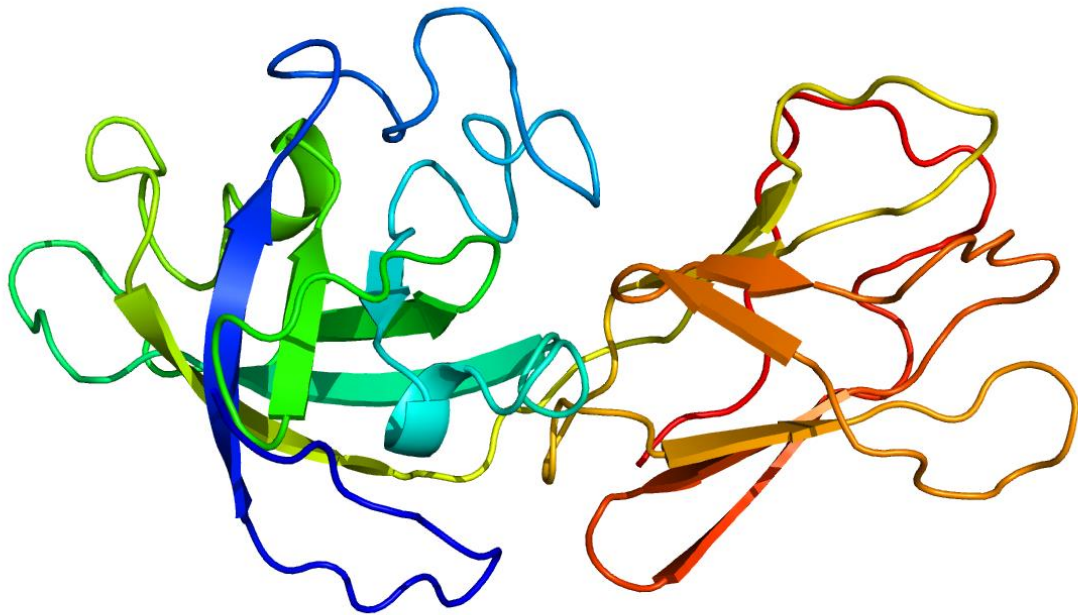
**Locus:** Prupe.6G075100

**Gene Model:** Prupe.6G075100.1.p

**Description:** PrpEXPA-16

**Family:** Alpha Expansin

**3D structure:**



## GENOME DATABASES

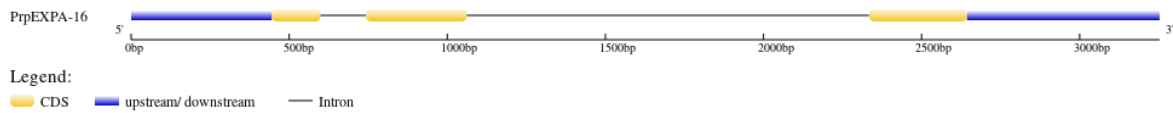
Phytozome: [https://phytozome-next.jgi.doe.gov/info/Ppersica\\_v2\\_1](https://phytozome-next.jgi.doe.gov/info/Ppersica_v2_1)

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

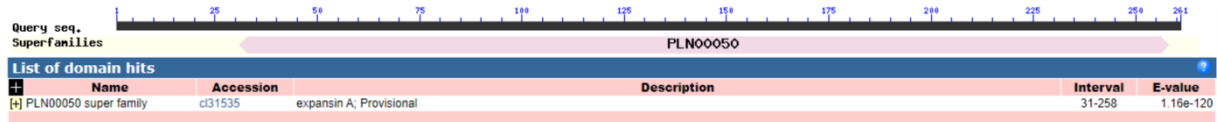
## EXTERNAL RESOURCES

[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-16

MGVVSVSACLASLLISLMWVAEARIPGVYSSGGAWEAAHATFYGGSDASGTMGGAC  
GYGNLYSQGYGVSTAALSTALFNGLSCGACFEIKCANDPNWCHSGSPSIFITATNFC  
PPNFAQPSDNGGWCNPPRPHFDLAMPMLKIAEYRAGIVPVS YRRVPCRKRGGIRFTI  
NGFRYFNLVLVSNVAGAGDIVRVS VKGSKTSWMSMRNWGQNWQSNV LVGQSL  
FRVRGSDRRTSTSWNVVPANWQFGQTFTGKNFRV\*

### CDS (coding sequence)

>PrpEXPA-16

ATGGGTGTGGTGAGTGTTTCTGCTTGCCTTGCCTCTCTACTCATCTCACTAATGTG  
GGTAGCTGAAGCAAGAATCCCAGGGGTGTACAGTGGGGGTGCATGGGAAGCAGC  
TCATGCCACCTTCTACGGAGGCTCTGATGCCTCTGGCACCATGGGTGGGGCTTGT  
GGATATGGAAATCTCTACAGCCAAGGCTATGGCGTGAGCACAGCTGCACTGAGC  
ACTGCCCTCTTCAACAATGGCCTCAGCTGCGGTGCCTGCTTTGAAATCAAGTGTG  
CAAACGACCCAAACTGGTGCCACTCTGGAAGCCCATCAATTTTCATCACTGCCAC  
CAACTTCTGCCCTCCAACTTTGCTCAACCAAGCGACAATGGCGGATGGTGCAAT  
CCTCCAGGCCGCACTTTGACCTGGCCATGCCCATGTTTCTCAAGATTGCCGAGTA  
CAGAGCTGGAATTGTCCCTGTTTCTTACCGTAGGGTGCCATGCCGCAAGCGCGGA  
GGGATCAGGTTCACTATCAACGGCTTCCGTTACTTCAACCTGGTTTTGGTAAGCA  
ACGTCGCGGGTGACAGGGGATATCGTGCGGGTGAGCGTGAAAGGATCCAAGACTA  
GCTGGATGAGCATGAGCCGTA ACTGGGGTCAA AACTGGCAGTCAAACGCCGTTCT  
GGTTGGTCAATCGTTGTCCTTCAGGGTCAGAGGCAGTGACAGGCGCACTTCCACC  
TCATGGAACGTTGTTCCGGCCAATTGGCAGTTCGGTCAAACATTCACCGGGAAGA  
ACTTCAGAGTCTGA

### Nucleotide

>PrpEXPA-16

CTCTAAATAAATTTTCCGGGAAAAATAGAGAAGAGAAAAGAAAAGAAAAGAGA  
AGAAAAGGTGAAGATACCGACACTCGCCTACAAGAGCTTGCATAAGCACCAACC  
TCCCATCAATTGGGAAATTGGTGAAGAACACAGGCAGGCCCCACACTTATCAGTA  
CAAGGTGCAATACAATTAGAGAGTGACATACAAGCGTTAGAGAATGAGAGTGGG  
GATGAAATTCATTTTATTTCTAGTTCTACATTTATGATGGGTTGAGTCTGAAAATT



AAAAGACAGGGTAACAAGTGTAAGGGAAATTAATTATTAAATTA AAAACCCAAG  
TGAGGAAATTGTAGAAGAGGAGGTTGAGGCGGCTGCAGAGAATTTGTAGCCCGC  
ACCCTATAAATACTGGCAAAGCTAAAGTTGTAGTATATTATTATGATTTATATGC  
ATGAGAAATGTATTTCTAGTAGTAAC TTTGTTATTTTCTTGTTTTGTTTTGATTTAC  
TTGGAAAGTATATTTGGTTTGT TTTCAATGGAAC TTTGGCTTTTTGTTAGTGGGTTTT  
GGCTTAATTCAACCAGCTTTACACGGTTTATATTGGATTTGAAGATGAAACGGAT  
TTGTAGCTCAAGTGTTTTAGACTATTTATCTCTGCATTCA