

IDENTIFICATION

Species: *Prunus persica*

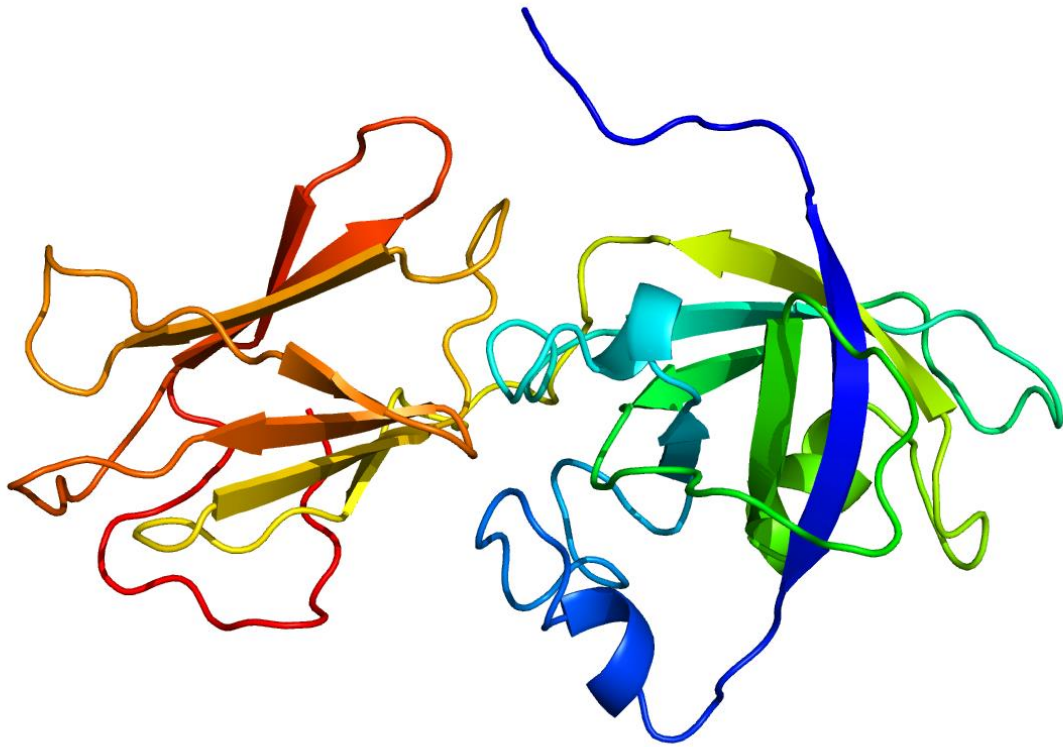
Locus: Prupe.3G265800

Gene Model: Prupe.3G265800.1.p

Description: PrpEXPA-10

Family: Alpha Expansin

3D structure:



GENOME DATABASES

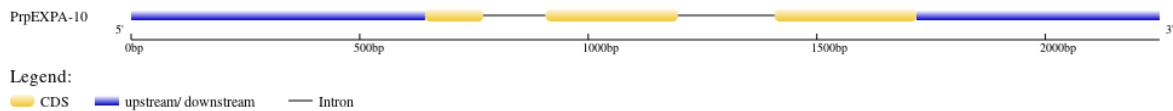
Phytozome: https://phytozome-next.jgi.doe.gov/info/Ppersica_v2_1

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

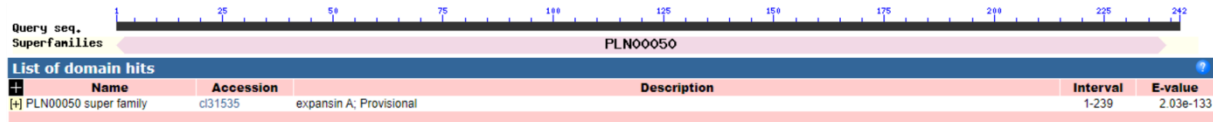
EXTERNAL RESOURCES

https://www.rosaceae.org/species/prunus_persica/genome_v2.0.a1

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>PrpEXPA-10

MTSLGILLGFLSVSSVNGYYGGWSNAHATFYGGGDASGTMGGACGYGNLYSQG
YGTNTAALSTALFNGLSCGACYEIRCVNDPQWCLPGTIVVTATNFCPPGGWCDPPQ
QHFDLSQPVFLHIAQYRAGVVPVSYRRVRCKRRGGIRFTVNGHSYFNLVLTNVGGA
GDVQSVAIKGSRTRWQLMSRNWGQNWQSNLNGQSLSFVTTSDGRRLVSYNVA
PPNWSFGQTYTGRQFLY*

CDS (coding sequence)

>PrpEXPA-10

ATGACTTCTTTGGGGATTCTTCTACTTGGGTTTCTCTCAGTTGTCTCCTCTGTCAAT
GGGTACTATGGGGGCTGGTCCAATGCTCATGCAACCTTTTATGGAGGTGGTGATG
CTTCAGGCACAATGGGTGGGGCTTGTGGCTATGGGAACCTGTACAGCCAGGGCTA
TGGGACTAACACAGCAGCACTAAGCACTGCATTGTTCAACAATGGCTTGAGCTGT
GGGGCATGCTATGAGATCAGGTGTGTAAATGACCCACAGTGGTGCCTCCCTGGCA
CCATTGTGGTCACAGCGACAAACTTTTGCCCACCAGGTGGCTGGTGTGATCCTCC
ACAGCAACACTTTGATCTCTCTCAGCCTGTCTTCCTGCACATTGCACAATACAGAG
CTGGAGTTGTCCCTGTATCATA CAGAAGGGTGAGATGCAAGAGAAGAGGAGGCA
TAAGGTTACAGTGAATGGCCATTCGTA CTTCAACTTAGTGCTTGTGACAAACGT
TGGTGGTGCTGGAGATGTGCAGTCTGTGGCCATCAAGGGCTCTAGGACCCGGTGG
CAACTAATGTCAAGAACTGGGGGCAAACTGGCAGAGCAACTCAAACCTAAAT
GGACAGAGCCTCTCTTTTCTTGTGACCACCAGTGATGGCCGCAGATTGGTTTCATA
TAACGTTGCCCTCCTAATTGGTCATTTGGGCAGACATATACTGGGAGACAGTTT
CTCTATTA

Nucleotide

>PrpEXPA-10

TGAATTAATAAGTTGGACAGTAAATAAATTCCATCATGGCAATAAAGAAGAATA
AATATGAGCAGCTCCTAAAATTTACCATTATCAGTATCTCTGTCTTCACATGGATG
AGTCTGAGAGACATATTTTCTACTTGGAGCAGTTGAGAGAGCCAAAGTTACTCTGT
CACAAATTTGTGGCAATTGCCAAATGGGAACTTCAAAAAACCACGCGTTTCAT
CCTTTAAAACCGCTCTCAGTCGAAAATACTGCATTGATTCTACTAACAGATCATG
AGAGTCCTAAAACCACTTAGCTCTGCTTGGTCCCAACAGCTCAAAATTGTCAGGT

TGTCATTTTCAGATGTGATGTGCGACCGACTTCTATTTATTCTTCTTCAAAGTTCAA
CAATCAAACCCTCCTCCCTCTTCATTTCAATTCCTCACTTCTGCGTGCTTGCTTTCA
AACTTCATCATTTTCTAATTGTAATAACTCTCTCTCTCTTTCTCCTAATTCCCTTTT
TTCTCTCATAAACATGAACATAAAAAGATTACATGTACAGTACACTACTGTACTA
GTTACTTACTCATAGCTAGACAAAGAGTTCTTCCTGCTATGAATGCCTAAAAGAG
CTCACAAACTTCACACGTCTTTGTGCGAGGAAAAATGACTTCTTTGGGGATTCTTCT
ACTTGGGTTTTCTCTCAGTTGTCTCCTCTGTCAATGGGTACTATGGGGGCTGGTCCA
ATGCTCATGCAACCTTTTATGGAGGTGGTGATGCTTCAGGCACAATGGGTATGTT
TAGCTTTATGATTTTTTTTCTTTCTTATTTAACTTATGATAGGTGACAAGCACCTTT
GCTGCAAAAAGATTAGAACTTTTCACTTCTGTTCCCTTCTACTTATTATATTTGGACA
TGCAATTTTTTTTTTAGGTGGGGCTTGTGGCTATGGGAACCTGTACAGCCAGGGCT
ATGGGACTAACACAGCAGCACTAAGCACTGCATTGTTCAACAATGGCTTGAGCTG
TGGGGCATGCTATGAGATCAGGTGTGTAAATGACCCACAGTGGTGCCTCCCTGGC
ACCATTGTGGTCACAGCGACAAACTTTTGCCACCAGGTGGCTGGTGTGATCCTC
CACAGCAACACTTTGATCTCTCTCAGCCTGTCTTCCTGCACATTGCACAATACAGA
GCTGGAGTTGTCCCTGTATCATAACAGAAGGTAAGCTAAATCTTATGTCTCTATTAA
TGCCAACCAGTGGAAAGAGGCCTTGACTTGCAGACAGTAGTCTTATGTTTCGAACC
ATGGCACAATGTGTACGAGAAAATCCCCCTCCCCCTTTCTAACTTTGGCCCAAAA
AAAAAAGTTCTCTAATAATTAGGTTTAAAGTGCTAATTAAGGCTTAATTATTAT
GATTATTATGTGTTTTGCAGGGTGAGATGCAAGAGAAGAGGAGGCATAAGGTTC
ACAGTGAATGGCCATTCGTACTTCAACTTAGTGCTTGTGACAAACGTTGGTGGTG
CTGGAGATGTGCAGTCTGTGGCCATCAAGGGCTCTAGGACCCGGTGGCAACTAAT
GTCAAGAACTGGGGGCAAACTGGCAGAGCAACTCAAACCTAAATGGACAGAG
CCTCTCTTTTCTTGTGACCACCAGTGATGGCCGCAGATTGGTTTCATATAACGTTG
CCCCTCCTAATTGGTCATTTGGGCAGACATATACTGGGAGACAGTTTCTCTATTAA
TTAATTAATCAATTAATTATCTGTCTGGGTGTGCTTAATGAAGCTTCTTTAGTCTT
CCACTTCGTTTAGTTATATGTGGTAAGTTTACTATCAGCAGACAAAAAGCTGAAG
TAATTCTGAGGAGGAAGGATGGAGTGTAGCTAATAGCTATAGTTGTTGGAAGAAT
ATGAAAAACGGTTTACTTTGAAGTGAGTGGCCCTTTTCATTATTTGATAATAGATT
GTGAGTTTTTGCAGTTCATGGCTGGGATTGTTCTGAAGCCTGATGGCCATATCTGC
TAGAGAGAGAGAAAGAGAGACAGAGAGAGATTATGTTTCTTAAGGCAGTTTGGC
AGTGAATTTTACCACCCGCTGTTAATTTTCATGAAGTTATGAATATTGAATAGAA
GAGGTGTGTTTTTACTAGTTACTAGCAAATGCTATATGGCAGAAGGTATGTTTGCT
AATTGCCTGTGTAATGTCAATAAACCTGCTTATGCGCCTTTTTATTACATTCCAGA
TACAATAACTAAAGGCAACAACCTTATTACGC