

IDENTIFICATION

Species: *Prunus persica*

Locus: Prupe.7G124900

Gene Model: Prupe.7G124900.1.p

Description: PrpEXPA-19

Family: Alpha Expansin

3D structure:



GENOME DATABASES

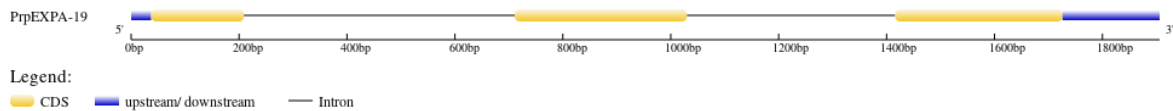
Phytozome: https://phytozome-next.jgi.doe.gov/info/Ppersica_v2_1

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

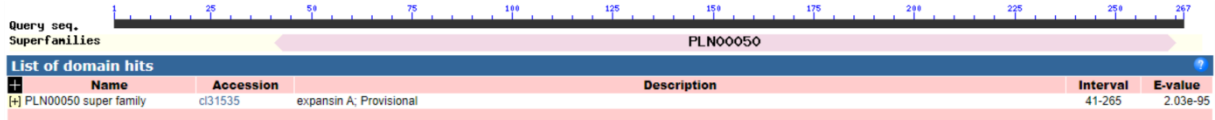
EXTERNAL RESOURCES

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

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>PrpEXPA-19

MAYKMCLLLPIFLCLVADGDGHDIVVSHNHHRPKFAPGAWKHAHATFYEGGSG
TFGGACGYEDVVQEGYGLETAALSEALFNKGQCGSCYEIKCVDDPKWCKPGQLTL
MVTGTNNCPPNWNQASDNGGWCNPPREHFDAKPAFAKIAEYKAGIVPIMYRRVPC
MKKGGIKFTITGNPYFNQVLVWNVGGAGEVTSLQVKGNKNLKW TAMKRLWGQKW
ETDAKMVGESLTFRVRGSDGRYSTSWHVAPNNWQFGQTFEGKNFK*

CDS (coding sequence)

>PrpEXPA-19

ATGGCATATAAAATGTGCTTGTTGCTGCCCATCTTTCTTTGTTTGGTGGCTGATGG
CGATGGGCATGACATTCATGTAGTTTCCACAACCACCACCACAGGCCAAAGTTC
GCTCCCGGTGCTTGGAAGCATGCTCATGCCACATTCTATGAAGGGGGCTCTGGAA
CCTTTGGGGGAGCTTGTGGATACGAGGACGTGGTACAAGAAGGATATGGCCTAG
AAACAGCAGCATTAAAGCGAGGCATTGTTCAACAAAGGGCAGGGATGCGGGTCAT
GCTACGAGATCAAATGCGTGGACGACCCTAAGTGGTGAAGCCAGGGCAGCTAA
CTCTCATGGTCACCGGTACCAACAATTGCCCGCCAAACTGGAACCAAGCAAGTGA
CAATGGAGGATGGTGAATCCTCCGCGCGAGCATTTTGACATAGCCAAGCCTGCC
TTCGCCAAAATTGCTGAGTACAAGGCTGGCATTGTTCCCTATCATGTACCGCAGAG
TCCCATGCATGAAGAAAGGAGGTATAAAGTTCACAATAACTGGGAACCCATATTT
CAACCAAGTGCTGGTGTGGAATGTGGGAGGAGCTGGGGAAGTGACGAGCTTGCA
AGTGAAGGGCAACAAGAACCTCAAATGGACAGCAATGAAGCGGCTGTGGGGTCA
GAAGTGGGAGACCGACGCCAAGATGGTCGGTGAGTCGTTGACCTTCCGAGTCAG
AGGGAGCGATGGAAGATACTCAACGTCATGGCATGTTGCCCAACAATTGGCA
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Nucleotide

>PrpEXPA-19

AAAAACCAAGAACCAAATCTTCTACATACAAATAAAAATGGCATATAAAATGTG
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GCATGCTCATGCCACATTCTATGAAGGGGGCTCTGGAACCTTTGGTATGAATATA
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TAACACACCAAATTCATATATGATCTCAATTAGGATATACTACTTATTCTCCAAA
AATCAAATCATTATCAAGACTAATGATTTTTGATGAATAATGCAGGGGGAGCTTGT
GGATACGAGGACGTGGTACAAGAAGGATATGGCCTAGAAAACAGCAGCATTAAAGC
GAGGCATTGTTCAACAAAGGGCAGGGATGCGGGTCATGCTACGAGATCAAATGC
GTGGACGACCCTAAGTGGTGCAAGCCAGGGCAGCTAACTCTCATGGTCACCGGTA
CCAACAATTGCCCGCCAAACTGGAACCAAGCAAGTGACAATGGAGGATGGTGCA
ATCCTCCGCGCGAGCATTTTTGACATAGCCAAGCCTGCCTTCGCCAAAATTGCTGA
GTACAAGGCTGGCATTGTTCCCTATCATGTACCGCAGGTAAATGTAATTACATTCTT
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