

IDENTIFICATION

Species: *Prunus persica*

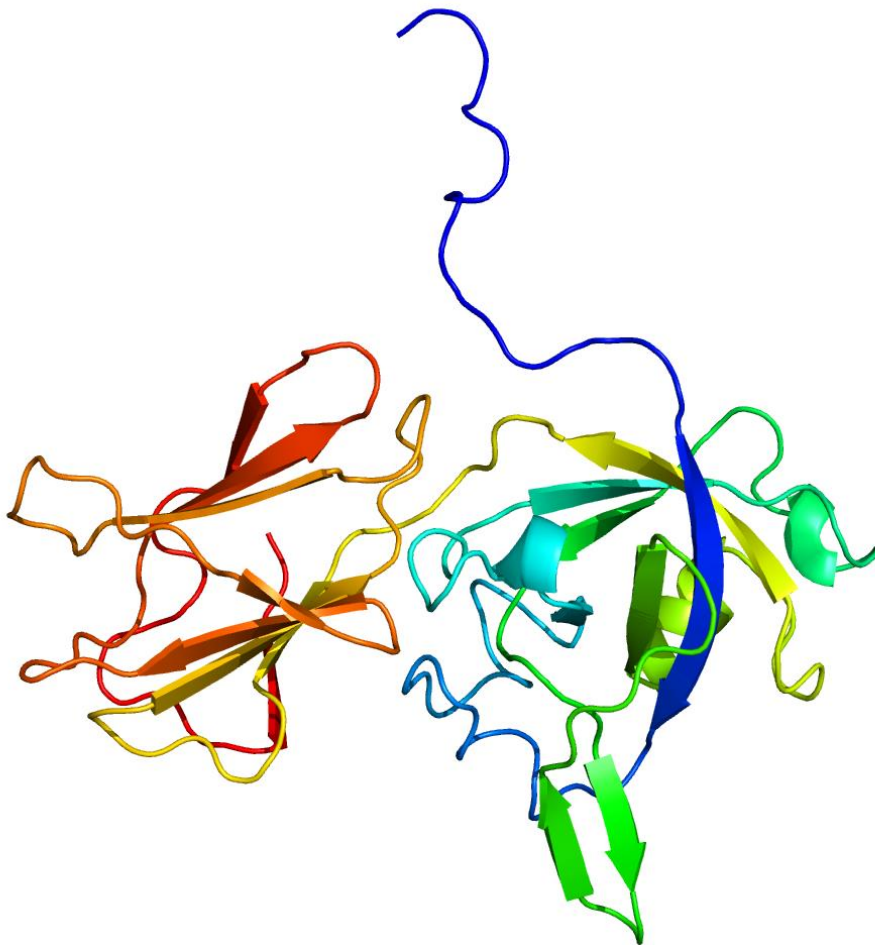
Locus: Prupe.1G516700

Gene Model: Prupe.1G516700.1.p

Description: PrpEXPA-04

Family: Alpha Expansin

3D structure:



GENOME DATABASES

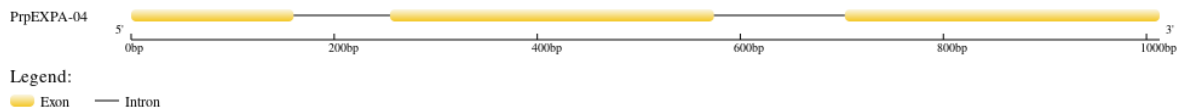
Phytozome: https://phytozome-next.jgi.doe.gov/info/Ppersica_v2_1

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

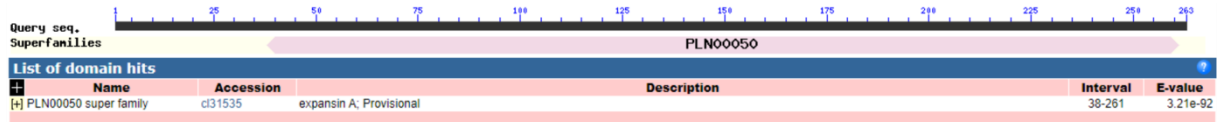
EXTERNAL RESOURCES

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

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>PrpEXPA-04

MRLPNLKALLGSLLLFLLAVFPDHAIAHHRPRFTAGPWKQSHATFYEGGSGTFFGAC
GYHDVVQEGYGLTVALSNALFNNGQSCGACYDIKCVDQPQWCKPGNPILHVTATN
NCPPNWNQASDNGGWCNPPREHFDAIKPVFLNIAEYKAGIPIEYRRVSCQKKGGRIF
TITGNPYFNEVLVWNVAGVGDVVSQVKGHDKLKWTMMKRMWGQRWVTDKLV
GESLTFRVLASDKRYSTSWHIAPKNWQFGQTFEGKNFR*

CDS (coding sequence)

>PrpEXPA-04

ATGAGATTGCCTAATTTGAAAGCCCTATTGGGTTTCATTGCTGCTCTTTCTTCTAGC
AGTATTTCCCGACCATGCCATTGCCACCATAGGCCAAGGTTCACTGCTGGCCCTT
GGAAGCAATCTCATGCCACATTCTATGAAGGAGGCTCCGGAACATTTGGTGGAGC
TTGTGGTTACCATGATGTTGTTCAAGAAGGATATGGCCTGGAGACAGTAGCATTG
AGCAATGCATTGTTCAACAATGGACAGTCATGTGGTGCATGCTACGATATCAAAT
GTGTAGACCAACCTCAATGGTGCAAGCCCAGGGAATCCGATTCTGCATGTTACGGC
GACTAACAATTGCCCCCGAATTGGAATCAGGCAAGCGACAATGGAGGATGGTG
CAATCCACCACGCGAGCATTTTGACATAGCCAAGCCTGTATTCCTCAATATTGCC
GAGTACAAGGCTGGCATCATCCAATTGAATATCGCAGGGTTTCATGCCAAAAGA
AAGGAGGTATTCGATTCACAATAACCGGGAACCCTTACTTCAACGAAGTGTGGT
GTGGAATGTGGCAGGAGTTGGGGATGTGGTCAGCGTGCAAGTGAAGGGCCACGA
CAAGTTGAAATGGACAATGATGAAGCGGATGTGGGGTCAGAGGTGGGTTACTGA
TGCCAAGTTGGTTGGTGAGTCACTCACCTTCCGAGTCCTAGCAAGTGATAAAAGA
TACTCCACCTCATGGCATATAGCCCCCAAGAATTGGCAGTTTGGCCAGACATTCG
AAGGCAAGA ACTTCCGATAG

Nucleotide

>PrpEXPA-04

ATGAGATTGCCTAATTTGAAAGCCCTATTGGGTTTCATTGCTGCTCTTTCTTCTAGC
AGTATTTCCCGACCATGCCATTGCCACCATAGGCCAAGGTTCACTGCTGGCCCTT
GGAAGCAATCTCATGCCACATTCTATGAAGGAGGCTCCGGAACATTTGGTACGAA
ATTCTAAACAACGTTGTTTTGAACACAAGAGCACTATATTTTAGTTACATTATATA
TATTTTGCAACTAATTGTTTTGAGCTTGTGAGGTGGAGCTTGTGGTTACCATGATG

TTGTTCAAGAAGGATATGGCCTGGAGACAGTAGCATTGAGCAATGCATTGTTCAA
CAATGGACAGTCATGTGGTGCATGCTACGATATCAAATGTGTAGACCAACCTCAA
TGGTGCAAGCCCGGAATCCGATTCTGCATGTTACGGCGACTAACAAATTGCCCC
CGAATTGGAATCAGGCAAGCGACAATGGAGGATGGTGCAATCCACCACGCGAGC
ATTTTGACATAGCCAAGCCTGTATTCTCAATATTGCCGAGTACAAGGCTGGCAT
CATCCCAATTGAATATCGCAGGTAAGTTTATTCATAACAGTGTAACAACATAACA
TGTCATAGTAAGTAGCAAGAGAATATTATCGATCAACCATTTTAATTATTATCTTC
ATGTTCAACATTGAATGAAGTGTTAATAATGTTTTACAGGGTTTCATGCCAAAAG
AAAGGAGGTATTCGATTCACAATAACCGGGAACCCTTACTTCAACGAAGTGTTGG
TGTGGAATGTGGCAGGAGTTGGGGATGTGGTCAGCGTGCAAGTGAAGGGCCACG
ACAAGTTGAAATGGACAATGATGAAGCGGATGTGGGGTCAGAGGTGGGTTACTG
ATGCCAAGTTGGTTGGTGAGTCACTCACCTCCGAGTCCTAGCAAGTGATAAAAG
ATACTCCACCTCATGGCATATAGCCCCAAGAATTGGCAGTTTGGCCAGACATTC
GAAGGCAAGAACTTCCGATAG