

IDENTIFICATION

Species: *Populus trichocarpa*

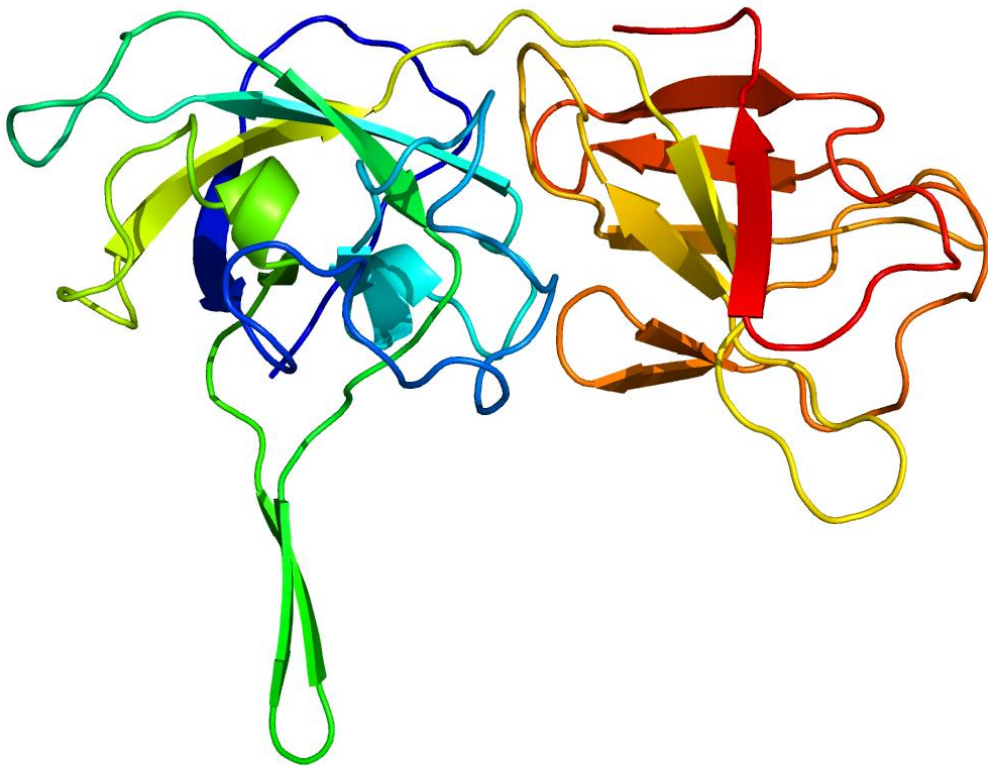
Locus: Potri.001G112901

Gene Model: Potri.001G112901.1.p

Description: PtEXPA-02

Family: Alpha Expansin

3D structure:



GENOME DATABASES

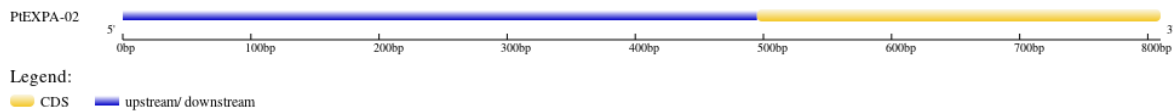
Phytozome: https://phytozome-next.jgi.doe.gov/info/Ptrichocarpa_v4_1

KEGG: <https://www.genome.jp/entry/gn:T01077>

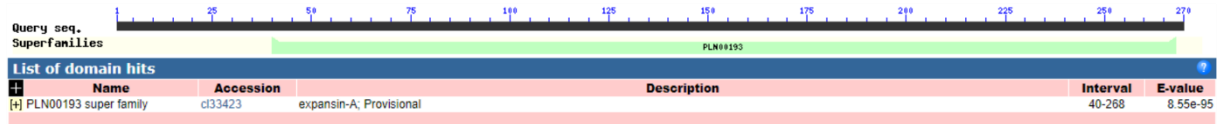
EXTERNAL RESOURCES

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GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>PtEXPA-02

MASFFHSWSFSLFLIVLTSAMFIGKSMVGYGKARVPTVFRPSQWSLAHATFYGDET
ARETMGGACGYGNLFQTGYGTNTAALSTTLFNNGYACGTCYQIKCTNAPACYGVIT
TVTATNICPPNWSQDSNNGGWCNPPRVHFDMSKPAFMKIAQWKAGIVPVMYRRVPC
ARTGGLRFLKLGNGYWLLVYVMNVGGGGDIASMWVKGSKTGWISMShNWGASY
QAFASLRGQALSFKITSYTTKQTVIALNVAPSTWGAGMTYKSTVNFS*

CDS (coding sequence)

>PtEXPA-02

ATGGCTTCCTTTTTTCATTCATGGAGCTTTAGCCTCTTCTTGATAGTGTTGACTTCA
GCAATGTTTCATCGGCAAATCAATGGCCGTAGGTTATGGTAAAGCACGCGTACCAA
CGGTGTTCCGGCCGAGCCAATGGTCGCTTGCCACGCCACCTTTTATGGCGATGA
GACCGCTCGCGAGACCATGGGAGGGGCTTGCGGGTATGGAAATTTGTTCCAAACT
GGATACGGAACCAATACTGCTGCATTGAGCACAACATTATTCAACAACGGATATG
CCTGTGGGACTTGTTACCAAATAAAATGTACGAATGCTCCTGCATGCTATGGGGT
AATTACAACGGTGACTGCTACAAACATCTGCCCTCCGAATTGGTCCCAGGATTCT
AACAAATGGTGGATGGTGAACCCTCCTCGAGTTCACCTTGACATGTCCAAGCCTG
CATTTCATGAAAATTGCTCAATGGAAGGCTGGCATCGTCCCAGTCATGTACCGAAG
AGTACCATGTGCAAGAACTGGCGGGCTTCGATTCAAGCTCCAAGGAAATGGGTA
CTGGTTGCTGGTGTATGTGATGAATGTAGGAGGAGGTGGTGACATTGCCAGCATG
TGGGTGAAGGGAAGCAAAACAGGATGGATAAGCATGAGCCATAACTGGGGAGCT
TCATAACCAGGCATTTGCTAGCCTTCGAGGACAAGCTCTATCTTTCAAGATCACTTC
TTACACAACCAAGCAGACTGTTATTGCATTGAATGTTGCTCCTTCAACCTGGGGT
GCAGGGATGACATATAAATCAACTGTGAACTTCAGTTAG

Nucleotide

>PtEXPA-02

TTCTCCATATTAACCAATAATTTTACTTGAGAGCCACCATCTTCGTGCCGTCAC
GAAGCCAATTTTTTGGAGAATGGGACATTATATAAGGATGTCAAGTACAAGAAC
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AGTCAACAGAAAAGCCATGGCTTCCTTTTTTCATTCATGGAGCTTTAGCCTCTTCT
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TAAAGCACGCGTACCAACGGTGTTCGGGCCGAGCCAATGGTCGCTTGCCCACGCC
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ATTCAACAACGGATATGCCTGTGGGACTTGTACCAAATAAAATGTACGAATGCT
CCTGCATGCTATGGGGTAATTACAACGGTGACTGCTACAAACATCTGCCCTCCGA
ATTGGTCCCAGGATTCTAACAATGGTGGATGGTGCAACCCTCCTCGAGTTCACTTT
GACATGTCCAAGCCTGCATTCATGAAAATTGCTCAATGGAAGGCTGGCATCGTCC
CAGTCATGTACCGAAGGTATGCCATCTTTCTTAGCTTTTCCATGCTTTTCAGAAGT
CAACTACATGTGGGCCAAACGCCACAAACGTTTTTTGAACGAGCTTGCTCGTGCTG
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ATCTAGTGGAAGATGTCCAGATTATTTGATCCTTCTTCTGCTGTGCTTCTTTTATT
CAAACCTCAATTAATCAAAATTCAAATCTA