

IDENTIFICATION

Species: *Arabidopsis thaliana*

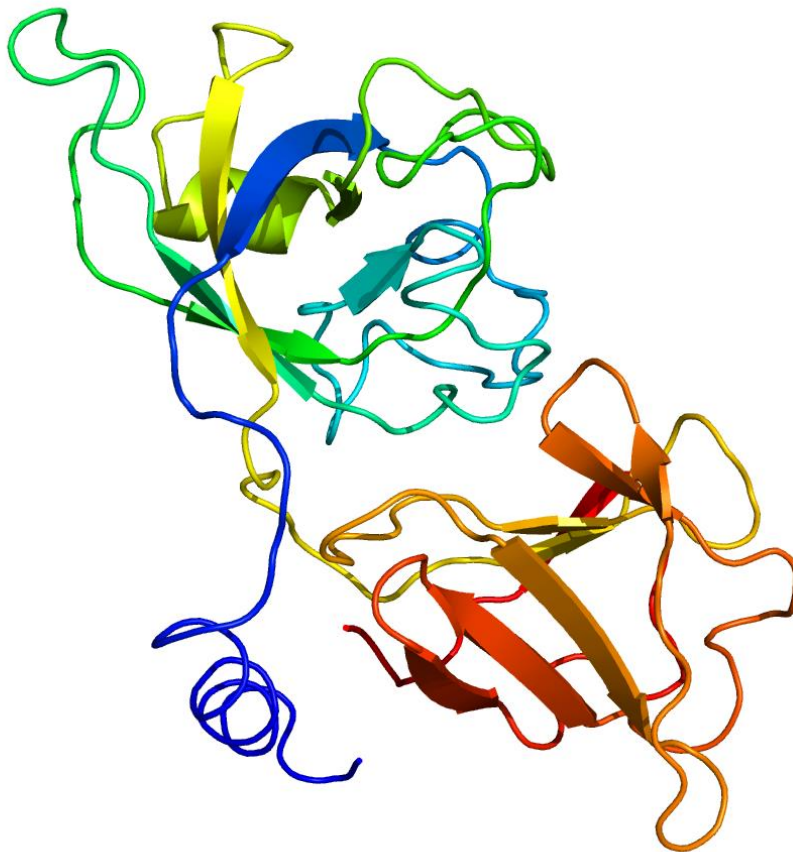
Locus: AT1G20190

Gene Model: AT1G20190.1

Description: AtEXPA-02

Family: Alpha Expansin

3D structure:



GENOME DATABASES

TAIR: <https://www.arabidopsis.org/>

KEGG: <https://www.genome.jp/entry/T00041>

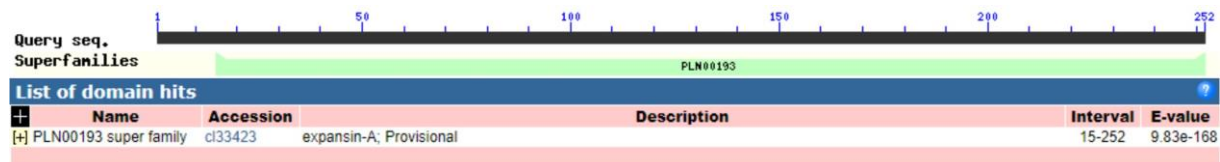
EXTERNAL RESOURCES

<https://www.gabipd.org/database/cgi-bin/GreenCards.pl.cgi?Mode=Show&QueryKey=197c0ef939ecd1d29302d8a4a92c1bc3&x.Overview=1&Start=1>

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>AtEXPA-02

MSKSLAGLAVLAALFIAVDAFRPSGLTNGHATFYGGSDASGTMGGACGYGDLYSAG
YGTMTAALSTALFNDGASCGEYRITCDHAADSRWCLKGASVVITATNFCPPNFALP
NNGGWCNPLKHFDMAQPAWEKIGIYRGGIVPVVFORVSCYKKGGRFRINGRDY
FELVNIQNVGGAGSIKSVSIKGSKTGWLAMSRNWGANWQSNAYLDGQALSFSITTTD
GATR VFLNVVPSSWSFGQIYSSNVQF

CDS (coding sequence)

>AtEXPA-02

ATGTCAAAGTCTCTAGCTGGATTGGCGGTTTTGGCCGCTCTTTTTATTGCGGTTGA
TGCGTTTAGGCCTTCTGGTTAACTAATGGTCACGCTACATTCTATGGAGGAAGTG
ACGCTTCTGGAACAATGGGTGGAGCTTGTGGTTACGGAGATCTTTACTCGGCGGG
GTACGGGACAATGACGGCGGCGTTAAGCACGGCTCTGTTCAACGACGGAGCTTCT
TGCGGAGAATGCTATAGGATAACGTGTGATCACGCGGCGGACTCACGGTGGTGCT
TGAAAGGAGCTTCTGTGGTTATTACAGCCACTAACTTTTGCCACCAAACCTTTGCT
TTGCCAACAACAACGGTGGTTGGTGAATCCGCCGCTTAAACATTTGACATGG
CACAACCCGCTTGGGAAAAGATCGGAATTTACAGAGGAGGAATCGTTCGTCGT
TTCCAAAGAGTAAGCTGTTACAAGAAAGGAGGAGTTAGATTCAGAATAAACGG
AAGAGACTACTTCGAGCTAGTGAATATTCAAATGTAGGAGGAGCAGGTTCTATT
AAATCTGTATCCATCAAAGGATCAAAGACTGGTTGGTTAGCCATGTCTCGTAACT
GGGAGCTAATTGGCAATCGAATGCTTATCTAGATGGTCAAGCTCTCTTTCTCC
ATTACCACTACTGATGGTGCTACTAGAGTCTTTCTCAATGTTGTTCTTCTTCTTG
TCTTTTGGACAGATTTATTCTTCCAACGTTTCAGTTTTAA

Nucleotide

>AtEXPA-02

CACATGTAAGGTTTTTGTGCTATACTACATTAGTTTACACTCGCTTCCCACCTTT
ATTTAAACAACCTCTCACCTCCTTCACTCGATCATCATCATCATCTCTTTCTTCT
TCCAAAAGTCATAATCATGTCAAAGTCTCTAGCTGGATTGGCGGTTTTGGCCGCT
CTTTTTATTGCGGTTGATGCGTTTAGGCCTTCTGGTTTAACTAATGGTCACGCTAC
ATTCTATGGAGGAAGTGACGCTTCTGGAACAATGGGTAATTTACACTTTAGTTT
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AGCTGTTACAAGAAAGGAGGAGTTAGATTCAGAATAAACGGAAGAGACTACTTC
GAGCTAGTGAATATTCAAATGTAGGAGGAGCAGGTTCTATTAATCTGTATCCA
TCAAAGGATCAAAGACTGGTTGGTTAGCCATGTCTCGTAACTGGGGAGCTAATTG
GCAATCGAATGCTTATCTAGATGGTCAAGCTCTCTCTTTCTCCATTACCACTACTG
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TCTTC