

## IDENTIFICATION

**Species:** *Arabidopsis thaliana*

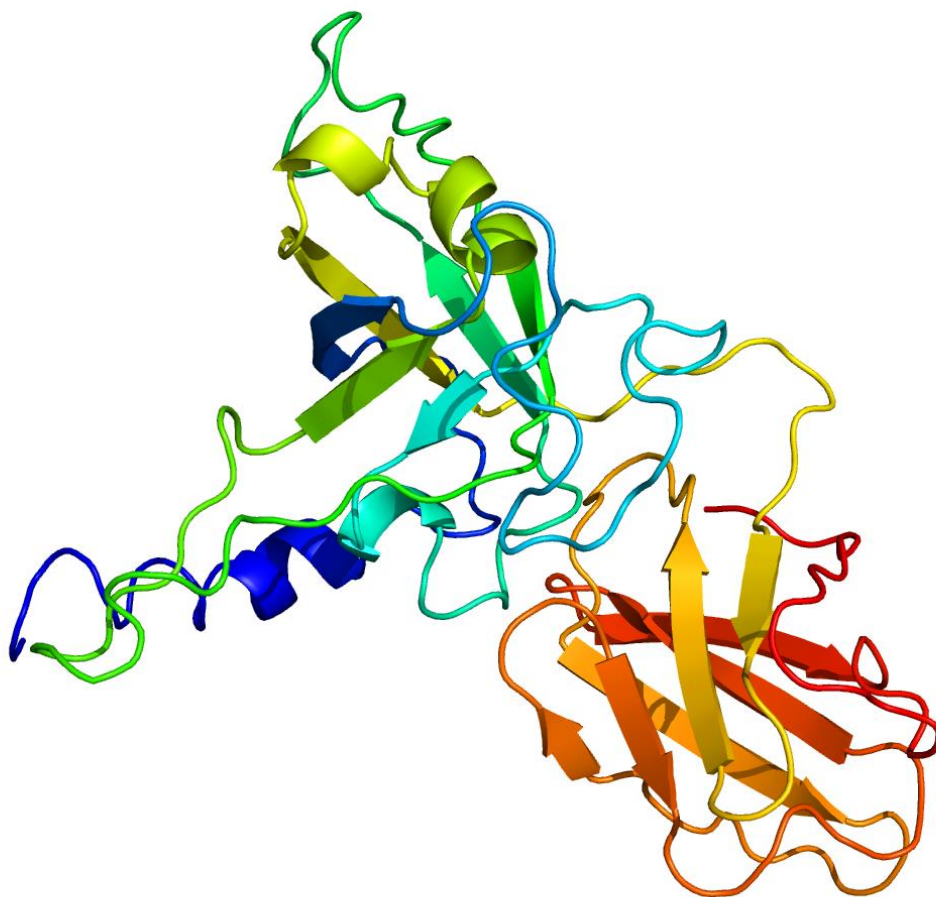
**Locus:** AT4G01630

**Gene Model:** AT4G01630.1

**Description:** AtEXPA-22

**Family:** Alpha Expansin

**3D structure:**



## GENOME DATABASES

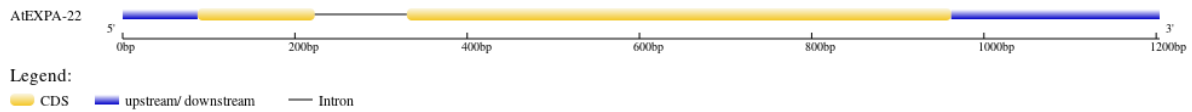
TAIR: <https://www.arabidopsis.org/>

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

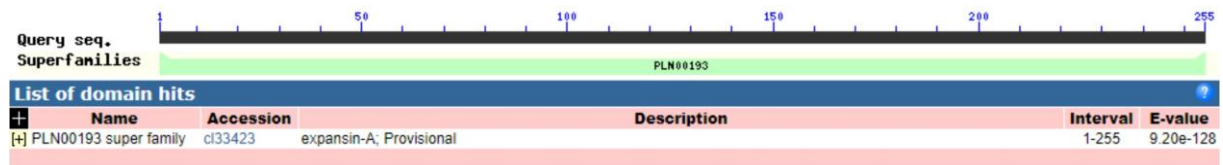
## EXTERNAL RESOURCES

<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-22

MTKIFSLLVAMIFSTMFFMKISSVSAGWLQAHATFYGGSDASGTMGGACGYGNLYT  
DGYKTNTAALSTALFNDGKSCGGCYQILCDATKVPQWCLKGKSITITATNFCPPNFA  
QASDNGGWCNPPRPHFDMAQPAFLTIAKYKAGIVPILYKKGVCRRSSGMRFTINGRN  
YFELVLISNVAGGGEISKVWIKGSKSNKWETMSRNWGANYQSNTYLNGQSLSFKVQ  
LSDGSIKAALNVVPSNWRFGQSFKSNVNF

### CDS (coding sequence)

>AtEXPA-22

ATGACGAAGATTTTCTCTCTATTGGTCGCAATGATCTTCTCCACAATGTTCTTCAT  
GAAGATCAGCTCAGTTTCTGCTGGTTGGTTGCAAGCTCATGCGACCTTTTATGGCG  
GAAGTGATGCCTCTGGTACAATGGGTGGAGCTTGTGGTTATGGAAACCTATACAC  
AGACGGCTACAAGACAAACACCGCGGCGTTAAGCACGGCCCTGTTCAACGACGG  
CAAGTCATGCGGTGGATGTTACCAAATCTTGTGTGATGCAACCAAAGTACCACAA  
TGGTGTCTTAAAGGCAAATCAATCACTATCACAGCTACAACTTCTGTCCACCGA  
ACTTTGCTCAGGCAAGCGACAATGGAGGTTGGTGCAACCCACCGAGACCTCATT  
CGACATGGCTCAGCCTGCGTTTCTCACCATCGCTAAGTACAAAGCTGGAATCGTC  
CCCATTCTTTACAAAAAAGTTGGATGTAGAAGAAGCGGAGGGGATGAGATTTACA  
ATAAACGGTAGAACTATTTTCGAGCTTGTTCATCTCAAACGTAGCAGGAGGGG  
GTGAGATCTCTAAAGTTTGGATCAAAGGATCTAAGAGCAACAAATGGGAGACAA  
TGTCAGAAGATTGGGGAGCTAATTATCAGAGTAATACTTACCTTAATGGTCAATC  
TCTATCTTTCAAAGTTCAACTTAGTGATGGAAGTATCAAAGCAGCTCTCAACGTT  
GTTCTTCGAATTGGCGGTTTGGTCAGAGCTTCAAGAGCAACGTTAACTTCTAA

## Nucleotide

>AtEXPA-22

CTAAAGCCTAAGTCTTATGCATCCAACAATCTTCAACTTCTTCTCTAATCAAAGT  
TAAAACACCTAAGAAATTGAAAGAAAACAAAATGACGAAGATTTTCTCTCTATTG  
GTCGCAATGATCTTCTCCACAATGTTCTTCATGAAGATCAGCTCAGTTTCTGCTGG  
TTGGTTGCAAGCTCATGCGACCTTTTATGGCGGAAGTGATGCCTCTGGTACAATG  
GGTAAGTCTCATAAACTAGACATGAACATTTGGTTTTACCCTAATGAGAGCTTTA  
AAAAATAATGTTCCCTTCTTCAACAAGAAACCTTCTCATAGCTTTCTTCTCAGGTG  
GAGCTTGTGGTTATGGAAACCTATACACAGACGGCTACAAGACAAACACCGCGG  
CGTTAAGCACGGCCCTGTTCAACGACGGCAAGTCATGCGGTGGATGTTACCAAAT  
CTTGTGTGATGCAACCAAAGTACCACAATGGTGTCTTAAAGGCAAATCAATCACT  
ATCACAGCTACAACTTCTGTCCACCGAAGCTTTGCTCAGGCAAGCGACAATGGAG  
GTTGGTGCAACCCACCGAGACCTCATTTGACATGGCTCAGCCTGCGTTTCTCACC  
ATCGCTAAGTACAAAGCTGGAATCGTCCCCATTCTTTACAAAAAAGTTGGATGTA  
GAAGAAGCGGAGGGATGAGATTTACAATAAACGGTAGAACTATTTGAGCTTG  
TTCTCATCTCAAACGTAGCAGGAGGGGGTGAGATCTCTAAAGTTTGGATCAAAGG  
ATCTAAGAGCAACAAATGGGAGACAATGTCAAGAAATTGGGGAGCTAATTATCA  
GAGTAATACTTACCTTAATGGTCAATCTCTATCTTTCAAAGTTCAACTTAGTGATG  
GAAGTATCAAAGCAGCTCTCAACGTTGTTCCCTTCGAATTGGCGGTTTGGTCAGAG  
CTTCAAGAGCAACGTTAACTTCTAATATCAATAACGGGTTTAGTCCACTTTTGTAT  
CTTTGTATTTACTTGCATTGGGTGTTTTTTTGCTTCCTCTGTTGCATCATCATCGTC  
TGCGATAAGCTGCTTGTTTTATAGCCTTATTATAGTCTTGCTTCCAGAGAGTTTAT  
AATCTGGAGAAGACTCAAGCAGTGATGATTGTATTTGTACATTTAAGGAAGATGT  
TACTATTATATATAAAGGATGTCTCAAACAACCTTACTTTTAA