

## IDENTIFICATION

**Species:** *Arabidopsis thaliana*

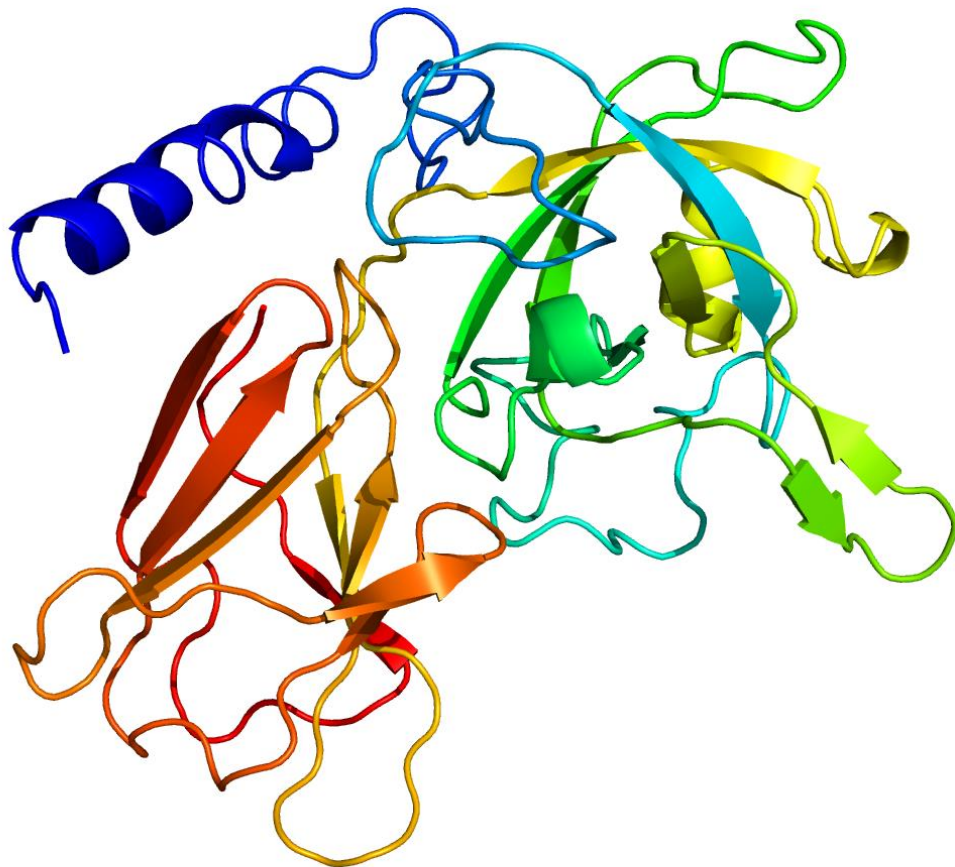
**Locus:** AT5G39300

**Gene Model:** AT5G39300.1

**Description:** AtEXPA-30

**Family:** Alpha Expansin

**3D structure:**



## GENOME DATABASES

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

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

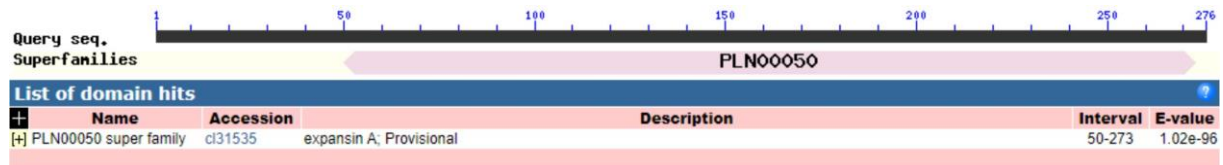
## EXTERNAL RESOURCES

<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-30

MKLLEQMVYVECFMIIMATLLVSMSYGHAMINDVAEAPVIDNVGSPTNGLDSSWY  
DARATFYGDIHGGETQQGACGYGDLFKQGYGLETAALSTALFNEG YTCGACYQIMC  
VHDPQWCLPGTIKITATNFCPPDYKTEGVWCNPPQKHFDLSLPMFLKIAQYKAGVV  
PVKYRRISCARTGGVKFETKGNPYFLMILPYNVGGAGDIKLMQVKGDKTGWITMQK  
NWGQNWTTGVNLTGQGISFRVTTSDGVTKDFNNVMPNNWGFQTFDGKINF

### CDS (coding sequence)

>AtEXPA-30

ATGAAACTCTTAGAACAAATGGTATACGTAGAATGTTTTATGATAATAATGGCTA  
CATTGTTAGTGTCCATGAGTTACGGTCATCGAGCGATGATTAATGATGTAGCCGA  
AGCACCCGTGATTGACAATGTAGGCAGCCCAACCAACGGACTCGACAGTTCTTGG  
TATGATGCACGAGCAACATTTTACGGTGATATCCATGGTGGAGAACTCAACAGG  
GAGCCTGTGGATACGGTGATTTATTCAAACAAGGCTATGGTCTAGAGACAGCGGC  
ATTGAGCACAGCACTCTTCAACGAAGGGTATACATGTGGGGCTTGTTACCAGATC  
ATGTGTGTGCACGACCCACAATGGTGTTTACCCGGAACCATCAAGATTACAGCAA  
CAAATTTCTGTCCACCAGATTACTCCAAAACCGAAGGCGTTTGGTGCAACCCACC  
ACAAAAGCACTTTGACCTCTCCCTACCAATGTTCTCAAGATCGCCCAATACAAA  
GCTGGAGTTGTCCCAGTTAAATACAGACGTATTTCTTGCAAGAACTGGTGGTG  
TCAAGTTTGAAACCAAAGGAAACCTTATTTCTTAATGATCTTGCCATACAATGT  
AGGAGGCGCTGGAGATATCAAGTTGATGCAAGTTAAAGGAGACAAGACCGGGTG  
GATAACAATGCAAAAGAACTGGGGACAAAACCTGGACCACTGGTGTTAATTTGAC  
TGGTCAGGGTATTTCAATTCAGGGTTACGACGAGTGATGGGGTTACAAAAGATTTT  
ATAATGTGATGCCAAACAATTGGGGATTTGGACAGACTTTTGATGGAAAGATTA  
ACTTTTAG

## Nucleotide

>AtEXPA-30

TCAAAGTTAAATAAGAAAAATATCATTCAAAGAAACAATAATCATGAAACTCTT  
AGAACAAATGGTATACGTAGAATGTTTTATGATAATAATGGCTACATTGTTAGTG  
TCCATGAGTTACGGTCATCGAGCGATGATTAATGATGTAGCCGAAGCACCCGTGA  
TTGACAATGTAGGCAGCCCAACCAACGGACTCGACAGTTCTTGGTATGATGCACG  
AGCAACATTTTACGGTGATATCCATGGTGGAGAACTCAACGTAAGTGTGAAAA  
AACTAATTATTGAATTTTTGTTTGGTTCATAAAAAATCATATACGCTGCGATTGTT  
TTAAATGATTACTTTTGAGTTTGGCGATTGCATTTACATATATCTTAATGTTTTGATC  
AAAGAAAAAATGTACATAAAATTAATGTTTATTTATTTTTATTCAATATAGAGG  
GAGCCTGTGGATACGGTGATTTATTCAAACAAGGCTATGGTCTAGAGACAGCGGC  
ATTGAGCACAGCACTCTTCAACGAAGGGTATACATGTGGGGCTTGTTACCAGATC  
ATGTGTGTGCACGACCCACAATGGTGTTTACCCGGAACCATCAAGATTACAGCAA  
CAAATTTCTGTCCACCAGATTACTCCAAAACCGAAGGCGTTTGGTGCAACCCACC  
ACAAAAGCACTTTGACCTCTCCCTACCAATGTTCCCTCAAGATCGCCCAATACAAA  
GCTGGAGTTGTCCAGTTAAATACAGACGTATTTCTTGTGCAAGAAGTGGTGGTG  
TCAAGTTTGAAACCAAAGGAAACCCTTATTTCTTAATGATCTTGCCATACAATGT  
AGGAGGCGCTGGAGATATCAAGTTGATGCAAGTTAAAGGAGACAAGACCGGGTG  
GATAACAATGCAAAAGAACTGGGGACAAAAGTGGACCACTGGTGTTAATTTGAC  
TGGTCAGGGTATTTCAATTCAGGGTTACGACGAGTGATGGGGTTACAAAAGATTTT  
AATAATGTGATGCCAAACAATTGGGGATTTGGACAGACTTTTGATGGAAAGATTA  
ACTTTTAGGAGAATGATTTCAAGTTTTGTATGCCAATGATTAATAATAAATGATATT  
ATTTATACTACTT