

## IDENTIFICATION

**Species:** *Arabidopsis thaliana*

**Locus:** AT5G39280

**Gene Model:** AT5G39280.1

**Description:** AtEXPA-28

**Family:** Alpha Expansin

**3D structure:**



## GENOME DATABASES

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

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

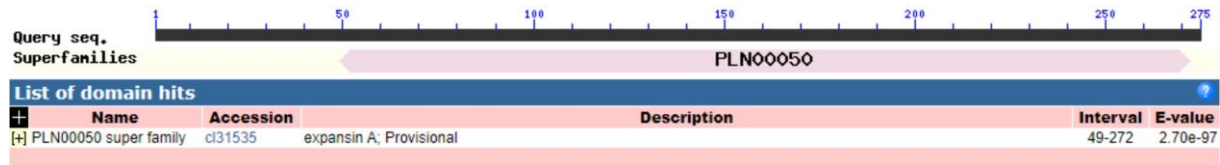
## EXTERNAL RESOURCES

<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-28

MNLLGKMIYVEGFMMIMATLLVSMSYGHRAMINDVAEAPVFDDV VSPNGLDSSWY  
DARATFYGDIHGGETQQGACGYGDLFKQGYGLETAALSTALFNEG YTCGACYQIMC  
VNDPQWCLPGSVKITATNFCPPDY SKTEGVWCNPPQKHFDLSLPMFLKIAQYKAGVV  
PVKYRRISCARTGGVKFETKGNPYFLMILPYNVGGAGDIKLMQVKGDKTGWITMQK  
NWXQNWTTGVNLTGQGISFRVTTSDGVTKDFNNVMPNNWGFQTFDGKINF

### CDS (coding sequence)

>AtEXPA-28

ATGAATCTCTTAGGAAAATGATATATGTAGAAGGTTTTATGATGATAATGGCTA  
CATTGTTAGTGTCCATGAGTTACGGTCATCGAGCGATGATTAATGATGTAGCCGA  
AGCACCCGTGTTTGACGATGTAGTCAGCCCAAACGGACTCGACAGTTCTTGGTAT  
GATGCACGAGCAACATTTTACGGTGATATCCATGGTGGAGAACTCAACAGGGA  
GCGTGTGGATACGGTGATCTATTCAAACAAGGCTATGGTCTAGAGACAGCGGCAT  
TGAGCACAGCACTCTTCAACGAAGGGTATACATGTGGGGCTTGTACCAGATCAT  
GTGTGTGAACGATCCACAATGGTGTTTACCCGGATCCGTC AAGATCACAGCAACT  
AATTTCTGTCCACCAGATTACAGCAAACCGAAGGCGTTTGGTGCAACCCACCAC  
AAAAGCACTTTGACCTCTCCCTACCAATGTTCCCTCAAGATCGCCCAATACAAAGC  
TGGAGTTGTCCCAGTTAAATACAGACGTATTTCTTGTGCAAGAACTGGTGGTGTC  
AAGTTTGAACCAAAGGAAACCCTTATTTCTTAATGATCTTGCCATACAATGTAG  
GAGGAGCTGGAGATATCAAGTTGATGCAAGTTAAAGGAGACAAGACCGGGTGA  
TAACAATGCAAAGA AACTGGGGACAAA AACTGGACCACTGGTGTTAATTTGACTG  
GTCAGGGTATTTCAATCAGGGTTACGACGAGTGATGGGGTTACAAAAGATTTTAA  
TAATGTGATGCCAAACAATTGGGGATTTGGACAGACTTTTGATGGAAAGATTAAC  
TTTTAG

## Nucleotide

>AtEXPA-28

AAATAAGAAAAATATCATTCAAGAGGGATAATAATCATGAATCTCTTAGGAAAA  
ATGATATATGTAGAAGGTTTTATGATGATAATGGCTACATTGTTAGTGTCCATGA  
GTTACGGTCATCGAGCGATGATTAATGATGTAGCCGAAGCACCCGTGTTTGACGA  
TGTAGTCAGCCCAAACGGACTCGACAGTTCTTGGTATGATGCACGAGCAACATTT  
TACGGTGATATCCATGGTGGAGAACTCAACGTAAGTGTGAAAACACTCATTATT  
GAATTTTTGTTTTGTTCTCAAATACCATATATGCTGCGATTGTTTTAAATGCTTA  
CTTTTGCGTTTGAGATTGCATTTACATTTATCTTAATGTTTGATAAAAAGAAAAAAT  
ATGTGTTTTCTCCGATAAGATATTATCATAAAAAAAAATATTTTATTTTTTTGTTCT  
ATATATTTCTATTCAATATAGAGGGAGCGTGTGGATACGGTGATCTATTCAAACA  
AGGCTATGGTCTAGAGACAGCGGCATTGAGCACAGCACTCTTCAACGAAGGGTA  
TACATGTGGGGCTTGTTACCAGATCATGTGTGTGAACGATCCACAATGGTGTTTA  
CCCGGATCCGTCAAGATCACAGCAACTAATTTCTGTCCACCAGATTACAGCAAAA  
CCGAAGGCGTTTGGTGCAACCCACCACAAAAGCACTTTGACCTCTCCCTACCAAT  
GTTCTCAAGATCGCCCAATACAAAGCTGGAGTTGTCCAGTTAAATACAGACGT  
ATTTCTTGTGCAAGAACTGGTGGTGTCAAGTTTGAAACCAAAGGAAACCCTTATT  
TCTTAATGATCTTGCCATACAATGTAGGAGGAGCTGGAGATATCAAGTTGATGCA  
AGTTAAAGGAGACAAGACCGGGTGGATAACAATGCAAAAAGAACTGGGGACAAA  
ACTGGACCACTGGTGTTAATTTGACTGGTCAGGGTATTTTCATTCAGGGTTACGAC  
GAGTGATGGGGTTACAAAAGATTTTAATAATGTGATGCCAAACAATTGGGGATTT  
GGACAGACTTTTGATGGAAAGATTAACCTTTTAGGAGAATGATTCAGTTTTGTAT  
GCCAATGTATTATTTGGGTGAAATGATTA AAAATAAAT