

## IDENTIFICATION

**Species:** *Arabidopsis thaliana*

**Locus:** AT5G02260

**Gene Model:** AT5G02260.1

**Description:** AtEXPA-24

**Family:** Alpha Expansin

**3D structure:**



## GENOME DATABASES

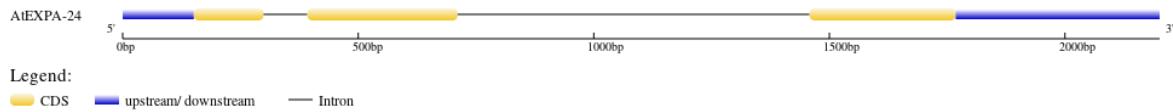
TAIR: <https://www.arabidopsis.org/>

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

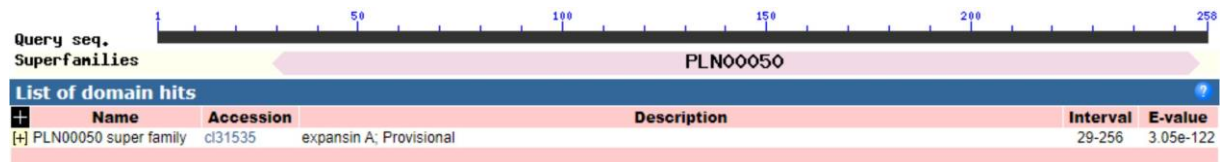
## EXTERNAL RESOURCES

<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-24

MAAKVITFMAMVMVVTAFANAKIPGVYTGGPWINAHATFYGEADASGTMGGACGY  
GNLYSQGYGVNTAALSTALFNGLSCGSCFELKCINDPGWCLPGNPSILITATNFCPP  
NFNQASDNGGWCNPPREHFDLAMPFLSLIAKYKAGIVPVS YRRIPCRKKGIRFTING  
FKYFNLVLTNVAGAGDVIKVS VKGSNTQWLDLSRNWQNWQSNALLVGQSLFR  
VKTS DGRSSTSNNIAPSNWQFGQTYSGKNFRV

### CDS (coding sequence)

>AtEXPA-24

ATGGCGGCGAAAGTAATTACATTTATGGCGGTTATGGTGGTACTGCCTTTACGG  
CCAACGCCAAAATCCCCGGAGTTTACACCGGTGGTCCTTGGATCAATGCTCACGC  
CACCTTCTACGGTGAAGCTGACGCTTCCGGCACTATGGGTGGTGC GTGTGGGTAC  
GGGAATTTGTATAGCCAAGGTTACGGAGTGAACACGGCGGCTTTAAGCACTGCCT  
TATTCAACAATGGTTTGAGTTGTGGCTCTTGCTTTGAGCTTAAGTGTATCAATGAT  
CCAGGATGGTGTCTTCTTGAAACCCATCAATTCTTATCACCGCCACTAATTTCTG  
CCCTCCTAACTTTAATCAAGCTAGCGACAATGGTGGTTGGTGAATCCTCCTCGTG  
AGCACTTTGATCTCGCTATGCCTATGTTTCTTCCATCGCTAAGTATAAGGCTGGT  
ATCGTCCCCGTCTCTTACCGCAGGATCCCATGTAGGAAGAAGGGAGGAATCAGAT  
TCACAATCAATGGATTCAAGTACTTCAACTTGGTGTGCTGGTCACTAACGTAGCCGG  
AGCTGGAGACGTCATTAAGGTGAGTGTGAAAGGATCCAACACACAATGGTTAGA  
TCTGAGCCGGA ACTGGGGACAAA ACTGGCAATCCAACGCACTTCTTGTGGCCAA  
TCTCTTTCTTCCGAGTCAAAACCTCTGATGGCCGAAGCTCCACCTCCAACAACAT  
TGCTCCCAGTAACTGGCAATTTGGCCAGACCTACTCCGGCAAGAACTTCCGCGTC  
TGA

## Nucleotide

>AtEXPA-24

CTTAAATTAGAAAAATAATTAAAAAAAGGCGTAAAGTCATTTGAAGCCTCCATAA  
GTAGCCTTCCTAGCTTCCCCTCTCCCTCTCACATTCCTCTCTTCTCTCTCTTTTC  
CAAAAACCAAAACCTTTTTTCCGTACCAAGGTCAACAAATGGCGGGCGAAAGTAAT  
TACATTTATGGCGGTTATGGTGGTACTGCCTTTACGGCCAACGCCAAAATCCCC  
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CTGACGCTTCCGGCACTATGGGTACACACACACACTCTCTCCCACCTCCTCTGT  
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GCTTAAGTGTATCAATGATCCAGGATGGTGTCTTCCTGGAAACCCATCAATTCTTA  
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GAGAAAATCCCATTTTTTTGGTTAGCTTATTTTCGAGATCGATCCTAGGAAATCGC  
CTAATGTTGCTTAGTCAAAGATGTTAAGTTATTTCTTAACTTTTTTTAGTAATTAG  
GATCCGAATGTAAGAATCTGTGAGCCTGAAGATTTTCGCATGTTCACTCTATTCTT  
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ACCTAAATCCTTTTCAATGTAAAATTACGAAAACACCCTTAAGCCCCGGGTCAGT  
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CAAAGGACCGACACTTCCTCACTCCACCACATACATTTGCCGGGTCAAATTTTTTA  
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CAAAACCTCTGATGGCCGAAGCTCCACCTCCAACAACATTGCTCCCAGTAACTGG  
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