

## IDENTIFICATION

**Species:** *Arabidopsis thaliana*

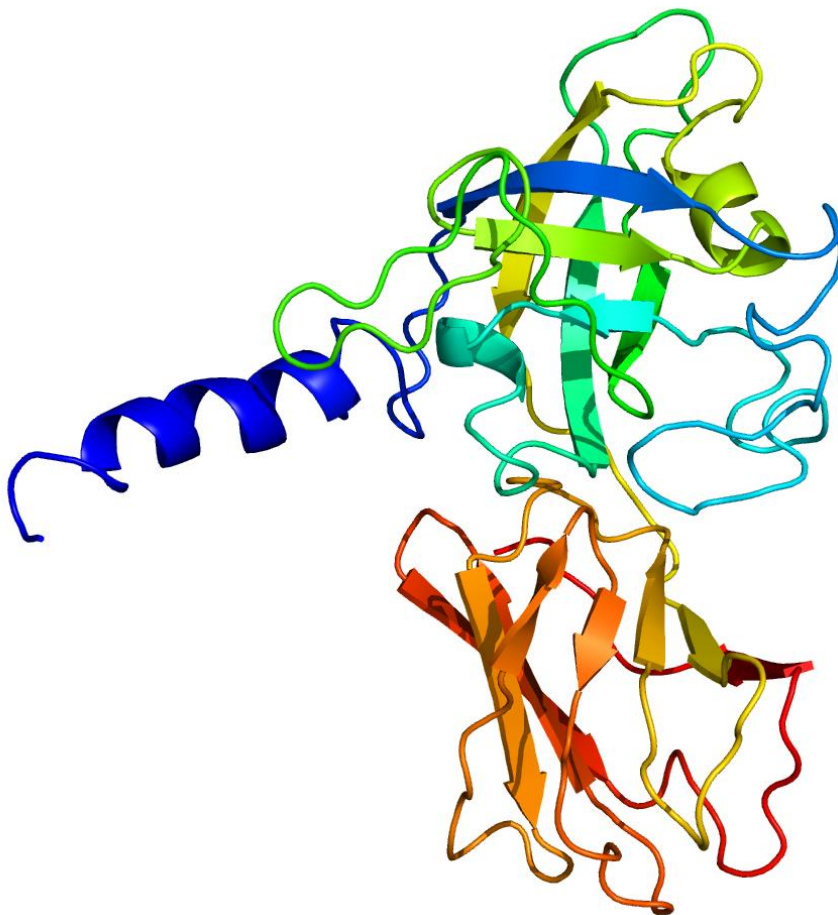
**Locus:** AT4G38210

**Gene Model:** AT4G38210.1

**Description:** AtEXPA-23

**Family:** Alpha Expansin

**3D structure:**



## GENOME DATABASES

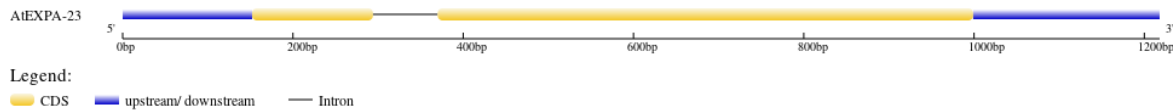
TAIR: <https://www.arabidopsis.org/>

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

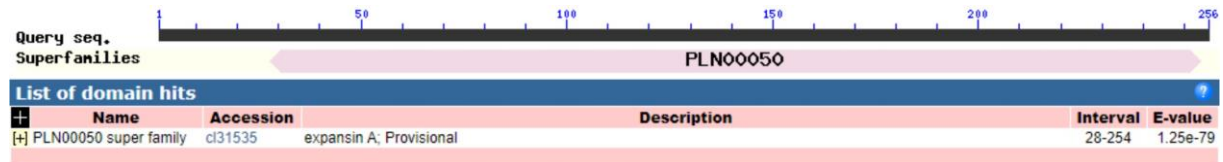
## EXTERNAL RESOURCES

<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-23

MDSGLQQLALCLFFILCRLFQATAEDDWKIATATLSRDRDGSSSVATGGACGYGDLR  
QSSFAGYSAGLSGKLFNRGSSCGACLEVRCVNHIRWCLQGSPSVVVTATDFCPPNSG  
LSSDYGGWCNFPKEHLELSHAAFTGIAETRAEMIQYRRVKCGRRGGLRFSLSGSSH  
FFQVLISNVGLDGEVVGVKVKGHTTAWIPMARNWGQNWSSLDLIGQSLSFEVTLK  
GGKTIASYDVAPPYWRFGMTYQGKQFHS

### CDS (coding sequence)

>AtEXPA-23

ATGGATTCTGGGCTTCAGCAACTCGCATTGTGCCTCTTCTTCATTCTCTGCCGCCT  
CTTTCAAGCCACTGCCGAAGATGACTGGAAGATAGCCACAGCCACGCTTTCTAGA  
GACAGAGACGGCTCCTCCTCCGTCGCTACTGGAGGCGCTTGTGGGTATGGAGATC  
TGAGGCAGAGCAGCTTTGCCGGCTACAGCGCAGGCCTGAGCGGGAAGCTGTTCA  
ACAGGGGAAGCAGCTGCGGAGCTTGTCTAGAAGTGCGGTGCGTGAACCACATCC  
GTTGGTGTCTTCAAGGCAGCCCCTCCGTGGTGGTCACCGCCACCGATTTCTGTCCT  
CCCAATTCGGGACTCTCCTCCGATTACGGAGGTTGGTGCAACTTCCCAAAGGAAC  
ACTTGGAATATCTCATGCCGCCTTACAGGGATCGCAGAAACCAGAGCTGAGAT  
GATACCTATACAGTATAGGAGGGTCAAGTGTGGGCGGAGAGGCGGGTTGAGATT  
CAGCTTGAGCGGGAGCTCCCACTTTTCCAGGTGTTGATAAGCAATGTGGGCCTC  
GACGGGGAAGTGGTTGGTGTGAAAGTGAAGGGCCACACAACGGCTTGGATCCCA  
ATGGCCAGAACTGGGGACAGA ACTGGCACTCCTCTCTCGATCTCATCGGACAGT  
CTCTCTTTTCGAGGTTACTCTCAAAGGCGGCAA AACCATTGCCTCTTATGATGTG  
GCTCCTCCGTATTGGCGCTTCGGAATGACATACCAAGGAAAGCAGTTCCACTCCT  
GA

## Nucleotide

>AtEXPA-23

AAAACATGTCAGAGCAATCTTTTGTTCGCATCCCCACAAGTCTTGAAAAGCGGAGC  
CTGATGATCAAAAGGAACCCCCAAAACCTCTCTCAAACGCATCACTTTTGTCTGCC  
ACCTGTGACTGACTGTGAGGATCCCAACAACACTTCTTGTTTCATGGATTCTGGGCT  
TCAGCAACTCGCATTGTGCCTCTTCTTCATTCTCTGCCGCCTCTTTCAAGCCACTG  
CCGAAGATGACTGGAAGATAGCCACAGCCACGCTTTCTAGAGACAGAGACGGCT  
CCTCCTCCGTCGCTACTGGTTCTCTTTTCTCTCTCTCCCCCTATTTTTCTTTCTTCT  
TTCATCAGGACTAACTAGACTAATTGGTTCTGATAGGAGGCGCTTGTGGGTATGG  
AGATCTGAGGCAGAGCAGCTTTGCCGGCTACAGCGCAGGCCTGAGCGGGAAGCT  
GTTCAACAGGGGAAGCAGCTGCGGAGCTTGTCTAGAAGTGCGGTGCGTGAACCA  
CATCCGTTGGTGTCTTCAAGGCAGCCCCTCCGTGGTGGTCACCGCCACCGATTTCT  
GTCCTCCCAATTCGGGACTCTCCTCCGATTACGGAGGTTGGTGCAACTTCCCAA  
GGAACACTTGGAATATCTCATGCCGCCTTACAGGGATCGCAGAAACCAGAGCT  
GAGATGATACCTATACAGTATAGGAGGGTCAAGTGTGGGCGGAGAGGCGGGTTG  
AGATTCAGCTTGAGCGGGAGCTCCCACTTTTTCCAGGTGTTGATAAGCAATGTGG  
GCCTCGACGGGGAAGTGGTTGGTGTGAAAGTGAAGGGCCACACAACGGCTTGG  
TCCAATGGCCAGAACTGGGGACAGAACTGGCACTCCTCTCTCGATCTCATCGG  
ACAGTCTCTCTTTTCGAGGTTACTCTCAAAGGCGGCAAAACCATTGCCTCTTATG  
ATGTGGCTCCTCCGTATTGGCGCTTCGGAATGACATACCAAGGAAAGCAGTTCCA  
CTCCTGACTCCTTTATCTTCTTCAAATCATGATTCACCTTTCGGTGACTTTATTATGA  
CTTTGGAGTCATTAGATATCATCACTTCATTTCAAGGAGGTATAAATGACTTTCCA  
CGAGTGGCTCATCTTTGTCTTCTCTTTTCTTTTTTCTTTTTATATAATATATCCTTCA  
CAATCCTTACTTGGACCGCATTTAGCTGTGTGAGAGTATATTATGCACATTGATC