

## IDENTIFICATION

**Species:** *Arabidopsis thaliana*

**Locus:** AT5G39290

**Gene Model:** AT5G39290.1

**Description:** AtEXPA-29

**Family:** Alpha Expansin

**3D structure:**



## GENOME DATABASES

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

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

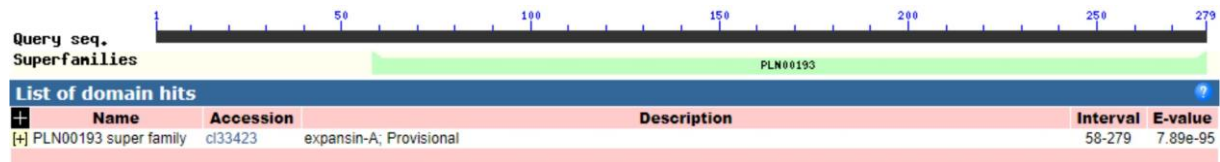
## EXTERNAL RESOURCES

<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-29

MKLLKMIYVEFLMIIMAMWVVPMSYGHGAMIGNAVEAPDVAEAPGINDPSKALDP  
NWDARATFYGDIHGGDTQQGACGYGNLFRQGYGLATAALSTALFNDGYTCGACY  
EIMCTRDPQWCLPGSVKITATNFCPANYSKTTDLWCNPPQKHFDLSLAMFLKIAKYK  
AGVVPVRYRRIPCSKTGGVKFETKGNPYFLMVLIYNVGGAGDIKYVQVKENKTGWI  
TMKKNWGQNWTSTVLTGQGLSFRVTTTDGITKDFWNVMPKNWGFQTFDGKINF

### CDS (coding sequence)

>AtEXPA-29

ATGAAACTCTTAGAAAAAATGATATATGTAGAATTTTGTATGATAATAATGGCGA  
TGTGGGTCGTGCCAATGAGTTACGGTCATGGAGCGATGATTGGTAATGCAGTCGA  
AGCACCTGATGTAGCCGAAGCACCCGGGATTAATGACCCAAGCAAGGCACTCGA  
CCCTAATTGGTATGACGCACGAGCCACGTTCTACGGTGACATCCATGGTGGAGAC  
ACTCAACAGGGAGCTTGTGGATACGGTAATCTATTCAGACAAGGCTATGGTCTAG  
CCACAGCAGCGTTAAGTACGGCACTCTCAACGACGGGTACACATGTGGGGCTTG  
TTATGAAATCATGTGCACGCGTGATCCACAATGGTGTTTACCCGGATCCGTC AAG  
ATCACAGCAACAACTTCTGTCCCGCAAATTACAGCAAAACCACAGACCTTTGGT  
GCAATCCACCACAGAAACACTTTGATCTCTCCTTAGCAATGTTTCTCAAGATTGCC  
AAGTACAAAGCCGGGGTTGTCCAGTTAGATACAGACGTATTCCTTGTAGCAAAA  
CTGGTGGTGTCAAGTTTGAACCAAAGGAAACCCTTATTTCTTAATGGTCTTGAT  
ATACAACGTAGGAGGAGCTGGAGATATTAAGTACGTGCAAGTTAAAGAAAACAA  
GACCGGGTGGATAACAATGAAAAAGA ACTGGGGGCAGAATTGGACCACTAGTAC  
AGTATTGACCGGCCAAGGTTTGTTCGTTTACGAGTTACGACGACTGATGGGATTACA  
AAAGATTTTTGGAATGTGATGCCAAAAAATTGGGGATTTGGACAGACTTTTGATG  
GTAAGATTAACCTTTTAA

## Nucleotide

>AtEXPA-29

ATCATTAAAGAGGGATAGTAATCATGAAACTCTTAGAAAAAATGATATATGTAG  
AATTTTTGATGATAATAATGGCGATGTGGGTCGTGCCAATGAGTTACGGTCATGG  
AGCGATGATTGGTAATGCAGTCGAAGCACCTGATGTAGCCGAAGCACCCGGGAT  
TAATGACCCAAGCAAGGCACTCGACCCTAATTGGTATGACGCACGAGCCACGTTC  
TACGGTGACATCCATGGTGGAGACACTCAACGTAAGATCAAATAATAATGTTTCT  
TTTTACTCTCATTACGAATTTGTTTTTTTTGTTAAAATTATATGGTTTTTGGTTACAA  
CGAATCTAATTATTGACTGCAAATTTTCAATATCAAAAAATCTCTATATGATAAC  
ATGTATATATAAAACCAACACACATGTAAGAAAAAAAACGAAAGCCATAATTAG  
TTTTTATGATTAACATATACATATACTCACTTTTTATCCTTATATATTCAATAGA  
GGGAGCTTGTGGATACGGTAATCTATTCAGACAAGGCTATGGTCTAGCCACAGCA  
GCGTTAAGTACGGCACTCTTCAACGACGGGTACACATGTGGGGCTTGTTATGAAA  
TCATGTGCACGCGTGATCCACAATGGTGTTTACCCGGATCCGTCAAGATCACAGC  
AACAAACTTCTGTCCCGCAAATTACAGCAAAACCACAGACCTTTGGTGCAATCCA  
CCACAGAAACACTTTGATCTCTCCTTAGCAATGTTTCTCAAGATTGCCAAGTACA  
AAGCCGGGGTTGTCCAGTTAGATACAGACGTATTCCTTGTAGCAAAACTGGTGG  
TGTCAAGTTTGAAACCAAAGGAAACCCTTATTTCTTAATGGTCTTGATATACAAC  
GTAGGAGGAGCTGGAGATATTAAGTACGTGCAAGTTAAAGAAAACAAGACCGGG  
TGGATAACAATGAAAAAGAAGTGGGGGCAGAATTGGACCACTAGTACAGTATTG  
ACCGGCCAAGGTTTGTCTGTTACAGAGTTACGACGACTGATGGGATTACAAAAGATT  
TTTGAATGTGATGCCAAAAAATTGGGGATTTGGACAGACTTTTGATGGTAAGAT  
TAACTTTTAAGAGAATGATTTGAATTTTATTATACGTGTCTTACACATAAGTGATG  
TATTACGTA CT T G C A A T A A T T T A A A A C T A