

## IDENTIFICATION

**Species:** *Arabidopsis thaliana*

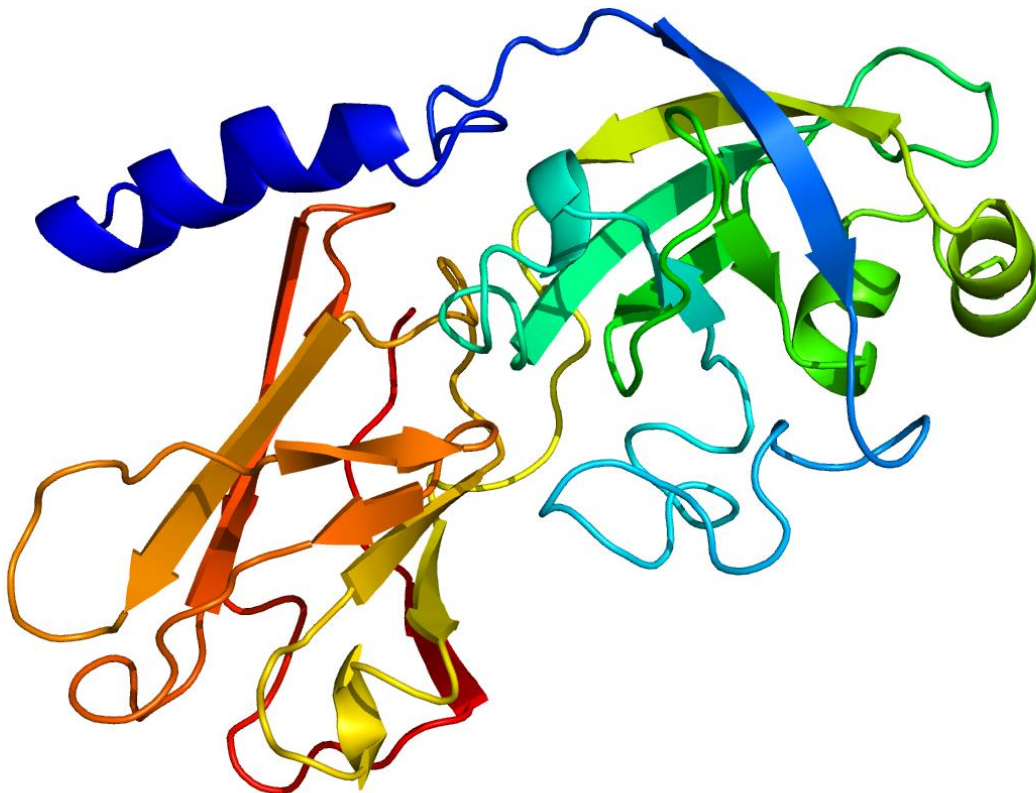
**Locus:** AT4G17030

**Gene Model:** AT4G17030.1

**Description:** AtEXLB-01

**Family:** Expansin Like Beta

**3D structure:**



## GENOME DATABASES

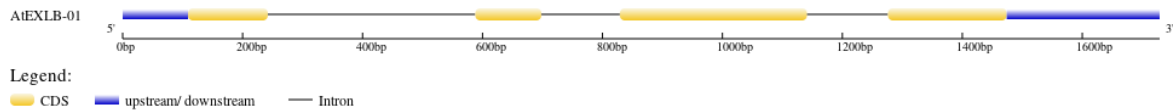
TAIR: <https://www.arabidopsis.org/>

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

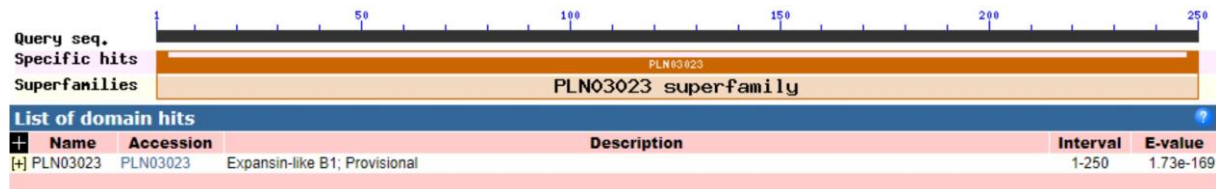
## EXTERNAL RESOURCES

<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

>AtEXLB-01

MKSHVLLLLLVQVIVLLPLLCLSDDFVNSRATYYGSPDCKANPRGHCGYGEFGRDI  
NNGEVSGVSWRLWNNGTGCGACYQVRCKIPPHCSEEGVYVVATDSGEGDGTDFILS  
PKAYGRMARPGTENQLYSFGVVNVEYQRIPCRYAGYNLVYKIHEKSYNPHYLAAILVL  
YVGGVNDILAVEVWQEDCKEWRMRVFGAVHDLQNPGRGLTLRFLVYGSAGIN  
WIQSPNAIPADWTAGATYDSNILLT

### CDS (coding sequence)

>AtEXLB-01

ATGAAGCATTCTCACGTTTTGCTTCTTCTATTTGTTCAAGTCATTGTCCTTTTGCCT  
CTCCTTTGTCTATCCGACGATTTTGTAACTCTAGAGCTACTTATTATGGCAGCCC  
CGATTGCAAAGCAAATCCTCGGGGACATTGTGGGTATGGAGAATTTGGAAGAGA  
TATCAATAACGGTGAAGTGAGTGGTGTTCATGGCGACTATGGAACAATGGA  
GGCTGTGGTGCTTGTACCAGGTGAGGTGCAAGATACCACCACACTGCAGTGAGG  
AAGGAGTATACGTAGTGGCTACGGACTCCGGAGAAGGAGATGGCACGGACTTCA  
TCTTAAGCCCTAAGGCGTACGGACGTATGGCGCGACCCGGCACAGAAAATCAGC  
TCTACTCCTTCGGTGTAGTCAACGTTGAGTACCAAAGGATCCCTTGCCGATACGC  
AGGGTATAATCTGGTGTATAAGATCCATGAGAAAAGCTACAATCCTCATTATCTT  
GCCATCCTTGTCTTGTACGTTGGTGGTGTAAATGACATCCTCGCCGTTGAAGTCTG  
GCAGGAGGATTGCAAAGAGTGGAGACGTATGAGAAGAGTGTGGAGCGGTTCA  
TGATTTGCAGAATCCACCTAGAGGCACTCTCACATTGAGGTTCTTAGTCTACGGA  
AGCGCAGGAATCAATTGGATCCAATCGCCAAACGCTATTCCCGCTGATTGGACTG  
CCGGAGCCACCTACGACTCCAACATTCTACTTACTTAA

## Nucleotide

>AtEXLB-01

CACTATCTTTTGTGATAAGAAATTCTATTATCAATTCCTATCATTTGTTAAGAAAA  
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ATGGAAGTGGCTGTGGTGCTTGTACCAGGTTATTATATATAGTTATCTACTTATC  
TCAATCAATATTTTCATCAAATATTATTATAGTATATGCTATGTCATTAATTACTAA  
ACTTATATTATGAAAGAAAAAAAACCTTATTTTATGAATTATAAAAAGGTGAGGT  
GCAAGATACCACCACACTGCAGTGAGGAAGGAGTATACGTAGTGGCTACGGACT  
CCGGAGAAGGAGATGGCACGGACTTCATCTTAAGCCCTAAGGCGTACGGACGTA  
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GTACCAAAGGATCCCTTGCCGATACGCAGGGTATAATCTGGTGTATAAGATCCAT  
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TGTGAAACAAAGTTAAACGTTATTATATGGTATGCATGTATATGTATGATTTTAG  
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TTGCAGAATCCACCTAGAGGCACTCTCACATTGAGGTTCTTAGTCTACGGAAGCG  
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AGCCACCTACGACTCCAACATTCTACTTACTTAATTGATTCACTTTTTCATCAGTGT  
GTTTTTATCATATAGTATTTATTATGGTTTCTGTATGCAATGGCTAATATATTTAA  
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ATTCATATATAATTTATGTATTGTGTCTCACTAAGAAGATTGTAATGGTTTGTATG  
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ACGTTTCGTAA