

## IDENTIFICATION

**Species:** *Arabidopsis thaliana*

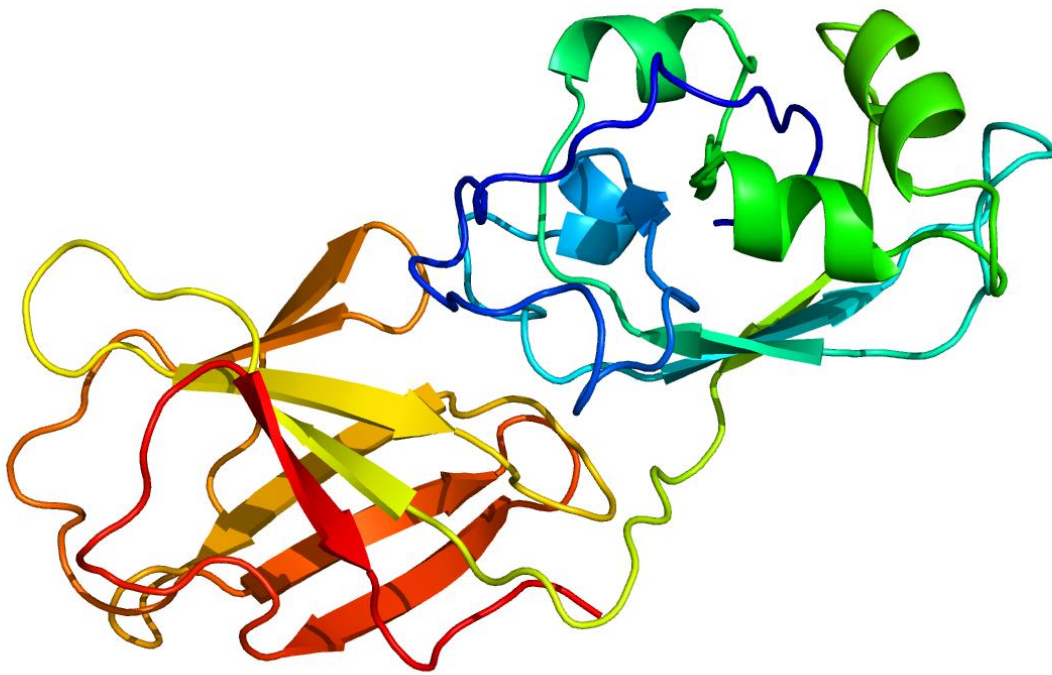
**Locus:** AT1G65681

**Gene Model:** AT1G65681.1

**Description:** AtEXPB-02

**Family:** Beta Expansin

**3D structure:**



## GENOME DATABASES

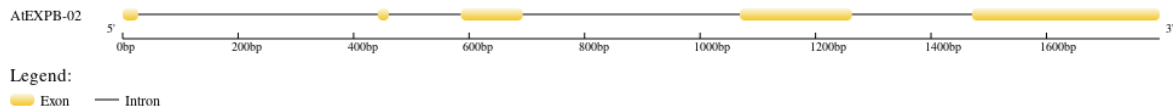
TAIR: <https://www.arabidopsis.org/>

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

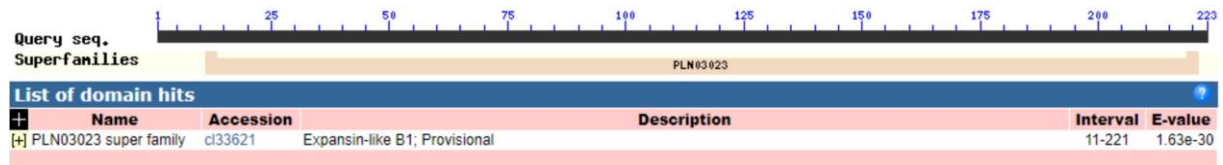
## EXTERNAL RESOURCES

<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

>AtEXPB-02

MIGELDFPFLGAGSTGGACGFAVANPPLYGMVSAGGPSVFNNGIGCGTCFQILCNGH  
PACSRRPITVTITDECPGGPCASEPAHFDSLKAMGALARPGQDRLRSAGVLRVYY  
RRVECLYRRTNIAFRMDPGANPYYSISVVEYENGDLAYIEIQPADGEFIPMQEMRS  
AVWKISSGSPLTGPFNIRL TSAESHKVVLA YNVIPANWKPNETYRSVVNFK

### CDS (coding sequence)

>AtEXPB-02

ATGATTGGAGAGCTTGATTTTCCATTTT TAGGCGCCGGTAGCACCGGAGGAGCTT  
GTGGTTTCGCAGTGGCTAATCCACCATTATACGGGATGGTTTCAGCTGGAGGTCC  
TTCAGTGTTCAACAATGGAATAGGATGTGGAACATGTTTT CAGATTCTATGCAAT  
GGGCATCCAGCATGCTCGAGGAGACCAATAACGGTGACGATAACCGACGAATGC  
CCTGGTGGTCTTGTGCCTCTGAACCAGCCACTTTGATCTTAGCGGCAAAGCCAT  
GGGTGCCTTAGCCAGACCTGGCCAAGGCGATCGACTTCGATCGGCTGGTGTCTA  
CGTGTTTACTACAGACGCGTGGAATGTTTATATCGAAGA ACTAACATAGCTTTCC  
GTATGGACCCTGGAGCAAATCCGTA CTACATTTCA TTTGTTGTCGAGTATGAAAA  
CGGTGATGGAGATTTGGCCTATATAGAAATTCAACCAGCCGACGGAGAATTCATC  
CCCATGCAAGAAATGAGGTCTGCTGTATGGAAGATCAGCTCTGGCAGTCCTCTAA  
CAGGACCATTCAACATCAGACTTACTTCTGCTGAATCTCATAAAGTAGTCCTAGC  
TTATAATGTTATTCCGGCGAATTGGAAACCTAATGAAACTTACCGTTCAGTTGTG  
AACTTTAAGTAG

### Nucleotide

>AtEXPB-02

ATGATTGGAGAGCTTGATTTTCCATTTGTAAGAAGTGACTCAGATTTT TAGTTTTCG  
GGTCTAAGTGTGGGAGAACTCGGTGAAAGAGAGGGTTCGAAGTCTGTTGTGAC

TAAAGTCATAACACGTGAGGCGAGCTGACTAAAGTCATAACACGTGAGGCGAGC  
TGACTAAGGTCATAACAAGCTTGAGGGCGTTTTGGTCTTTTCGCATGAGCTCTGTA  
ACTATATCTTCTTCTTCTTCTCTGTAATTCTGTTAGATCGGAGATAGAGAAAGAGA  
GAGAATTGTAATCAAGTTCTAGAGAGAACTAGAGAGAGAAAACCTTGTAAGATA  
CATTGTAAAGAAAGGTTCTAGTGGATTTCCGGAGAGATTCTCCGGCGAGACGTAG  
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GGCTAATCCACCATTATACGGGATGGTTTCAGCTGGAGGTCCTTCAGTGTTCAAC  
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CTTTGTTAATGCTTTTTTAGGTAATATATTAGTTAGAATAGTATTTTCAGAAAAGAT  
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AGGCGATCGACTTCGATCGGCTGGTGTCTACGTGTTTACTACAGACGGTACTTAT  
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ACATAGCTTTCCGTATGGACCCTGGAGCAAATCCGTACTACATTTTCATTTGTTGTC  
GAGTATGAAAACGGTGATGGAGATTTGGCCTATATAGAAATTCAACCAGCCGAC  
GGAGAATTCATCCCATGCAAGAAATGAGGTCTGCTGTATGGAAGATCAGCTCTG  
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CGTTCAGTTGTGAACTTTAAGTAG