

## IDENTIFICATION

**Species:** *Eucalyptus grandis*

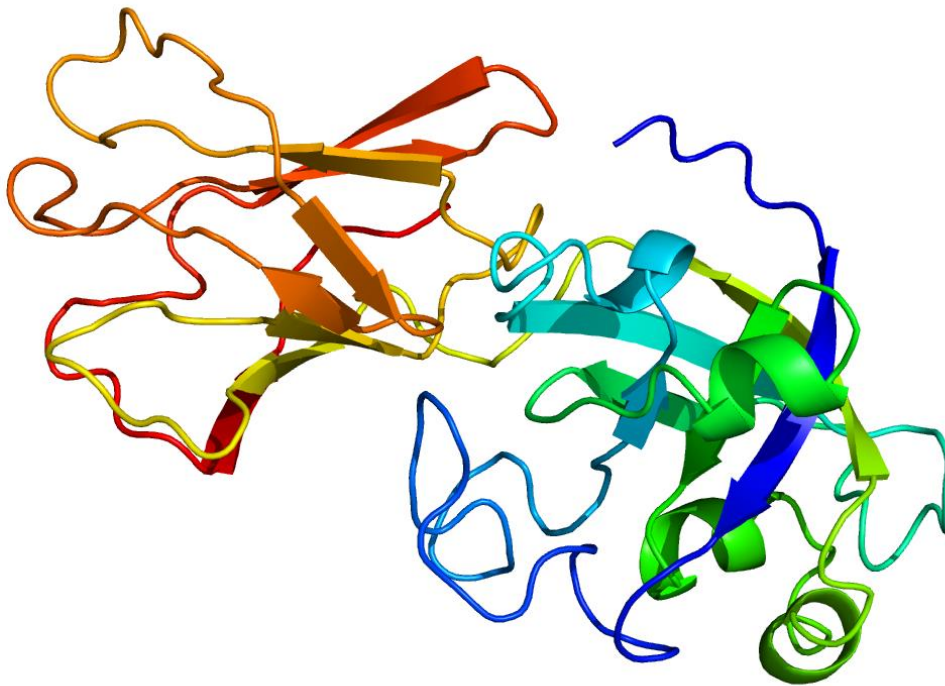
**Locus:** Eucgr.K00177

**Gene Model:** Eucgr.K00177.1.p

**Description:** EgrEXPB-11

**Family:** Beta Expansin

**3D structure:**



## GENOME DATABASES

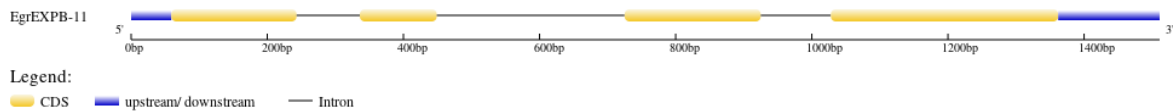
Phytozome: [https://phytozome-next.jgi.doe.gov/info/Egrandis\\_v2\\_0](https://phytozome-next.jgi.doe.gov/info/Egrandis_v2_0)

KEGG: <https://www.genome.jp/entry/T03547>

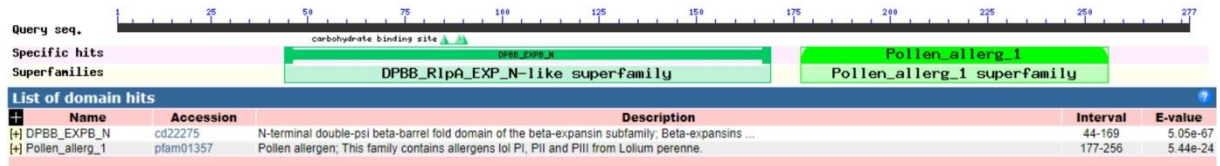
## EXTERNAL RESOURCES

<https://eucgenie.org/>

## GENE STRUCTURE



## DOMAIN ARCHITECTURE



## SEQUENCES

### Peptide

>EgrEXPB-11

MAALHSFRFHPSIFLCLVASFCFSRTCFCGSKAKHSNLTTFGTRWSWAGATWYGSPDG  
AGSDGGACGYGNAVSQPPFSSMVTGIGPSLYKSGKECGACYKIKCTKRMHPPSCSGPK  
VRVIITDFCPGGPCATNSAHFDLSGTAFGAMAKAGEEVAFRDAGVLKIRYARVACDY  
SGRTIAFHVDPGSNSNYFAAVIEYEEGDGDLAGVSLKEASMGPEEWRSMQQSWGAV  
WKLDAGSEMQPPFSIRLTSQYSRETIVAKNVIPENWKPGSTYRSLVNYL\*

### CDS (coding sequence)

>EgrEXPB-11

ATGGCCGCTCTTCACTCGTTTCGATTTACCCCTTCGATCTTCTTGTGTTTGGTAGCC  
TCGTTTTGCTTCAGCCGGACGTGCTTCGGCTCAAAGCCAAGCACTCGAACTTAA  
CAACATTCGGAACCCGCTGGTCTTGGGCCGGAGCGACCTGGTATGGTAGTCCCGA  
TGGAGCCGGCAGCGACGGCGGAGCCTGTGGATACGGGAATGCGGTGTCGCAACC  
GCCGTTCTCTTCCATGGTGACTGGAATCGGCCCTTCTCTGTACAAATCGGGCAA  
GAGTGTGGAGCTTGCTACAAGATCAAATGTACAAAAGAATGCATCCATCCTGTT  
CGGGCAAACCGGTAAGGGTGATCATCACGGACTTTTGCCCCGGAGGTCCCTGCGC  
GACTAATTCCGCCCATTTGACCTCAGCGGGACCGCATTTCGGTGCTATGGCTAAA  
GCAGGAGAAGAAGTCGCATTCCGGGATGCTGGAGTCCTCAAATCCGATATGCTC  
GAGTCGCGTGCGATTACTCAGGAAGAACCATAGCATTCCATGTTGATCCAGGGTC  
CAACTCCAACTACTTTGCGGCGGTGATTGAGTATGAAGAGGGAGATGGCGACCTT  
GCAGGAGTATCACTAAAGGAAGCTTCGATGGGGCCTGAGGAGTGGAGGTCGATG  
CAACAGTCATGGGGTGCTGTTTGAAGCTGGACGCTGGCTCAGAGATGCAACCTC  
CGTTCTCAATTCGGCTGACATCGCAATACTCAAGAGAGACCATAGTGGCCAAGAA  
CGTGATTCCGGAAAACCTGGAAGCCTGGTTCAACCTATAGATCTCTAGTCAACTAC  
TTGTAA

### Nucleotide

>EgrEXPB-11

AAACAAAGCTCTTTCATTACTATAACATGCGAAAGTCCTTGTAATAAAGATCACT  
AAACATGGCCGCTCTTCACTCGTTTCGATTTACCCCTTCGATCTTCTTGTGTTTGGT  
AGCCTCGTTTTGCTTCAGCCGGACGTGCTTCGGCTCAAAGCCAAGCACTCGAAC  
TTAACAACATTCGGAACCCGCTGGTCTTGGGCCGGAGCGACCTGGTATGGTAGTC

CCGATGGAGCCGGCAGCGACGGTATGGAATGTACGGGGAGAGAGAGAGAGGGA  
GGGTCTGGTTGTTTCTTATGTGATTCATGCAAGAATGACATCCTATGTTGGCATGC  
TGCAGGCGGAGCCTGTGGATACGGGAATGCGGTGTTCGCAACCGCGTTCTCTTCC  
ATGGTGACTGGAATCGGCCCTTCTCTGTACAAATCGGGCAAAGAGTGTGGAGCTT  
GCTACAAGGTACGCTCCATTTATATCGCCAACCTTTGCGAACACAATAGAGTAGAT  
TCGCACGTCGAGTGCATGTTGATGCCTGAAAATCTCGCGTTACAATTGGAACAAA  
GCGACATTCTGTCTGGTCCAAAAATTCTTGATTTCCGAAGTTAGGCTTTGACATCGC  
ACGCTTACCTTCATCATCTGCTGGCAAATGTAGCAGATGGAGGTGAACTTGTCC  
GGGTATATATCAGCTTGCATAACCTACTAATGTAGAGTCCTGGGTTCTATGTTTAC  
TCGATAGATCAAATGTACCAAAGAATGCATCCATCCTGTTCTGGGCAAACCGGTA  
AGGGTGATCATCACGGACTTTTGCCCCGGAGGTCCCTGCGCGACTAATTCCGCCC  
ATTTGACCTCAGCGGGACCGCATTCCGGTGCTATGGCTAAAGCAGGAGAAGAAG  
TCGCATTCCGGGATGCTGGAGTCCTCAAATCCGATATGCTCGGTAACCTCATCTA  
ACATAACCAGAAAATGCTTCTGGCTCAGCGAGGGTCTCGATTTGTATTGCCAATT  
CAGTTGACACCTTCCATGCATTTCTTACATTTCCAGAGTCGCGTGCGATTACTCAG  
GAAGAACCATAGCATTCCATGTTGATCCAGGGTCCAACTCCAACTACTTTGCGGC  
GGTGATTGAGTATGAAGAGGGAGATGGCGACCTTGCAGGAGTATCACTAAAGGA  
AGCTTCGATGGGGCCTGAGGAGTGGAGGTCGATGCAACAGTCATGGGGTGCTGTT  
TGGAAGCTGGACGCTGGCTCAGAGATGCAACCTCCGTTCTCAATTCGGCTGACAT  
CGCAATACTCAAGAGAGACCATAGTGGCCAAGAACGTGATTCCGGAAAACCTGGA  
AGCCTGGTTCAACCTATAGATCTCTAGTCAACTACTTGTAAATTGTCTGGCACACTA  
CAAAGGCCTTCAAGCGCTATTGGCTCAGTGTCAAAGAACTAGATTAGCATAAGCA  
CGAGATGTTGGTTAGTGTATTGGGCACTGTAGTTTTTGGCTATCGTAGTATTTGAG  
GATTGCAGACTTCAGTTACCGTC