

## IDENTIFICATION

**Species:** *Eucalyptus grandis*

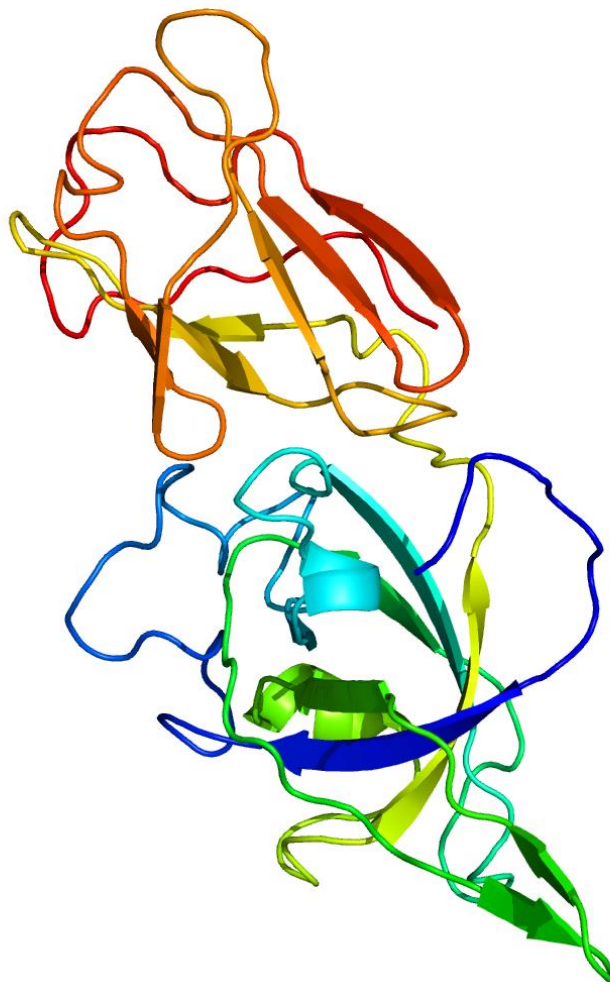
**Locus:** Eucgr.E03359

**Gene Model:** Eucgr.E03359.1.p

**Description:** EgrEXPA-10

**Family:** Alpha Expansin

**3D structure:**



## GENOME DATABASES

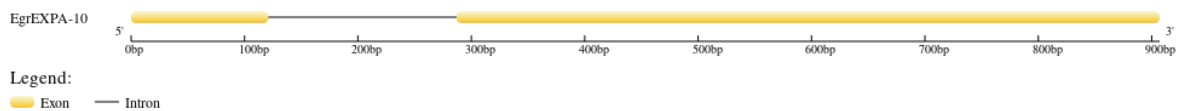
Phytozome: [https://phytozome-next.jgi.doe.gov/info/Egrandis\\_v2\\_0](https://phytozome-next.jgi.doe.gov/info/Egrandis_v2_0)

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

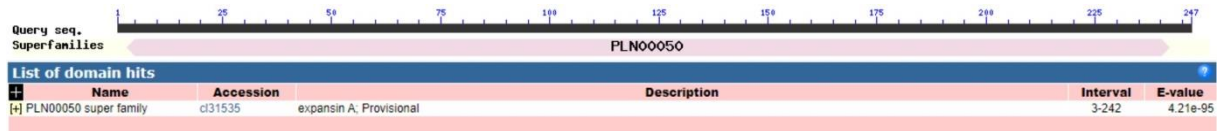
## EXTERNAL RESOURCES

<https://eucgenie.org/>

## GENE STRUCTURE



## DOMAIN ARCHITECTURE



## SEQUENCES

### Peptide

>EgrEXPA-10

MAVHEVFLILAMAVVVS AIDGTWYDARATFYGDMGGGETMQGACGYGDLIKQGY  
GLATTALSTALFNEGLSCGACFEIYCSNAPKSCIPKAAPIIVTATNFCPPNYTKTKDIW  
CNPPQKHFDSLMPMFTKIAYYKAGVIPVRYRRVLC SKRGGVKFEIKGNPNWTLVLIY  
NVGGAGDVNAVSIKGSNTQWIAMTRNWGQNWQTGTVLTGQSLSFQVTVSDGTKIEF  
DNAVPAGWQFGQTYDGGKNF\*

### CDS (coding sequence)

>EgrEXPA-10

ATGGCTGTTCACGAGGTCTTCCTCATATTAGCTATGGCGGTGGTAGTTTCTGCTAT  
AGATGGTACTTGGTACGATGCGCGTGCGACTTTTTACGGTGACATGGGCGGTGGC  
GAAACCATGCAGGGAGCTTGCGGATATGGAGATCTCATCAAACAAGGTTATGGA  
CTAGCGACAACAGCACTAAGCACCGCCCTTTCAACGAAGGACTTAGCTGCGGTG  
CTTGTTCGAGATCTACTGTAGCAACGCCCCAAGTCGTGCATTCCAAGGCTGCT  
CCAATCATAGTCACGGCAACAAATTTTTGCCCTCCGA ACTACACTAAGACGAAGG  
ACATCTGGTGCAATCCTCCGCAAAAGCATTTCGACCTGTCTATGCCCATGTTACC  
AAGATCGCGTACTATAAGGCCGGCGTCATTCTGTCCGCTATCGCCGCGTCTTGT  
GTTCCAAGCGAGGAGGAGTCAAGTTCGAGATTAAGGAAATCCGA ACTGGACCC  
TTGTGCTAATCTATAACGTCGGTGGCGCCGGCGACGTGAATGCAGTGAGCATCAA  
GGGCTCGAACACGCAATGGATTGCTATGACTCGTAACTGGGGGCAAACTGGCA  
GACTGGA ACTGTTTTGACGGGGCAGAGCTTGTCAATCCAAGTCACCGTGAGTGAC  
GGGACGAAGATAGAATTTGATAATGCGGTGCCTGCAGGGTGCCAATTTGGGCAG  
ACATATGATGGGGGAAAGA ACTTCTAG

### Nucleotide

>EgrEXPA-10

ATGGCTGTTCACGAGGTCTTCCTCATATTAGCTATGGCGGTGGTAGTTTCTGCTAT  
AGATGGTACTTGGTACGATGCGCGTGCGACTTTTTACGGTGACATGGGCGGTGGC  
GAAACCATGCGTAAGTAAAATCTCTTGGCAAGGAGAAAGAAAGGAGAGCCTTTT  
CCTAATTTTATTATCCTTTTTTTGTACTCCTTTGCGGGGACCTTTAGGCAGATGGAT  
GATTGAGCTATTTTCATGTCACTGGTGTACTGATTTGTTTCTCGTTCATGGTCATT  
GCCTGCAGAGGGAGCTTGCGGATATGGAGATCTCATCAAACAAGGTTATGGACT

AGCGACAACAGCACTAAGCACCGCCCTTTTCAACGAAGGACTTAGCTGCGGTGCT  
TGTTTCGAGATCTACTGTAGCAACGCCCCCAAGTCGTGCATTCCCAAGGCTGCTC  
CAATCATAGTCACGGCAACAAATTTTTGCCCTCCGAACTACACTAAGACGAAGGA  
CATCTGGTGCAATCCTCCGCAAAGCATTTCGACCTGTCTATGCCCATGTTACCA  
AGATCGCGTACTATAAGGCCGGCGTCATTCCTGTCCGCTATCGCCGCGTCTTGTGT  
TCCAAGCGAGGAGGAGTCAAGTTCGAGATTAAAGGAAATCCGAACTGGACCCTT  
GTGCTAATCTATAACGTTCGGTGGCGCCGGCGACGTGAATGCAGTGAGCATCAAG  
GGCTCGAACACGCAATGGATTGCTATGACTCGTAACTGGGGGCAAACTGGCAG  
ACTGGAAGTGTGACGGGGCAGAGCTTGTCATTCCAAGTCACCGTGAGTGACG  
GGACGAAGATAGAATTTGATAATGCGGTGCCTGCAGGGTGGCAATTTGGGCAGA  
CATATGATGGGGGAAAGAACTTCTAG