

## IDENTIFICATION

**Species:** *Eucalyptus grandis*

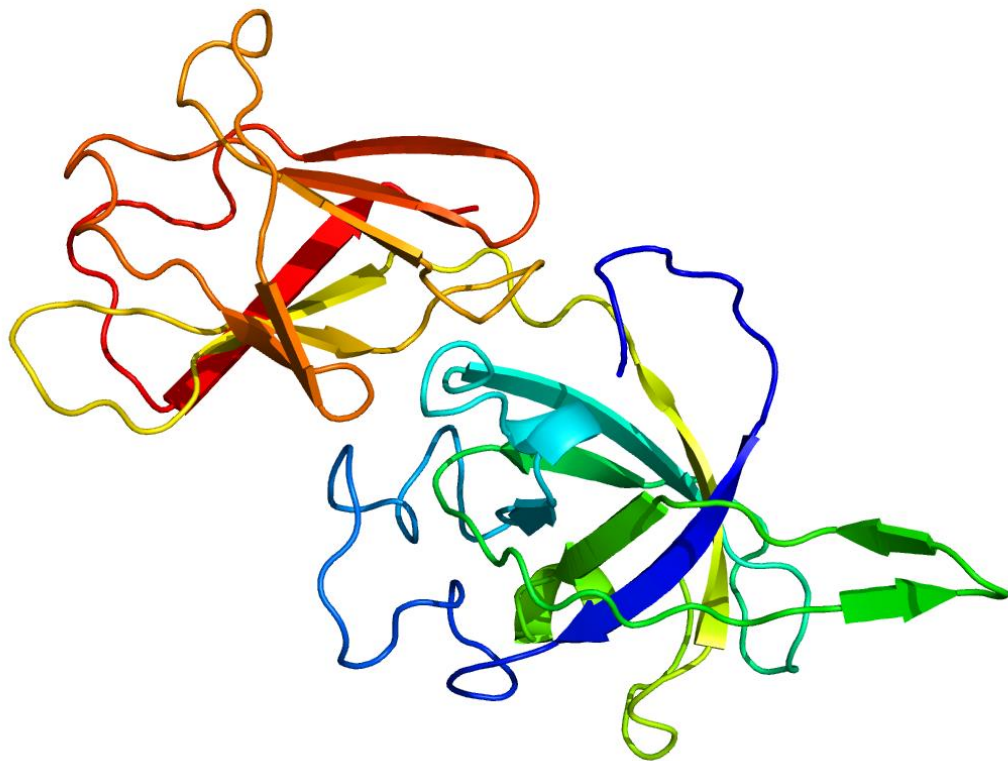
**Locus:** Eucgr.L02610

**Gene Model:** Eucgr.L02610.1.p

**Description:** EgrEXPA-25

**Family:** Alpha Expansin

**3D structure:**



## GENOME DATABASES

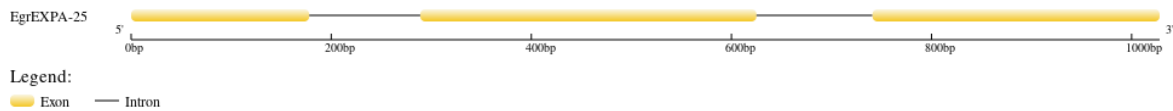
Phytozome: [https://phytozome-next.jgi.doe.gov/info/Egrandis\\_v2\\_0](https://phytozome-next.jgi.doe.gov/info/Egrandis_v2_0)

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

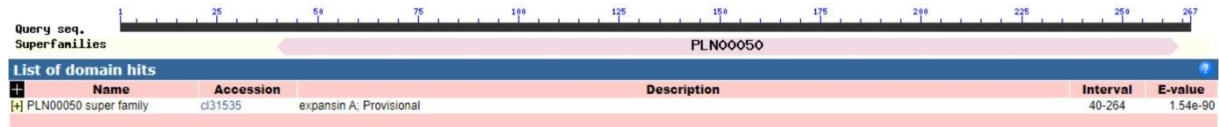
## EXTERNAL RESOURCES

<https://eucgenie.org/>

## GENE STRUCTURE



## DOMAIN ARCHITECTURE



## SEQUENCES

### Peptide

>EgrEXPA-25

MARPEYPHQSTVVLGSLALMMVLLFGVAGGNSHNGGSLQGWDS SAHATFYGDMR  
GNETMKGACGYGDLFKQGYGLKTTALSTVLFNDGATCGACYVIICIHSPWCLPNRPII  
RVTATNFCPPNYSKPTEVWCNPPQKHFDLSLPMFLKIARYRAGIVPVAFRRVKCGPK  
QGGMKFEMKGNWWLLVLVYNVGGDGQVVDVKIKGTRTGWVGMTRNWWGQNWQ  
TSVDLRGQALSFRVTTSDRMVLQSDNVAPPDWQFGRTYEGRNFAD\*

### CDS (coding sequence)

>EgrEXPA-25

ATGGCTCGGCCTGAGTACCCTCATCAGTCAACAGTGGTGCTCGGAAGTCTTGCAT  
TGATGATGGTTCTTTTGTTCGGGTGTCGCCGGCGGCAACAGCCACAATGGTGGCAG  
CCTCCAAGGATGGGATTCCAGCGCTCATGCCACATTCTACGGCGACATGCGTGCC  
AATGAGACCATGAAGGGAGCTTGTGGGTATGGCGACCTGTTCAAGCAAGGGTAT  
GGACTGAAGACAACAGCCCTAAGCACCGTCCTCTTCAACGACGGAGCGACTTGC  
GGAGCCTGCTACGTGATAATTTGCATCCATTCCCCCTGGTGCTTACCCAACCGGCC  
CATCATCCGCGTCACTGCCACCAACTTTTGCCCGCCAACTACTCCAAACCGACT  
GAGGTCTGGTGCAACCCGCCCAAAGCACTTTGATCTCTCCCTGCCCATGTTCCCT  
CAAGATCGCTCGCTATCGTGCCGGGATCGTGCCCTGTGGCATTCCGCCGAGTGAAG  
TGTGGTCCGAAGCAAGGAGGGATGAAGTTCGAGATGAAAGGGAACGAGTGGTGG  
CTGCTGGTGCTTGTGTACAATGTTCGGGGGAGACGGGCAAGTGGTGGACGTGAAG  
ATCAAGGGGACGAGGACGGGCTGGGTTCGGGATGACTCGGAATTGGGGTCAGAAT  
TGGCAAACCTCGGTTCGACCTCCGAGGCCAGGCCTTGTCTTCCGGGTCACCACCA  
GTGACCGGATGGTGCTCCAGTCCGACAACGTGGCGCCCGCCGATTGGCAGTTTGG  
CCGACTTATGAGGGCAGGAATTTGCCCGATTGA

### Nucleotide

>EgrEXPA-25

ATGGCTCGGCCTGAGTACCCTCATCAGTCAACAGTGGTGCTCGGAAGTCTTGCAT  
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CCTCCAAGGATGGGATTCCAGCGCTCATGCCACATTCTACGGCGACATGCGTGCC  
AATGAGACCATGAGTAAGCTACTTTAACTGCAAACCTGCACTGACTCTAATCACGC  
ACACGCACAAGTCCCTCAACGTGACATATATTTATATTATATATCATTCTTGTGG  
CTTTTGCACATAGAGGGAGCTTGTGGGTATGGCGACCTGTTCAAGCAAGGGTATG  
GACTGAAGACAACAGCCCTAAGCACCGTCCTCTTCAACGACGGAGCGACTTGGC

GAGCCTGCTACGTGATAATTTGCATCCATTCCCCCTGGTGCTTACCCAACCGGCC  
ATCATCCGCGTCACTGCCACCAACTTTTGCCCGCCCAACTACTCCAAACCGACTG  
AGGTCTGGTGCAACCCGCCCAAAAGCACTTTGATCTCTCCCTGCCCATGTTCCCTC  
AAGATCGCTCGCTATCGTGCCGGGATCGTGCCTGTGGCATTCCGCCGAGTGAAGT  
GTGGTCCGAAGCAAGGAGGTATGCATACATATAGTCACGCAAGAACTAAAAAGA  
GGCCTCGAGTCCGATTCCTGCGTTATGTGTAATCCTATTTAATGTTATAAGTGAAG  
TGATATGGGTGAGCATAACGAACAGGGATGAAGTTCGAGATGAAAGGGAACGAGT  
GGTGGCTGCTGGTGCTTGTGTACAATGTCGGGGGAGACGGGCAAGTGGTGGACG  
TGAAGATCAAGGGGACGAGGACGGGCTGGGTCTGGGATGACTCGGAATTGGGGTC  
AGAATTGGCAAACCTCGGTCGACCTCCGAGGCCAGGCCTTGTCTTCCGGGTCAC  
CACCAGTGACCGGATGGTGCTCCAGTCCGACAACGTGGCGCCGCCCGATTGGCAG  
TTTGGCCGGACTTATGAGGGCAGGAATTCGCCGATTGA