

## IDENTIFICATION

**Species:** *Eucalyptus grandis*

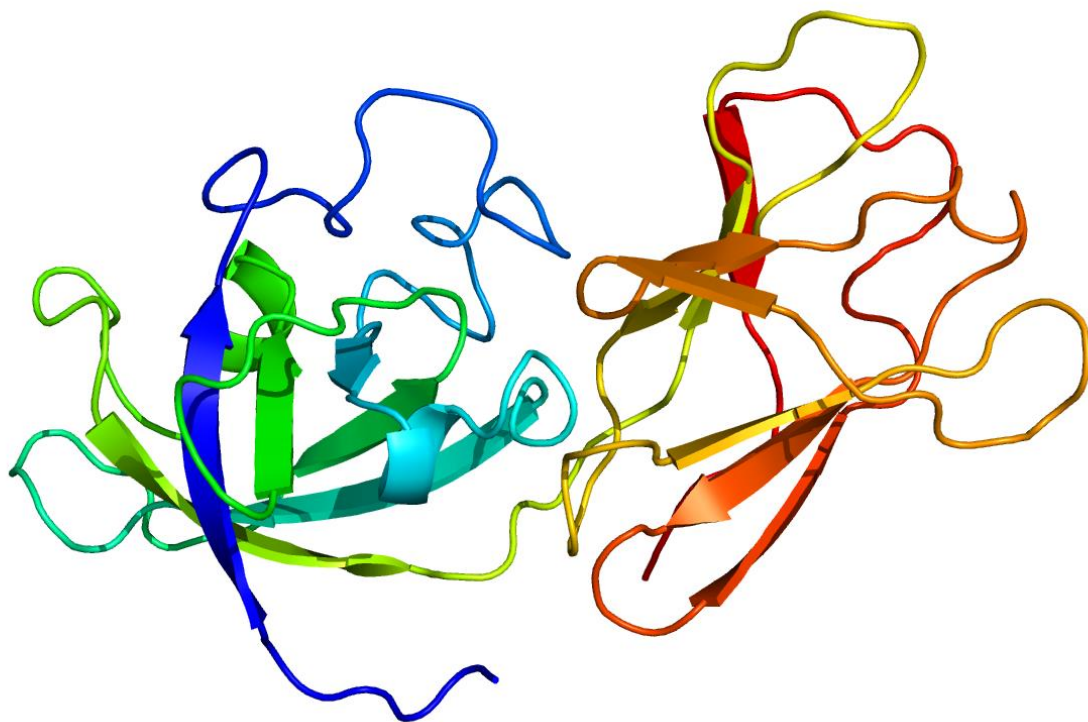
**Locus:** Eucgr.D01943

**Gene Model:** Eucgr.D01943.1.p

**Description:** EgrEXPA-08

**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>

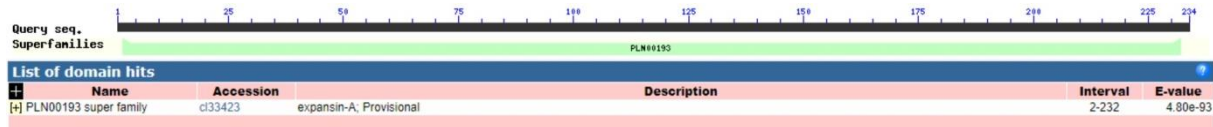
## EXTERNAL RESOURCES

<https://eucgenie.org/>

## GENE STRUCTURE



## DOMAIN ARCHITECTURE



## SEQUENCES

### Peptide

>EgrEXPA-08

GFQPSWSLAHATFYGDETASETMGGACGYGNLFLNGYGTATAALSSTLFNDGYAC  
GTCYQIKCVQSPWCFSGSPFTTVTATNLCPPNWSQDSNNGGWCNPPRTHFDMSKPAF  
MKIAQWKAGIVPVMYRRVPCIKPGGLRFQFQNGYWLLVYVMNVGGGGDIASMW  
VKGSKTDWISMHNWGASYQAFSSLGGQSLFKLTSYTTRETIAYNVAPANWNVGL  
TYQATVNFH\*

### CDS (coding sequence)

>EgrEXPA-08

GGGTTTCAACCTAGCCCATGGTCCCTTGCTCATGCCACTTTCTATGGGGACGAGA  
CTGCCTCCGAGACCATGGGAGGGGCATGTGGGTACGGGAATTTGTTCCCTCAATGG  
GTACGGCACCGCGACGGCGGCTCTGAGCTCGACCCTTTTCAACGATGGGTACGCT  
TGTGGGACATGCTACCAGATCAAGTGCCTGCAGTCGCCCTGGTGCTTCAGCGGCT  
CACCTTTCACTACTGTCACGGCCACCAACCTCTGCCACCCAACCTGGTCCCAGGA  
CTCCAACAACGGTGGGTGGTGCAACCCGCCCGCACCCATTTTGACATGTCCAAG  
CCCGCCTTCATGAAGATCGCTCAGTGGAAGGCCGGCATTGTCCCTGTCATGTATA  
GAAGAGTACCCTGCATAAAGCCAGGAGGGCTCAGATTCCAGTTCCAAGGGAACG  
GTTACTGGCTTTTGGTGTACGTGATGAATGTGGGAGGAGGGGGCGACATCGCCAG  
CATGTGGGTCAAAGGAAGCAAGACTGATTGGATCAGCATGAGCCACAACCTGGGG  
CGCTTCGTACCAAGCCTTCTCAAGCCTTGAGAGCCAGTCTCTCTCCTTCAAGCTCA  
CCTCCTACACCACCGAGAGACCATCATTGCCTACAACGTTGCTCCTGCCAACTG  
GAACGTAGGGTTGACTTACCAAGCCACTGTCAATTTCCACTAG

### Nucleotide

>EgrEXPA-08

GGGTTTCAACCTAGCCCATGGTCCCTTGCTCATGCCACTTTCTATGGGGACGAGA  
CTGCCTCCGAGACCATGGGTACGGCTGTTGTTCCATGTGATCACCGTCTTAATCAA  
TTGCTTTTATAATTTGCATTGCAAATTTGCAATGGCCATACTTCTTTGTTATGTCCA  
TCCTCTCTGGTCCATTGTTCAAGTATTTTTGTAACCTGATATCATTTTAAGTACATA  
AACATGAAGTACATATCTATTCATTAGAGAAATCAACCGTGCCTCCGTTTCCAAT  
TTCCAGGAGGGGCATGTGGGTACGGGAATTTGTTCCCTCAATGGGTACGGCACCGC  
GACGGCGGCTCTGAGCTCGACCCTTTTCAACGATGGGTACGCTTGTGGGACATGC  
TACCAGATCAAGTGCCTGCAGTCGCCCTGGTGCTTCAGCGGCTCACCTTTCTACTA  
CTGTCACGGCCACCAACCTCTGCCACCCAACCTGGTCCCAGGACTCCAACAACGG

TGGGTGGTGCAACCCGCCCCGCACCCATTTTGACATGTCCAAGCCCGCCTTCATG  
AAGATCGCTCAGTGGAAGGCCGGCATTGTCCCTGTCATGTATAGAAGGTAAACAC  
CAACATTTTCTCTAGCCCCTACTTAGTGTATGGCACTAAATTATACACAGCTTCTG  
GTTATAATGAACTCCTTAAAGACATGCATGTGACAATTCGCCCTCGGGCCGCACT  
CAATACCCGACCAAGGTTACATCCAAATCCATTCGTGACTTGAAAAGCTGTGGC  
AATATTTGCAGAGTACCCTGCATAAAGCCAGGAGGGCTCAGATTCCAGTTCCAAG  
GGAACGGTTACTGGCTTTTGGTGTACGTGATGAATGTGGGAGGAGGGGGCGACA  
TCGCCAGCATGTGGGTCAAAGGAAGCAAGACTGATTGGATCAGCATGAGCCACA  
ACTGGGGCGCTTCGTACCAAGCCTTCTCAAGCCTTGGAGGCCAGTCTCTCTCCTTC  
AAGCTCACCTCCTACACCACCCGAGAGACCATCATTGCCTACAACGTTGCTCCTG  
CCA ACTGGAACGTAGGGTTGACTTACCAAGCCACTGTCAATTTCCACTAG