

## IDENTIFICATION

**Species:** *Eucalyptus grandis*

**Locus:** Eucgr.A00986

**Gene Model:** Eucgr.A00986.1.p

**Description:** EgrEXPA-03

**Family:** Alpha Expansin

**3D structure:**



## GENOME DATABASES

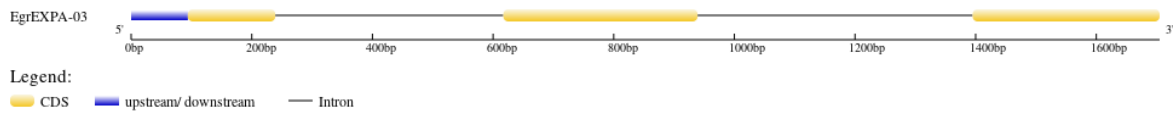
Phytozome: [https://phytozome-next.jgi.doe.gov/info/Egrandis\\_v2\\_0](https://phytozome-next.jgi.doe.gov/info/Egrandis_v2_0)

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

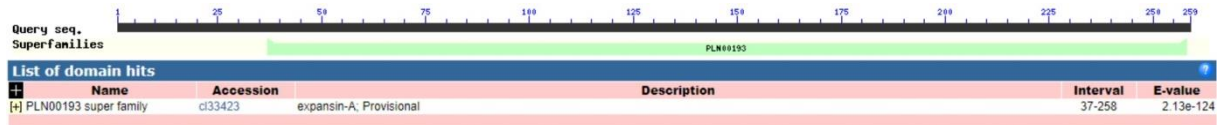
## EXTERNAL RESOURCES

<https://eucgenie.org/>

## GENE STRUCTURE



## DOMAIN ARCHITECTURE



## SEQUENCES

### Peptide

>EgrEXPA-03

MEKVSMHGGGLILSLGLVLMITVQPNGAAAAWLKAHATFYGGSDASGTMGGACGYG  
NLNTDGYGIKTAALSTALFNDGKSCGGCYQIVCDAAQVPQWCLKGTYITITATNFCP  
PNYALPSDNGGWCNPPRPHFDMSQPAFETIAKYSAGIVPILYRKVGCKRNGGIRFTIN  
GRDYFELVLISNVGGAGEILNVWIKGSKMNNWETMSRNWGANWQSLSYLNQSLSRF  
RVQASNGRTVTALNVVPSNWNFGQSFSSTQF\*

### CDS (coding sequence)

>EgrEXPA-03

ATGGAAAAGGTGTCCATGCACGGTGGTCTTATACTTAGTCTTGGCCTGGTGTGGA  
TGATCACTGTGCAACCAAATGGAGCAGCGGCTGCTTGGCTTAAAGCCCACGCAAC  
TTTCTATGGCGGAAGCGATGCTTCAGGAACAATGGGAGGAGCATGTGGATATGG  
GAATCTGAACACAGATGGCTATGGAATCAAGACGGCGGCGCTGAGTACGGCTTT  
GTTCAATGATGGCAAGTCGTGTGGTGGATGTTATCAAATAGTCTGTGATGCCGCA  
CAGGTTCCCTCAGTGGTGTCTCAAGGGCACTTACATTACCATCACTGCCACCAATTT  
CTGCCCGCCAAATTATGCTCTCCCCAGTGACAATGGCGGGTGGTGAATCCCCCA  
AGGCCTCACTTTGACATGTCTCAACCTGCATTTGAGACCATTGCCAAGTACAGTG  
CCGGAATTGTTCCATTTTTGTACAGGAAGGTTGGATGCAAGAGAAATGGAGGCAT  
CAGATTTACCATCAACGGAAGGGACTACTTCGAGCTCGTCCTCATATCTAATGTA  
GGGGGAGCTGGAGAAATCTTGAATGTTTGGATCAAAGGGTCCAAGATGAACAAT  
TGGGAAACCATGTGCGAGAACTGGGGGGCAAAGTGGCAAAGCCTCAGCTATCTC  
AACGGCCAGAGCCTGTCCTTCAGAGTCCAGGCCAGCAATGGCCGAACCGTCACA  
GCCCTTAATGTGGTGCCTTCAAATTGGAATTTTGGCCAGTCCTTTTCTAGCAGCAC  
CCAATTTAA

### Nucleotide

>EgrEXPA-03

GCAATAACAAGAAGAAGAAGAAGGAGGAGGAGGGGAGACACAGAGAGAGAGA  
GAGAGAGACAGAGAGAGAGAGAGACAGAGAGAGACAGAGAGAATGGAAAAGG  
TGTCCATGCACGGTGGTCTTATACTTAGTCTTGGCCTGGTGTGATGATCACTGTG  
CAACCAAATGGAGCAGCGGCTGCTTGGCTTAAAGCCCACGCAACTTTCTATGGCG  
GAAGCGATGCTTCAGGAACAATGGGTGAGTACTGCCTCTTTTTCTTCCTTTCATAT  
TCACCTAATTATGCTCAAGCCACGATCATGTCCAATATTCGAAATGCATAAATGA  
CCTGCAGCTACTTTCACAAAGCCTCATTCTTCTCCTGCAGCATTTCATGATCATCTG  
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TGGATGTTATCAAATAGTCTGTGATGCCGCACAGGTTCCCTCAGTGGTGTCTCAAG  
GGCACTTACATTACCATCACTGCCACCAATTTCTGCCC GCCAAATTATGCTCTCCC  
CAGTGACAATGGCGGGTGGTGCAATCCCCCAAGGCCTCACTTTGACATGTCTCAA  
CCTGCATTTGAGACCATTGCCAAGTACAGTGCCGGAATTGTTCCATTTTGTACAG  
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TTGTCTAGGTTGCAACATGATTCAAGAAAGTTTATTAAGTGGTTTTCCCGGGCCA  
TAATGCTATACAAAAAAAAAAAAAAAAAATTCAGGTGAAACCAGACCGAGCCAATG  
ATTTCTTTATGTCCTTTTCTGGCTTCTCAGTATTTTTTAAATTGCAAGTTGGGTTC  
TTAAAAGTAGAAGCTTTTTCTGCTTTTGGCCC GCTGAATCCAATTTGGTCTTCTTA  
ACTGGACAAGAATATGTAGACTGAAGACCCAACCTCTAGTTTCGGCACAAATTTG  
GCCATAAGAAAATCCGAAGAACTTGCTTAACCAGATTGTA CTACATTATACTGAA  
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AGAAACTGGGGGGCAA ACTGGCAAAGCCTCAGCTATCTCAACGGCCAGAGCCTG  
TCCTTCAGAGTCCAGGCCAGCAATGGCCGAACCGT CACAGCCCTTAATGTGGTGC  
CTTCAAATTGGAATTTTGGCCAGTCCTTTTCTAGCAGCACCCAATTTTAA