IDENTIFICATION

Species: *Eucalyptus grandis*

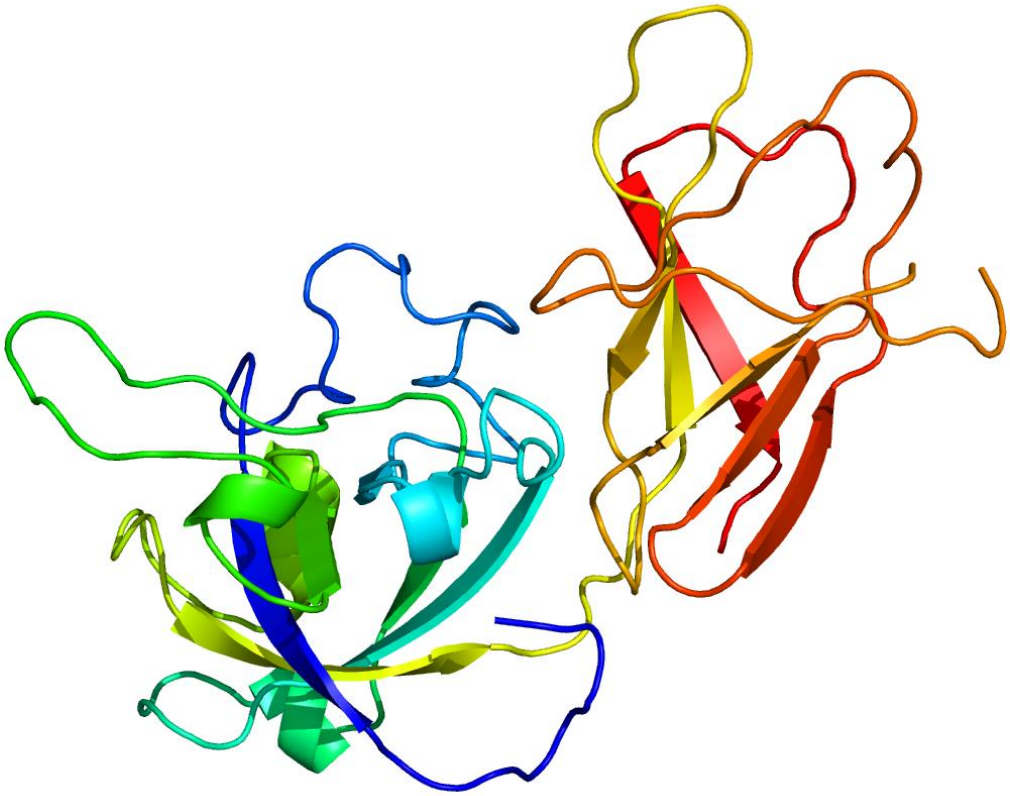
Locus: Eucgr.H05003

Gene Model: Eucgr.H05003.1.p

Description: EgrEXPA-16

Family: Alpha Expansin

3D structure:



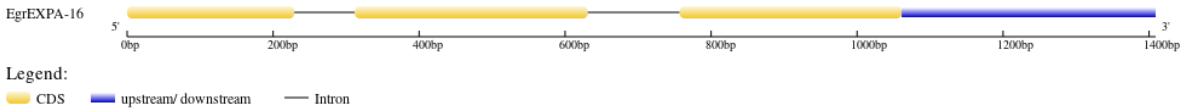
GENOME DATABASES

Phytozome: https://phytozome-next.jgi.doe.gov/info/Egrandis_v2_0
KEGG: https://www.genome.jp/entry/T03547

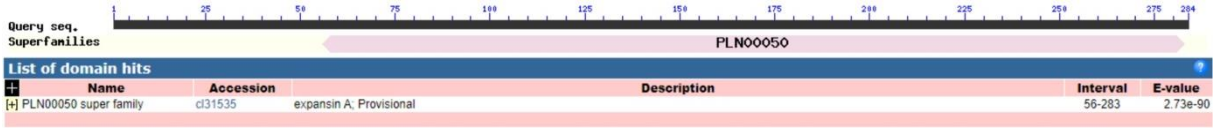
EXTERNAL RESOURCES

https://eucgenie.org/

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>EgrEXPA-16

MSKSPWQCEEKVRNPKRSTKPNFLGSIDPQMGVLRSAFLCLMLVQSCELVASSDSGG
EWKTATATYSVETDGSLITEGACGYGDLHRATYGKYSAGLSSMLFNRGSTCGACFEL
RCVDHILWCLPGSPSVILTATDFCPPNYGLAADYGGWCNFPQEHFEMSEAAFAEIAV
RRADVVPIQYRRVNCLRSGGLRFTLSGNSHFFQVLVTNVGLDGEVIAMKMKGSKTG
WIPMARNWGQSWQSNVDLRGQPLSFEVTTSDRRTLTSYNVAPPSWQFGQTFEGKQF
*

CDS (coding sequence)

>EgrEXPA-16

ATGTCCAAATCCCCATGGCAATGCGAAGAAAAGGTGAGGAATCCTAAGAGAAGT
ACGAAGCCGAACTTCCTAGGAAGCATTGATCCTCAAATGGGTGTTCTTCGGTCCG
CGTTTCTCTGTTTGATGCTCGTGCAAAGCTGCGAGCTTGTCGCCTCCTCTGACTCT
GGTGGCGAATGGAAGACTGCTACCGCGACATACTCTGTAGAGACGGATGGATCTT
TGATAACGGAAGGGGCTTGTGGTTATGGGGACCTTCACAGGGCCACCTATGGCAA
GTACAGTGCCGGCTTGAGCTCGATGCTGTTCAACAGAGGGAGTACCTGCGGGGCT
TGCTTCGAGCTCCGGTGCGTCGACCACATTTTGTGGTGCCTCCCTGGTAGCCCGTC
GGTGATCCTCACCGCCACCGACTTCTGCCCTCCGAACTACGGGCTCGCGGCAGAT
TACGGCGGATGGTGCAACTTCCCGCAGGAGCACTTCGAGATGTCGGAGGCAGCCT
TCGCCGAGATTGCGGTGCGAAGGGCTGATGTGGTGCCTATCCAGTACAGGAGGGT
GAACTGTCTGAGAAGCGGTGGTCTGAGATTCACATTGAGCGGAAACTCTCACTTC
TTTCAGGTCTTGGTGACGAATGTAGGCCTAGATGGGGAGGTGATTGCCATGAAAA
TGAAGGGATCGAAAACAGGGTGGATACCGATGGCAAGAAACTGGGGCCAAAGTT
GGCAATCCAACGTCGACCTTAGAGGACAGCCTCTCTCTTTCGAGGTGACCACCAG
CGACAGAAGAACCCTCACATCTTACAATGTGGCTCCGCCGAGCTGGCAGTTCGGT
CAGACATTTGAAGGGAAACAGTTCTAA

Nucleotide

>EgrEXPA-16

ATGTCCAAATCCCCATGGCAATGCGAAGAAAAGGTGAGGAATCCTAAGAGAAGT
ACGAAGCCGAACTTCCTAGGAAGCATTGATCCTCAAATGGGTGTTCTTCGGTCCG
CGTTTCTCTGTTTGATGCTCGTGCAAAGCTGCGAGCTTGTCGCCTCCTCTGACTCT
GGTGGCGAATGGAAGACTGCTACCGCGACATACTCTGTAGAGACGGATGGATCTT
TGATAACGGGTACTGGTAGTCCCTCTTGTCTTCCTTGCGCTAGTTCCCCTGTTTTC

AGGCATTTGCTCAACCTCTGTTTCCGGTGCTAGCAGAAGGGGCTTGTGGTTATGG
GGACCTTCACAGGGCCACCTATGGCAAGTACAGTGCCGGCTTGAGCTCGATGCTG
TTCAACAGAGGGAGTACCTGCGGGGCTTGCTTCGAGCTCCGGTGCGTCGACCACA
TTTTGTGGTGCCTCCCTGGTAGCCCGTCGGTGATCCTCACCGCCACCGACTTCTGC
CCTCCGAACTACGGGCTCGCGGCAGATTACGGCGGATGGTGCAACTTCCCGCAGG
AGCACTTCGAGATGTCGGAGGCAGCCTTCGCCGAGATTGCGGTGCGAAGGGCTG
ATGTGGTGCCTATCCAGTACAGGAGGTATGGTGAAAGCAACCCACGCAAATGCA
GCTACTTTTTTTTTGGTCGTAAAATGCAGCTACTTTAACGGATGTATTTGTGAGAC
TTGATTCCTAACATCTTTCGACTCTGTGTAAACATCTGCAGGGTGAACTGTCTGAG
AAGCGGTGGTCTGAGATTCACATTGAGCGGAAACTCTCACTTCTTTCAGGTCTTG
GTGACGAATGTAGGCCTAGATGGGGAGGTGATTGCCATGAAAATGAAGGGATCG
AAAACAGGGTGGATACCGATGGCAAGAAACTGGGGCCAAAGTTGGCAATCCAAC
GTCGACCTTAGAGGACAGCCTCTCTCTTTCGAGGTGACCACCAGCGACAGAAGAA
CCCTCACATCTTACAATGTGGCTCCGCCGAGCTGGCAGTTCGGTCAGACATTTGA
AGGGAAACAGTTCTAACATGGAAAACCATGAAGAACAGGAACTGTATACTGCAA
GCTTCTCCCAAGCTTCAGGGCAACGCATTCATAGTAGAAGCAGAATTCTATCATG
TCTTCTCTGTACCATGAACATAGTAGCGACGAAAAGAGAGTAGCAAAGTTGCCTA
AGACAGTTGAAAAGACTATGAATGCAAGGCCCTAGTTTTGTCTCATTGTATTGTG
TTAATGATCGAAAGGTAGAGGCATGCCTTCATTGCTAAGCAATGCATTTACATTG
GGCAATTGGAGTATGTGTATTTCCATCATACCTTCCTAATGTTATAAGGAGTATCT
ATTGCTAAGTGACGCCATTGGCTTGCCCAAGCTC