

IDENTIFICATION

Species: *Eucalyptus grandis*

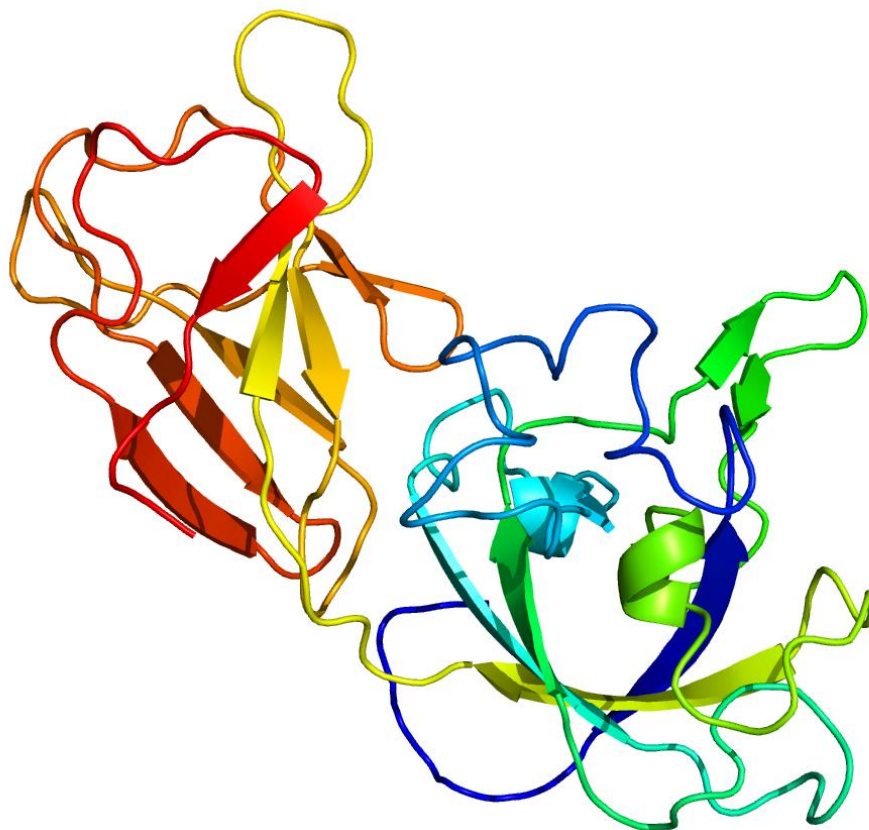
Locus: Eucgr.F02618

Gene Model: Eucgr.F02618.1.p

Description: EgrEXPA-12

Family: Alpha Expansin

3D structure:



GENOME DATABASES

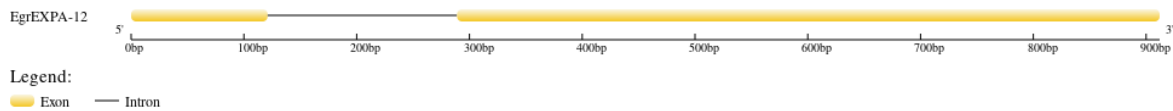
Phytozome: https://phytozome-next.jgi.doe.gov/info/Egrandis_v2_0

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

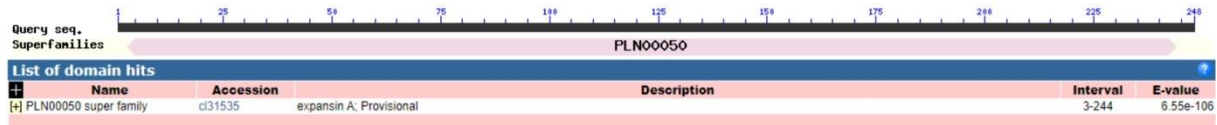
EXTERNAL RESOURCES

<https://eucgenie.org/>

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>EgrEXPA-12

MAVYEVFLALAMATVVS/AIDSWYDAHATCYGDMGGGETMQGACGYGDLFKQG
YGLKTAALSTALFNDGLTCGACFEIYCHNDPQWCIPNAGSIKITATNFCPPNYTPNKP
DAWCNPPQKHFDLSVKMFTKLAEYRAGIIPVR YRRISCSKHGGIKFEINGNPYFTLVLI
YNVGGAGDVNAVKIKGSNTQWIAMSRNWGQNWQTGTVLTGQSLSFQVTVSDGKK
VKLNNVAPAGWQFRHTYNGRNNI*

CDS (coding sequence)

>EgrEXPA-12

ATGGCTGTTTACGAGGTTTTCTCGCATTGGCTATGGCCACGGTAGTGTCTGCCAT
AGACAGTGATTGGTACGATGCGCATGCGACTTGTTACGGCGACATGGGCGGCGG
AGAAACCATGCAGGGAGCTTGTGGATATGGAGATCTTTTCAAACAAGGATATGG
ACTAAAGACCGCAGCACTGAGTACGGCCCTTTTCAATGATGGACTTACCTGTGGC
GCTTGTTTCGAGATCTATTGTCACAACGACCCGCAGTGGTGCATTCCGAATGCGG
GTTCAATCAAATCACTGCAACAACTTCTGCCCTCCGAACTACACCCCAAATAA
ACGGGACGCCTGGTGCAATCCTCCGCAGAAGCACTTCGACCTTCCGTGAAAATG
TTCACGAAGCTTGCGGAGTACAGGGCCGGAATCATCCCCGTCCGCTATCGCCGCA
TCTCGTGTTCCAAGCATGGAGGAATCAAGTTCGAGATCAACGGGAACCCGTA
TACCCTCGTGCTAATTTACAACGTGGGCGGCGCCGGGGACGTGAACGCCGTGAAG
ATCAAGGGCTCGAACACTCAATGGATCGCGATGAGTCGTA
ACTGGGGGCAA
AAT
TGGCAGACCGGA
ACTGTCTTGACGGGGCAAAGCTTATCGTTTCAAGTCACCGTGA
GTGACGGGAAGAAAGTAAA
ACTCAATAATGTGGCGCCTGCTGGGTGGCAATTTA
GGCATA
ACATA
CAACGGGAGAAACAATATCTAG

Nucleotide

>EgrEXPA-12

ATGGCTGTTTACGAGGTTTTCTCGCATTGGCTATGGCCACGGTAGTGTCTGCCAT
AGACAGTGATTGGTACGATGCGCATGCGACTTGTTACGGCGACATGGGCGGCGG
AGAAACCATGCGTAAGTAAAAATCTCTAGGCAAGGAGAAAGTAGGAAGAGCCTT
GCCCTAGCCTTATCATCCTTTCTTGTGCTACTTTGCGCGAGGACATATGTACAGAT
GGATAATGAGGCTACTTCATTTGCTAATGTTTGTGATCTGTTCCCTCGTTCGTGG
TCATCACATGCAGAGGGAGCTTGTGGATATGGAGATCTTTTCAAACAAGGATATG
GACTAAAGACCGCAGCACTGAGTACGGCCCTTTTCAATGATGGACTTACCTGTGG
CGCTTGTTTCGAGATCTATTGTCACAACGACCCGCAGTGGTGCATTCCGAATGCG

GGTTCAATCAAATCACTGCAACAAACTTCTGCCCTCCGAACTACACCCCAAATA
AACCGGACGCCTGGTGCAATCCTCCGCAGAAGCACTTCGACCTTTCCGTGAAAAT
GTTACGAAGCTTGCGGAGTACAGGGCCGGAATCATCCCCGTCCGCTATCGCCGC
ATCTCGTGTTCCAAGCATGGAGGAATCAAGTTCGAGATCAACGGGAACCCGTACT
TTACCCTCGTGCTAATTTACAACGTGGGCGGGCGCCGGGGACGTGAACGCCGTGAA
GATCAAGGGCTCGAACACTCAATGGATCGCGATGAGTCGTA ACTGGGGGCAAAA
TTGGCAGACCGGAACTGTCTTGACGGGGCAAAGCTTATCGTTTCAAGTCACCGTG
AGTGACGGGAAGAAAGTAAACTCAATAATGTGGCGCCTGCTGGGTGGCAATTT
AGGCATACATACAACGGGAGAAACAATATCTAG