

IDENTIFICATION

Species: *Eucalyptus grandis*

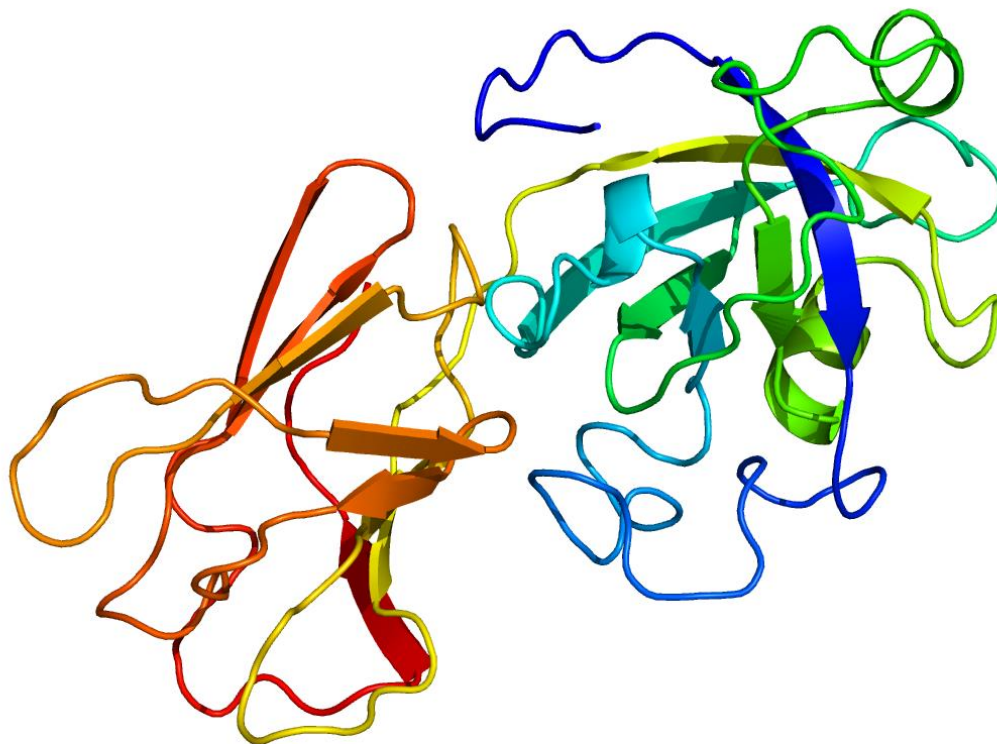
Locus: Eucgr.F02621

Gene Model: Eucgr.F02621.1.p

Description: EgrEXPA-13

Family: Alpha Expansin

3D structure:



GENOME DATABASES

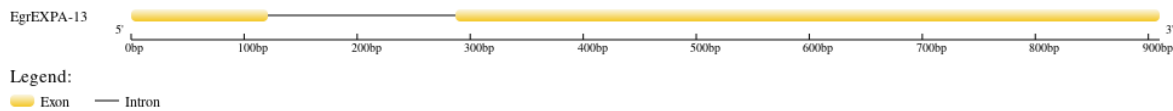
Phytozome: https://phytozome-next.jgi.doe.gov/info/Egrandis_v2_0

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

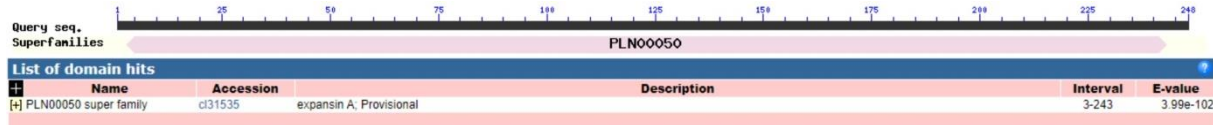
EXTERNAL RESOURCES

<https://eucgenie.org/>

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>EgrEXPA-13

MSVYKVFPLAMAMVVS AIDSNWYDAHATCYGDMGGGETMQGACGYGDLFKQG
YGLETAALSTALFNDGLTCGACFEIYCTNAPQSCIPKAGSIITATNFCPPNYTPHKPDA
WCNPPQKHFDLSMKMFTKLA YYKAGIIPVRYRRVLCSKQGGVKFEINGNPYFTLVLI
YNVGGAGDVNAV KIKGSNTQWITMSRNWGQNWQTGIVLTGQSLSFQVTVSDGKT
EFDNAAPAGWQFGQTYDGGKNF*

CDS (coding sequence)

>EgrEXPA-13

ATGTCTGTTTACAAGGTTTTTTTCCCATTGGCTATGGCTATGGTAGTTTCTGCCAT
AGACAGTAATTGGTACGATGCGCATGCGACTTGTTACGGCGACATGGGCGGTGG
AGAAACCATGCAGGGAGCTTGTGGATATGGAGATCTTTCAAACAAGGATATGG
ACTGGAGACCGCAGCGTTGAGCACGGCCCTTTTCAATGATGGACTTACCTGTGGC
GCTTGTTCGAAATCTATTGTACCAACGCTCCGCAATCGTGCATCCCGAAGGCCG
GTCCATTATAATCACCGCGACAACTTCTGCCACCAAACACTACTCCACATAA
ACCGGACGCCTGGTGCAACCCTCCGCAAAGCATTTCGACCTGTCCATGAAAATG
TTCACGAAGCTTGCCTACTATAAGGCCGGAATCATTCCCGTCCGCTATCGCCGCG
TCCTATGTTCCAAGCAAGGAGGAGTCAAGTTCGAGATCAACGGGAACCCTTACTT
TACCCTCGTGCTAATTTACAACGTGGGCGGCGCCGGGGACGTGAACGCCGTGAAG
ATCAAGGGCTCGAACACCCAGTGGATCACAATGAGTCGTAACCTGGGGGCAAAT
TGGCAGACCGGAATTGTCTTGACGGGGCAAAGCTTGTCTGTTCCAAGTCACCGTGA
GTGACGGGAAGACAGTAGAATTTCGATAATGCGGGCGCCTGCTGGGTGGCAATTTG
GGCAGACATACGACGGGGGCAAGAATTTCTAG

Nucleotide

>EgrEXPA-13

ATGTCTGTTTACAAGGTTTTTTTCCCATTGGCTATGGCTATGGTAGTTTCTGCCAT
AGACAGTAATTGGTACGATGCGCATGCGACTTGTTACGGCGACATGGGCGGTGG
AGAAACCATGCGTAAGTTAAAATCTCTAGGCAAGGAGAAAGTAGGAAGAGCCTT
GCCCTGATCTTATTATCCTTTCTCGTCCTACTTTGCAAGCACATATGTACAGATGG
ATAATGAGACTATTTACGTCGCTAATGTTTGTGATTCTTTTCTCGTTTGTGGTCA
TCGCATGCAGAGGGAGCTTGTGGATATGGAGATCTTTCAAACAAGGATATGGAC
TGGAGACCGCAGCGTTGAGCACGGCCCTTTTCAATGATGGACTTACCTGTGGCGC
TTGTTTCGAAATCTATTGTACCAACGCTCCGCAATCGTGCATCCCGAAGGCCGTT

CCATTATAATCACCGCGACAAACTTCTGCCACCAAACCTACACTCCACATAAACC
GGACGCCTGGTGCAACCCTCCGCAAAAGCATTTCGACCTGTCCATGAAAATGTTC
ACGAAGCTTGCGTACTATAAGGCCGGAATCATTCCCGTCCGCTATCGCCGCGTCC
TATGTTCCAAGCAAGGAGGAGTCAAGTTCGAGATCAACGGGAACCCTTACTTTAC
CCTCGTGCTAATTTACAACGTGGGCGGCGCCGGGGACGTGAACGCCGTGAAGATC
AAGGGCTCGAACACCCAGTGGATCACAATGAGTCGTAACGGGGGCAAAATTGG
CAGACCGGAATTGTCTTGACGGGGCAAAGCTTGTTCGTTCCAAGTCACCGTGAGTG
ACGGGAAGACAGTAGAATTCGATAATGCGGGCGCCTGCTGGGTGGCAATTTGGGC
AGACATACGACGGGGGCAAGAATTTCTAG