

IDENTIFICATION

Species: *Eucalyptus grandis*

Locus: Eucgr.B03214

Gene Model: Eucgr.B03214.1.p

Description: EgrEXPA-07

Family: Alpha Expansin

3D structure:



GENOME DATABASES

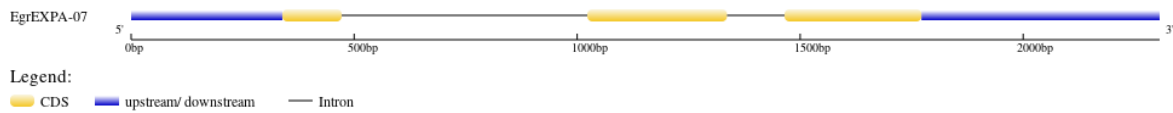
Phytozome: https://phytozome-next.jgi.doe.gov/info/Egrandis_v2_0

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

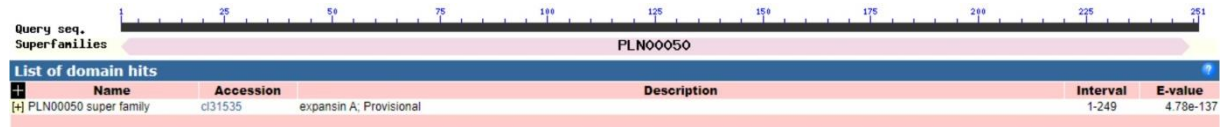
EXTERNAL RESOURCES

<https://eucgenie.org/>

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>EgrEXPA-07

MAVVGLLLVGCLAMWVCSVDGYGGGGWINAHATFYGGSDASGTMGGACGYGNL
YSQGYGTNTAALSTALFNGLSCGSCYEIRCVNDRQWCLPASIVVTATNFCPPNNAL
PSNAGGWCNPPLQHFDLSEPVFEHIARYRAGIVPVA YRRVPCRRRGGIRFTINGHSYF
NLVLITNVGGAGDVHAVSVKGSRTGWMSMSRNWQNWQSNNYLNGQSLSFKVT
SDGRSVMSYNAAPAHWSFGQTFSGAQFR*

CDS (coding sequence)

>EgrEXPA-07

ATGGCCGTGGTTGGGTTGCTGTTGGTGGGTTGCCTCGCAATGTGGGTGTGCTCCGT
CGACGGGTATGGAGGAGGAGGGTGGATCAATGCTCATGCCACTTTCTACGGAGG
CAGTGACGCTTCTGGGACAATGGGTGGAGCCTGCGGGTATGGGAAGTGTACAGC
CAGGGCTACGGCACCAACACCGCGGCGCTGAGCACGGCCCTCTTCAACAACGGC
CTGAGCTGCGGGTCGTGCTACGAGATCCGGTGCCTGAACGACCGCCAGTGGTGCC
TCCCTGCGAGCATCGTGGTCACCGCCACCAACTTCTGCCCGCCCAACAACGCTCT
CCCCAGCAACGCGGGCGGGTGGTGCAACCCCCCTCTCCAACACTTCGACCTCTCT
GAGCCCGTCTTCGAGCACATTGCACGGTACCGGGCTGGGATCGTACCCGTCGCAT
ACCGGAGGGTGCCCTGCCGGAGGAGGGGAGGCATAAGGTTACGATCAACGGCC
ACTCCTACTTCAACCTGGTCCTCATCAACAACGTCGGCGGGGCCGGCGACGTCCA
TGCTGTGTCCGTGAAAGGGTCCAGGACCGGGTGGATGTCCATGTTCGAGGAAGTGG
GGCCAGAACTGGCAGAGCAACAACCTCAACGGCCAGAGCCTCTCCTTCAAG
GTCACCACCAGCGACGGTTCGACGCGTCATGTCCTACAACGCGGGCGCCCGCCACT
GGTCCTTCGGGCAGACCTTCTCAGGAGCCCAGTTCCGCTAG

Nucleotide

>EgrEXPA-07

CAACCCCTCTTCCCAGAACTCCCTATAAATCCCCGCTCAAGCTCCCTTCATTTCC
CTACTCCATTCCCCTCTCTCCTCCCCTCTCTCGCTCTCTCTCTCTCTCTCGGT
CTGTGTGAAGACTGAAGTCTGCTCAGTCTTTTGCAGGTAATAATCACCCCAACC
CCATTTGGGTCATTGCTCTAACTCCAAGAAGCCTCTTTCTTTTCGTCTATACTTATG
CTAGGCTTGGAGAGTGCAGGTGCTTGAACCTGGAGTCCTTTTTTTTACCCAAA
ATGCTGCATTGCATAATTTGGTTGATTTGGTCTTTGGCATGCGCAGGGGAAGCAA
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AGGCAGTGACGCTTCTGGGACAATGGGTAACCAGCCCTTCCCCACTTCGACGCCT
CCCTCTCTTCTTCCTCCTCCGCTTCTTCATTTTCAAGCTCTTTTGCTCTGTTTTGTCT
CGCTAGCACTGTACACAGCTACTCACTCTGCTAATAGTAACAATGATAAAGGTAA
CGACATCCGACAGGAACGTGTCGATGAAGTCCATTGTCTTCCACGTTTTTCATTGC
GGTCCCTACTGTGCTGGTACATCTGACGCAGAAAAGAAAAGAAAACAGGGGAAATT
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CTCAAATTACATTTTCAGGACATGAAAGATGGTGAAGTACAGTACTCATAACAT
CATTAGAAAAAGAAGAGGGCAAAAGACATTGCTTTTTTTTTTTATTTTCCACGTTTCC
CAGAATTTGTAGGTTGACAGGCATTTTAAAGGGAAGTCGCCAGCACAACAGAAG
GGTCCCTCTGCATTTTGCTCTCCTATAGGTGGAGCTCATCTCTAAACTCCGTCTCAT
CCTTAAATTTTTGGTCACATTAGGTGGAGCCTGCGGGTATGGGAAC TTGTACAGC
CAGGGCTACGGCACCAACACCGCGGGCTGAGCACGGCCCTCTTCAACAACGGC
CTGAGCTGCGGGTCGTGCTACGAGATCCGGTGC GTGAACGACCGCCAGTGGTGCC
TCCCTGCGAGCATCGTGGTCACCGCCACCAACTTCTGCCCGCCAACAACGCTCT
CCCCAGCAACGCGGGCGGGTGGTGAACCCCCCTCTCCAACACTTCGACCTCTCT
GAGCCCGTCTTCGAGCACATTGCACGGTACCGGGCTGGGATCGTACCCGTCGCAT
ACCGGAGGTACGTGCATTGCAACGCTAGGCCCAGTTTTTTTTGGTCGCGTGAAAAA
GTTAGGCGCGTGTGTTAAGCACATGAACTCTTTGGTCCGACTAGTCAATTTACAA
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CCCGCATTTGGCTGTTTATGTCCACGACTGTAATATGTTTGTATTGGAAACATCAA
GTCATTCTATTCAGATCGAAAGACTTTGCATTTTAATTTTT