

IDENTIFICATION

Species: *Eucalyptus grandis*

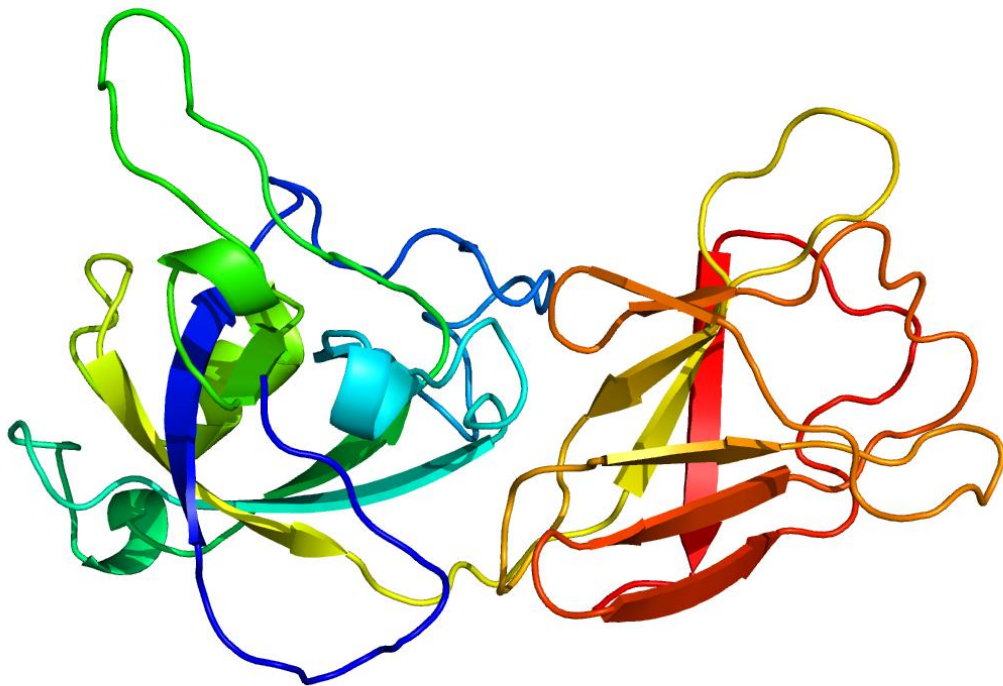
Locus: Eucgr.K02434

Gene Model: Eucgr.K02434.1.p

Description: EgrEXPA-24

Family: Alpha Expansin

3D structure:



GENOME DATABASES

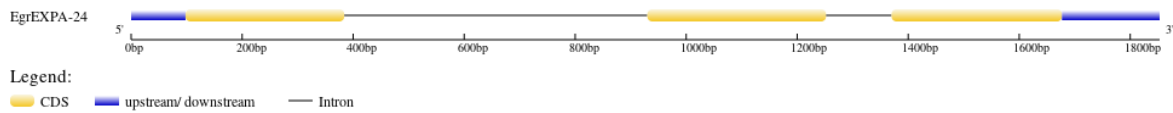
Phytozome: https://phytozome-next.jgi.doe.gov/info/Egrandis_v2_0

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

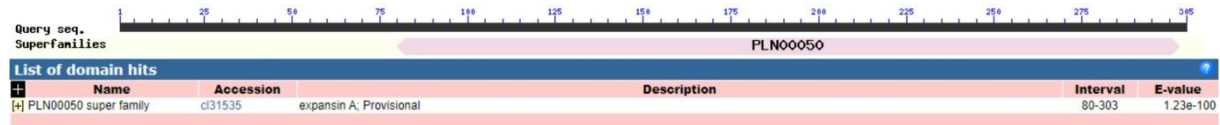
EXTERNAL RESOURCES

<https://eucgenie.org/>

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>EgrEXPA-24

MALPLKALFASLLIAASTLSDLRVATAAAV AHRSSWRHAAHRVAGNRMHYHHPRR
AHVHSGNHHSHPAKHNRPKFAPGPWKQAHATFYEGSGTFFGACGYQDVVQQGYG
YQTTAVSTAMFNNGQTCGACYEVKCVDPNPWCQLGQPSLFVTATDLCPPNYNLPSD
NGGWCNSPREHFDLAKPVFTTLAKDYTAGIVPVQYRRVPCRKQGGVRFITGNPYFN
LVLVSNVGGAGEVVSQVKGDKVPWTTMQRNWGQKWETNAMLVGQSLTFRVRAS
DGRFTTAWHVAPPNWQFGQTFEGKNFK*

CDS (coding sequence)

>EgrEXPA-24

ATGGCATTGCCTTTGAAAGCCCTCTTTCCTCACTGCTTGCCATTGCCTCGACGTT
GTCCGATCTTCGCGTTGCGACTGCCGCAGTCGCTCATCATCGTTCCTCCTCGTGGC
GACATGCCGCTCACCGTGTGGCTGGAAACAGAATGCATTACCACCATCCCCGGAG
GGCTCATGTCCATTCCGGAAACCACCACTCTCCCGCTAAGCATAACCGGCCCAAG
TTCGCGCCAGGCCCTTGAAGCAGGCTCATGCCACCTTTTATGAGGGGGGCTCCG
GTACATTTGGAGGAGCCTGCGGTTATCAGGACGTGGTGCAGCAAGGCTACGGCTA
TCAGACGACGGCGGTGAGCACGGCAATGTTCAACAACGGGCAGACGTGTGGGGC
GTGCTACGAGGTGAAGTGCCTGACAACCTCAGTGGTGGCAGCTTGGCCAGCCT
TCCCTCTTCGTACGGCCACCGACCTCTGCCCTCCCAACTACAACCTGCCAGCGA
CAACGGTGGATGGTGCAACTCGCCCCGCGAGCACTTTGACCTCGCCAAGCCGTT
TTCACCACGCTGGCCAAGGACTACACTGCTGGCATTGTCCCGGTCCAGTACCGCA
GGGTTCATGCCGGAAGCAAGGAGGGGTCCGGTTCACCATAACTGGGAACCCGT
ACTTCAACCTAGTGCTGGTGTGCAATGTGGGTGGAGCCGGTGAAGTCGTGAGCGT
ACAGGTGAAGGGCGATAAGGTGCCATGGACTACAATGCAGCGCAACTGGGGCCA
GAAGTGGGAGACCAACGCCATGTTGGTCGGGCAGTCCCTGACCTTCCGGGTTAGA
GCAAGCGACGGCCGATTCACAACCGCCTGGCACGTCGCCCCACCTAACTGGCAAT
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Nucleotide

>EgrEXPA-24

TTTTAACTTGTTTATTTTTTTTTTCCAAAAGGAGAGACAAAACCTTGCAAAGGTCGTG
CCAAAATCCCTCTACTCATTGCTGCTTAGCTCCAACATCAACATGGCATTGCCTTT
GAAAGCCCTCTTTGCCTCACTGCTTGCCATTGCCTCGACGTTGTCCGATCTTCGCG
TTGCGACTGCCGCAGTCGCTCATCATCGTTCCTCCTCGTGGCGACATGCCGCTCAC

CGTGTGGCTGGAAACAGAATGCATTACCACCATCCCCGGAGGGCTCATGTCCATT
CCGGAAACCACCCTCTCCCGCTAAGCATAACCGGCCCAAGTTCGCGCCAGGCC
TTGGAAGCAGGCTCATGCCACCTTTTATGAGGGGGGCTCCGGTACATTTGGTACG
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CCTCAAACCCCGCGATGTTTGTATGACAAGCATTGGTTTGATCGTTTCATAAG
CATGCAGCTTGGTTTTTAAGGAACCAGGAAATACAAGCACGATCAAATAGATTA
ACCAAGATTCAACTTGTGTGTAGGATGACAAACATAGCCATGACCGATGTTGGC
TCAACTAAGAGAGAAATGGGTAGTTTTAGGATTTGTATGCCCCACGACCCCATG
TATAGTAAGTAGATACATTCGAAAACAACAAAAACCTCTTACAAATAAGTTGTTG
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AAGAGTTTACATGTTTGCCTTAAGTTGTGTAACATCAAGAAAATTCAGGGG
AGAGGCAATTTTACGAGACAAGTTAGAGAACCGAGTTGTTATCACGTATTCAGTG
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CTCCCAGCGTTGTAGTATAAGTATCGGCAAATT