

IDENTIFICATION

Species: *Eucalyptus grandis*

Locus: Eucgr.I01954

Gene Model: Eucgr.I01954.1.p

Description: EgrEXPA-20

Family: Alpha Expansin

3D structure:



GENOME DATABASES

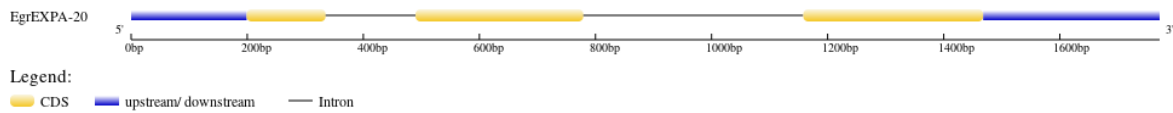
Phytozome: https://phytozome-next.jgi.doe.gov/info/Egrandis_v2_0

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

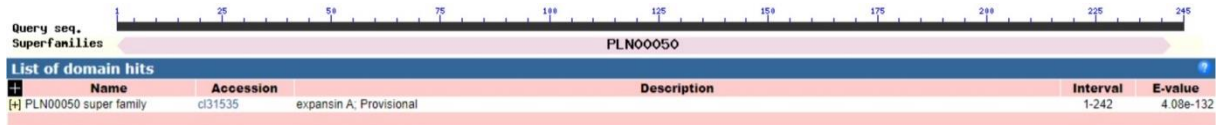
EXTERNAL RESOURCES

<https://eucgenie.org/>

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>EgrEXPA-20

MVPLGFLVVGLLSQFVPSRAYGYGGWTNAHATFYGGSDASGTMGGACGYGNLY
SQYGTNTAALSTALFNGLSCGACFELRCVNDPQWCLPGAIVVTATNFCPPGGWC
DPPQLHFDLSQPVFQHIAQYRAGIVPVAYRRVRCRRSGGIRFTVNGHSYFNLVLITNV
GGAGDVHLSVAIKGSRTRWQPMsrNWGQNWQNSDLNGQSLFLVTASDGRSVVSY
NVAPSGWSFGQTYTGGQFRY*

CDS (coding sequence)

>EgrEXPA-20

ATGGTTCCTCTAGGATTCCTGGTGGTTCGGCTTGCTCTCGCAATTCGTGCCGGTTTC
TCGCGCCTATGGATATTACGGCGGGTGGACGAATGCTCATGCCACATTCTATGGA
GGGAGCGATGCTTCCGGAACAATGGGAGGGGCTTGTGGGTATGGGAATCTATAC
AGCCAAGGGTACGGCACAAACACAGCTGCACTGAGCACTGCATTGTTCAACAAT
GGGCTGAGCTGCGGCGCGTGTCTTGGAGCTCCGGTGCCTGAACGACCCGCAGTGGT
GCCTCCCGGGCGCCATTGTGGTCACGGCGACCAACTTCTGCCCTCCAGGAGGGTG
GTGCGACCCTCCTCAACTCCATTTGACCTCTCCAGCCGGTCTTCCAGCACATTG
CGCAGTACAGGGCCGGGATCGTCCCGGTGGCCTACCGAAGAGTGAGGTGCAGGA
GAAGCGGAGGGATCCGGTTCACCGTCAACGGCCATTCTTATTTCAACCTCGTGCT
CATAACCAATGTCGGCGGAGCCGGGGATGTGCACTCCGTGGCCATCAAAGGATC
AAGGACCCGGTGGCAACCCATGTCGAGAACTGGGGACAGAACTGGCAGAGCAA
CTCCGACCTCAATGGGCAGAGCCTCTTTTCTAGTCACCGCCAGCGACGGCCGG
AGCGTCGTGTCCTACAACGTCGCCCTTCTGGTTGGTCCCTTCGGTCAGACTTATAC
CGGAGGCCAATTCCGATACTAA

Nucleotide

>EgrEXPA-20

GCAATTCCTGGGCAGCCTCTCCTCTCTCAAAGGGTTCGAGTTTTGATTCCTTCCA
TACACGGTCTCTACTTGCTTTCTCTTCTGTTTTGGCTCCGGTTCTGAGGTATGCA
GACGTTGATAATGGGGTTGTATCAATCCAATGTCAACAAAGCAAACATCTCATG
AAAAAATCGTGTTGGTACAGGGCGAAAAGAGATGGTTCCTCTAGGATTCCTGGTG
GTCGGCTTGCTCTCGCAATTCGTGCCGGTTTCTCGCGCCTATGGATATTACGGCGG
GTGGACGAATGCTCATGCCACATTCTATGGAGGGAGCGATGCTTCCGGAACAATG
GGTACGTGTTACATGGAACAAGTACTTAAACAAACCCAAAAGCTTAACATACT
GAGTTAGGAATTCGACGTATTAATTGTTTAATCTCACTCTTCTTAGCAGTACCAA

AATAATGTGCTTTGCTTTTACTTCTTATTTTCTTTGTGACATTAGGAGGGGCTTGTG
GGTATGGGAATCTATACAGCCAAGGGTACGGCACAAACACAGCTGCACTGAGCA
CTGCATTGTTCAACAATGGGCTGAGCTGCGGGCGCGTGCTTTGAGCTCCGGTGCGT
GAACGACCCGCAGTGGTGCCTCCCGGGCGCCATTGTGGTCACGGCGACCAACTTC
TGCCCTCCAGGAGGGTGGTGCAGCCCTCCTCAACTCCATTTTCGACCTCTCCAGCC
GGTCTTCCAGCACATTGCGCAGTACAGGGCCGGGATCGTCCCGGTGGCCTACCGA
AGGTATACCCTAGACATCAATTACTTCCCTGCTGTGAGGTCTAATGTATGGGTCCA
CAAACATGCTCCTACTTGGGTAGTATAATTATATTTAAAATCTAGCGAGCTCAAGT
AACATAGTTCATTTTTTACGTAGTAGAAATTATTAATCGATTTGTTCGAGTTCGAA
TTTTGGCTTTCTTTTAGCAGAAGAAAACAAAATTCTATGGATCAAGTTGTAATA
AAATATAATATATTTGGAGTCTTACCCTTTGTTTGTCAATTGGTTCAACTAATACA
AGGGAGACTAGACAAATGTTACACTGGATTAATTGAAAACCTGATTTCTCCATGCT
TTCACGGGGCTAATCGCGTGCTTCCGTCGCGACGGGTACTTCTTTGCAGAGTGAG
GTGCAGGAGAAGCGGAGGGATCCGGTTCACCGTCAACGGCCATTCTTATTTCAAC
CTCGTGCTCATAACCAATGTTCGGCGGAGCCGGGGATGTGCACTCCGTGGCCATCA
AAGGATCAAGGACCCGGTGGCAACCCATGTCGAGAACTGGGGACAGAACTGGC
AGAGCAACTCCGACCTCAATGGGCAGAGCCTCTCTTTCCTAGTCACCGCCAGCGA
CGGCCGGAGCGTCGTGTCCTACAACGTCGCCCCTTCTGGTTGGTCCTTCGGTCAG
ACTTATACCGGAGGCCAATTCCGATACTAATTATCGAACCCTGCTTACAACCTTT
TACTAGCACAAGTCGTGAAAACATTATAAGTATGAAAATCCAACCTTGGATTTCT
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TTTGCTTGCTGAGTTTGGGCTGCTTCTGTAATCCTAAATGTCCTGCTGAATGGATA
AAAGCCCTCATAATTTTACCGGGCGTGAGTATCATCTTGGCTTGTTAGTGTTCCCTC
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