

IDENTIFICATION

Species: *Eucalyptus grandis*

Locus: Eucgr.G03134

Gene Model: Eucgr.G03134.1.p

Description: EgrEXPA-19

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

Query seq. SQGYGTNTAALSTALFNDGLSCGSCYEMKCNDDPKWCLPGSITVTATNFCPPNYALS
Superfamilies PLN0193

Name	Accession	Description	Interval	E-value
PLN00193 super family	cl33423	expansin-A, Provisional	1-170	6.54e-100

SEQUENCES

Peptide

>EgrEXPA-19

SQGYGTNTAALSTALFNDGLSCGSCYEMKCNDDPKWCLPGSITVTATNFCPPNYALS
NDNGGWCNPLQHFDMAEPAFLQIAQYKAGIVPISFRRVPCVKKGGVRFITINGHSYF
NLVLISNVAGAGDVHSVSIKGSKTGWQTM SRNWGQNWQSN SYLNGQSLSFQVTTSDS*

CDS (coding sequence)

>EgrEXPA-19

ATGGCGGTTCGCGGCGTTCTCGGCATTCTCTCCTCATGTTGGCGGTGGTCGGTTT
GTGCCTCCGAGGTGCTTATGCCGACTCCGGCGGGTGGCAAAGCGCTCACGCCACC
TTCTACGGCGGTGGTGTATGCATCCGGCACCATGGGGGGCGCTTGTGGGTACGGCA
ACTTGTACAGCCAGGGCTACGGCACCAACACCGCGGCCCTCAGCACCGCCCTGTT
CAACGACGGCCTGAGCTGCGGGTCTGCTACGAGATGAAGTGCAACGACGACCC
CAAGTGGTGCCTCCCCGGCAGCATCACCGTCACCGCCACCAACTTCTGCCCTCCT
AACTACGCCCTTTCCAACGACAACGGCGGCTGGTGCAACCCCCCGCTCCAGCACT
TCGATATGGCCGAGCCGGCATTCTCCAAATCGCCAATACAAAGCCGGGATCGT
CCCCATCTCCTTCAGAAGGGTCCCCTGTGTGAAGAAAGGAGGCGTGAGGTTACG
ATCAACGGCCACTCCTACTTCAACCTGGTGCTGATCTCGAACGTGGCCGGGGCCG
GAGACGTGCACTCGGTGTGATCAAGGGCTCGAAGACCGGGTGGCAGACCATGT
CCCGAACTGGGGCCAGA ACTGGCAGAGCAACTCCTACCTAACGGCCAGTCCCT
CTCCTTCCAGGTCACCACCAGCGACAGCTAG

Nucleotide

>EgrEXPA-19

GCACCCACCAAGCCTCCAAGCAACAAGAAGCCTCTCTCCCTCTCCTTTTCTCTCC
CTCCCTCCCTCCCTCCCTCCTTACAATTCTAGTTTTGAGTAGCGAAGAGAGGCAAT
GGCGGTTCGCGGCGTTCTCGGCATTCTCTCCTCATGTTGGCGGTGGTCGGTTTGT
GCCTCCGAGGTGCTTATGCCGACTCCGGCGGGTGGCAAAGCGCTCACGCCACCTT
CTACGGCGGTGGTGTATGCATCCGGCACCATGGGTACGTCTATCTTACAAGCCCAT
ATGCCCTTCACTTATCATCGCTCAATATTCCCCGCTTGTCTTTACTGAAGAGCTCG
CCTAATGTGCCAAATTTGCCGCCCTCCCCAGAAATCCACTGATTAAGGAAGATAA
TTGTCTAAGGAGTGGTTACGATGAATTTACGATTGTACCCTCACCTCTTCTGAATT
GACTTTTGCATGCTAAAGTAGGGATTTTTTGCATTTAATCCACTAAATTAATTCT
CTTTATTCTATTTTTATGCAGGGGGCGCTTGTGGGTACGGCAACTTGTACAGCCAG

GGCTACGGCACCAACACCGCGGCCCTCAGCACCGCCCTGTTCAACGACGGCCTGA
GCTGCGGGTCCTGCTACGAGATGAAGTGCAACGACGACCCCAAGTGGTGCCTCCC
CGGCAGCATCACCGTCACCGCCACCAACTTCTGCCCTCCTAACTACGCCCTTTCCA
ACGACAACGGCGGCTGGTGCAACCCCCGCTCCAGCACTTCGATATGGCCGAGCC
GGCATTCTCCAAATCGCCCAATACAAAGCCGGGATCGTCCCCATCTCCTTCAGA
AGGTAACACAAAACCTCGAACCCGAGCCCTTCCCTTGCCTCCAAAATCAATCAACC
AATCACAAAAGTTTTTTAGAAAGTTAGATTTGCTGATTTATATATATGGTCATGGGC
GTTGACGCTGCAGGGTCCCCTGTGTGAAGAAAGGAGGCGTGAGGTTACGATCA
ACGGCCACTCCTACTTCAACCTGGTGCTGATCTCGAACGTGGCCGGGGCCGGAGA
CGTGC ACTCGGTGTCGATCAAGGGCTCGAAGACCGGGTGGCAGACCATGTCCCG
GAACTGGGGCCAGAACTGGCAGAGCAACTCCTACCTCAACGGCCAGTCCCTCTCC
TTCCAGGTCACCACCAGCGACAGCTAGACCATCACCAGCTACAACGTCCTGCCCT
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AACTTGGCGTCCAGATGGGAACATGGTGGAGCCAGAAGCAGGGTTAGGAGAAGA
AATTCAACGTTTTTGGCCACTTTTGGCCGGCTATTGCTGAGGTGGCCGTTGTGCACC
CGCTAGGCATTTTACTTTATTTATATGTAATGATTTATATATACAGATAGATATAG
TGAAGAAGGGTTATCACAAATCAAGAAAAGAACAGGGGGGGTATTCTTAGTTGCC
TTTGGATTGAGTGGAAGGCCATGGATACCACTCCGAGGTCTGCAGATTGTAATT
CCAAAAGTTGGGTTTGAATTTGGACGACTTTTTTATGGTATCTAGTCGGATTGATG
ATC