

IDENTIFICATION

Species: *Eucalyptus grandis*

Locus: Eucgr.G02938

Gene Model: Eucgr.G02938.1.p

Description: EgrEXPA-18

Family: Alpha Expansin

3D structure:



GENOME DATABASES

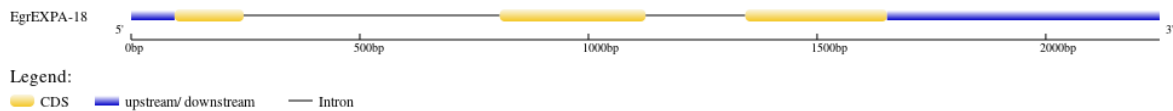
Phytozome: https://phytozome-next.jgi.doe.gov/info/Egrandis_v2_0

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

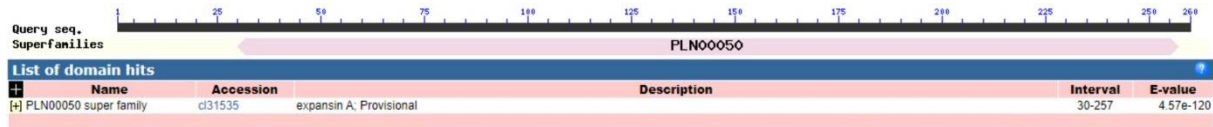
EXTERNAL RESOURCES

<https://eucgenie.org/>

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>EgrEXPA-18

MASVSRVVGVLVSLILFSTLAEARIPGVYTGPPWQSAHATFYGGSDASGTMGGACGY
GNLYSQGYGVNTAALSTALFNNGFSCGACFEIKCANEPQWCHSGSPSILVTATNFCPP
NYALPNDNGGWCNPPRPHFDLAMPMLKIAEYRAGIVPVS YRRVPCRKQGGIRFTIN
GFRYFNLVLVTNVAGAGDINKLWVKGSKTGWMSMSRNWGQNWQSNVLAGQSL
FRVTAGDRRTSTSWNIVPSNWQFGQTFTGKNFRV*

CDS (coding sequence)

>EgrEXPA-18

ATGGCTAGTGTTCCTCGTGTGGTGGCCTTGTCTCTCTGATACTGTTTTTCGACGCT
GGCCGAGGCCAGAATCCCGGGTGTCTACACCGGCGGTCCGTGGCAGAGTGCCCA
TGCCACATTTTATGGTGGCAGCGACGCATCCGGGACTATGGGTGGCGCGTGCAGG
TACGGCAACCTGTACAGCCAGGGCTACGGCGTCAACACCGCCGCGCTGAGCACG
GCGCTGTTCAACAACGGGTTTCAGCTGCGGCGCGTGTCTTCGAGATCAAGTGCGCGA
ACGAGCCCCAGTGGTGCCACTCCGGCAGCCCGTCCATCCTGGTGACGGCGACCAA
CTTTTGCCCCCGAACTACGCCCTGCCCAACGACAACGGCGGGTGGTGCAACCCC
CCGCGGCCGCACTTCGATCTCGCCATGCCCATGTTCTCAAATCGCCGAGTACC
GCGCAGGGATCGTCCCGTGTCTACCGCCGCGTGCCTGCGGCAAGCAAGGAG
GGATCAGGTTACGATCAACGGGTTTCAGGTAACCTGGTGCTGGTCCACCAA
CGTGGCCGGCGCAGGGGACATCAACAAGCTGTGGGTGAAAGGGTTCGAAGACCGG
GTGGATGAGCATGAGCCGCAACTGGGGCCAGAAGTGGCAGTCCAACCTCCGTCCTC
GCCGGCCAGTCCCTCTCCTTCCGGGTACCGCCGGCGACCGCCGACCTCCACCT
CCTGGAACATCGTCCCGTCCAATTGGCAGTTCGGCCAGACCTTCACCGGCAAGAA
CTTCAGGGTCTAG

Nucleotide

>EgrEXPA-18

CTCACAAGTCACGCACACCCCCACCACAACCTGCTCTAACAGCTCCTCCACTTCCT
TTCCGTTTCCTGATACTGACTCTAGGAGGAGCCAAGCCCATGGCTAGTGTTTCCCG
TGTGGTTGGCCTTGTCTCTCTGATACTGTTTTTCGACGCTGGCCGAGGCCAGAATCC
CGGGTGTCTACACCGGCGGTCCGTGGCAGAGTGCCCATGCCACATTTTATGGTGG
CAGCGACGCATCCGGGACTATGGGTACTATAATTGGTCTCAGTCTGATTCTTCAA
AATCTTGTCTCTTTCAATCTTGGTTATCATGAGTTTCTTCACTTTCCGTTCCGTTC
AGCAAATCTCTGGTTGACCTGAGAGAACTTTTCAAATGATGTCCCTCATCTGC

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GACAGTTAGGATCACAACCCTCAATTTCAAGCTACATTCCACGAAACTGCTTTGG
CAGAGTGCATCTTAACAAGAAGCCGACTTTACCACTTGGACTTCCTTCCCATTTTC
CCAAACACCTAGCAAGCATTGTTGTGTTCTTGGCGATCCGCTATTCAGATGTCAG
ACCCTAATTTGAAATCAAGCACATTATTCTGTTTTGGACCAAATCTGGTTTTACTA
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GCACTTCATCAAACACCTCGCACACAGCAAACGCATTTACGAAAAACAGTCGCTC
ACCCGCTTTTTTCCCTGACTCTTCGCAGGTGGCGCGTGCGGGTACGGCAACCTGTA
CAGCCAGGGCTACGGCGTCAACACCGCCGCGCTGAGCACGGCGCTGTTCAACAA
CGGGTTCAGCTGCGGCGCGTGCTTCGAGATCAAGTGCGCGAACGAGCCCCAGTG
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AACTACGCCCTGCCAACGACAACGGCGGGTGGTGCAACCCCCCGCGGCCGCAC
TTCGATCTCGCCATGCCATGTTCCCTCAAATCGCCGAGTACCGCGCAGGGATCG
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TACGGTCGTCTTTCTTGAATTTGCCAATGAACATATTA
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CTCG
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ATTA
TCGTGTCCCTCCTTCATTTCCA
ACTTTCTTGATTGCCCC