

IDENTIFICATION

Species: *Eucalyptus grandis*

Locus: Eucgr.A00721

Gene Model: Eucgr.A00721.1.p

Description: EgrEXPA-01

Family: Alpha Expansin

3D structure:



GENOME DATABASES

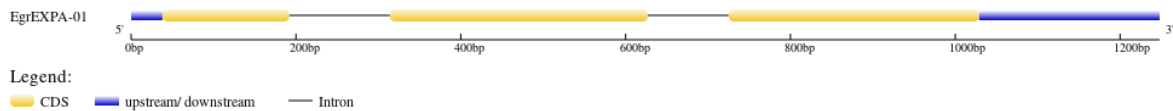
Phytozome: https://phytozome-next.jgi.doe.gov/info/Egrandis_v2_0

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

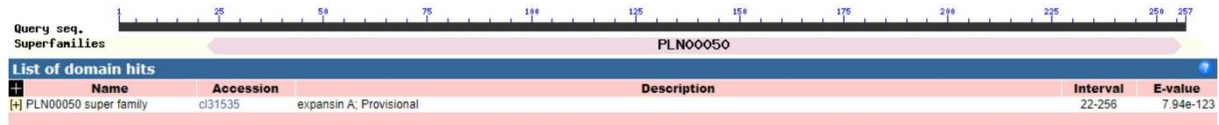
EXTERNAL RESOURCES

<https://eucgenie.org/>

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>EgrEXPA-01

MRTPSAIPSLPLLSLLFIMHAALFRSVAGNYGPWQSAHATFYGGHDASGTMGGACGY
GNLYSQGYGTQTAALSTALFNGLSCGSCYELRCSGDPKWCLPHAIMVTATNFCPPN
YALAGDNGGWCNPPRAHFDLAEP AFLQIAQYRAGIVPVSFRRVPCVKKGGMRFTING
HSYFNLVLTNVAGAGDVRSVSIKGSRTGWPMSRNWQNWQSN SYLNGQSLSFT
VTASNGRTLTTYNVVPAGWQFGQTFEGDQF*

CDS (coding sequence)

>EgrEXPA-01

ATGAGAACTCCTAGTGCTATTCCAAGCTTGCCACTACTCTCTCTCTTGTTCATCAT
GCATGCTGCGCTCTTTTCGGAGCGTCGCCGCAACTACGGCCCCTGGCAGAGTGCC
CACGCGACGTTCTACGGCGGCCATGATGCATCCGGCACGATGGGAGGAGCGTGC
GGCTACGGCAACTTGTACAGCCAGGGCTACGGGACCCAAACGGCGGGCTCTGAGC
ACCGCTCTGTTCAACAGCGGCTTGAGCTGTGGGTCGTGCTACGAGCTCCGATGCA
GCGGCGACCCGAAATGGTGCCTCCCCACGCGATCATGGTGACCGCCACCAACTT
CTGCCCCCTAACTACGCGTTGGCCGGCGACAACGGAGGGTGGTGCAACCCTCCT
CGCGCGCACTTCGACTTGGCCGAGCCC GCGTTCCTTGCAGATCGCCCAGTACCGGG
CCGGGATTGTTCCCGTGAGCTTCAGGAGGGTCCCCTGTGTGAAGAAAGGAGGCAT
GAGGTTACGATCAATGGCCATTCATACTTCAACCTGGTGCTGGTCACCAATGTG
GCTGGTGCAGGGGATGTCCGATCGGTGTCCATCAAGGGTTCAAGGACTGGGTGG
ATGCCAATGTCAAGGAACTGGGGCCAGAATTGGCAGAGCAATTCGTACCTGAAC
GGCCAGAGCCTCTCCTTCACGGTCAACGCCAGCAACGGCCGGACCCTCACGACCT
ACAACGTTGTCCCGGCAGGTTGGCAGTTCGGACAGACTTTCGAAGGCGACCAGTT
TTAG

Nucleotide

>EgrEXPA-01

CCTCCTCCTCCTCCCTCTCTTTTTGTCTACAGTAGAAAATGAGAACTCCTAGTGCT
ATTCCAAGCTTGCCACTACTCTCTCTCTTGTTCATCATGCATGCTGCGCTCTTTTCGG
AGCGTCGCCGCAACTACGGCCCCTGGCAGAGTGCCACGCGACGTTCTACGGCG
GCCATGATGCATCCGGCACGATGGGTAAGTTAGAACGTGGCGAGAATTTTCATAT
ATACAGTCGAACCGGCTAGACATTGTCTTTGGCATCACATATTGGCATGAGAAAA

TAGCATAGAAGATGAGTGTCTTTTCCTCTGTTGCAGGAGGAGCGTGCGGCTACGG
CAACTTGTACAGCCAGGGCTACGGGACCCAAACGGCGGCTCTGAGCACCGCTCTG
TTCAACAGCGGCTTGAGCTGTGGGTCGTGCTACGAGCTCCGATGCAGCGGCGACC
CGAAATGGTGCCTCCCCACGCGATCATGGTGACCGCCACCAACTTCTGCCCCC
TAACTACGCGTTGGCCGGCGACAACGGAGGGTGGTGCAACCCTCCTCGCGCGCAC
TTCGACTTGGCCGAGCCCGCGTTCTTGCAGATCGCCCAGTACCGGGCCGGGATTG
TTCCCGTGAGCTTCAGGAGGTAATTACATGACTCAAACTAACGATCGAGCTTG
AGCTTGCCCGTTTCCGATGCGCTAACCATCGTTCGGCTGCATTGCGCCGTGCCATTG
TGACAGGGTCCCCTGTGTGAAGAAAGGAGGCATGAGGTTCACGATCAATGGCCA
TTCATACTTCAACCTGGTGCTGGTCACCAATGTGGCTGGTGCAGGGGATGTCCGA
TCGGTGTCCATCAAGGGTTCAAGGACTGGGTGGATGCCAATGTCAAGGAACTGG
GGCCAGAATTGGCAGAGCAATTCGTACCTGAACGGCCAGAGCCTCTCCTTCACGG
TCACCGCCAGCAACGGCCGGACCCTCACGACCTACAACGTTGTCCCGGCAGGTTG
GCAGTTCGGACAGACTTTCGAAGGCGACCAGTTTTAGGTGAATGAAAATGATCTA
TCCGAGGAGGGCGTAGATCGATGTATAACACATAAACATGTATCCCTAGTTCATA
TATGAGACGAGGCTTATAAATGTACAATCCTGGAATCTACCTAAAAAGGAAATG
GAAAACCAGTCATTAAGTATTATCGCTTGTGTGTTCTTTTTATGTACTTAC
AAAACCTGAATGCTTAGAAAGTTGCCTTGATCAGGC