

IDENTIFICATION

Species: *Eucalyptus grandis*

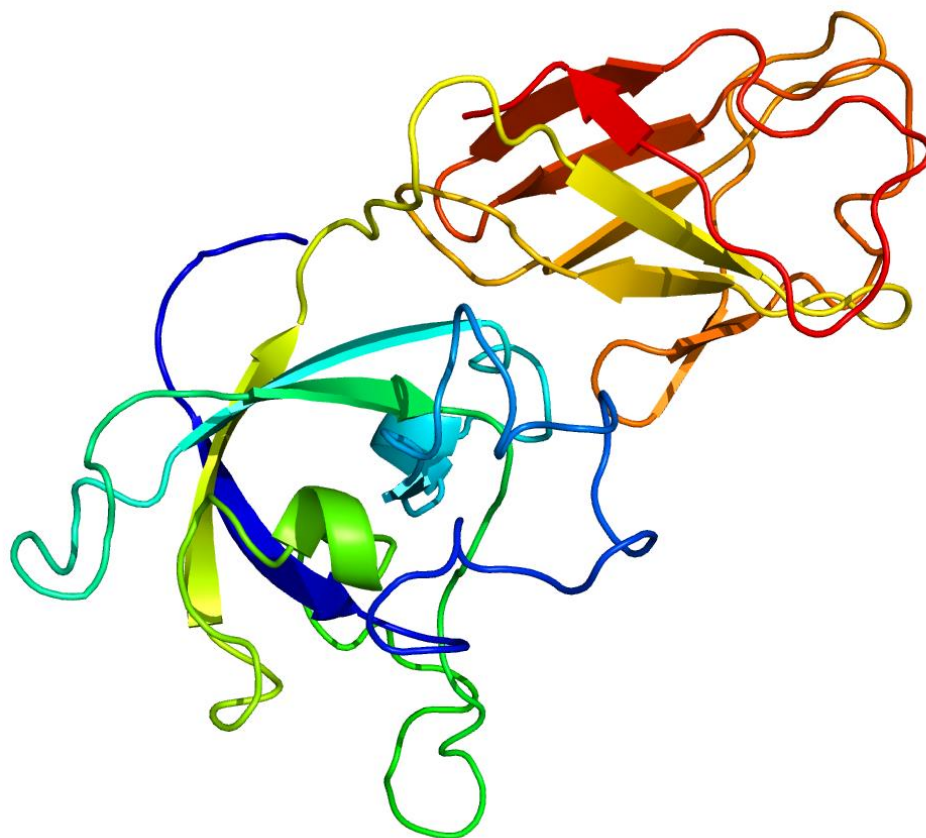
Locus: Eucgr.J01729

Gene Model: Eucgr.J01729.1.p

Description: EgrEXPA-22

Family: Alpha Expansin

3D structure:



GENOME DATABASES

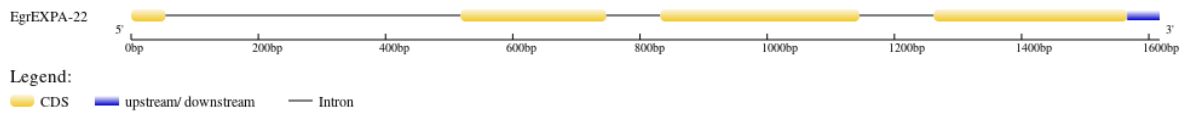
Phytozome: https://phytozome-next.jgi.doe.gov/info/Egrandis_v2_0

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

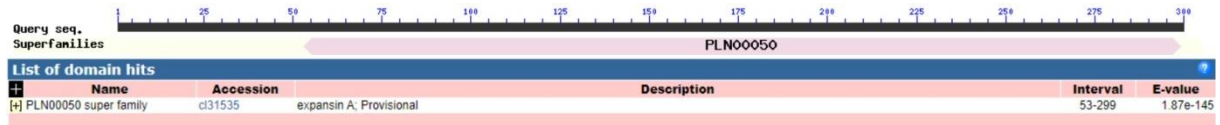
EXTERNAL RESOURCES

<https://eucgenie.org/>

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>EgrEXPA-22

MKMLLMQLKGFVVGQVEQALSLRSSKLFPLSISLSLSPSVILGCKFLLQKPEMGS LGF
TIV AFLTLLKTVQSDGSGWTS AHATFYGGSDASGTMGGACGYGNLISQGYGTNTAA
LSTALFNNGQSCGACYEIQCVSDNQWCLSGSITITATNFCPPNPSLPNDNGGWCNPPL
EHFDLAEPVFQQIAQYKAGIVPVQYRRVACARKGGIRFTVNGHSYFNLVLITNVGGS
GDVVSASIKGSNTGWQAMSRNWGQNWQSN SYLNGQALSFKVTTSDGRVSVSNAAA
PPNWSFGQTFSGSQF*

CDS (coding sequence)

>EgrEXPA-22

ATGAAGATGCTGCTCATGCAATTA AAAAGGTGACTTTGTTGGGCAAGTTGAGCAAG
CTCTTTCACTCAGAAGTTCCAAGCTGTTCCCTCTCTCCATCTCTCTCCCTCTCTC
CCTCTGTCATCTTGGGCTGCAAATTCCTGCTGCAA AAGCCAGAAATGGGTTCTCTC
GGATTCACCATTTGTGGCCTTCCTGACATTGCTGAAGACAGTCCAGAGCGATGGGA
GCGGATGGACCTCTGCCACGCCACTTTCTATGGGGGCAGTGATGCTTCTGGAAC
AATGGGTGGGGCTTGCGGGTATGGGAATCTGATTAGCCAGGGGTACGGCACCAA
CACGGCCGCCCTGAGCACCGCCCTGTTCAACAACGGGCAGAGCTGCGGAGCGTG
CTACGAGATCCAGTGCGTGAGTGACAACCAAGTGGTGCTTGTCCGGCTCCATCACC
ATCACTGCCACCAATTTCTGCCCTCCTAACCCTAGCCTCCCGAACGACAATGGAG
GATGGTGTAATCCCCCTCTCGAGCACTTCGACCTCGCCGAGCCGGTCTTCCAGCA
GATCGCTCAGTACAAAGCCGGAATAGTTCCTGTT CAGTACAGAAGGGTTGCTTGT
GCGAGGAAGGGTGGGATCAGATTCACCGTCAATGGCCACTCCTACTTCAACCTCG
TCCTGATAACCAACGTCCGGTGGCTCTGGGGACGTGGTGTCGGCGTCCATCAAAGG
CTCCAACACCGGCTGGCAAGCCATGTCCAGGAACTGGGGCCAGA ACTGGCAGAG
CAACTCGTACCTCAACGGCCAGGCCCTCTTTTCAAGGTTACCACCAGCGACGGC
CGCGTCTCAGTCTCAACGCTGCCGCCCGCCCAACTGGTCCTTCGGCCAGACAT
TCAGCGGGTCCCAATTCTAA

Nucleotide

>EgrEXPA-22

ATGAAGATGCTGCTCATGCAATTA AAAAGGTGACTTTGTTGGGCAAGTTGAGCAAG
TACAAATGCTGCAATTA AATGC ACTTGTGGGCATCTCAACACCACCACCACCA
CCCTCAAGAATCAA AATTCAATTCCTTTCTCTCACCCCAAATTGCCACCAGCCCT
CTGACCGGTCTTCAGCTGAACCACCGGGCTCTTCCAATGTGCCTTGGTCCTCACG

AACTAAAAAGGTCAAAAAGTCCACTCAGATGGATCATAAATCTAGGCAGAATAT
GGGGAATTCCAAAAAGAAAAGTTAAAAAAAATTTGGAGTCCTCTCCGCTCCAT
GTCGACAAGCGCTTTGCTTTAATTTTTTTTCTTTTAGCAGTTTTTTTCTGTTTCGGTT
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ATCTCTCTCTCCCTCTCTCCCTCTGTCATCTTGGGCTGCAAATTCTTGCTGCAAAA
GCCAGAAATGGGTTCTCTCGGATTCACCATTGTGGCCTTCCTGACATTGCTGAAG
ACAGTCCAGAGCGATGGGAGCGGATGGACCTCTGCCACGCCACTTTCTATGGGG
GCAGTGATGCTTCTGGAACAATGGGTAAGTTATCATCAGAAGAATCACATTGTCT
GCAACATCATTTTCGGTTCCTGAGTTAAGACGAATTCTTTTGGATCTGCTTTCAGGT
GGGGCTTGCGGGTATGGGAATCTGATTAGCCAGGGGTACGGCACCAACACGGCC
GCCCTGAGCACCGCCCTGTTCAACAACGGGCAGAGCTGCGGAGCGTGCTACGAG
ATCCAGTGCGTGAGTGACAACCAGTGGTGCTTGTCCGGCTCCATCACCATCACTG
CCACCAATTTCTGCCCTCCTAACCCTAGCCTCCCGAACGACAATGGAGGATGGTG
TAATCCCCCTCTCGAGCACTTCGACCTCGCCGAGCCGGTCTTCCAGCAGATCGCTC
AGTACAAAGCCGGAATAGTTCCTGTTCAGTACAGAAGGTGAGCAACTAATTGAAT
AGATCATGGCACTTTCTGTTCTGTCAGAAAACACTAATTGAAGCCCTTTCAACTCT
TCCATCATCAGCAAGCACGCTAACGATGTATGTGTTTCGTACAGGGTTGCTTGTGC
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CCAACACCGGCTGGCAAGCCATGTCCAGGAACTGGGGCCAGAACTGGCAGAGCA
ACTCGTACCTCAACGGCCAGGCCCTCTCTTTCAAGGTTACCACCAGCGACGGCCG
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AGCGGGTCCCAATTCTAAACCCGACCCTGGGGCCGGAAAAACCGTGAAAAGCTA
ACTCCAAAAAAAACC