

IDENTIFICATION

Species: *Eucalyptus grandis*

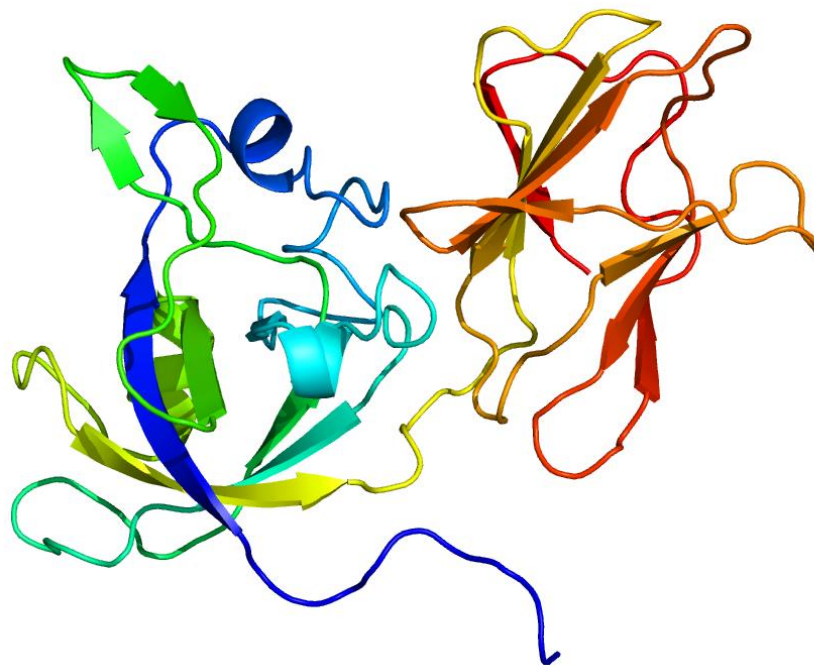
Locus: Eucgr.A00988

Gene Model: Eucgr.A00988.1.p

Description: EgrEXPA-04

Family: Alpha Expansin

3D structure:



GENOME DATABASES

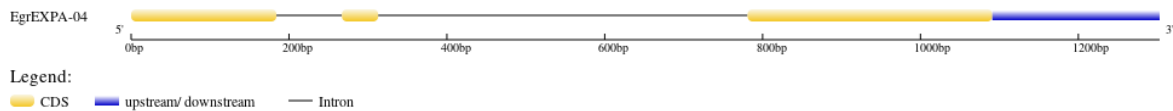
Phytozome: https://phytozome-next.jgi.doe.gov/info/Egrandis_v2_0

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

EXTERNAL RESOURCES

<https://eucgenie.org/>

GENE STRUCTURE



DOMAIN ARCHITECTURE

Query seq. MGIKTAVMSTALFNDSKSCSGCYQIVCDIAIQVHQWCLRGTSTITMPPISARQTMLAPM
Superfamilies PLN0193

Name	Accession	Description	Interval	E-value
PLN00193 super family	cl33423	expansin-A, Provisional	2-179	7.06e-65

SEQUENCES

Peptide

>EgrEXPA-04

MGIKTAVMSTALFNDSKSCSGCYQIVCDIAIQVHQWCLRGTSTITMPPISARQTMLAPM
TMADDLAKYRAGIVPILYRKVGCRRDGGIRLTFNSRDHFELFLISNVGGAGEISNVSIGK
GSKMNEWETISRNEWANWQSLSYLNGQSLFRLEASNGRTITALNVAPSDWKFGQSF
SSSTQF*

CDS (coding sequence)

>EgrEXPA-04

ATGGGAATCAAGACGGCGGTGATGAGTACGGCTCTGTTCAATGACAGCAAGTCG
TGCAGCGGATGTTATCAGATAGTCTGTGATGCCATACAGGTTTCATCAGTGGTGTG
TCAGGGGCACTTCTATAACCATGCCACCAATTTCTGCCCCGCCAACTATGCTCGC
CCCAATGACAATGGCGGATGACCTTGCCAAGTACAGGGCCGGAATTGTTCCAATT
TTGTACAGGAAGGTTGGATGCAGGAGAGATGGAGGTATAAGGTTGACATTCAAC
AGTAGGGACCACTTCGAGCTCTTCTCATATCCAATGTAGGGGGAGCCGGTGAAA
TCTCGAACGTATCGATCAAAGGGTCCAAGATGAACGAGTGGGAAACCATATCGA
GAAACTGGGAGGCGAACTGGCAAAGCCTCAGCTATCTCAACGGCCAGAGCCTGT
CCTTCAGACTCGAGGCCAGCAATGGCCGAACCATCACAGCCCTTAACGTGGCACC
TTCAGATTGGAAGTTTGGCCAGTCCTTCTCCAGCAGCACCCAATTTTAA

Nucleotide

>EgrEXPA-04

ATGGGAATCAAGACGGCGGTGATGAGTACGGCTCTGTTCAATGACAGCAAGTCG
TGCAGCGGATGTTATCAGATAGTCTGTGATGCCATACAGGTTTCATCAGTGGTGTG
TCAGGGGCACTTCTATAACCATGCCACCAATTTCTGCCCCGCCAACTATGCTCGC
CCCAATGACAATGGCGGATGGTGCAATCCCCCAAGGCCCTCACTTGGACATGTCTC
AACCTGCATTTGAGACCTTGCCCTGGACATGTCTCAACCTGCATTTGAGACCTTGCC
AAGTACAGGGCCGGAATTGTTCCAATTTTGTACAGGAAGTGTGTCCTATTCTTGT
GCACTCGTACAGTTTCTCGGTCTTTTCTGAAGTTAGTTTGCCTAGTTTGAACATG
ATTCGAGAAAATTTATTAACCGGGTTTTCCCGGGCCATAGTGCTAGACGAGAAAT
TCCAGTGAAACCAGACTAAGCCGATCATTTCATATGTTTTTTCTGGCTTCTGAGT
ATATTTCAAATTGCAAGTTGGGTTACTTAAATATAGAACCTTCTTCTGCATTTGGC
CTGCTGAATCCCATTTAGTCTTCTTAACTGGACAAGGATATGTAGACTGGAGACT
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GGACGAAGAGAAAGGATTTTCGATGAGATTAACATATTCTATTTCTCCCGTATCTT
TCATCAGGGTTGGATGCAGGAGAGATGGAGGTATAAGGTTGACATTCAACAGTA
GGGACCACTTCGAGCTCTTCCTCATATCCAATGTAGGGGGAGCCGGTGAAATCTC
GAACGTATCGATCAAAGGGTCCAAGATGAACGAGTGGGAAACCATATCGAGAAA
CTGGGAGGCGAACTGGCAAAGCCTCAGCTATCTCAACGGCCAGAGCCTGTCCTTC
AGACTCGAGGCCAGCAATGGCCGAACCATCACAGCCCTTAACGTGGCACCTTCAG
ATTGGAAGTTTGGCCAGTCCTTCTCCAGCAGCACCCAATTTTAAGAAGAAGGGTG
CAAATACTACTATTGATGCAGCCTCATCAATCAACTATAGAAAGGTTGTGCTTAT
CTCCCTTTGCCGTATGTATCTACACTTCATTTTACAATTGTATATATGGGGTTGTG
CCGAGTACCTTCAAGGACCAACCCGTGATGCAGAACTTTTTGAAGCTGGAGCTGT
TAGCTGATGTTCAAAGGTTCAAGAAAGCAAAAGAA