

IDENTIFICATION

Species: *Eucalyptus grandis*

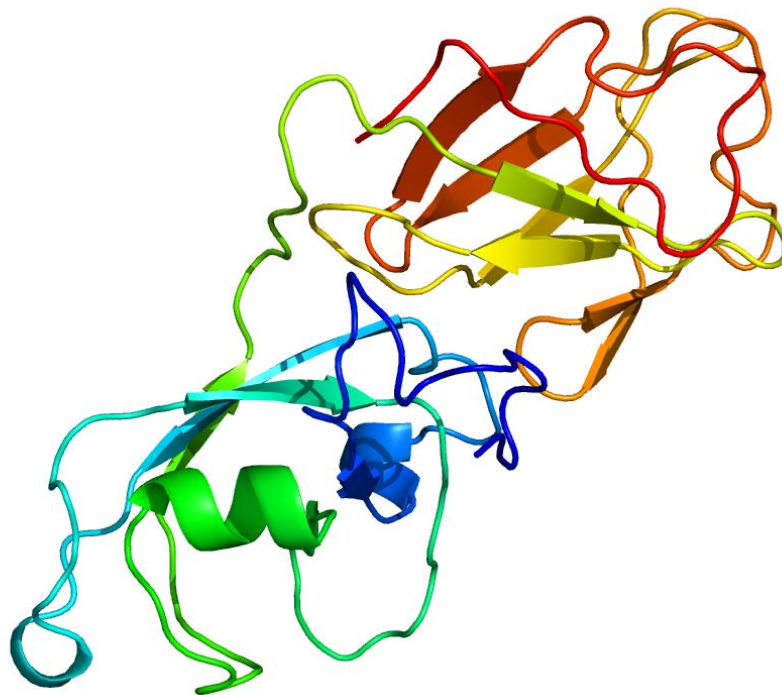
Locus: Eucgr.F01688

Gene Model: Eucgr.F01688.1.p

Description: EgrEXPA-11

Family: Alpha Expansin

3D structure:



GENOME DATABASES

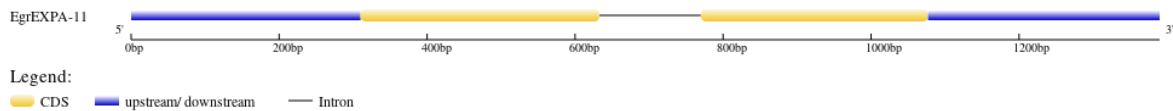
Phytozome: https://phytozome-next.jgi.doe.gov/info/Egrandis_v2_0

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

EXTERNAL RESOURCES

<https://eucgenie.org/>

GENE STRUCTURE



DOMAIN ARCHITECTURE

Query seq. MGGACGYGDLYSTGYGTRTAALSTALFSDGASCGQCYRIVCDYKTDSRWCIKGTSTITATNFCPPNSALPNDNGGWCNPPLQHFDMAQPAWEKIGIYRGGIIPVLFQRVPCKKHGGVRFINGRDYFELVLISNVAGAGSIKSVSIKGSTTGWTAMSRNWGANWQSNSYLN GQSLSFQVTTTDGVTKIFTDIVPPNWTFGQTFSSSVQF*

Superfamilies ■ PLN0193

Name	Accession	Description	Interval	E-value
PLN00193 super family	cl33423	expansin-A, Provisional	1-210	2.11e-151

SEQUENCES

Peptide

>EgrEXPA-11

MGGACGYGDLYSTGYGTRTAALSTALFSDGASCGQCYRIVCDYKTDSRWCIKGTSTITATNFCPPNSALPNDNGGWCNPPLQHFDMAQPAWEKIGIYRGGIIPVLFQRVPCKKHGGVRFINGRDYFELVLISNVAGAGSIKSVSIKGSTTGWTAMSRNWGANWQSNSYLN GQSLSFQVTTTDGVTKIFTDIVPPNWTFGQTFSSSVQF*

CDS (coding sequence)

>EgrEXPA-11

ATGGGAGGAGCTTGTGGCTATGGGGACTTGTACTCGACTGGGTATGGCACCCGAACTGCAGCGTTGAGCACCGCGTTGTTACGCGACGGGGCTTCGTGTGGGCAGTGCTACAGGATCGTCTGTGACTACAAAAGTACTCCAGGTGGTGCATCAAAGGAAGTCCATCACGATCACTGCCACCAATTTCTGCCCTCCGAACTCCGCTCTCCCGAACGACAATGGTGGGTGGTGCAACCCGCCCTCCAGCATTTTCGACATGGCTCAGCCCGCTTGGAAAAGATCGGCATCTACAGAGGAGGAATCATAACCGTCTCTGTTCCAAAGGGTTCCATGCAAGAAACATGGTGGAGTAAGGTTACCATCAACGGGAGAGACTACTTTGAGCTGGTCCTCATAAGCAATGTTGCCGGAGCTGGGTTCGATCAAGTCCGTCTCGATCAAAGGCTCGACCACAGGATGGACCGCCATGTCAAGGAACTGGGGGGCTAATTGGCAGTCGAATTCGTACCTCAATGGCCAATCCCTTTCTTTTCAGGTCACCACCACTGATGGAGTGACCAAGATTTTCACAGACATCGTGCCACCAAAGTGGACATTTGGCCAAACCTTCTCTAGCTCGGTTCAATTCTAG

Nucleotide

>EgrEXPA-11

GTCATGCCACCTTCTACGGTGGAAAGCGACGCCTCTGGCACCATGGGTAAGTTTAA GAATATAACTTGTCTCTCTTGTGAAACGACTCGCCGGTCCACATGGACCCGGT AGTCACGAAACCTTTCGATACAGATGCCTAGATTAGGTAATGGAATCAACGAACT TTGATTTCAAGAATGCTTTGGCTTCTGTAGGCTCATTGTTGACTACTTTGTAGGGT ATAGAATGAGGTGATCTTTGTTTAGTAAGACAATTTACTGATGCCCAGATTAGGG GCTCTCGAGTTAACATTAGTCGGTGACGTGCAGGAGGAGCTTGTGGCTATGGGG ACTTGTACTCGACTGGGTATGGCACCCGAACTGCAGCGTTGAGCACCGCGTTGTT CAGCGACGGGGCTTCGTGTGGGCAGTGCTACAGGATCGTCTGTGACTACAAAAGT GACTCCAGGTGGTGCATCAAAGGAACTTCCATCACGATCACTGCCACCAATTTCT GCCCTCCGAACTCCGCTCTCCCGAACGACAATGGTGGGTGGTGCAACCCGCCCT CCAGCATTTTCGACATGGCTCAGCCCGCTTGGGAAAAGATCGGCATCTACAGAGGA

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TCAAAGGCTCGACCACAGGATGGACCGCCATGTCAAGGAACTGGGGGGCTAATT
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AAACCTTCTCTAGCTCGGTTCAATTCTAGTCGAATTCGAGAGCAGCTTTGGAGGTT
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GATTCGCCTT