

IDENTIFICATION

Species: *Eucalyptus grandis*

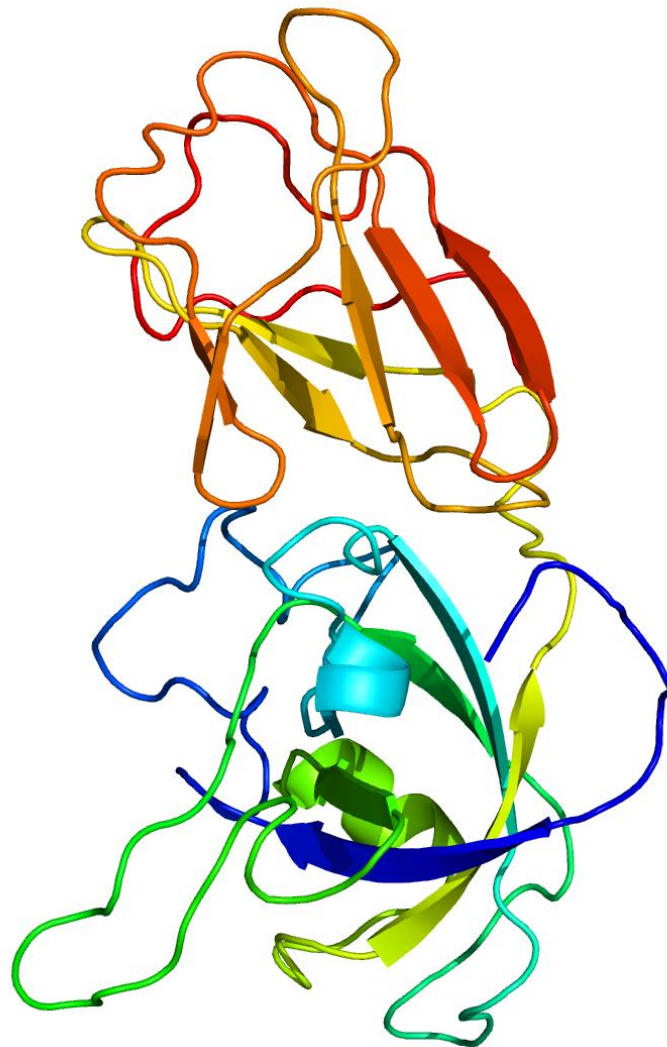
Locus: Eucgr.F03723

Gene Model: Eucgr.F03723.1.p

Description: EgrEXPA-15

Family: Alpha Expansin

3D structure:



GENOME DATABASES

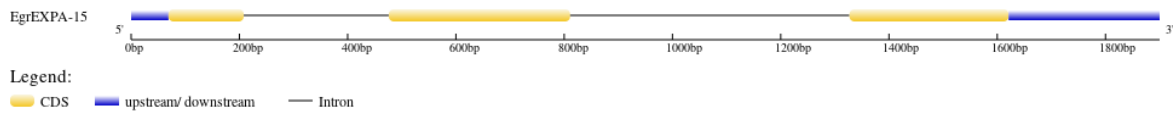
Phytozome: https://phytozome-next.jgi.doe.gov/info/Egrandis_v2_0

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

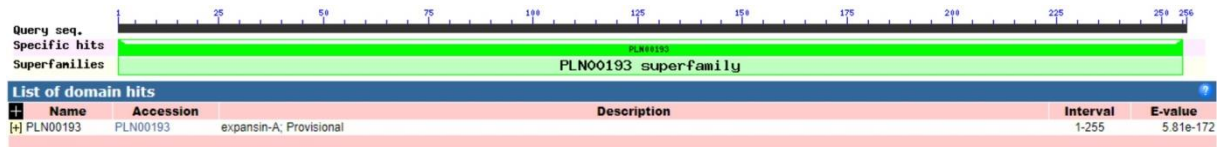
EXTERNAL RESOURCES

<https://eucgenie.org/>

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>EgrEXPA-15

MAKPTLAVAALLACSYLAVTVNAFSPSGWTKGHATFYGGSDASGTMGGACGYGDL
YSAGYGTRTAALSTALFNDGASCGQCYRMICDHIADPKWCRPGASVTITATNFCPPN
FALPSNNGGWCNPLQHFDMAEPAWEKIGIYRGGIVPILFQRPVCKKHGGVRFTINGR
DYFELVLITNVAGSGSIQSVSIKGSKTAWMAMSRNWGANWQSNNSYLNQSLFRVT
TTDGATRVFEDIVQSNWAFGQTYSSSIQF*

CDS (coding sequence)

>EgrEXPA-15

ATGGCAAACCCACTCTTGCAGTAGCGGCTCTTCTCGCGTGCTCTTACCTTGCCGT
GACTGTCAATGCCTTCTCTCCCTCGGGGTGGACTAAAGGCCATGCCACCTTCTATG
GAGGGAGTGATGCTTCTGGAACCATGGGGGGAGCGTGTGGATACGGGGATTGT
ATTCAGCTGGGTATGGGACTAGAACAGCTGCCCTGAGCACTGCCCTTTTCAATGA
CGGCGCTTCGTGCGGACAGTGCTACAGGATGATATGCGACCACATTGCGGACCCC
AAGTGGTGCAGGCCGGGCGCGTCCGTGACCATCACCGCGACCAACTTTTGCCCTC
CAAACCTTCGCTCTTCCGAGCAATAACGGTGGTTGGTGCAACCTCCCCTCCAACA
CTTTGACATGGCTGAGCCCGCGTGGGAAAAGATCGGCATCTACAGAGGCGGGAT
CGTCCCCATCTTGTTCCAAAGGGTCCCCTGCAAGAAGCACGGCGGGGTGAGATTC
ACCATCAACGGTCGAGACTACTTCGAGCTCGTCCTCATCACCAATGTCGCGGGAA
GCGGATCGATCCAATCTGTTTCGATCAAAGGGTCGAAAACGGCCTGGATGGCGAT
GTCAAGGAAGTGGGGGGCCAATTGGCAGTCCAATTCCTATCTGAACGGCCAGTCT
CTATCTTTCAGGGTCACTACTACTGACGGAGCGACTCGAGTCTTTGAAGACATCG
TGCAGTCGAACTGGGCTTTCGGCCAAACATATTCGAGCTCTATACAGTTTTGA

Nucleotide

>EgrEXPA-15

CCCCATTTTCTTGCTCTTCTCACGTCTCCTCCCTCCTCTCTGTTTCTTCCATCTTGG
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CCACCTTCTATGGAGGGAGTGATGCTTCTGGAACCATGGGTAACCTCACCTTTCTTT
TGCCTTTCATGCTTCAAGATATAGAAAATTGTAGTTTTCTCGATACAAGGAAGTTC
CGAAAGATTCCCTCAGATGTCAGATTTGTCTCTAATCTCGCGTTGCTTGCTTTCGG
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CATGGACAATGTCATGTTGGCTCGGCGGCTGGTAGTTCGGGGCTTCTTGGTATTA
CTAATGGCTCATCCGTCTTTGGTTTGCAGGGGGAGCGTGTGGATACGGGGATTTG
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TCGTCCCCATCTTGTTCCAAAGGCATGTTCTTCTTGTTGCTCTCTGTCTTCCCAT
CGGAATCTAAGATAAACTACCGTAACCATGGTTGGGCTTTAATGAAATAACAGAG
CACTTGTGATGCATATTCAGTAGGAAACACAATCGCTGATGACTGACTACTCTTA
ATGAATCACGCGGTATGAACTTTTTGATAGGGATTTATTCAACTAGTTCTTGACAA
AAGTAGTGTGATATGTAAGAGAATACAGATGTCAATCAGTCCGATGAATGAACTT
TCATTTAACTAAAATGCGGTCTCCTTTGGTAATAGACAAAATTGTAGTCGTAGCA
AGGATGAGAACAAAATTGCAATTTCTGGGATTCAATTGGTGCGCCGCGTAGTTAC
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CACAATCTTCAGGCTTTTTAACTAGTTGAGGTGAAACTTGAATCTGCCACTTCATA
TCTCCTCTGTCTCATGCTTCAGAGTTATAAATCTTGCAGGGTCCCCTGCAAGAAGC
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