

IDENTIFICATION

Species: *Eucalyptus grandis*

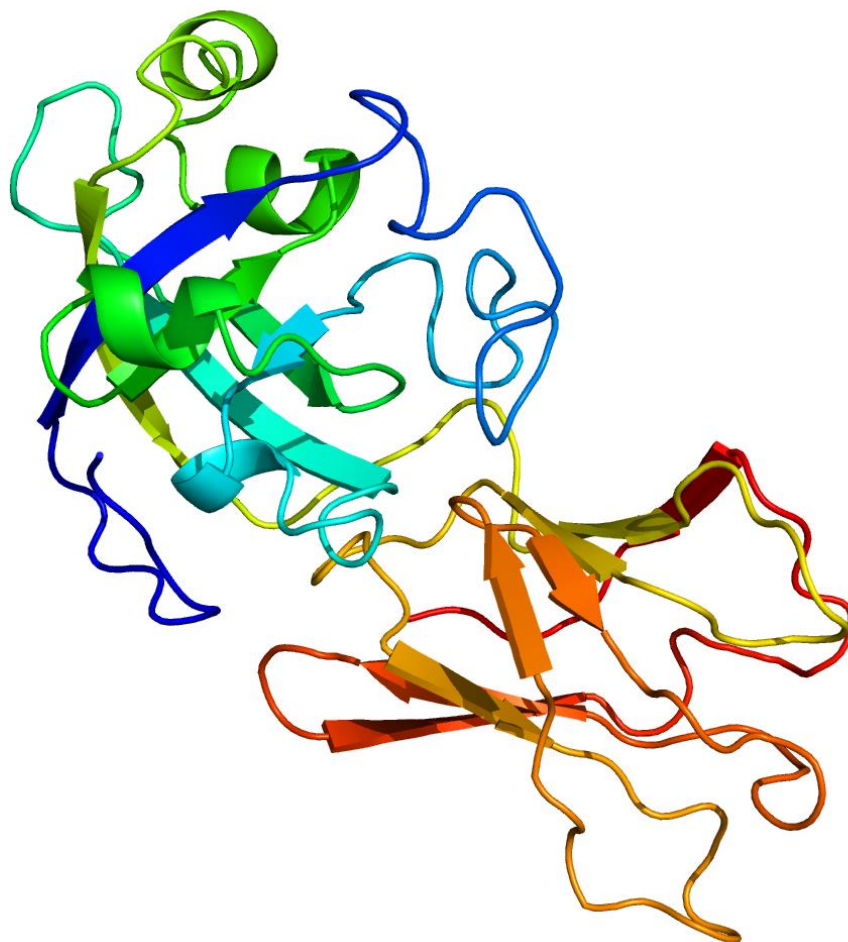
Locus: Eucgr.E01622

Gene Model: Eucgr.E01622.1.p

Description: EgrEXPB-04

Family: Beta Expansin

3D structure:



GENOME DATABASES

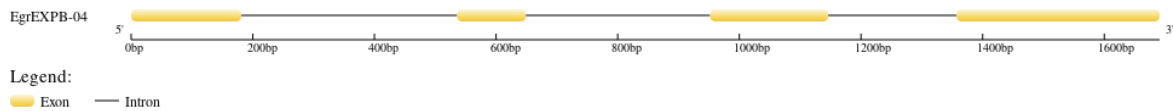
Phytozome: https://phytozome-next.jgi.doe.gov/info/Egrandis_v2_0

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

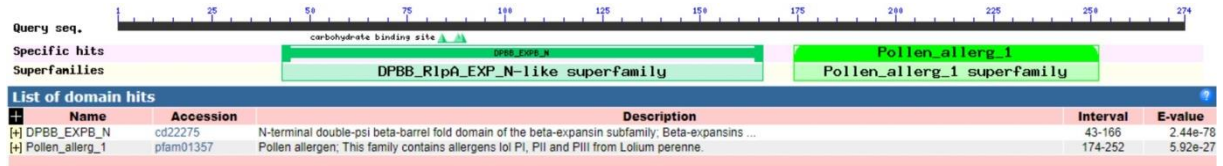
EXTERNAL RESOURCES

<https://eucgenie.org/>

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>EgrEXPB-04

MALLQSPSICFPLALLLSLLINSSHCFKPKSLNISKVQSNGDWSPAGATWYGSPNGAG
SDGGACGYGSGVAQAPFASMVSAGGPSLFKSGKGCACGYQVKCTENAACSGNPVT
VVITDECPGGPCVAESAHFDSLSTAFGAMASSGKADELNRNAGVLRQIQYKKVKCKFPK
VKEAFHVDSGSNPYYFAALIEYANGDGELSAVNLRKQALDSDSWLPMQQSWGAIWK
LDGAGQLRAPFSIKLTSLSGKTLVANNVIPAGWQPGQTYRSDVNFV*

CDS (coding sequence)

>EgrEXPB-04

ATGGCGCTTCTTCAATCTCCATCGATTTGCTTCCCTCTCGCCCTTCTGCTTTCTCTC
CTCATAAACTCGTCTCATTGCTTCAAACCCAAATCGCTTAACATCTCGAAGGTTCA
GTCCAACGGTGATTGGTCGCCGGCAGGTGCGACGTGGTACGGGAGTCCCAATGG
CGCTGGAAGCGATGGTGGTGCATGTGGGTATGGGAGTGGGGTCGCCCAAGCTCC
ATTCGCTTCAATGGTGTCCGCAGGAGGGCCTTCTCTTTTCAAATCAGGCAAAGGA
TGTGGAGCTTGTTACCAGGTGAAATGCACCGAAAACGCGGCTTGTTCTGGGAACC
CAGTGACGGTCGTTATAACTGATGAATGCCCTGGTGGCCCTTGTTGTTGCTGAATCT
GCTCACTTCGATTTGAGCGGCACGGCTTTTGGAGCTATGGCGAGCTCTGGCAAGG
CCGATGAACTTCGCAACGCTGGGGTGCTGCAAATTCAATACAAAAAAGTAAAGT
GCAAGTTCGCCGGCGTGAAGGAGGCATTCCACGTTGACTCCGGCTCGAACCCCTA
CTATTTCGCTGCGCTAATTGAGTACGCGAATGGGGATGGCGAGCTCAGCGCCGTC
AACCTGAAGCAGGCTCTAGACTCTGACTCTTGGCTTCCGATGCAACAGTCGTGGG
GCGCGATTTGGAAGCTGGATGGCGCGGGCCAGCTGCGCGCCCCATTCTCGATCAA
GCTCACCTCTTTGACTCCGGCAAGACCCTGGTTGCCAACACGTGATCCCCGCT
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Nucleotide

>EgrEXPB-04

ATGGCGCTTCTTCAATCTCCATCGATTTGCTTCCCTCTCGCCCTTCTGCTTTCTCTC
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GTCCAACGGTGATTGGTCGCCGGCAGGTGCGACGTGGTACGGGAGTCCCAATGG
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CAAAGTTAATATATGTTACGAGATATGATTTTCCTAAATTAACAATCGTGGAAT
AGAATTCATGAAAACATCTACTGCGGCAAGCTTTCTAGACTTCCATTA AAAAGTAG
CTTGACTTCTTCGTATTTAAACAGATTATTTGACTCGGTACATATTGTCCTATTCA
AACAGATTATTTAGTAGTAGTTAGGAAGTGCAGTCTTTTGAGCTCTTGTTGATTAA
ATTTCAGGTGAAATGCACCGAAAACGCGGCTTGTTCTGGGAACCCAGTGACGGTC
GTTATAACTGATGAATGCCCTGGTGGCCCTTGTTGCTGAATCTGCTCACTTCGA
TTTGAGCGGCACGGCTTTTGGAGCTATGGCGAGCTCTGGCAAGGCCGATGAACTT
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CCAGACTTATACTAATCAGCAAATAGTCTAACTTGCTTATTA AAAAGTCTATTTATG
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CTGACTCTTGGCTTCCGATGCAACAGTCGTGGGGCGCGATTTGGAAGCTGGATGG
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