

IDENTIFICATION

Species: *Eucalyptus grandis*

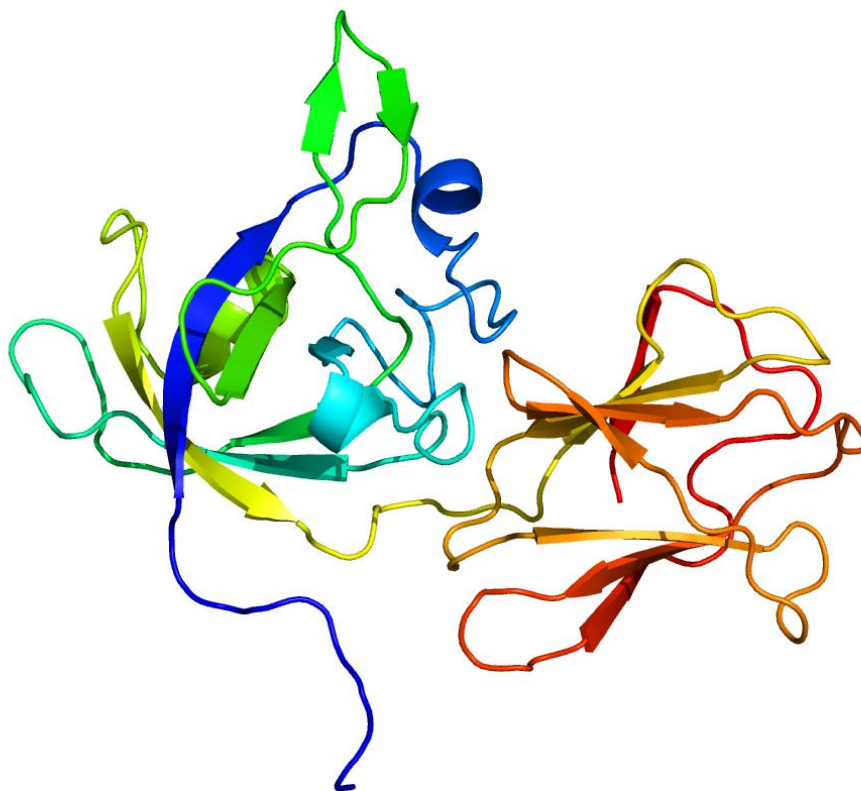
Locus: Eucgr.B00524

Gene Model: Eucgr.B00524.1.p

Description: EgrEXPA-05

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>

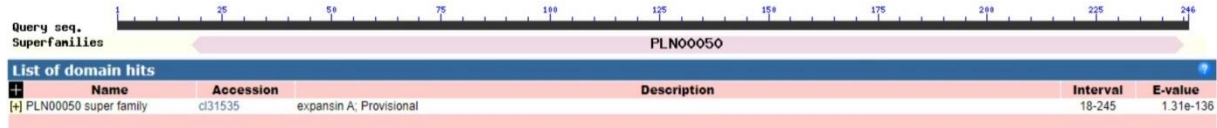
EXTERNAL RESOURCES

<https://eucgenie.org/>

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>EgrEXPA-05

MAFLGVLLVGLLCLGSSVHGYGDGWIDAHATFYGGGDASGTMGGACGYGNLYSQG
YGTNTAALSTALFNLSGLSCGACFEIKCVNDPRWCNPASIVVTATNFCPPNNALPNN
GGWCNPPLHHFDLSQPVFQQAQYSSGIVPVA YRRVPCQKKGIRFTINGHSYFNLVL
ITNVGGAGDVRVSISIKSRTGWQPMSRNWQNWQSNLNLDGQSLSFSVTTSDGRTV
VSNNVAPPNWSFGQTFAGR*

CDS (coding sequence)

>EgrEXPA-05

ATGGCTTTTCTTGGGGTGCTCCTGGTGGGATTGCTCTGTTTGGGCTCATCTGTTCA
TGGATATGGTGATGGCTGGATCGATGCGCATGCGACCTTCTACGGCGGTGGCGAC
GCTTCTGGCACAATGGGCGGGGCTTGTGGCTACGGGAACCTTGTACAGCCAGGGCT
ACGGCACGAACACAGCGGCCCTGAGCACTGCCCTGTTCAACAGCGGGCTGAGCT
GCGGGGCCTGCTTCGAGATCAAGTGCCTCAACGACCCACGGTGGTGAACCCGG
CCTCGATTGTGGTCACCGCCACCAACTTCTGCCCGCCGAACAATGCGCTCCCCAA
CAATGCCGGCGGCTGGTGCAACCCACCTCTCCATCACTTCGATCTCTCCAGCCA
GTGTTCCAGCAGATTGCCAGTACAGCTCTGGGATTGTCCCTGTGGCTTATAGGA
GGGTACCATGTCAAAGAAGGGAGGCATCAGATTCACCATCAATGGTCACTCCTA
CTTCAACTTGGTCTGATCACCAACGTTGGAGGTGCAGGGGACGTCCGCTCTGTT
TCGATCAAGGGCTCGCGGACCGGCTGGCAACCCATGTCCCGGAACCTGGGGCCAG
AACTGGCAGAGCAATTCGAACCTCGACGGACAGAGCCTCTCCTTTTTCGGTCACCA
CCAGTGATGGCCGGACTGTGGTCTCCAACAACGTGGCACCCCCCAATTGGTCTT
CGGCCAGACCTTCGCCGGCCGG

Nucleotide

>EgrEXPA-05

ATGGCTTTTCTTGGGGTGCTCCTGGTGGGATTGCTCTGTTTGGGCTCATCTGTTCA
TGGATATGGTGATGGCTGGATCGATGCGCATGCGACCTTCTACGGCGGTGGCGAC
GCTTCTGGCACAATGGGTA ACTTAACTAGTTCTTTTGAATATGTTCAATTTTGGCAA
ATAATCGGTTATGTAGCCGAATGTAACAGGACATAACTCTTTACACGATGAGTT
TTAGTCATTCTGCTAATGGTCGCCAGGAAGATTTTATTTCGCGTTGGTTCGATCCATA
AAATCAGCCCTGAGGGCTTAAAGTCATACACGTATTGCATTGCATTAGTTTAAATGA
GAGCCATTTGACAAAATTGAAACGATATACTGAGGCAATAAATTCAATTTGGCAA
TGCTTTCTGTTGTGGCAAGGCGGGGCTTGTGGCTACGGGAACCTTGTACAGCCAGG

GCTACGGCACGAACACAGCGGCCCTGAGCACTGCCCTGTTCAACAGCGGGCTGA
GCTGCGGGGCCTGCTTCGAGATCAAGTGCGTCAACGACCCACGGTGGTGCAACCC
GGCCTCGATTGTGGTCACCGCCACCAACTTCTGCCCCGCCGAACAATGCGCTCCCC
ACAATGCCGGCGGCTGGTGCAACCCACCTCTCCATCACTTCGATCTCTCCCAGC
CAGTGTTCCAGCAGATTGCCCAGTACAGCTCTGGGATTGTCCCTGTGGCTTATAG
GAGGTTGCCAATTTATCACGCTCTGTGTTAATTCAATTTAATTCTGTGTGAAAAGT
TATGGGAGCTTTGATTTTAAAATTGAATTCATGATGTTACACATAATTGCATAGAT
ATACTAAACAATTGAAGAATTTATTGGCACAGCTAATCTTTGCAATGTTTCATGTG
GTAGGGTACCATGTCAAAAGAAGGGAGGCATCAGATTCACCATCAATGGTCACT
CCTACTTCAACTTGGTCCTGATCACCAACGTTGGAGGTGCAGGGGACGTCCGCTC
TGTTTCGATCAAGGGCTCGCGGACCGGCTGGCAACCCATGTCCCGGAACTGGGGC
CAGAACTGGCAGAGCAATTCGAACCTCGACGGACAGAGCCTCTCCTTTTCGGTCA
CCACCAGTGATGGCCGGACTGTGGTCTCCAACAACGTGGCACCCCCCAATTGGTC
CTTCGGCCAGACCTTCGCCGGCCGG