

IDENTIFICATION

Species: *Eucalyptus grandis*

Locus: Eucgr.E00357

Gene Model: Eucgr.E00357.1.p

Description: EgrEXLB-02

Family: Expansin Like Beta

3D structure:



GENOME DATABASES

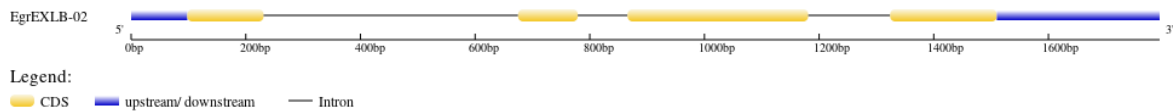
Phytozome: https://phytozome-next.jgi.doe.gov/info/Egrandis_v2_0

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

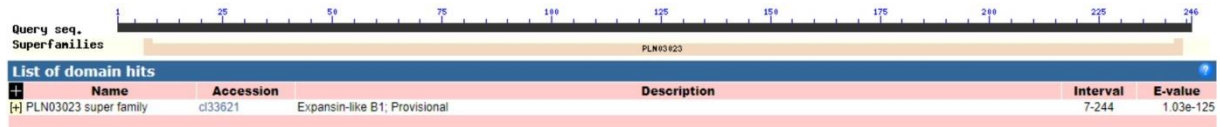
EXTERNAL RESOURCES

<https://eucgenie.org/>

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>EgrEXLB-02

MKSAMNYSCLLCILVLLPALCHCQDPFTPSRATYYGSPYCYGTPTGACGYGEYGRTI
DGYVTGVSRLYRNGSGCGACYQVRCTEPQCTGEGAYVVVTDYGEDRTDFILSTRS
YAKMAKPDDYQTKQLFAYGVVEVEFRRVPCRYPGQNLLVSVNEHSRNPSYLAIIILY
VGGTNDVTA AEYWQDDYQGWNRMRVYGAVFDTQTTPRGLYLRFRVGGSWVQP
KRALPADWKAGAVYDSQVQLN*

CDS (coding sequence)

>EgrEXLB-02

ATGAAATCTGCAATGAACTATAGTTGTCTTCTTTGTATCCTGGTGCTCTTGCCAGC
ACTTTGTCACTGTCAAGATCCATTTACACCATCGAGAGCTACTTACTATGGCAGTC
CTTACTGCTATGGGACTCCA ACTGGAGCTTGTGGGTACGGTGAGTATGGCAGGAC
CATCGATGGCTATGTGACTGGAGTTTCGAGGCTATACAGAAATGGATCTGGATGT
GGTGCCTGCTATCAGGTGAGGTGCACGGAACCGCAGTGCACGGGCGAAGGAGCG
TACGTGGTGGTGACGGACTATGGAGAAGGAGACAGGACGGACTTCATCCTGAGC
ACCAGATCTTATGCGAAGATGGCAAACCGGACGACTACCAAACCAAGCAGCTG
TTTGCCTACGGCGTGGTTGAGGTGCAATTCAGAAGGGTTCGGTGCCGATACCCCG
GCCAAAACCTCCTTGTCAGCGTCAATGAACACAGCAGAAACCTTCTTACTTAGC
TATCATCCTTTTATACGTCCGGCGGCACAAATGACGTACAGCTGCGGAGTATTGG
CAGGATGACTATCAAGGGTGAACCGGATGCGCCGAGTGTACGGAGCAGTGTTTC
GACACGCAAACCTCCGCCAAGAGGCGATTTGTACCTGAGGTTCCGAGTGGGTGGGT
CTTGGGTGCAGCCAAAGCGCGCCCTCCCTGCTGACTGGAAAGCTGGTGCTGTTTA
TGACTCCCAAGTGCAGCTGAACTAG

Nucleotide

>EgrEXLB-02

ATCTCAAGACCACCTTGTCCATTTCCCTCTCTCTCTAGTCGAGTCCTCTAGGCTTG
AGTTTACTTGTCTTGCATTAGGATCAGTACATTGAGTGAGACATGAAATCTGCAA
TGA ACTATAGTTGTCTTCTTTGTATCCTGGTGCTCTTGCCAGCACTTTGTCACTGTC
AAGATCCATTTACACCATCGAGAGCTACTTACTATGGCAGTCCTTACTGCTATGG
GACTCCAAGTATGTGCACGCTCCGTCTTGTGATAGAAACAAACTTGCATCAG
CCACCGCACCACACAAGCGCTGCACATAAATTATGTTACACATTAGTGTGAAGC
TAGTAGAGCACTAGTCGCTAAAATAGTATCGTGTCATGAAAAGTACACAAAACA
ACGTTTCTTGTCTTTCAATTA ACTTCTTTAACTATGTTTATGGTCATGTGGCATGCT
CCATTACATCATGAATAACTTTTTGCGGGTATGCACTCTTCCCTTGATACTCGGT

AGAGCGCAATATAACATGAGAAGATCTGTGTAGTAGCATATCTCACTCGGTACTT
GAAGGCTTGGTTGTTACATGCACTCTTTGAACCGCTCCATTTTCATTACGCCAAA
CCAAACACTTGAAACAGAACAATTTTTGCTAGAGAAGATCTAATGAGTGCAATGT
TCATGGCAGCTGGAGCTTGTGGGTACGGTGAGTATGGCAGGACCATCGATGGCTA
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CAGGTTTTAACTTCATATAGACTGCACATATATAGATGATGACTCTTTTTAACTTT
TTCATTAGTCTAATTTTGTGTTTAAAGTATAGGTGAGGTGCACGGAACCGCAGT
GCACGGGCGAAGGAGCGTACGTGGTGGTGACGGACTATGGAGAAGGAGACAGG
ACGGACTTCATCCTGAGCACCAGATCTTATGCGAAGATGGCAAACCGGACGACT
ACCAAACCAAGCAGCTGTTTGCCTACGGCGTGGTTGAGGTTCGAATTCAGAAGGGT
TCCGTGCCGATACCCCGGCCAAAACCTCCTTGTGTCAGCGTCAATGAACACAGCAGA
AACCCTTCTTACTTAGCTATCATCCTTTTATACGTGGCGGCACAAATGACGTCAC
AGCTGCGGAGTATTGGCAGGTATTCAGTCATCCATTATCCCATGAGTTTGCTACA
ATTTGGTTTCAAGTAGAATCAAATTAACCATAAATCGACATAAACACGAACAAG
AGACCACTACTCAACAAGACAATGACCTTGCTTTCTCGTAATTTTCGATTCAGGAT
GACTATCAAGGGTGGAAACCGGATGCGCCGAGTGTACGGAGCAGTGTTTCGACACG
CAAACCTCCGCCAAGAGGCGATTTGTACCTGAGGTTCCGAGTGGGTGGGTCTTGGG
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CTATAATAAATGAGATTGGTGTTCCCTT