

IDENTIFICATION

Species: *Eucalyptus grandis*

Locus: Eucgr.E00358

Gene Model: Eucgr.E00358.1.p

Description: EgrEXLB-03

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>

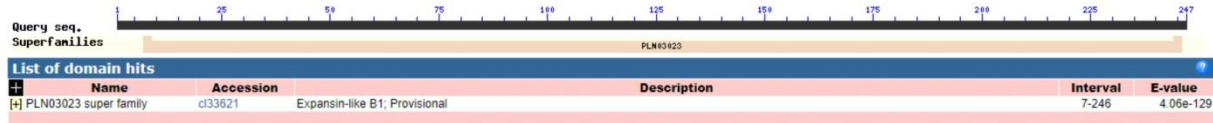
EXTERNAL RESOURCES

<https://eucgenie.org/>

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>EgrEXLB-03

MKSAMSYSCLLCILVLLPALCHSENSFTPSRATYYGSPDCYGTPTGACGYGEYGRTV
YDGYVTGVSRLYRNGSGCGACYQVRCTKPQCTGEGAYVAVTDYGEGRDTRDFILSTR
AYAKMAKPDYQTEQLFAYGVVEVEFRRVPCRYPGQNLLVSVSEHSRNPSYLAVILL
YVAGKDDVIAAEYWQEDCQEWKPMRRVYGA VFDQTTPPIGELYLRFQVGGSWVHP
KYALPADWKAGAVYDSQVQLD*

CDS (coding sequence)

>EgrEXLB-03

ATGAAATCTGCAATGAGCTATAGTTGTCTTCTCTGTATCCTGGTGCTCTTGCCAGC
ACTTTGTCACTCTGAAAATTCATTTACGCCCTCGAGAGCCACTTACTATGGCAGCC
CTGACTGCTATGGGACTCCAAGTGGAGCTTGTGGGTACGGCGAGTATGGCAGGAC
CGTCTACGATGGCTATGTGACTGGAGTTTCGAGGCTATACAGAAATGGATCTGGA
TGTGGTGCTTGTATCAGGTGAGGTGCACGAAACCGCAGTGCACGGGCGAAGGA
GCGTACGTGGCGGTGACGGACTATGGAGAGGGAGACAGGACGGACTTCATCCTG
AGCACCAGAGCCTATGCGAAGATGGCAAACCGGACGACTACCAAACCGAGCAG
CTGTTTCGCCTACGGCGTGGTTGAGGTCGAATTCAGAAGGGTTCCGTGTCGATACC
CCGGCCAAAACCTCCTTGTGACGTCAGTGAACACAGCAGAAACCTTCTTACTT
AGCTGTCATCCTTTTATACGTCGCCGGCAAAGATGACGTCATAGCTGCGGAGTAT
TGCCAGGAGGACTGCCAAGAGTGGAAGCCGATGCGCCGAGTGTACGGAGCAGTG
TTCGACACGCAAACCTCCGCAATAGGCGAGTTGTACCTGAGGTTCCAAGTGGGTG
GGTCTTGGGTGCATCCAAAGTACGCCCTCCCTGCTGACTGGAAAGCTGGTGCTGT
TTATGATTCCCAAGTGCAGCTGGACTAG

Nucleotide

>EgrEXLB-03

ATCCCAAACCTTCTTGTCCATTTCCCTCTCTCTCTAGTCGAGTCCTCTAGGCTT
GAGTTTACTTGTCTTGCATTAGGATCAGTACATTGAGTGAGACATGAAATCTGCA
ATGAGCTATAGTTGTCTTCTCTGTATCCTGGTGCTCTTGCCAGCACTTTGTCACTCT
GAAAATTCATTTACGCCCTCGAGAGCCACTTACTATGGCAGCCCTGACTGCTATG
GGACTCCAAGTATGTGCACGCTCCGTCTCCTGTGATAGAAACCAAGCTTGCATCA
GCCACCGCACCAACAAGCGCCGCACATAAATTATGTTACACATTAGTGTGAAG
CTAGTAGAGCACTAGTCGCTAAAATAGTATCGTGTCATGAAAAGTACACAAAAC
AACATTTCTTGTCTTTAAAGTAACTTTTTTAACTTCGTTTATGGTCATGTGGCATGC
TCTGTTACATCATGAATAACTTTTCGTGGGTATGCGCTCTTCCCTTGATACTCAG

CAGAACGCAATATAACATGAGAAGATCTGTGTAGTGGCATGTCTCGCTCGGTACT
TGAAGGCTTGGTTGTTACATGCACTCTTTGAACCACTCCATTTTCATTATGCCCAA
ACCAAACATTTGAAACAGAACAATTTTTGCTAGAGAAGATCTAATGAGTGCAATG
TTTATGGCAGCTGGAGCTTGTGGGTACGGCGAGTATGGCAGGACCGTCTACGATG
GCTATGTGACTGGAGTTTCGAGGCTATACAGAAATGGATCTGGATGTGGTGCTTG
CTATCAGGTTTAACTTCATATAGACTACACATAAATAGATGATGACTCTTTTTGAC
TTTTTCATCAGTCTAATTTTACTTTTTTTTTAAGTATAGGTGAGGTGCACGAAACCG
CAGTGCACGGGCGAAGGAGCGTACGTGGCGGTGACGGACTATGGAGAGGGAGAC
AGGACGGACTTCATCCTGAGCACCCAGAGCCTATGCGAAGATGGCAAAACCGGAC
GACTACCAAACCGAGCAGCTGTTTCGCCTACGGCGTGGTTGAGGTGCAATTCAGAA
GGGTTCCGTGTCGATACCCCGGCCAAAACCTCCTTGTGTCAGCGTCAGTGAACACAG
CAGAAACCTTCTTACTTAGCTGTCATCCTTTTATACGTCGCCGGCAAAGATGACG
TCATAGCTGCGGAGTATTGGCAGGTATTCAGTCATCCATTATCCCATGAGTTTGCT
ACAATTTGGTTACAAGTAGAATCAAATTGAACCATAAATCGACATAAACACGTTT
TAGAGACCACTAGTCGACAAGACAATAATGACCTTGCTTTCTCGTAATTTTCGATT
CAGGAGGACTGCCAAGAGTGGAAGCCGATGCGCCGAGTGTACGGAGCAGTGTTT
GACACGCAAACCTCCGCCAATAGGCGAGTTGTACCTGAGGTTCCAAGTGGGTGGGT
CTTGGGTGCATCCAAAGTACGCCCTCCCTGCTGACTGGAAAGCTGGTGCTGTTTA
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TTGATTGGGAAAGTGCG