

IDENTIFICATION

Species: *Eucalyptus grandis*

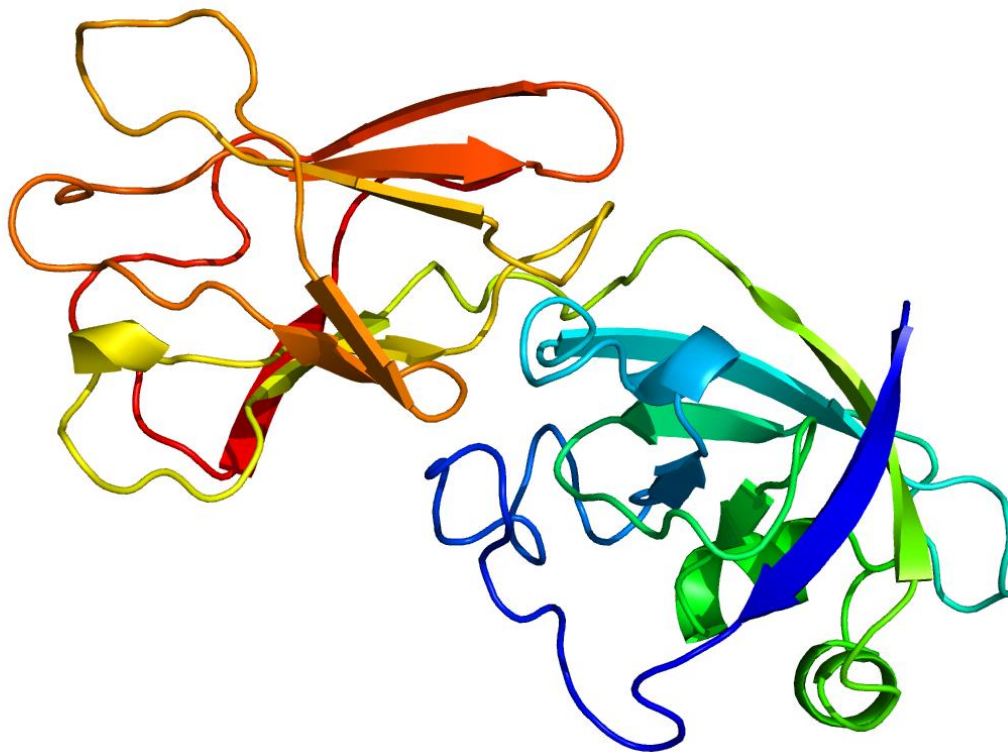
Locus: Eucgr.I01493

Gene Model: Eucgr.I01493.1.p

Description: EgrEXLA-01

Family: Expansin Like Alpha

3D structure:



GENOME DATABASES

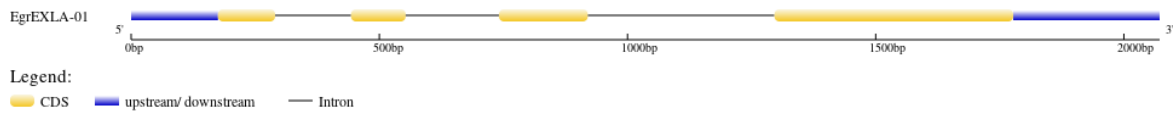
Phytozome: https://phytozome-next.jgi.doe.gov/info/Egrandis_v2_0

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

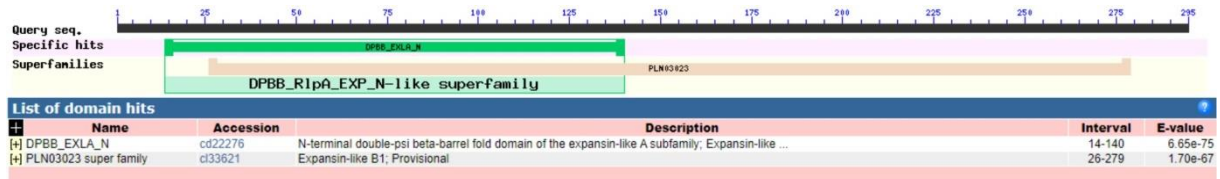
EXTERNAL RESOURCES

<https://eucgenie.org/>

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>EgrEXLA-01

MALLLCFLLSLFISSATACDRCVHQSKAAYFSKASALSSGACGYGSLAVGFNSGFLAA
AIPSLYKDGAGCGACFQIRCKNANLCTKGGTRVIVTDLNRNNNTDFVLSSRAFAAMA
RQGMSQDILRQGIVDVEYKRVPCDYKDRNLAVRVEESSRKPNYLAIKVLVYQGGQTEI
VAMDVAQVSLHPLYHQIHFPFKSIRHFLGPSCQITSRFPYSQVGSSYWTYMSRNYGA
VWNTSRVPD GALQFRFVVTSGYDGKWIWAKSVLPADWQNGVVYDSGIQITDIAQEG
CSQCDDGSW*

CDS (coding sequence)

>EgrEXLA-01

ATGGCCTTGCTTCTCTGCTTCCTCCTCTCTCTTCATCTCATCCGCCACTGCTTGC
GATCGCTGCGTCCACCAGTCCAAGGCCGCTTACTTCAGCAAGGCCTCTGCACTTT
CGTCTGGAGCATGTGGGTATGGCTCTTTGGCTGTGGGCTTCAACAGTGGCTTTCTC
GCAGCAGCCATTCCTTCCCTTTACAAAGATGGTGCTGGTTGTGGTGCTTGCTTTCA
GATAAGGTGCAAGAACGCCAATCTGTGCACCAAAGGAGGGACTAGAGTGATCGT
GACCGATCTCAACCGCAACAACAACACAGACTTCGTGCTCAGCAGCCGAGCTTTC
GCGGCCATGGCTCGCCAGGGGATGAGCCAGGACATCTTGAGACAAGGCATTGTC
GACGTCGAATATAAAAGAGTCCCTTGCGACTACAAGGACCGGAATCTGGCCGTTCC
GGGTGGAGGAGTCGAGCCGAAAGCCAAATTACCTCGCCATCAAAGTGCTGTACC
AAGGCGGCCAGACCGAAATCGTGGCCATGGACGTAGCACAAGTGAGCCTCCACC
CTTTATATCACCAAATCCACTTTCCTTCAAATCAATCCGACATTTTCTTGCCCCG
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CTACATGAGCAGGAACACTACGGCGCTGTTTGGAACACGAGCCGCGTCCCCGATGG
GGCATTGCAGTTCCGGTTCGTGGTGACCTCTGGCTACGATGGGAAGTGATCTGG
GCCAAGAGCGTCCTTCCC GCGGATTGGCAGAACGGGGTTCGTCTACGATTCAGGAA
TCCAAATTACCGATATCGCACAAGAGGGTTGCTCTCAATGTGACGACGGGAGCTG
GTGA

Nucleotide

>EgrEXLA-01

GTCCGACCCGAAGGAAAAAATAAAGAATCGTTGTCAATCCAAATCCTTTTTGG
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ATAAATACCGCGTTTCTCCATCAGTCTTTCATTTCGACACTGACTCGACAACAATAA

GAACCAAGATGGCCTTGCTTCTCTGCTTCCTCCTCTCTCTCTTCATCTCATCCGCCA
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TGCACTTTCGTGTAAGCAATCGGTTCTTGGTCTTCTCGTTTGTTCGTTCCCTTTCTTC
AAAACCCAGATGGATTTTATGGCGAAATGTGTAGTTTTGGCTCGGACCCAGATGA
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TCTCGAAATTTCTTTCCCTTTCTACCATCCTCGGTAGACTCAGCTGATCACAGTACG
ACATCGATGGATGTGATGGGCCAAATTTTCTAAATTATTAAGCTGTTAGTATAGT
GTGTACATGCCTTTTTAATGTTGTTTGTGACACCTTTTTGACTGATCCGTGGAAAA
AACTATTGATTTGCAGATAAGGTGCAAGAACGCCAATCTGTGCACCAAAGGAGG
GACTAGAGTGATCGTGACCGATCTCAACCGCAACAACAACACAGACTTCGTGCTC
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TTTTCTTAAAGTATCAGTGATACAAATTGTA CTCTGGTGACATGTTAATGAGAATG
TTTGGTAATAAGTTTCATATA