

IDENTIFICATION

Species: *Eutrema salsugineum*

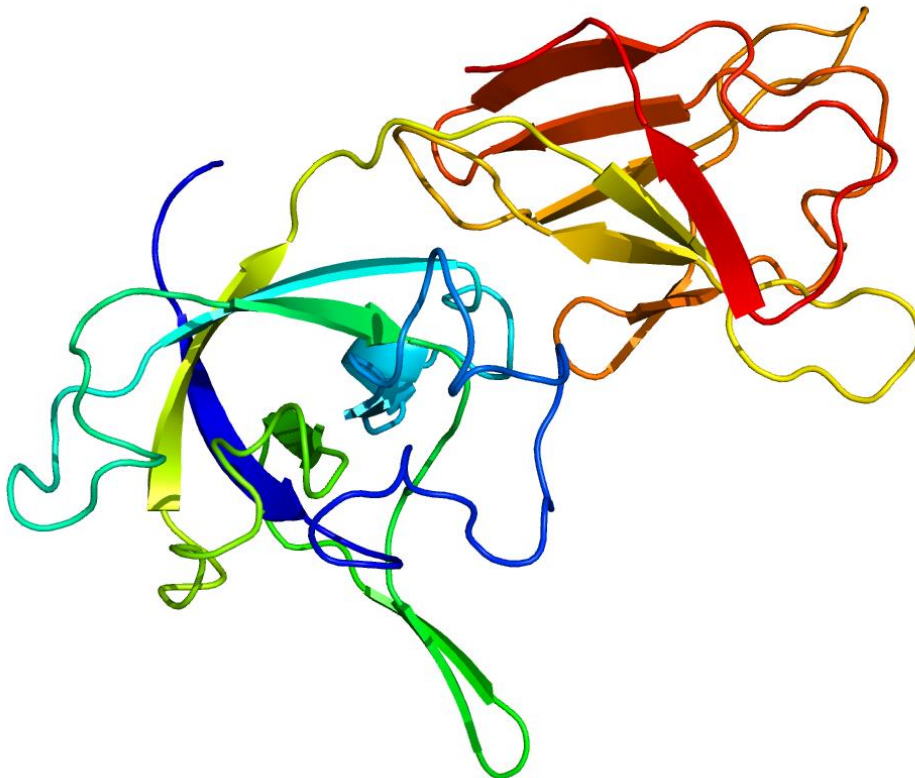
Locus: Thhalv10028899m

Gene Model: Thhalv10028899m

Description: EsEXPA-06

Family: Alpha Expansin

3D structure:



GENOME DATABASES

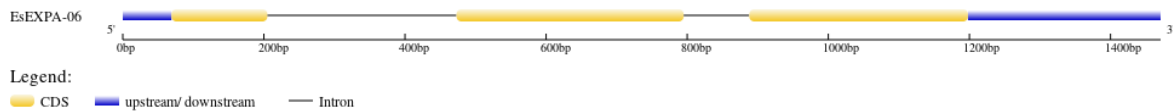
Phytozome: https://phytozome-next.jgi.doe.gov/info/Esalsugineum_v1_0

KEGG: <https://www.genome.jp/entry/T02985>

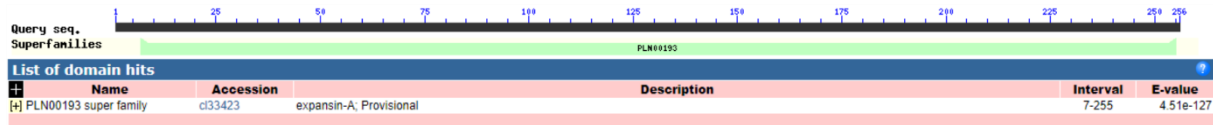
EXTERNAL RESOURCES

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GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>EsEXPA-06

MTKIISLSVA AIFSIMFFTKISSVSAGWLR AHATFYGGSDASGTMGGACGYGNLYTDG
YKTNTAALSTALFNDGKSCGGCYQIVCDASKVPQWCIRGRSITITATNFCPPNFAQAS
DNGGWCNPPRPHFDMAQPAFLTI AKYKAGIVPIIYRRVGCRRSGGMRFTMNGRNYFE
LVLISNVGGAGEISKVWIKGSKSNKWETMSRNWGANWQSNTYLNQSLSFKVQLSN
GRIKAALNVIPSNWRFGQSFKSRINF*

CDS (coding sequence)

>EsEXPA-06

ATGACAAAGATCATCTCTCTTTTCAGTCGCAGCTATCTTCTCCATAATGTTCTTCAC
GAAGATCAGCTCGGTTTCTGCAGGTTGGTTACGAGCTCATGCGACCTTCTATGGC
GGAAGTGATGCTTCTGGTACAATGGGAGGAGCTTGTGGTTATGGAAACCTATACA
CGGACGGTTACAAGACAAACACCGCAGCATTAAAGCACGGCACTGTTCAACGACG
GCAAGTCTTGTGGTGGATGTTACCAGATCGTCTGCGACGCGAGCAAAGTGCCACA
ATGGTGTATTAGAGGCAGATCAATCACAATCACTGCCACAAACTTTTGTCCACCA
AACTTTGCTCAGGCAAGCGACAATGGAGGATGGTGTAAACCCACCAAGACCTCACT
TCGACATGGCTCAGCCTGCTTTTCTCACCATCGCTAAGTACAAAGCTGGAATCGT
CCCAATCATCTACAGAAGGGTTGGATGTAGAAGAAGCGGAGGGATGAGATTTAC
AATGAATGGTAGAACTATTTTCGAGCTAGTCCTCATCTCAAACGTTGGAGGAGCT
GGTGAGATCTCTAAAGTTTGGATCAAAGGCTCTAAGAGCAACAAATGGGAGACA
ATGTCAAGAACTGGGGAGCTAATTGGCAGAGTAATACTTACCTTAATGGTCAAT
CGCTCTCTTTCAAAGTTCAACTCAGCAATGGAAGAATCAAAGCAGCTCTCAACGT
TATTCCTTCGAATTGGCGGTTTGGTCAGAGCTTCAAGAGCAGAATCAACTTCTGA

Nucleotide

>EsEXPA-06

TAATCATCAACCTCTCTTCTTAAAAGAAAGAATCAAAGCTCATTAAACACCTAAG
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ACGGCAAGTCTTGTGGTGGATGTTACCAGATCGTCTGCGACGCGAGCAAAGTGCC
ACAATGGTGTATTAGAGGCAGATCAATCACAATCACTGCCACAAACTTTTGTCCA
CCAAACTTTGCTCAGGCAAGCGACAATGGAGGATGGTGTAACCCACCAAGACCT
CACTTCGACATGGCTCAGCCTGCTTTTCTCACCATCGCTAAGTACAAAGCTGGAA
TCGTCCCAATCATCTACAGAAGGTAAATGATATTACATATCATATATATAGATCA
AGAATGTCACATTAATTAAGAGAGTGTGCTTAATTAAGGGTATTTCTTCTTCTTA
ATAGGGTTGGATGTAGAAGAAGCGGAGGGATGAGATTTACAATGAATGGTAGAA
ACTATTTGAGCTAGTCCTCATCTCAAACGTTGGAGGAGCTGGTGAGATCTCTAA
AGTTTGGATCAAAGGCTCTAAGAGCAACAAATGGGAGACAATGTCAAGAACTG
GGGAGCTAATTGGCAGAGTAATACTTACCTTAATGGTCAATCGCTCTCTTTCAA
GTTCAACTCAGCAATGGAAGAATCAAAGCAGCTCTCAACGTTATTCCTTCGAATT
GGCGGTTTGGTCAGAGCTTCAAGAGCAGAATCAACTTCTGATAATGATGATTGTA
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AGCTGTATGATAGTCTTGATTCCAGAGTGTTTATAATCTGGAGAAGACTCGAGCA
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