IDENTIFICATION

Species: *Eutrema salsugineum*

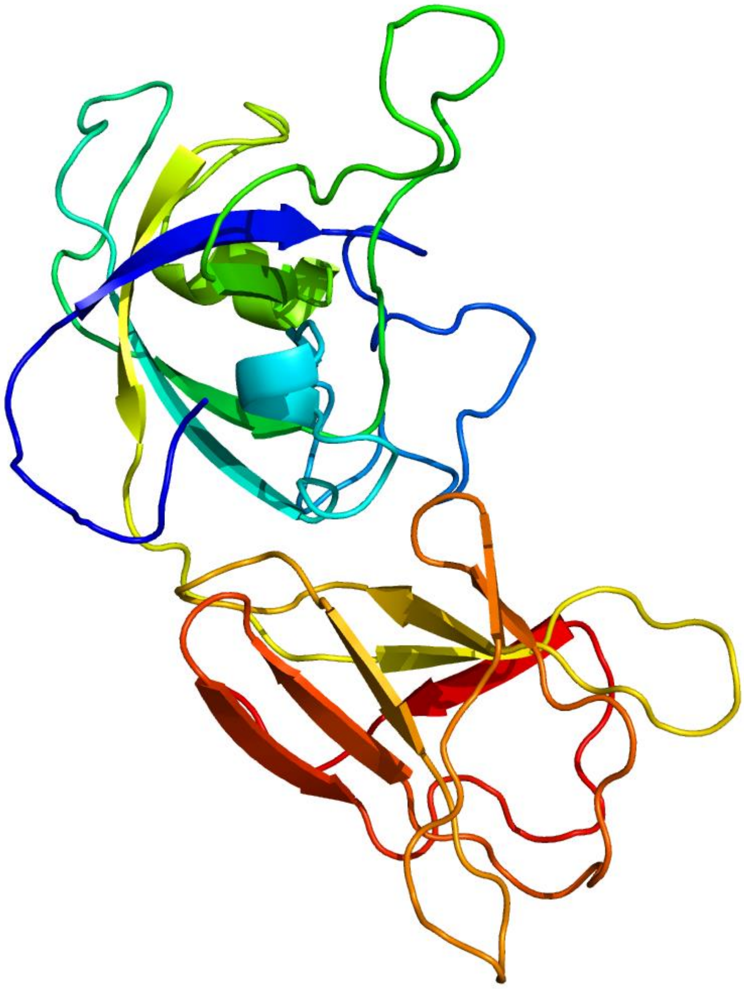
Locus: Thhalv10009820m

Gene Model: Thhalv10009820m

Description: EsEXPA-10

Family: Alpha Expansin

3D structure:



GENOME DATABASES

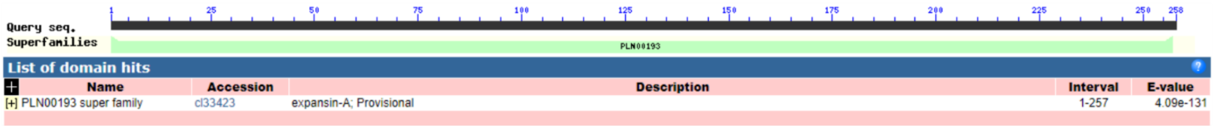
Phytozome: https://phytozome-next.jgi.doe.gov/info/Esalsugineum_v1_0
KEGG: https://www.genome.jp/entry/T02985

EXTERNAL RESOURCES

-

GENE STRUCTURE

DOMAIN ARCHITECTURE



List of domain hits

Name	Accession	Description	Interval	E-value
[+] PLN00193 super family	cl33423	expansin-A; Provisional	1-257	4.09e-131

SEQUENCES

Peptide

>EsEXPA-10

MTKILSFSIVVNFLLAMFCTNMISSVSAGWMQAHATFYGGSDASGTMGGACGYGNL
YTDGYGTNTAALSTALFNDGKSCGGCYQMVCDATKVPQWCRKGKWITITATNFCPP
NYALPNDDGGWCNPPRSHFDLAQPAFETIAIYRAGIVPVFYRRVGCRRSGGMRFTMN
GRDYFELVLISNVGGAGEISQVWIKGSKSNKWETMSRNWGANWQSLTYLNGQSLSF
KIQTSNGKIKSALDVVPSNWQFGQSFKSNLNF*

CDS (coding sequence)

>EsEXPA-10

ATGACGAAGATTTTATCTTTTTCGATAGTGGTCAACTTCCTCCTCGCGATGTTCTG
CACGAATATGATCAGCTCGGTTTCTGCAGGTTGGATGCAAGCTCATGCAACCTTC
TATGGAGGAAGTGATGCTTCGGGTACAATGGGCGGAGCGTGTGGTTACGGCAAC
CTCTACACCGATGGTTACGGGACAAACACGGCAGCGTTAAGCACCGCACTGTTCA
ACGACGGCAAATCTTGTGGCGGTTGTTACCAAATGGTCTGCGATGCGACCAAAGT
GCCACAATGGTGTCGTAAAGGCAAATGGATAACAATCACGGCTACGAATTTCTGT
CCTCCAAACTACGCTTTACCAAATGACGATGGAGGTTGGTGTAATCCTCCCAGGT
CTCATTTCGATTTGGCTCAGCCTGCGTTTGAGACCATCGCCATCTACAGAGCCGG
AATCGTCCCTGTTTTCTATAGAAGGGTCGGATGTAGAAGAAGCGGAGGAATGAG
ATTCACGATGAACGGTAGAGATTACTTCGAGCTTGTCCTCATCTCAAACGTAGGA
GGTGCAGGTGAGATTTCCCAAGTATGGATCAAAGGCTCCAAAAGCAACAAATGG
GAGACGATGTCAAGAAACTGGGGAGCTAATTGGCAAAGCCTTACTTACCTCAAC
GGACAAAGTCTCTCGTTTAAAATCCAAACCAGTAATGGCAAAATCAAGAGTGCG
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ACTTCTGA

Nucleotide

>EsEXPA-10

ATGACGAAGATTTTATCTTTTTCGATAGTGGTCAACTTCCTCCTCGCGATGTTCTG
CACGAATATGATCAGCTCGGTTTCTGCAGGTTGGATGCAAGCTCATGCAACCTTC
TATGGAGGAAGTGATGCTTCGGGTACAATGGGTAAGTAATTTAATTTTTTTTTTTT
TTTTTTAACATAGTAATTTAATTTTCTAAAGCATCTTCTTTCATTCTTCTCCAAGAA
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CTTGTGGCGGTTGTTACCAAATGGTCTGCGATGCGACCAAAGTGCCACAATGGTG
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TTCTATAGAAGGTGATATAAAAAAACTGCCCTTCAAGACCTCATTTCAATATCAG
TTCTTTGTGCTAATAAATAAAAGGGTTTCTTGGGGATGATTGTTATCTCTTGTAGG
GTCGGATGTAGAAGAAGCGGAGGAATGAGATTCACGATGAACGGTAGAGATTAC
TTCGAGCTTGTCCTCATCTCAAACGTAGGAGGTGCAGGTGAGATTTCCCAAGTAT
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GCTAATTGGCAAAGCCTTACTTACCTCAACGGACAAAGTCTCTCGTTTAAAATCC
AAACCAGTAATGGCAAAATCAAGAGTGCGCTCGATGTTGTTCCTTCGAATTGGCA
GTTTGGTCAAAGCTTCAAGAGCAACCTAAACTTCTGA