

IDENTIFICATION

Species: *Eutrema salsugineum*

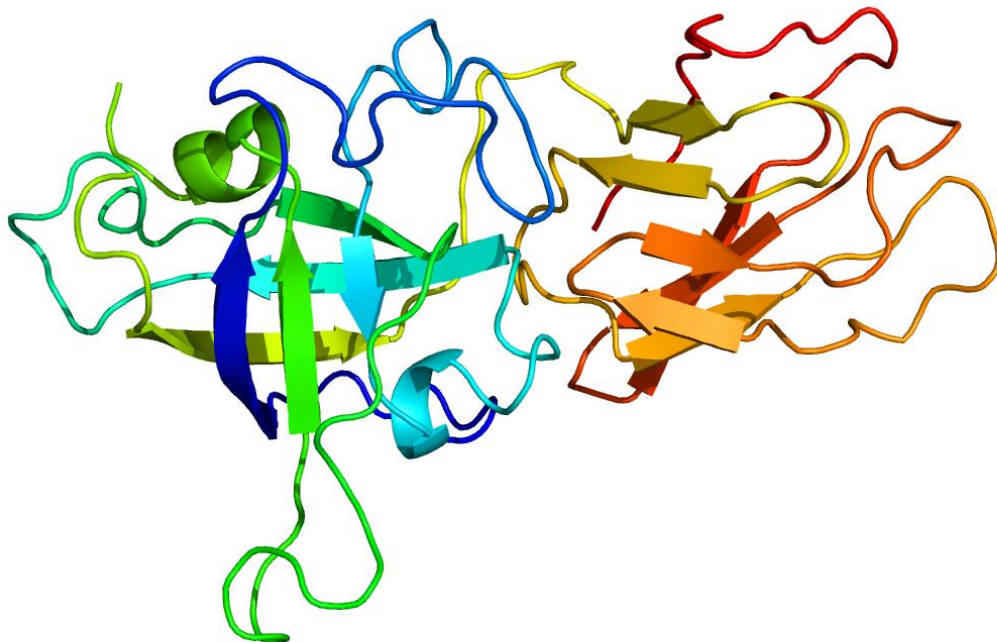
Locus: Thhalv10022301m

Gene Model: Thhalv10022301m

Description: EsEXPA-20

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>

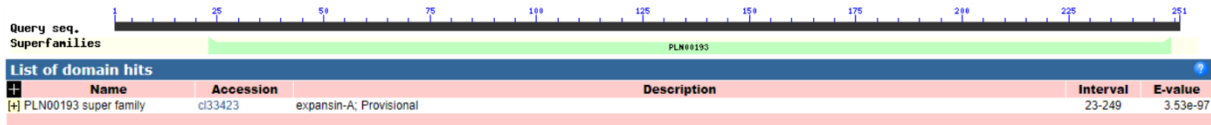
EXTERNAL RESOURCES

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GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>EsEXPA-20

MKGKYLVTVILLVGTLSSEGMCSNGWIRAHATFYGVNDSPASLGGACGYDNPYHAGF
GAHTAALSGALFRSGESCGGCYQVRCDYWADPKWCLRGAAVTVTATNFCPSSNNN
GGWCNLPRHHFDMSPAFFRIARRGNEGIVPVFYRRVGCKRRGGVRFMTMRGQGNFN
MVILSNVGGGAVKAVAVRGRGKTWLQMTRNWGANWQSSGDLRGQRLSFRVTL
FDRKTMFLNVVPSWWFGQTFSSRGQFL*

CDS (coding sequence)

>EsEXPA-20

ATGAAGGGGAAATATTTGGTAACGGTTATTCTCTTGGTTGGCACATTAAGTGAGG
GGATGTGTTCTAATGGTTGGATTAGGGCTCATGCAACATTTTATGGTGTTAATGAT
AGCCCTGCTTCACTTGGAGGAGCTTGTGGATATGACAATCCTTACCACGCCGGAT
TCGGAGCCCATACGGCGGCGCTAAGCGGTGCGCTATTCAGAAGCGGCGAGTCAT
GTGGTGGTTGCTACCAAGTGAGGTGCGACTATTGGGCGGATCCTAAGTGGTGTCT
CCGAGGAGCCGCCGTGACGGTGACAGCTACAACTTTTGTCCGTCGTCGAACAAC
AACGGAGGTTGGTGCAATCTCCCTCGCCACCCTTTGACATGTCAATGCCCGCTTT
CTCCGCATTGCCCGTCGCGGCAACGAAGGCATCGTCCCCGTCTTCTATCGCCGG
GTGGGATGCAAAGGAGAGGTGGTGTGAGGTTACGATGAGAGGTCAAGGGAAC
TTCAATATGGTAATACTGTCAAACGTTGGCGGGGGCGGCGCGGTGAAAGCGGTTG
CGGTGAGAGGGTCAAGGGGAAAGACTTGGCTTCAGATGACTCGTAATTGGGGTG
CCAAGTGGCAGAGCTCCGGCGACCTCCGGGGACAGAGACTCTCCTTTAGAGTTAC
TCTTTTGTACCGCAAACGATGACTTTTTTAAACGTTGTCCCTTCTTCTTGGTGGT
CGCCAAACCTTCTTCTCGAGGCCAATTCCTCTGA

Nucleotide

>EsEXPA-20

ATGAAGGGGAAATATTTGGTAACGGTTATTCTCTTGGTTGGCACATTAAGTGAGG
GGATGTGTTCTAATGGTTGGATTAGGGCTCATGCAACATTTTATGGTGTTAATGAT
AGCCCTGCTTCACTTGGTAAAAAGTCCTTAATAGATTAATACTTGTGTTTCTTACT
TTAGCTTTTGTATATAGTAAATTCACTTTATTGATGTATTTGTTTATAGGAGGAG
CTTGTGGATATGACAATCCTTACCACGCCGGATTCGGAGCCCATACGGCGGCGCT
AAGCGGTGCGCTATTCAGAAGCGGCGAGTCATGTGGTGGTTGCTACCAAGTGAG
GTGCGACTATTGGGCGGATCCTAAGTGGTGTCTCCGAGGAGCCGCCGTGACGGTG
ACAGCTACAACTTTTGTCCGTCGTCGAACAACAACGGAGGTTGGTGCAATCTCC

CTCGCCACCACTTTGACATGTCAATGCCCCGCTTTCTTCCGCATTGCCCGTCGCGGC
AACGAAGGCATCGTCCCCGTCTTCTATCGCCGGTAACATATACTTTTCTATTTAGC
ATTGACATTAAAAAAAAAAAAAAAAAACGATGTAGAGAATGATAAATTATAACGTTG
TCGTAGTAACATATTAATATTCGCAACACATAAAAACGCCAACACAAATAAACAA
ACAATCTATCCCCCATAACCACATAATACAGCAAATATGTTTCTAATAGAATATT
TAATTAGCTTCGTTACATAAAAAAAGATTTATAGCATCATGTAATATGAGCAAAT
ATTTTAATATTTTGTCTTTTTTTTTTCGGGTTTTCAAAAATCTGTTACTAATTTTTGT
TTTTTGATTACAACATTTATATAGGGTGGGATGCAAAGGAGAGGTGGTGTGAG
GTTACGATGAGAGGTCAAGGGAACCTCAATATGGTAATACTGTCAAACGTTGGC
GGGGCGGCGCGGTGAAAGCGGTTGCGGTGAGAGGGTCAAGGGGAAAGACTTG
GCTTCAGATGACTCGTAATTGGGGTGCCAACTGGCAGAGCTCCGGCGACCTCCGG
GGACAGAGACTCTCCTTTAGAGTTACTCTTTTTGACCGCAAACGATGACTTTTTT
AAACGTTGTCCCTTCTTCTTGGTGGTTCGGCCAAACCTTCTCTTCTCGAGGCCAAT
TCCTCTGA