

IDENTIFICATION

Species: *Eutrema salsugineum*

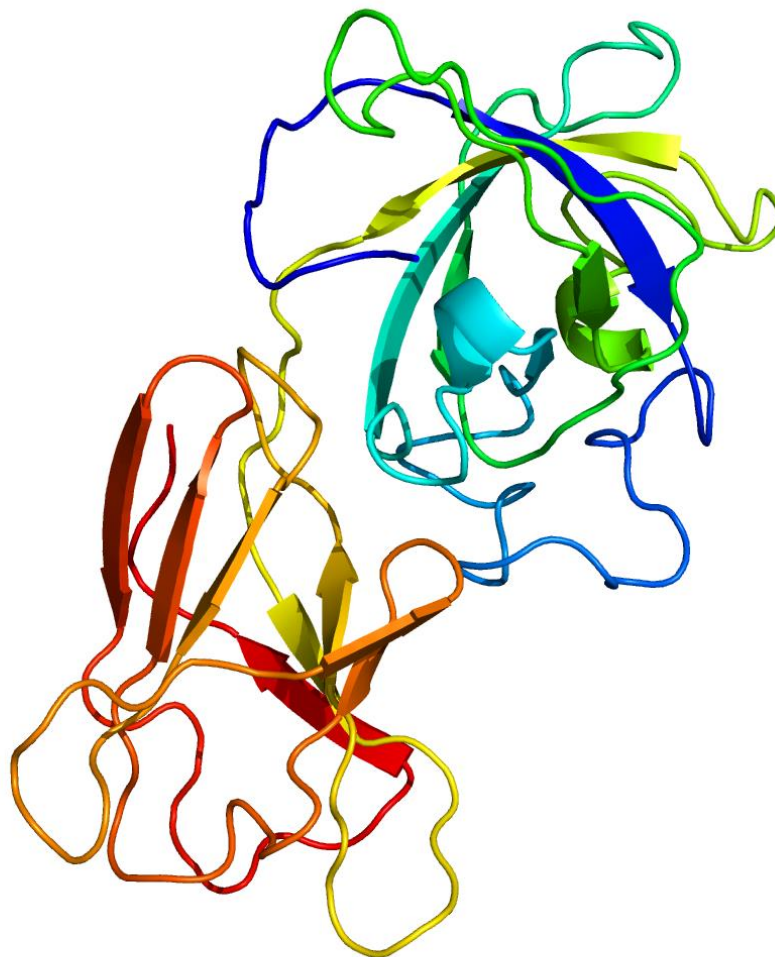
Locus: Thhalv10014522m

Gene Model: Thhalv10014522m

Description: EsEXPA-04

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>

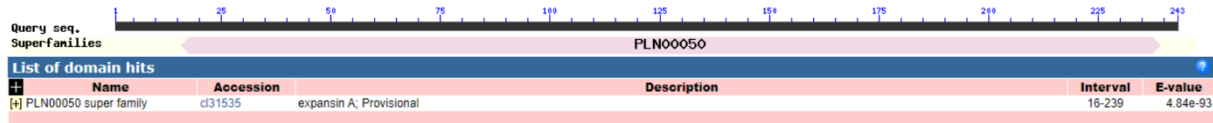
EXTERNAL RESOURCES

-

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>EsEXPA-04

MGHRLRSTDTAISDENGWEDAHATFYGGLKGEETMQGACGYQNLFEQGYGLET
LSTVLFKDGATCGACFELRCVNDPQWCIKGAGTIRVTATNFCPPNYTKTVGVWCNPP
QKHFDLSLPMFLKFAKYKAGIVPVQYRRVLCPPKQGGVKFRLTGNPYFLMVLVFN
GRAGVVTEVKVKGSKTGWIQMRRNWGQVWDTGTVLTGQSLSFSAVSDGKRLKFD
NVAPPNWQFNQTFAGKSNF*

CDS (coding sequence)

>EsEXPA-04

ATGGGCCACCGACTAAGAAGCACTGATACCGCCATTAGTGATGAAAACGGATGG
GAGGATGCTCACGCCACATTTTACGGTGGTTTGAAGGGCGAAGAAACCATGCAA
GGAGCATGTGGGTACCAAATCTATTCGAGCAAGGCTACGGTTTAGAGACGACG
GCTCTAAGCACGGTTTTGTTCAAAGACGGAGCCACGTGCGGTGCATGCTTCGAGC
TTCGATGCGTCAACGATCCACAATGGTGCATCAAAGGAGCCGGAACATAACGCGT
GACAGCCACCAATTTCTGCCACCAAACACTACCAAACCGTAGGTGTTTGGTGC
AATCCACCGCAGAAACATTTTCGATCTTTCGCTACCGATGTTTCTCAAGTTCGCTAA
GTACAAAGCCGGGATCGTTCCGGTGCAATACAGGCGAGTTTTATGCCCAAAAAA
CAAGGCGGTGTCAAGTTCGGTTAACCGGAAATCCTTATTTCTTGATGGTCTTGT
TTTCAACGTTGGACGTGCTGGTGTGTGACCGAGGTTAAGGTGAAAGGTTCTGAAG
ACCGGTTGGATTCAGATGAGGAGGAACACTGGGGACAGGTTTGGGATACCGGTACG
GTGTTAACCGGACAGAGTTTGTCTGTTTTCGGTTGCTGTCAGTGATGGGAAACGTTT
GAAGTTTGATAATGTTGCTCCACCTAATTGGCAGTTTAATCAAACCTTTTGCTGGCA
AGAGTAATTTCTAG

Nucleotide

>EsEXPA-04

ATGGGCCACCGACTAAGAAGCACTGATACCGCCATTAGTGATGAAAACGGATGG
GAGGATGCTCACGCCACATTTTACGGTGGTTTGAAGGGCGAAGAAACCATGCGTA
TGTTTTTTTATTCATCGAATTAATATCTGTGTGTGTGTGTGTGTCTATTTATCTA
TGGTTCCTTTTTTTTTCATTTGCAAGAAATGCAAGTGAGTACTGATTCAAAATTTAA
CATATATGTTTTAGAAACAAAATTGATTTTTTTTTTTGTGGGATTTGTTTTATAAA
TCAATGAGTTGGATTTTAAAACCTTTTTTGTGGTTATAATTTAACTTATGTCATG
CAACTCAATTTGTGCTGAATCGTATTATATAACAATCATTTACTCAATGACATCATT
TTGAAATTGTTAAAAGAAATGCATGCAGTTCTGTTTATTATTAGTAGAAAATATG

GTATTTCAACGAAGTCTAAACCATACATGTATTTTTATGTATCAACCAACGTAACC
AGAAGGAGCATGTGGGTACCAAAAATCTATTCGAGCAAGGCTACGGTTTAGAGAC
GACGGCTCTAAGCACGGTTTTGTTCAAAGACGGAGCCACGTGCGGTGCATGCTTC
GAGCTTCGATGCGTCAACGATCCACAATGGTGCATCAAAGGAGCCGGA ACTATA
CGCGTGACAGCCACCAATTTCTGCCACCAA ACTACACCAAACCGTAGGTGTTT
GGTGCAATCCACCGCAGAAACATTTTCGATCTTTTCGCTACCGATGTTTCTCAAGTTC
GCTAAGTACAAAGCCGGGATCGTTCGGTGCAATACAGGCGAGTTTTATGCCCA
AAAAACAAGGCGGTGTCAAGTTCCGGTTAACCGGAAATCCTTATTTCTTGATGGT
TCTTGTTCACGTTGGACGTGCTGGTGTGTGACCGAGGTAAAGGTGAAAGGT
TCGAAGACCGGTTGGATTCAGATGAGGAGGAACTGGGGACAGGTTTGGGATACC
GGTACGGTGTTAACCGGACAGAGTTTGTCTTTTCGGTTGCTGTCAGTGATGGGA
AACGTTTGAAGTTTGATAATGTTGCTCCACCTAATTGGCAGTTTAATCAA ACTTTT
GCTGGCAAGAGTAATTTCTAG