

IDENTIFICATION

Species: *Eutrema salsugineum*

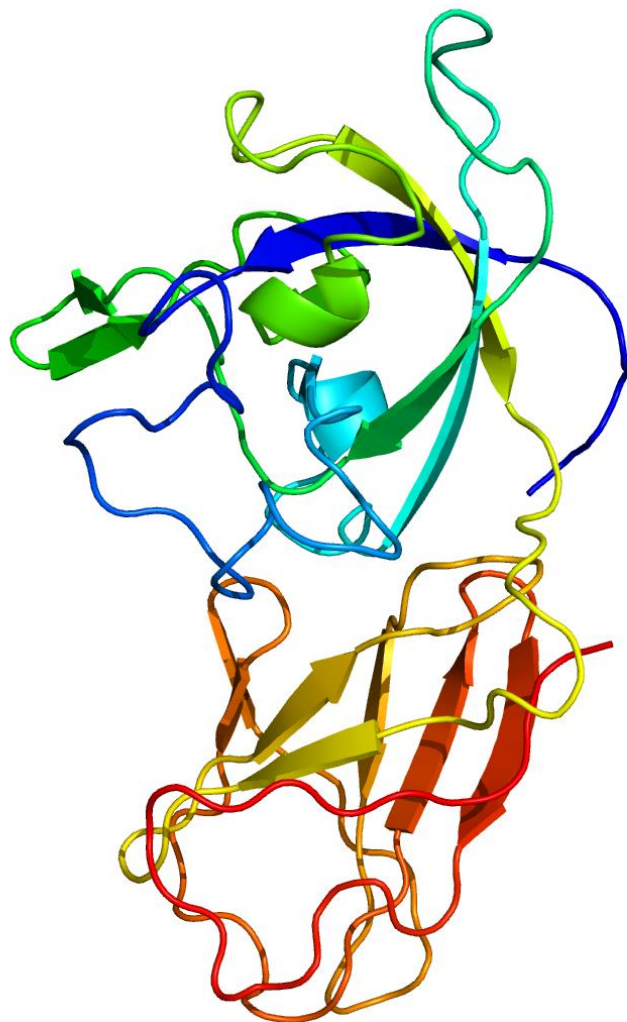
Locus: Thhalv10014463m

Gene Model: Thhalv10014463m

Description: EsEXPA-05

Family: Alpha Expansin

3D structure:



GENOME DATABASES

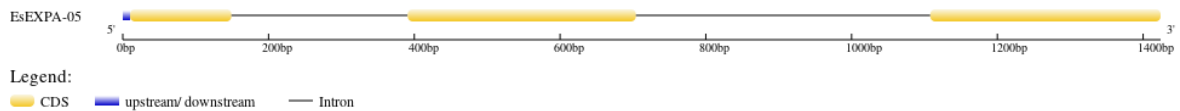
Phytozome: https://phytozome-next.jgi.doe.gov/info/Esalsugineum_v1_0

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

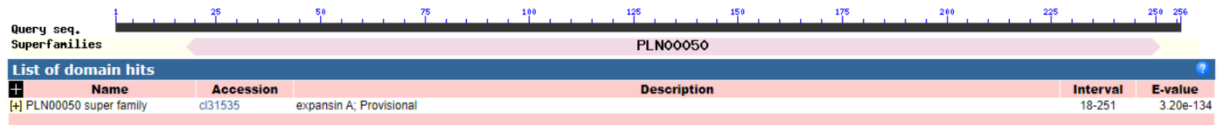
EXTERNAL RESOURCES

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GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>EsEXPA-05

MEIFGKLLMSLSLMMMVMWKCVDGYSSGWVSARATFYGGADASGTMGGACGYG
NLYSQGYGTNTAALSTALFNQGGQSCGACFQIKCVNDPKWCLGGTITVTGTNFCPPNF
AQANNAGGWCNPPQHFDLAQPIFLRIAKYKAGVVPVQYRRVACRRKGGMRFTING
HSYFNLVLVTNVAGAGDVVSVSIIKGRTRGWQMSRNWQNWQSNANLDGQALSFK
VTSDGRTVVSNNATPRNWSFGQTYTGKQFRSQR*

CDS (coding sequence)

>EsEXPA-05

ATGGAGATTTTGGAAAATTGTTAATGTCATTGAGTCTTATGATGATGGTGTATGTG
GAAGTGTGTAGATGGTTACAGTAGTGGTTGGGTCAGTGCTCGAGCCACATTCTAT
GGAGGTGCTGATGCTTCTGGCACCATGGGCGGCGCGTGTGGCTACGGGAATTTAT
ACAGTCAAGGTTATGGCACGAACACGGCGGCGCTAAGTACGGCTCTGTTCAACG
GCGGCCAAAGTTGCGGCGCTTGTTCAGATAAAATGTGTAACGATCCAAAATG
GTGTCTTGGAGGAACAATCACGGTCACCGGAACAACTTTTGTCCGCCGAACCTT
GCTCAGGCCAACACGCCGGAGGTTGGTGTAACTCCTCCGCAACATCACTTCGATT
TGGCTCAGCCATCTTCTCCGCATCGCTAAATACAAAGCCGGCGTCGTCCCTGTC
CAATACCGGCGAGTGGCTTGCCGGAGAAAGGGAGGGATGCGATTCACGATCAAC
GGACTCATACTTCAACCTCGTACTCGTAACTAACGTCGCCGGCGCCGGAGATG
TTGTCTCCGTCTCTATTAAGGAACAAGGACAGGTTGGCAAAGCATGTCGAGAAA
CTGGGGACAGAACTGGCAAAGCAACGCGAATCTCGACGGTCAAGCTCTCTCCTTC
AAAGTAACAACCAGCGATGGCCGCACAGTCGTCTCCAATAACGCTACTCCTCGTA
ACTGGAGCTTCGGACAGACTTATACCGGCAAACAGTTCCGGTCTCAGAGGTGA

Nucleotide

>EsEXPA-05

GGCGAAGAAAATGGAGATTTTGGAAAATTGTTAATGTCATTGAGTCTTATGATG
ATGGTGTATGTGGAAGTGTGTAGATGGTTACAGTAGTGGTTGGGTCAGTGCTCGAG
CCACATTCTATGGAGGTGCTGATGCTTCTGGCACCATGGGTAATTTCTTCTCTT
CTCTCAAAGACTCAAATAATAATACTCCAGCTTAATTCAAACTTAAAACCTTT
GACGAATCCTTTTCATAATAGACTCAATTTAGTGCTATTGAATAGTAAAACAAA
AAATCTTAATGACGTTTTTATACTTACTTTGAAGATTCTAAATTACACTAATTTGT
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GCGGCGCTAAGTACGGCTCTGTTCAACGGCGGCCAAAGTTGCGGCGCTTGTTTTTC
AGATAAAATGTGTAAACGATCCAAAATGGTGTCTTGGAGGAACAATCACGGTCA
CCGGAACAAACTTTTTGTCCGCCGA ACTTTGCTCAGGCCAACACGCCGGAGGTTG
GTGTAATCCTCCGCAACATCACTTCGATTTGGCTCAGCCCATCTTTCTCCGCATCG
CTAAATACAAAGCCGGCGTCCCTGTCCAATACCGGCGGTACGTTTTCCGGTC
TCGGTTTAGCTCGGTTTCGCTGAAATCACAGACTAGAGTGACATTTCAACTTTTCAT
TTTGATGGAGTATATTTTTTAATTTTCGAGTGTATAAAAGTCCACAATCGATTTTCT
CGAGAACATGCATTTTAAAACCTTTAAAAAATTATCAATTTTTGGAGGAAAAATC
AAAATTTTTGACACAGACTTAATGTTTTCTCGTTTTGGTTTTCGTTTTTCATCTGAATT
TTCTCCAAAAGAAAATGCATGAACTCAGAAAAAGGTTTGATCAGATTCAGAAAA
AGTTATAAAATCCAAGAAAATTGGCAGATTAATTAATCTTCATGTGTTTGCCCCC
CCAAAAAAAAATAAAATAAATAATCTTTTTGTATACTCTGTTTTTGATGGAAACA
GAGTGGCTTGCCGGAGAAAGGGAGGGATGCGATTCACGATCAACGGGACACTCAT
ACTTCAACCTCGTACTCGTAACTAACGTCGCCGGCGCCGGAGATGTTGTCTCCGT
CTCTATTAAGGAACAAGGACAGGTTGGCAAAGCATGTCGAGAACTGGGGACA
GAACTGGCAAAGCAACGCGAATCTCGACGGTCAAGCTCTCTCCTTCAAAGTAACA
ACCAGCGATGGCCGCACAGTCGTCTCCAATAACGCTACTCCTCGTAACTGGAGCT
TCGGACAGACTTATACCGGCAAACAGTTCCGGTCTCAGAGGTGA