

IDENTIFICATION

Species: *Eutrema salsugineum*

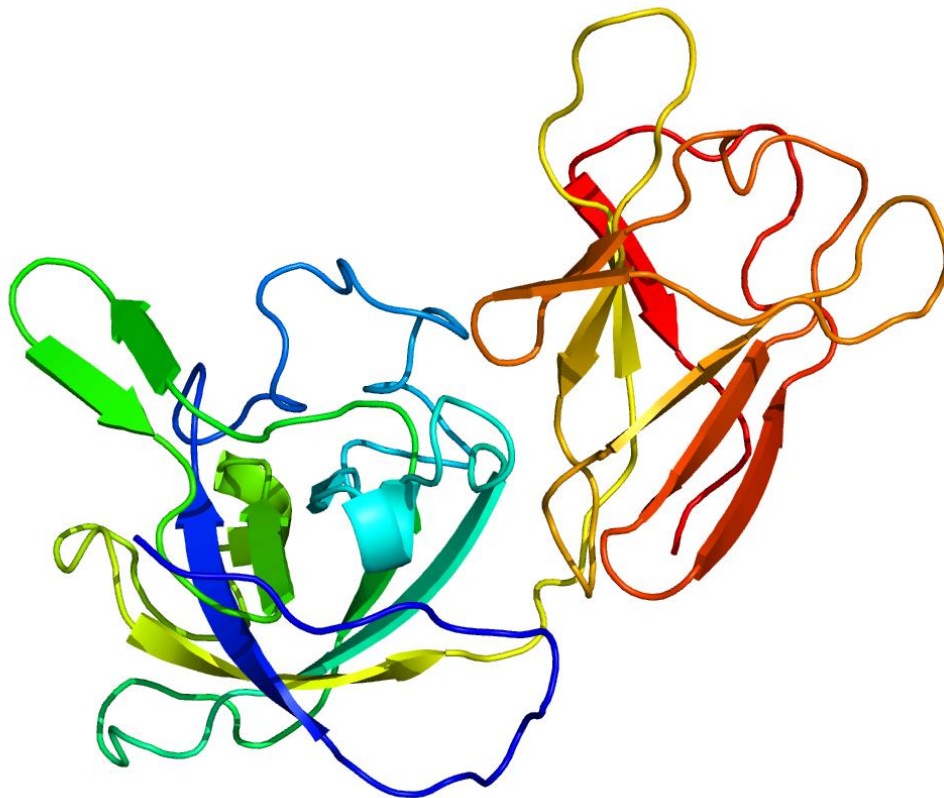
Locus: Thhalv10028333m

Gene Model: Thhalv10028333m

Description: EsEXPA-27

Family: Alpha Expansin

3D structure:



GENOME DATABASES

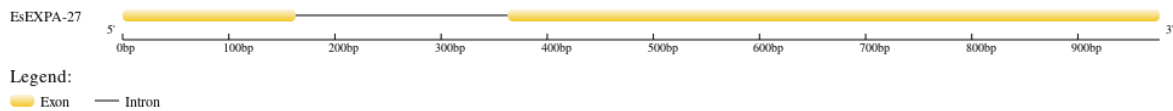
Phytozome: https://phytozome-next.jgi.doe.gov/info/Esalsugineum_v1_0

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

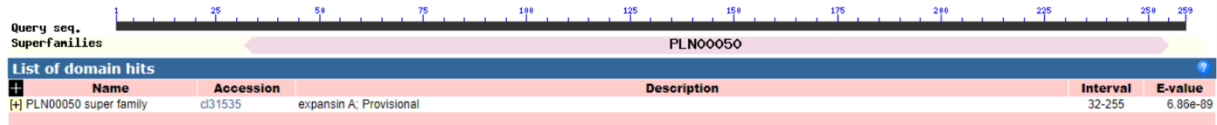
EXTERNAL RESOURCES

-

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>EsEXPA-27

MAIWFVPISYGHGAEAPMVGDVANSPGSGTNGLDPTWYDARATFYGDIHGGGTQQ
GACGYGDLNKQGYGLATAALSQALFNDGYTCGACFEIMCTNDPKWCLPGSIKITAT
NFCPANYTKTTGVWCNPPQKHFDLSLPIFLKIAQYEAGVVPVKYRRIPCAKTGGVKF
ETKGNPNFLMILPYNVGGAGDIKAMQIKGSGTGWITMKKNWGQNWVTDVVLTGQG
LSFRVVMDSGISKDFINVVQKNWGFQDQTFDGKINF*

CDS (coding sequence)

>EsEXPA-27

ATGGCGATATGGTTCGTGCCCATCAGTTACGGTCATGGAGCCGAGGCCCCCGATGG
TTGGTGATGTAGCCAACTCACCTGGAAGTGAACCAATGGACTCGACCCTACTTG
GTATGACGCACGAGCCACATTTTACGGTGATATCCATGGTGGAGGCACTCAGCAG
GGAGCTTGTGGATACGGTGACCTAAACAAACAAGGCTATGGTCTAGCCACGGCG
GCGTTGAGCCAGGCGCTTTTCAATGACGGGTACACGTGTGGGGCTTGTTTCGAGA
TCATGTGCACGAATGATCCAAAATGGTGTGGCCCGGATCCATCAAGATTACAGC
TACAAATTTCTGTCCAGCAAACACTACACCAAGACGACAGGCGTATGGTGCATCCA
CCACAGAAACACTTTGACCTCTCCTTACCAATATTCCTCAAGATCGCACAATACG
AAGCTGGGGTTGTCCCGGTTAAATACAGGCGTATTCCTTGCGCAAAAACCGGCGG
TGTC AAGTTCGAAACCAAAGGAAACCCTAATTTCTTAATGATCTTGCCGTACAAT
GTAGGAGGAGCCGGAGATATCAAGGCCATGCAGATTAAGGAAGCGGAACTGGA
TGGATAACCATGAAGAAGAATTGGGGACAGA ACTGGGTC ACTGATGTTGTGTTA
ACCGGACAAGGCTTATCGTTTAGGGTTGTGATGAGTGATGGGATTAGTAAGGATT
TTATTAATGTGGTACAAAAAATTGGGGATTTGATCAGACTTTTGATGGGAAGAT
TAACTTTTAG

Nucleotide

>EsEXPA-27

ATGGCGATATGGTTCGTGCCCATCAGTTACGGTCATGGAGCCGAGGCCCCCGATGG
TTGGTGATGTAGCCAACTCACCTGGAAGTGAACCAATGGACTCGACCCTACTTG
GTATGACGCACGAGCCACATTTTACGGTGATATCCATGGTGGAGGCACTCAGCGT
AAGTCTTCAATTGCCAATATTTTATTTCGAATTAATTATTGAGATAATGTAATTCA
TTTGGAGCTTGTTTGAAATATCTAAAATTCTTAAGGCGTAATTCATTTGGAGGAGC
AAAACATTATACTATAATTATCATATACTTCTGTTCCATCTTTTTTTTTATCGTACA
CTCACTTTTTTTCATTGTAAATTCAATAGAGGGAGCTTGTGGATACGGTGACCTAA

ACAAACAAGGCTATGGTCTAGCCACGGCGGCGTTGAGCCAGGCGCTTTTCAATGA
CGGGTACACGTGTGGGGCTTGTTTCGAGATCATGTGCACGAATGATCCAAAATGG
TGTTTGCCCGGATCCATCAAGATTACAGCTACAAATTTCTGTCCAGCAAACACTACA
CCAAGACGACAGGCGTATGGTGCAATCCACCACAGAAACACTTTGACCTCTCCTT
ACCAATATTCCTCAAGATCGCACAATACGAAGCTGGGGTTGTCCCGGTTAAATAC
AGGCGTATTCCTTGCGCAAAAACCGGCGGTGTCAAGTTCGAAACCAAAGGAAAC
CCTAATTTCTTAATGATCTTGCCGTACAATGTAGGAGGAGCCGGAGATATCAAGG
CCATGCAGATTAAAGGAAGCGGAACTGGATGGATAACCATGAAGAAGAATTGGG
GACAGAACTGGGTCACTGATGTTGTGTTAACCGGACAAGGCTTATCGTTTAGGGT
TGTGATGAGTGATGGGATTAGTAAGGATTTTATTAATGTGGTACAAAAAATTGG
GGATTTGATCAGACTTTTGATGGGAAGATTAACTTTTAG