

IDENTIFICATION

Species: *Eutrema salsugineum*

Locus: Thhalv10028120m

Gene Model: Thhalv10028120m

Description: EsEXPA-26

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>

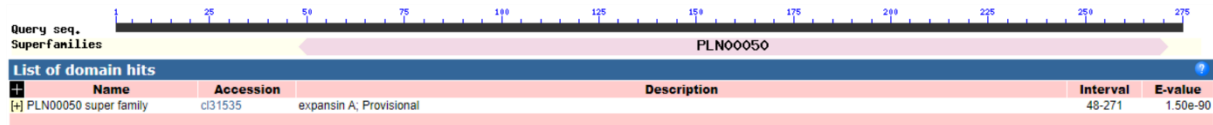
EXTERNAL RESOURCES

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GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>EsEXPA-26

MKLEIMICTNVLLITMAIWVFPISYGHGAEAPMVGDVANSPGSGTNGLDPTWYDAR
ATFYGDIHGGGTQQGACGYGDLNKQGYGLATAALSQALFNDGYTCGACFEIMCTN
DPKWCLPGSIKITATNFCLANYTKTTGVWCNPPQKHFDLSLPIFLKIAQYKAGVIPVK
YRRIPCAKTGGVKFETKGNPNFLMILPYNVGGAGDIKAMQIKSGTGWITMKNWG
QNWVTDVVLVTGQGLSFRVVTSDGISKDFINVVPKNWGFDTFDGKINF*

CDS (coding sequence)

>EsEXPA-26

ATGAAACTCTTAGAAATAATGATATGTACAAATGTTTTGTTGATAACAATGGCGA
TATGGTTCGTGCCCATCAGTTACGGTCATGGAGCTGAGGCCCCGATGGTTGGTGA
TG TAGCCA ACTCACCTGGAAGT GGAACCAATGGACTCGACCCTACTTGGTATGAC
GCACGAGCCACATTTTACGGTGATATCCATGGTGGAGGCACTCAGCAGGGAGCTT
GTGGATACGGTGACCTAAACAAACAAGGCTATGGTCTAGCCACGGCGGCGTTGA
GCCAGGCGCTTTTCAATGACGGGTACACGTGTGGGGCTTGTTTCGAGATCATGTG
CACGAATGATCCAAAATGGTGTGTTGCCCGGATCCATCAAGATTACAGCTACAAAT
TTCTGTCTAGCAA ACTACACCAAGACGACAGGCGTATGGTGCAATCCACCACAGA
AACACTTTGACCTCTCCCTACCAATATTCCTCAAGATCGCACAATACAAAGCTGG
GGTTATCCCGGTTAAATACAGGCGTATTCCTTGCGCAAAAACCGGCGGTGTCAAG
TTCGAAACCAAAGGAAACCCTAATTTCTTAATGATCTTGCCGTACAATGTAGGAG
GAGCCGGAGATATCAAGGCCATGCAGATTAAGGAAGCGGAACTGGATGGATAA
CCATGAAGAAGAATTGGGGACAGAACTGGGTC ACTGATGTTGTGTTA ACCGGAC
AAGGCTTATCGTTT AGGGTTGTGACGAGTGATGGGATTAGTAAGGATTTTATTAA
TGTGGTACCAAAA AATTGGGGATTTGATCAGACTTTTGATGGGAAGATTA ACTTT
TAG

Nucleotide

>EsEXPA-26

ATGAAACTCTTAGAAATAATGATATGTACAAATGTTTTGTTGATAACAATGGCGA
TATGGTTCGTGCCCATCAGTTACGGTCATGGAGCTGAGGCCCCGATGGTTGGTGA
TG TAGCCA ACTCACCTGGAAGT GGAACCAATGGACTCGACCCTACTTGGTATGAC
GCACGAGCCACATTTTACGGTGATATCCATGGTGGAGGCACTCAGCGTAAGTCTT
CAATTGCCAATATTTTATTCGAATTAATTATTGAGATAATGTAATTCATTTGGAG
CTTGTTCAA AATATCTAAAATTCCTTAAGGCGTAATTCATTTGGAGGAGCAAACA

TTATACTATAATTATCATATACTTCTGTTCTATTTTTTTTTTATCGTACACTCACTTTT
TTTCATTGTAAATTCAATAGAGGGGAGCTTGTGGATACGGTGACCTAAACAAACAA
GGCTATGGTCTAGCCACGGCGGGCGTTGAGCCAGGCGCTTTTCAATGACGGGTACA
CGTGTGGGGCTTGTTTCGAGATCATGTGCACGAATGATCCAAAATGGTGTGTTGCC
CGGATCCATCAAGATTACAGCTACAAATTTCTGTCTAGCAAACCTACACCAAGACG
ACAGGCGTATGGTGCAATCCACCACAGAAACACTTTGACCTCTCCCTACCAATAT
TCCTCAAGATCGCACAAATACAAAGCTGGGGTTATCCCGGTTAAATACAGGCGTAT
TCCTTGCGCAAAAACCGGCGGTGTCAAGTTCGAAACCAAAGGAAACCCTAATTTTC
TTAATGATCTTGCCGTACAATGTAGGAGGAGCCGGAGATATCAAGGCCATGCAG
ATTAAAGGAAGCGGAACCTGGATGGATAACCATGAAGAAGAATTGGGGACAGAAC
TGGGTCACTGATGTTGTGTTAACCGGACAAGGCTTATCGTTTAGGGTTGTGACGA
GTGATGGGATTAGTAAGGATTTTATTAATGTGGTACCAAAAAATTGGGGATTTGA
TCAGACTTTTGATGGGAAGATTAACCTTTAG