

IDENTIFICATION

Species: *Eutrema salsugineum*

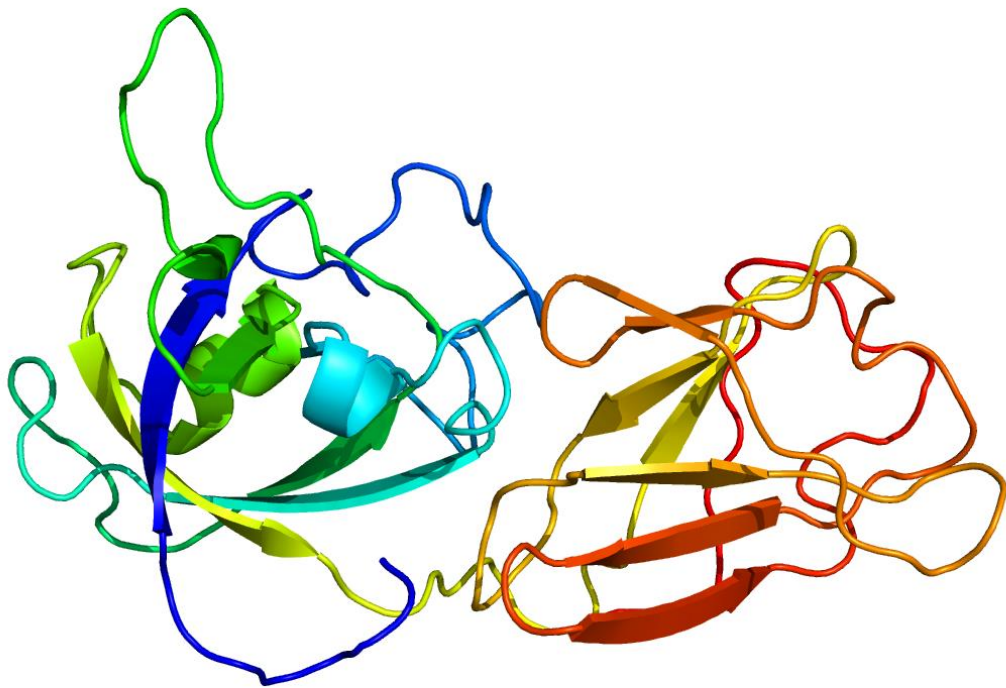
Locus: Thhalv10028134m

Gene Model: Thhalv10028134m

Description: EsEXPA-23

Family: Alpha Expansin

3D structure:



GENOME DATABASES

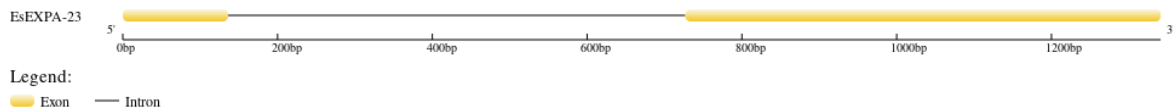
Phytozome: https://phytozome-next.jgi.doe.gov/info/Esalsugineum_v1_0

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

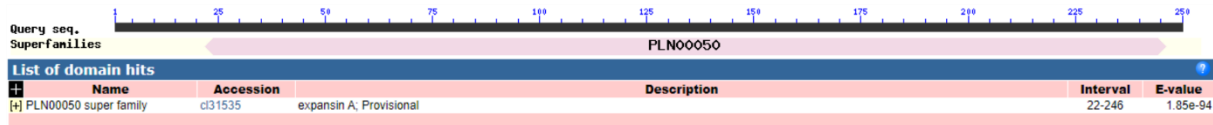
EXTERNAL RESOURCES

-

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>EsEXPA-23

MSYGYGAEAPTNGDAANSLGGDAFNNGWDNARATFYGDIHGGGTQQGACGYGNL
NKQGYGLATAALSTALFNNGYTCGACFEIMCTQDPKWCLPGSIKITATNFCPANYTK
KTDIWCNPPQKHFDLSLPMFLKIAKYKAGVIPVRYRRVPCVKTGGVKFEIKGNRYFL
MILPYNVGGAGDIKAMQIKRSRTGWITMKNWQNWTTNVVLTGQGLSFRIMTSD
GVSKDFINVPKNWGFQTFDGRINF*

CDS (coding sequence)

>EsEXPA-23

ATGAGTTACGGTTATGGAGCCGAGGCACCAACCAATGGTGATGCAGCCAATTCAC
TTGGAGGTGACGCCTTCAACAATGGTTGGGATAACGCACGAGCCACATTTTACGG
TGACATTCATGGTGGAGGCACTCAACAGGGAGCTTGTGGATATGGTAATCTAAAC
AAACAAGGCTATGGTCTAGCAACGGCAGCGTTGAGCACAGCACTCTTCAACAAT
GGGTACACGTGCGGGGCTTGTTCGAGATCATGTGCACGCAGGATCCAAAATGGT
GTTTGCCCGGATCCATTAAGATTACAGCTACAAATTTCTGTCCAGCAAACACTACAC
CAAGAAGACAGACATTTGGTGAACCCACCACAGAAACACTTTGATCTCTCCCTA
CCAATGTTCTCAAGATCGCCAAGTACAAAGCCGGGTTATTCCGGTTAGATACA
GACGTGTTCTTGTGTGAAAACCGGCGGTGTCAAGTTCGAAATCAAGGGAAACCG
TTATTTCTTAATGATCTTGCCGTACAATGTAGGAGGGGCTGGAGATATTAAGGCC
ATGCAGATTAAGAAGCAGAACCGGATGGATTACGATGAAGAAGAATTGGGGA
CAGAACTGGACCACCAATGTTGTATTGACCGGACAAGGTTTATCATTGAGGATTA
TGACGAGTGATGGGGTTAGTAAAGATTTTATTAATGTGGTACCAAAGAATTGGGG
ATTTGGTCAGACTTTTGATGGAAGGATTAACATTTTAG

Nucleotide

>EsEXPA-23

ATGAGTTACGGTTATGGAGCCGAGGCACCAACCAATGGTGATGCAGCCAATTCAC
TTGGAGGTGACGCCTTCAACAATGGTTGGGATAACGCACGAGCCACATTTTACGG
TGACATTCATGGTGGAGGCACTCAACGTAAGTTATTCAATTCCTAATATTTTATAT
TCTAATTATTGAGATATTTTTTTTTGTTTAAGAAAACAACAACAACATTATGC
TACTTTAGTGGCATTGGTTCAATCTGACTGAAATTTGCAAAACAATTAATAATA
TTAAAATATCCAATGTCACAATATACACGAAAGTTTGGTTCCAATATATATTTCCA
GTGTCACATTGTACACATTCAAACATGATTCATTCAATATTGTATAGGTTGCGAGT
GTTTTAAATGCTAATTCTGCAACTGTGATTGCATTTACATTTTTTTCTTTTTTAGA

TAAAACTATATTTTTTTTCATGAAACATTCTTACAGAGTATAACACAAACACCAA
GTTACCAACGTAACGTAGTTTCTTCTTACGTGCGTTTGCATTTACAACGTGACCAAG
GAAAATGTTTAAAGGGACCCCTTGTTTAAAATACATATAAATTACAATTCATGTG
TTAATTTTTGTTTTAAAAAATTATATTATAACATGCAAACACAAAAGTAAACAA
ACAAACAAAGCCATATCTATTAATTATTAACTCACTTTTTCCATTATATAATTCAA
TAGAGGGAGCTTGTGGATATGGTAATCTAAACAAACAAGGCTATGGTCTAGCAA
CGGCAGCGTTGAGCACAGCACTCTTCAACAATGGGTACACGTGCGGGGCTTGTTT
CGAGATCATGTGCACGCAGGATCCAAAATGGTGTTTGCCCGGATCCATTAAGATT
ACAGCTACAAATTTCTGTCCAGCAAACCTACACCAAGAAGACAGACATTTGGTGCA
ACCCACCACAGAAACACTTTGATCTCTCCCTACCAATGTTCCCTCAAGATCGCCAA
GTACAAAGCCGGGGTTATTCCGGTTAGATACAGACGTGTTCCCTTGTGTGAAAACC
GGCGGTGTCAAGTTCGAAATCAAGGGAAACCGTTATTTCTTAATGATCTTGCCGT
ACAATGTAGGAGGGGCTGGAGATATTAAGGCCATGCAGATTAAGAAGCAGAA
CCGGATGGATTACGATGAAGAAGAATTGGGGACAGAACTGGACCACCAATGTTG
TATTGACCGGACAAGGTTTATCATTCAGGATTATGACGAGTGATGGGGTTAGTAA
AGATTTTATTAATGTGGTACCAAAGAATTGGGGATTTGGTCAGACTTTTGATGGA
AGGATTAACTTTTAG