

IDENTIFICATION

Species: *Eutrema salsugineum*

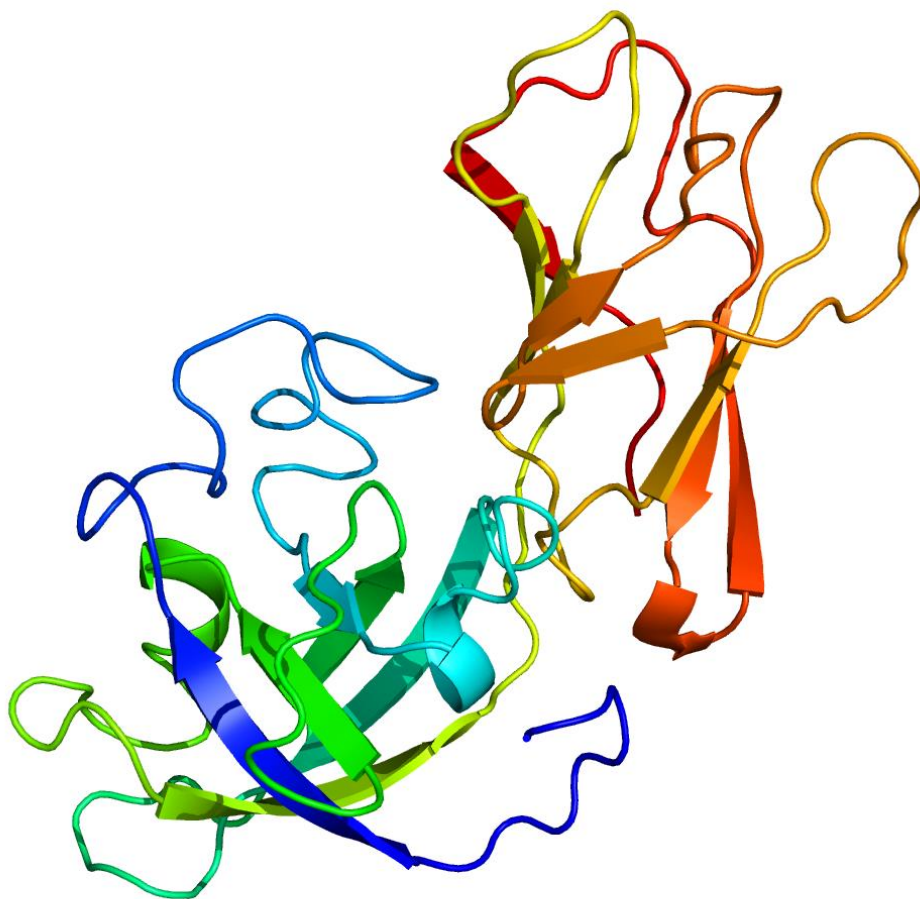
Locus: Thhalv10008503m

Gene Model: Thhalv10008503m

Description: EsEXPA-09

Family: Alpha Expansin

3D structure:



GENOME DATABASES

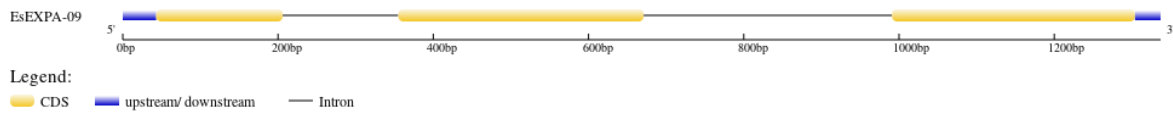
Phytozome: https://phytozome-next.jgi.doe.gov/info/Esalsugineum_v1_0

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

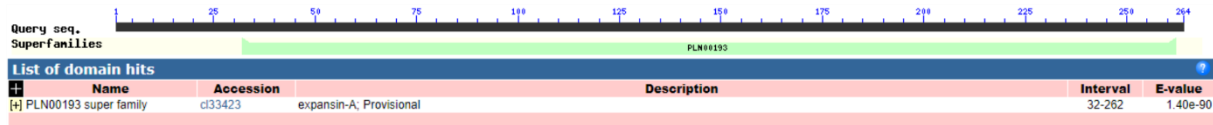
EXTERNAL RESOURCES

-

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>EsEXPA-09

MGPTSSWSFNKFFAIVFVVSFVSGEFVAGYYRSPWRF AHATFYGDETA SETMGGA
CGYGNLFNSGYGVATAALSATMFKDGYGCGQCFQIMCYKSPHCYYGNPTTVVTAT
NLCPPN WYQDSNNGGWCNPPRTHFDMAKPAFMKLANWKAGIIPVAYRRVPCKRIG
GMRFQFQGNAYWLLIFVMNVGGAGDIKSMAVKGSRTNWISMSHWNWGASYQAFSSL
YGQSLSRVTSYTTGQTLYAWN VAPSNWNAGMTYKTTVNFR*

CDS (coding sequence)

>EsEXPA-09

ATGGGTCCGACCTCAAGTTCTTGGAGCTTCAACAAATTTTTTGCAATAGTTTTTCGT
CGTTTTCTCAGTCTCCGGTGAGTTCGTTCGCCGGATATTACAGGCCGAGCCCGTGG
AGATTCGCTCATGCCACATTCTACGGCGACGAGACAGCTAGTGAAACCATGGGTG
GTGCATGTGGGTACGGAAATCTATTTAACAGCGGCTACGGCGTAGCCACGGCGGC
GCTAAGCGCGACGATGTTCAAAGATGGTTACGGTTGTGGCCAATGTTTCAAATA
ATGTGTTATAAGTCGCCACATTGTTACTACGGAAACCCTACAACGGTGGTTACAG
CCACCAACCTTTGCCCTCCAATTGGTACCAAGACTCCAACAATGGTGGTTGGTG
CAATCCTCCTAGAACCCATTTGATATGGCTAAACCGGCTTTCATGAAACTCGCT
AATTGGAAGGCCGGTATCATCCCTGTTGCATACCGCAGAGTCCCATGCAAAGGA
TTGGAGGTATGAGGTTCAATTCCAAGGCAATGCTTATTGGCTTCTCATCTTCGTC
ATGAATGTCGGCGGTGCCGGAGACATCAAGAGCATGGCCGTGAAAGGTAGCCGG
ACGAATTGGATAAGCATGAGCCATAACTGGGGAGCCTTTACCAAGCTTTTTCT
CTCTCTACGGTCAATCTCTCTTTCCGGGTCACCTTCTTACACCACCGGTCAAACC
CTCTATGCCTGGAACGTTGCTCCGTCTAACTGGAACGCCGGTATGACTTACAAGA
CCACTGTTAATTTCCGTTGA

Nucleotide

>EsEXPA-09

CAAACCCCAAGATAACCCTTCGAAAAGGAAAAGGAACTAAAGATGGGTCCGAC
CTCAAGTTCTTGGAGCTTCAACAAATTTTTTGCAATAGTTTTTCGTCTTTTTCTCAGT
CTCCGGTGAGTTCGTTCGCCGGATATTACAGGCCGAGCCCGTGGAGATTCGCTCAT
GCCACATTCTACGGCGACGAGACAGCTAGTGAAACCATGGGTACGTAAGATTAA
TATTATTTCACTTTCTCATGTATATACAATATATAATCACCAAGGCCTGATATAAT

AACAATATCAGTTACATACATGACCATACATACATTAATCAGTTAATGACATAAT
CACTTTACACGTATATATATATGCAGGTGGTGCATGTGGGTACGGAAATCTATTTAA
CAGCGGCTACGGCGTAGCCACGGCGGGCGCTAAGCGCGACGATGTTCAAAGATGG
TTACGGTTGTGGCCAATGTTTCCAAATAATGTGTTATAAGTCGCCACATTGTTACT
ACGGAAACCCTACAACGGTGGTTACAGCCACCAACCTTTGCCCTCCAAATTGGTA
CCAAGACTCCAACAATGGTGGTTGGTGCAATCCTCCTAGAACCATTTCGATATG
GCTAAACCGGCTTTCATGAAACTCGCTAATTGGAAGGCCGGTATCATCCCTGTTG
CATACCGCAGGTATATATGTCTCATGTCTGAATATTTTCACAAATTTAGCTATCATA
CAAACATTTTCAGCTAAAAATTTAAAATTATTTTTACCGGGGCTAATTTAAAAGTATA
TATAAATATATGTATATATATGTTCTAATTCCACAATCGATGAATGTTTATGTTGA
TAGATATTATTTGAGAAGAGGCACGTCTCTATAGTCCCCTTACTATATATACCGAT
ACGACACATAGAGATACAATATTCACATGCATAACATAACGACTTTATAAATAGT
TCAAAACTATGGAATTCTAAAATATTATATTTAATGCGATTGATATATGTAGAGT
CCCATGCAAAAGGATTGGAGGTATGAGGTTTCAATTCCAAGGCAATGCTTATTGG
CTTCTCATCTTCGTCATGAATGTCGGCGGTGCCGGAGACATCAAGAGCATGGCCG
TGAAAGGTAGCCGGACGAATTGGATAAGCATGAGCCATAACTGGGGAGCCTCTT
ACCAAGCTTTTTCTCTCTCTACGGTCAATCTCTCTCTTTCCGGGTCACTTCTTACA
CCACCGGTCAAACCCTCTATGCCTGGAACGTTGCTCCGTCTAACTGGAACGCCGG
TATGACTTACAAGACCACTGTTAATTTCCGTTGAAATTACGATTTTGCCCTTGCAG
CAAACCCAAA