

IDENTIFICATION

Species: *Eutrema salsugineum*

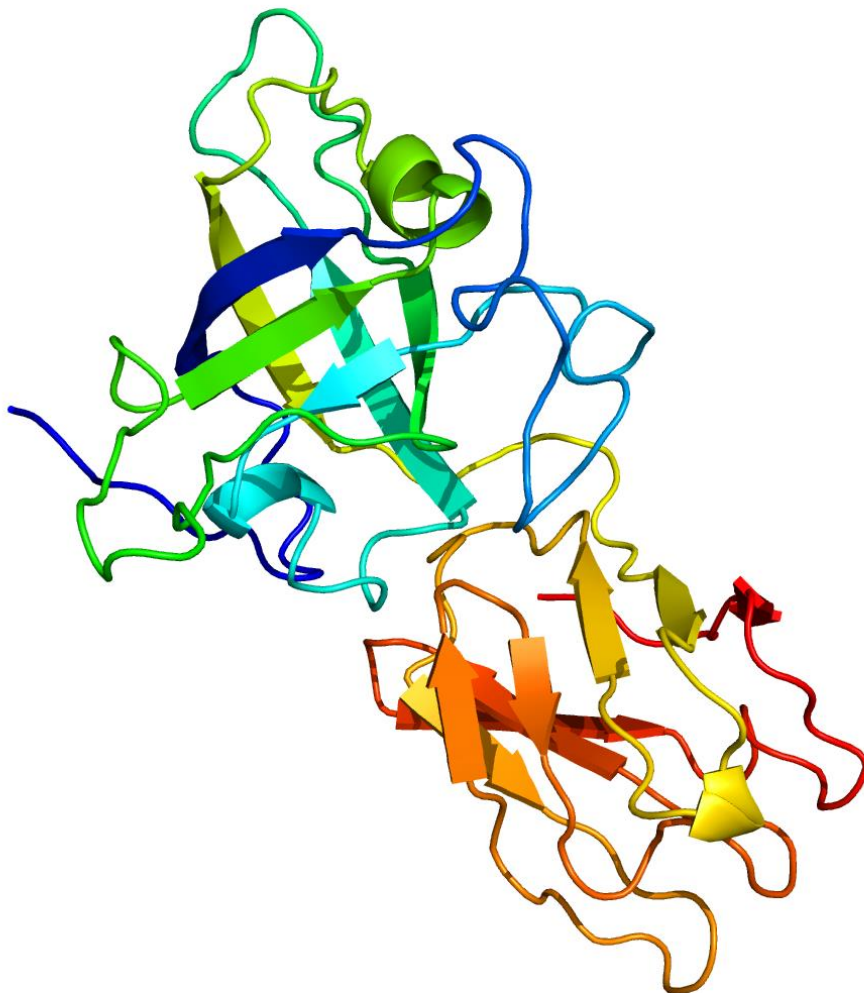
Locus: Thhalv10028214m

Gene Model: Thhalv10028214m

Description: EsEXPA-24

Family: Alpha Expansin

3D structure:



GENOME DATABASES

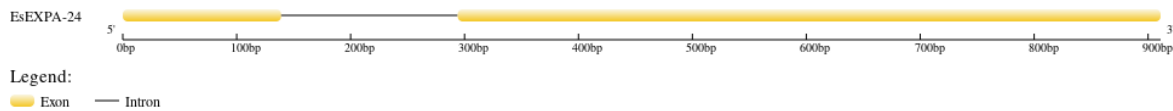
Phytozome: https://phytozome-next.jgi.doe.gov/info/Esalsugineum_v1_0

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

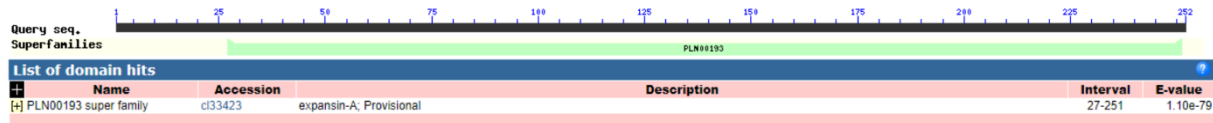
EXTERNAL RESOURCES

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GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>EsEXPA-24

MAIWVVPMIYGDVAEPRSGGGTKELDTAWYDARATFYGDIHGGGTQDGACGYGDP
NKEGYGLATTALSTALFNDGYTCGACYEIMCARDSQWCLPGSINITATNFCPPSYSKT
QDQSCNPPNKHFEELSQPMFLKIAKDKAKNVPLRYRRVPCAKTGGVKFETKRGPQNH
LTILPYNVGGAGDIKAVEVKGSKTGWIPMTKIFGQIWTISKVVLGTGQGISLRIMTSDGV
SKDFINVIPPNWGFGQTDFDGKINF*

CDS (coding sequence)

>EsEXPA-24

ATGGCAATATGGGTCGTGCCCATGATTTACGGTGATGTAGCCGAACCACGCAGTG
GTGGTGGAAACCAAGAAGACTCGACACTGCTTGGTATGACGCACGAGCCACATTTTA
TGGTGACATTCATGGTGGAGGCACTCAAGACGGAGCTTGTGGATACGGTGACCCA
AACAAAGAAGGCTACGGTTTAGCCACGACGGCGTTGAGCACGGCGCTCTTTAAC
GACGGGTACACGTGTGGTGTCTTGTATGAGATCATGTGCGCTCGTGATTCACAAT
GGTGTGTTGCCCGGGTCGATCAATATCACAGCTACAAATTTTTGTCCACCAAGTTAC
TCTAAGACCCAAGACCAGTCGTGCAACCCACCAAAACAACACTTTGAACTCTCCC
AACCAATGTTCTCAAGATCGCAAAAGACAAAGCCAAGAATGTCCCGCTTAGAT
ACAGACGTGTTCTTGTGCGAAAACCGGTGGTGTCAAGTTCGAAACCAAAAGAG
GCCACAGAATCACTTAACGATCTTGCCTTACAATGTTGGCGGGGCCGGAGATAT
TAAGCCGTGGAGGTTAAAGGAAGTAAGACCGGATGGATACCGATGACGAAGAT
TTTTGGACAGATTTGGACCAGTAAAGTCGTGTTAACCGGTCAAGGTATATCGTTG
AGGATTATGACAAGTGATGGGGTTAGTAAAGATTTTATTAATGTGATACCACCGA
ATTGGGGATTTGGACAGACTTTTGATGGAAAGATTAACCTTCTAA

Nucleotide

>EsEXPA-24

ATGGCAATATGGGTCGTGCCCATGATTTACGGTGATGTAGCCGAACCACGCAGTG
GTGGTGGAAACCAAGAAGACTCGACACTGCTTGGTATGACGCACGAGCCACATTTTA
TGGTGACATTCATGGTGGAGGCACTCAAGGTAAGTTTGGTTATTGAAATGATGTT
TTGTTTTCAAATAATTAATAAAAAAATAAAAAATGACATGGAAACACAAAAG
TAAACAAACAATCAAAACAAAAGACACATATTATTATTACATGCTCAGTTTTTT
TCAATTATAAATTTTAATAGACGGAGCTTGTGGATACGGTGACCCAAACAAAGAA
GGCTACGGTTTAGCCACGACGGCGTTGAGCACGGCGCTCTTTAACGACGGGTACA
CGTGTGGTGTCTTGTATGAGATCATGTGCGCTCGTGATTCACAATGGTGTGTTGCC

GGGTCGATCAATATCACAGCTACAAATTTTTGTCCACCAAGTACTCTAAGACCC
AAGACCAGTCGTGCAACCCACCAAACAAACACTTTGAACTCTCCCAACCAATGTT
CCTCAAGATCGCAAAAAGACAAAGCCAAGAATGTCCCGCTTAGATACAGACGTGT
TCCTTGTGCGAAAACCGGTGGTGTCAAGTTCGAAACCAAAAGAGGCCACAGAA
TCACTTAACGATCTTGCCTTACAATGTTGGCGGGGCCGGAGATATTAAGGCCGTG
GAGGTTAAAGGAAGTAAGACCGGATGGATACCGATGACGAAGATTTTTGGACAG
ATTTGGACCAGTAAAGTCGTGTTAACCGGTCAAGGTATATCGTTGAGGATTATGA
CAAGTGATGGGGTTAGTAAAGATTTTATTAATGTGATACCACCGAATTGGGGATT
TGGACAGACTTTTGATGGAAAGATTAACCTTCTAA