IDENTIFICATION

Species: *Eutrema salsugineum*

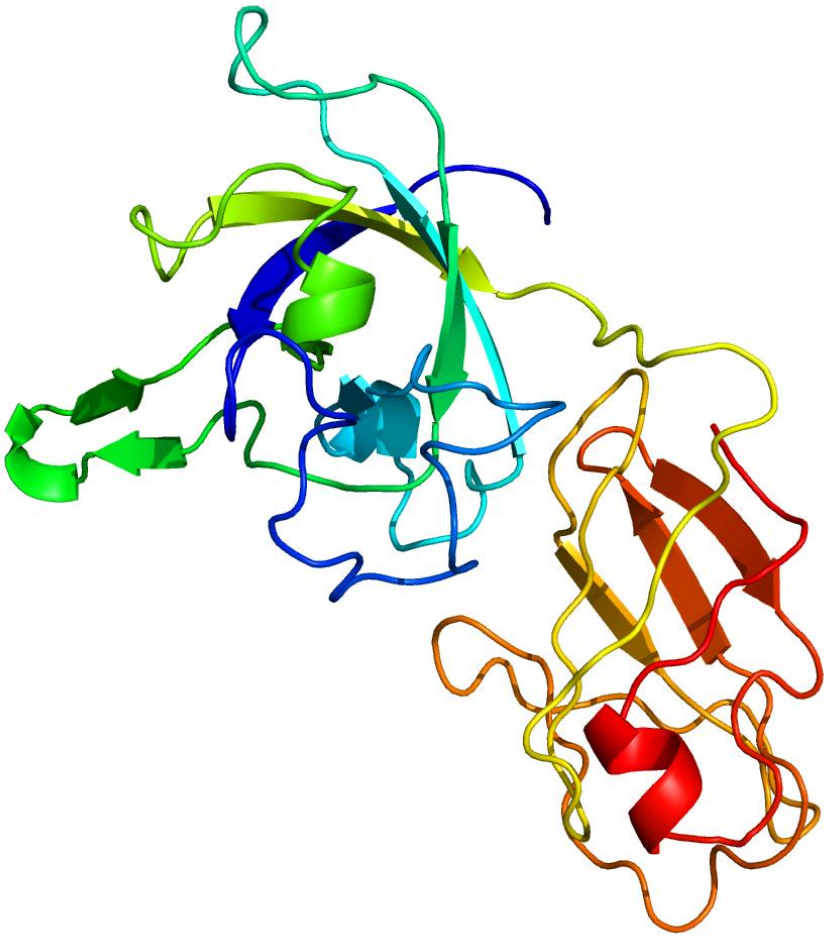
Locus: Thhalv10027877m

Gene Model: Thhalv10027877m

Description: EsEXPA-22

Family: Alpha Expansin

3D structure:



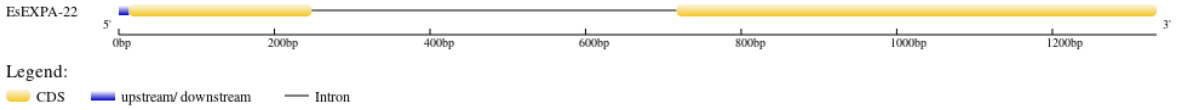
GENOME DATABASES

Phytozome: https://phytozome-next.jgi.doe.gov/info/Esalsugineum_v1_0
KEGG: https://www.genome.jp/entry/T02985

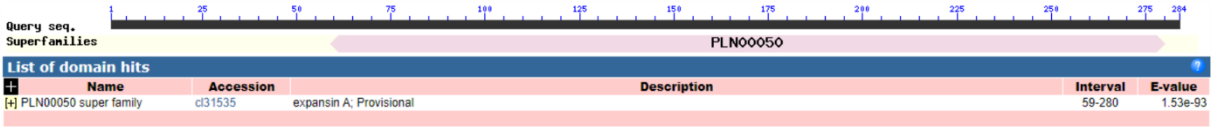
EXTERNAL RESOURCES

-

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>EsEXPA-22

MKLLEKFVYAQVLMMLMVIWAMPMTYGHGDNVPMPGHESVAGDGANPPNGGDG
TDAPESGWHDARATFYGDINGGETQQGACGYGDLHKQGYGLATAALSTALFNDGY
TCGACYEIQCVNAPQWCLPGTIKITATNFCPPDFSKTQDNWCNPPQKHFDLSQPMFL
KIAKYKAGVVPVRYRRVPCAKTGGVKFEIKGNPHFLMILPYNVGGAGDIKTMQIKGT
KTEWITMKKNWGQIWSSGVVLTGQCLSFRITTSDGITKDFMDVTPPTWGCNGQSFDG
KVNF*

CDS (coding sequence)

>EsEXPA-22

ATGAAACTCTTAGAAAAATTTGTGTATGCACAAGTTTTGATGATGTTAATGGTGA
TATGGGCCATGCCCATGACTTACGGTCATGGTGACAACGTGCCGATGCCTGGTCA
TGAATCCGTGGCTGGTGATGGAGCCAACCCACCAAATGGTGGCGACGGAACAGA
CGCACCCGAATCCGGTTGGCATGACGCTCGTGCCACCTTTTACGGTGACATCAAT
GGTGGAGAAACTCAACAGGGAGCTTGTGGATATGGTGATTTACACAAACAAGGT
TATGGTCTAGCCACAGCAGCACTAAGCACCGCGCTATTCAACGACGGATACACAT
GTGGAGCTTGTTACGAGATCCAGTGCGTGAATGCACCACAATGGTGTTTGCCCGG
AACCATCAAGATCACAGCTACAAACTTCTGTCCACCAGATTTCAGCAAGACTCAA
GACAACTGGTGCAACCCGCCACAGAAACACTTTGATCTCTCCCAACCAATGTTCC
TTAAGATCGCCAAATACAAAGCCGGGGTTGTCCCGGTTAGATACAGGCGTGTTCC
TTGCGCCAAAACCGGTGGTGTCAAGTTTGAAATCAAGGGGAACCCTCATTTCTTA
ATGATCTTGCCGTACAATGTAGGAGGAGCCGGAGATATCAAGACCATGCAGATT
AAGGGAACCAAGACCGAGTGGATAACCATGAAGAAGAATTGGGGACAGATTTGG
AGCTCTGGTGTTGTGTTGACCGGACAATGCTTATCGTTTAGGATCACAACAAGTG
ATGGCATTACGAAAGACTTTATGGACGTGACACCGCCAACTTGGGGATGTAATGG
ACAGAGTTTTGATGGAAAGGTCAACTTTTAG

Nucleotide

>EsEXPA-22

AAAATCTGAAATCATGAAACTCTTAGAAAAATTTGTGTATGCACAAGTTTTGATG
ATGTTAATGGTGATATGGGCCATGCCCATGACTTACGGTCATGGTGACAACGTGC
CGATGCCTGGTCATGAATCCGTGGCTGGTGATGGAGCCAACCCACCAAATGGTGG
CGACGGAACAGACGCACCCGAATCCGGTTGGCATGACGCTCGTGCCACCTTTTAC
GGTGACATCAATGGTGGAGAAACTCAACGTTAGTTTCAAGACCTCTAATTGAGAT

GTGAAGGTTTTGTTGTTACTATTTAGGAACTATACATTAGCCAACAATAACATGA
ACACATAGTAAACGAGACTCAATCTTTGAAAACGACCTATATATCTTTTATAAAT
CTCTTTAGAAGATTTTTTTTTTTTTCTTGTAAATCTTTTTGGGATATAGAAATGCAA
ATGCCAACATAGTTTTCTGTTTATTATTTTTTTTTTGTGTGTTCTACGTATGCATTT
ACATTAACATAAACAAAATTTAGAAAACGTTACTATTGAGCCCATTGAATTGAAA
CATTTGAATAGGGTCACCAAATATGGGGTCCCTATATAAAAAAAATGATTTTTTT
TTTCAGCTTAGTATGCAGTTATTCTATATATTGCTAATTAAACAAACGAATTGGGG
ATTTAAAAAATAATACATACTCACTTTTTTTTTTCATTTTATATTTGGATAGAGGG
AGCTTGTGGATATGGTGATTTACACAAACAAGGTTATGGTCTAGCCACAGCAGCA
CTAAGCACCGCGCTATTCAACGACGGATACACATGTGGAGCTTGTTACGAGATCC
AGTGCGTGAATGCACCACAATGGTGTTTGCCCGGAACCATCAAGATCACAGCTAC
AAACTTCTGTCCACCAGATTTCAGCAAGACTCAAGACAACTGGTGCAACCCGCCA
CAGAAACACTTTGATCTCTCCCAACCAATGTTCCTTAAGATCGCCAAATACAAAG
CCGGGGTTGTCCCGGTTAGATACAGGCGTGTTCCTTGCGCCAAAACCGGTGGTGT
CAAGTTTGAAATCAAGGGGAACCCTCATTTCTTAATGATCTTGCCGTACAATGTA
GGAGGAGCCGGAGATATCAAGACCATGCAGATTAAGGGAACCAAGACCGAGTGG
ATAACCATGAAGAAGAATTGGGGACAGATTTGGAGCTCTGGTGTTGTGTTGACCG
GACAATGCTTATCGTTTAGGATCACAACAAGTGATGGCATTACGAAAGACTTTAT
GGACGTGACACCGCCAACTTGGGGATGTAATGGACAGAGTTTTGATGGAAAGGT
CAACTTTTAG