

IDENTIFICATION

Species: *Eutrema salsugineum*

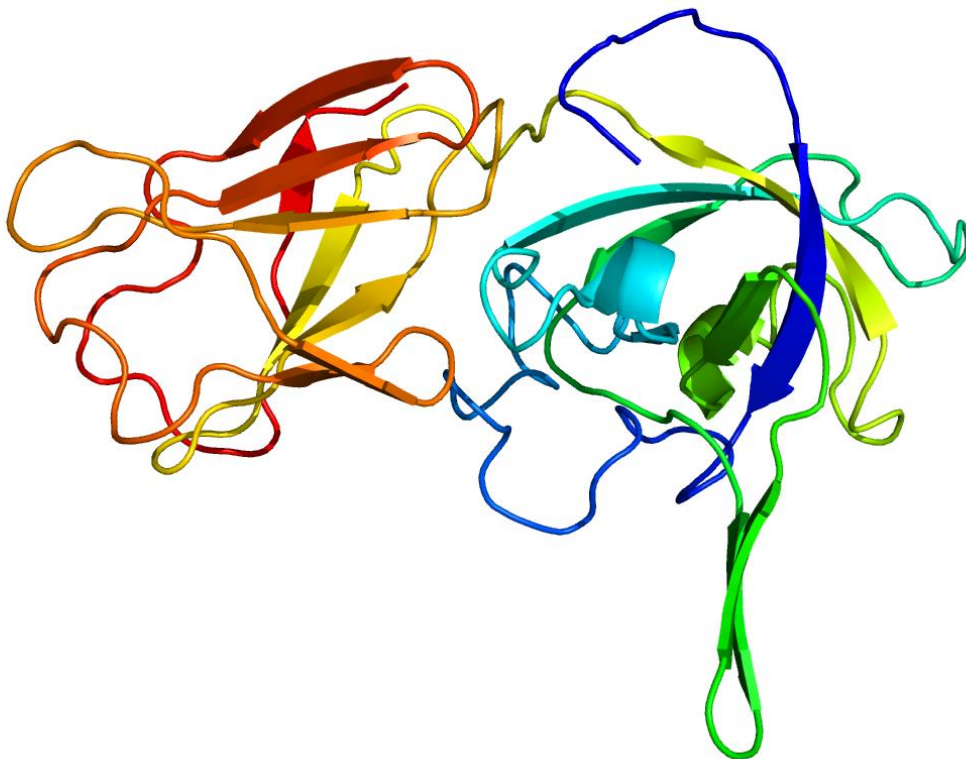
Locus: Thhalv10008578m

Gene Model: Thhalv10008578m

Description: EsEXPA-07

Family: Alpha Expansin

3D structure:



GENOME DATABASES

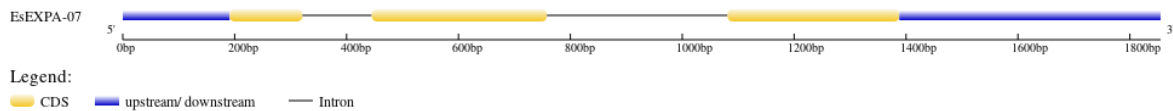
Phytozome: https://phytozome-next.jgi.doe.gov/info/Esalsugineum_v1_0

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

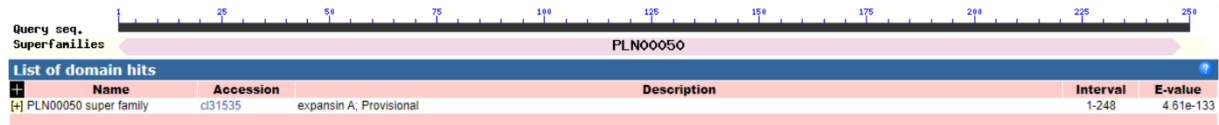
EXTERNAL RESOURCES

-

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>EsEXPA-07

MGPVGLVTVLIGVMASVSGYGGGWINAHATFYGGGDASGTMGGACGYGNLYSQ
GYGTNTAALSTALFNGLSCGSCFEIRCENDGKWCLPGSIVVTATNFCPPNNALPNN
NGGWCNPPLQHFDLAQPVFQRIAQYRAGIVPVAYRRVPCRRRGGIRFTINGHSYFNL
VLITNVGGAGDVHSAAIKGSRTGWQAMSRNWGQNWQSNLYNGQALSFKVTTSDG
RTVVSFNAAPSGWSFGQTFAGGQFR*

CDS (coding sequence)

>EsEXPA-07

ATGGGTCCTGTCCGGTTCCTAGTTACGGTTTTGATAGGAGTAATGGCTTCTTCTGT
GAGCGGCTATGGTGGCGGTTGGATCAACGCTCACGCCACTTCTACGGTGGTGGC
GATGCTCCGGCACAATGGGTGGTGGCTTGTGGATACGGCAATCTATATAGCCAAG
GTTATGGGACGAACACGGCGGCTTTGAGCACGGCTCTGTTCAATAACGGACTTAG
CTGCGGTTCTTGCTTTGAGATAAGATGTGAAAACGATGGTAAATGGTGTCTACCT
GGCTCAATCGTTGTAACCGCTACTAACTTTTGCCCGCCAAACAACGCTTTACCTAA
CAACAATGGCGGTTGGTGTAAATCCTCCTCTTCAACACTTTGATCTCGCTCAGCCTG
TTTTTCAACGCATTGCTCAATACAGAGCTGGAATCGTCCCTGTTGCATACAGGAG
GGTCCGTGTAGGAGAAGGGGAGGAATAAGATTTACGATAAATGGTCACTCATA
TTTTAACCTCGTTCTGATCACAAACGTCGGAGGCGCCGGAGACGTACACTCGGCG
GCGATCAAGGTTCAAGAACAGGTTGGCAAGCGATGTCAAGGAACTGGGGGCAA
AATTGGCAAAGCAACTCTTACCTTAACGGTCAAGCACTTTCCTTTAAAGTCACCA
CCAGCGACGGTTCGACCGTCTCCTTCAACGCCGCTCCTTCCGGCTGGTCCTTC
GGCCAGACCTTCGCCGGTGGACAGTTCCGCTAA

Nucleotide

>EsEXPA-07

CAAAGCTCTCTTCTTCTCGTATCTCTTGAAGGAAAGAAGAAGAATAACCTT
TAAGTCTCAACTCCCAAGTAACTACTTTCTCTATCTACATTCAATATTATCTTCTC
ATTTTCTCTAACACACATTCAATTGAGCTAAAAGCCATCGACTTTATCACTCCTGT
GCAGGTTAATAACAAGAACTAAAACATGGGTCCTGTCGGGTTCTTAGTTACGGTTT
TGATAGGAGTAATGGCTTCTTCTGTGAGCGGCTATGGTGGCGGTTGGATCAACGC
TCACGCCACTTTCTACGGTGGTGGCGATGCTTCCGGCACAATGGGTAATTTGCTC
AAAACAATATACAAAACCATTTTTTTTTTTTGGTTAATGTTAACCAAGGACTTCTC
CATCCATTTCTTACCAAATTATCAAGTTTTACTGATCCTAAATCTACTTCTATTA

GGTGGTGCTTGTGGATACGGCAATCTATATAGCCAAGGTTATGGGACGAACACGG
CGGCTTTGAGCACGGCTCTGTTCAATAACGGACTTAGCTGCGGTTCTTGCTTTGAG
ATAAGATGTGAAAACGATGGTAAATGGTGTCTACCTGGCTCAATCGTTGTAACCG
CTACTAACTTTTGCCCGCCAAACAACGCTTTACCTAACAACAATGGCGGTTGGTG
TAATCCTCCTCTTCAACACTTTGATCTCGCTCAGCCTGTTTTTCAACGCATTGCTCA
ATACAGAGCTGGAATCGTCCCTGTTGCATACAGGAGGTAACAAAAATTGTAGCTT
TCTCTGTTTTGAAGCTTTTTACATCTGCTCTGTTTTTCTTATAATACATAGTATATC
GTAATAAATCAGAACTATTTTCTTGGATTCAATTGATCAAAACAGAATAATTCGAT
TGAATTTTCATGATTGAAGGATAAATTATGCTCCAAGTTTCAATATTTAGATATCTG
TTCAAATTTTTTTCGGTTGCTCTGTTTTGTTTTAGTTTCTTAGGTTGCTCTGTTTTTTA
CCAAAGCAGAGTAATACGTAACCTTTCCAATACTTTATCCGTTTTGTTTGATGAACA
TGAATTTGTGGTGTTTTTTGCAGGGTTCCGTGTAGGAGAAGGGGAGGAATAAGATT
TACGATAAATGGTCACTCATATTTTAAACCTCGTTCTGATCACAAACGTCCGGAGGC
GCCGGAGACGTACACTCGGCGGCGATCAAGGGTTCAAGAACAGGTTGGCAAGCG
ATGTCAAGGAACTGGGGGCAAATTTGGCAAAGCAACTCTTACCTTAACGGTCAA
GCACTTTCCCTTTAAAGTCACCACCAGCGACGGTCGCACCGTCGTCTCCTTCAACGC
CGCTCCTTCCGGCTGGTCCTTCGGCCAGACCTTCGCCGGTGGACAGTTCCGCTAA
AAGGGACAATTTGGTCATTTTCTACTCTACTTTTATAGCTAAAAGTAATAGTAAA
ATTGTTTGTGTGGTGTGTAGAGGGCATATTGGTAAATTGGGTTCTTGCGAACTCTC
GGTTCTTGTTGAGAGAGTGATGCGTCGAGGGCTCGGTTTTGCAGAAGACCTTGAT
GACGTCTATCTTTTTTGGACCTCTTTTATTTGTTTACGTTCTTACAAAAATAGTTTT
TTACTAAGAGTGGGAAAAAAGAAGAAGAGAAAAGCATGGTAGTTATTGTATTA
CTAATGCAGAGGTGGAGTTTTAACTACCACCCGCTAGTAGTAATGAGTAACCCAT
TTACCCTTTAAGGCGTGAGAGATGGGATTATGAGGGTTTTTCAATTGTATTTTG
TGATGTTGTTTGTATGAGATCAAGAGAACACTATCAATTTTACAGTATATCAATA
AAAAGATGCAACTTCTTTCCGAG