

IDENTIFICATION

Species: *Eutrema salsugineum*

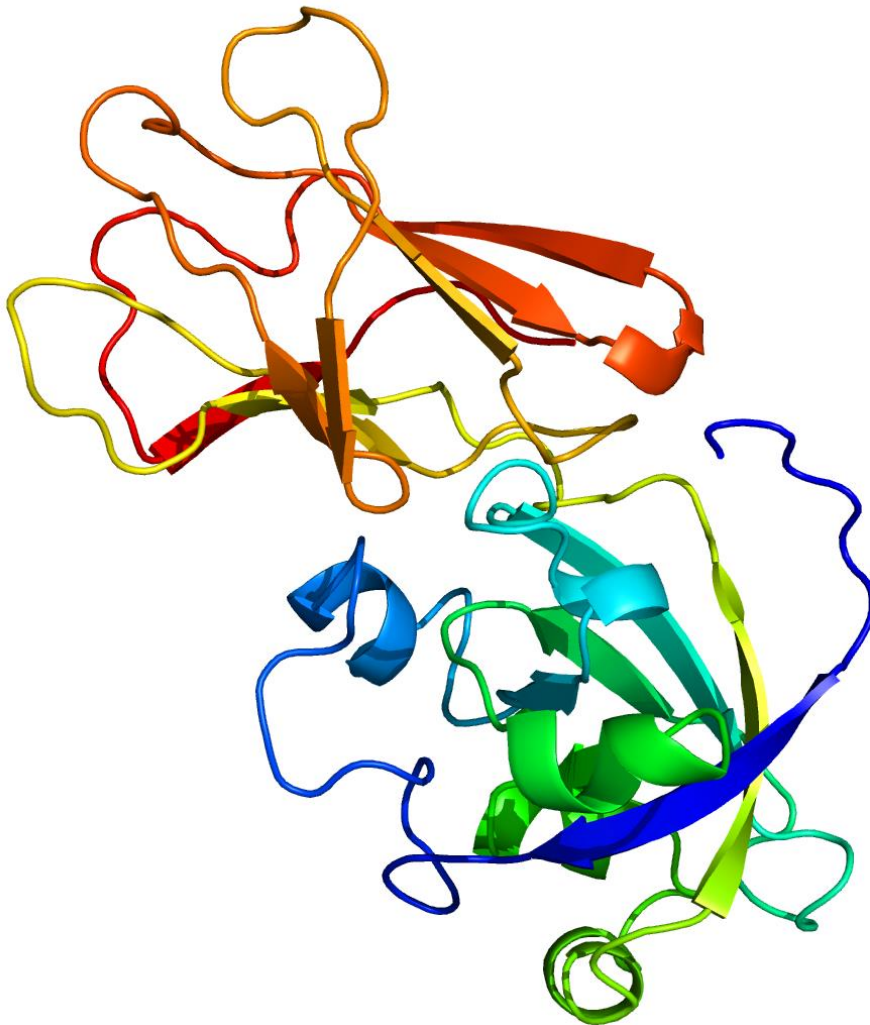
Locus: Thhalv10006139m

Gene Model: Thhalv10006139m

Description: EsEXPB-04

Family: Beta Expansin

3D structure:



GENOME DATABASES

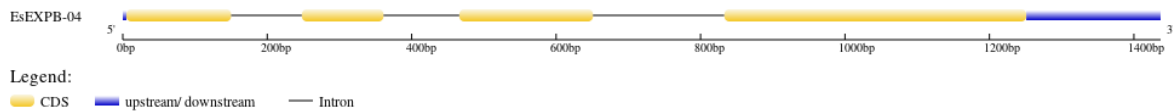
Phytozome: https://phytozome-next.jgi.doe.gov/info/Esalsugineum_v1_0

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

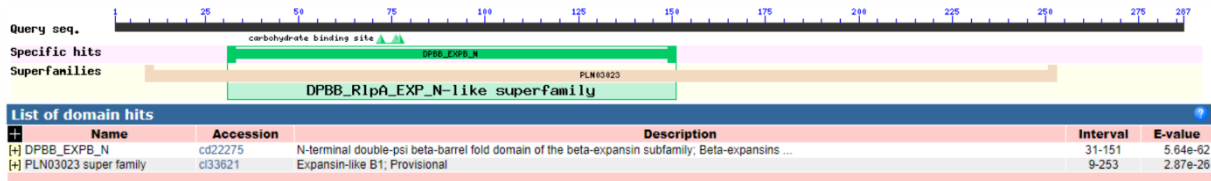
EXTERNAL RESOURCES

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GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>EsEXPB-04

MAFFSGKKICFIVALFAISLKPFCFCTNTRWNTAGITWYGDREGPGSTGGACGYGDA
VAKHPYNCMISAGGPSLYQDGKGCCTCYRLVCDHPMCTKKPIKVMISDECPGCTKE
AVHFDLSGKAFGALAKHGKADQLRNLGELKVRYKRACCKHPKSKIAIHVDAGANPY
YMSFAVKYANGDGNFACVEIQPAGGKYLKMEEMRSAVWKLNPGCALKGPFNVRLT
SAVTKNVLVAKAVIPEKWNPGAIYHSLVNFAPKKS VHKKS VHKKS VHKKS VHKKS
VHKHKH*

CDS (coding sequence)

>EsEXPB-04

ATGGCATT TTTTTCAGGCAAAAAAATTTGCTTTATCGTTGCTCTCTTTGCAATCTC
ATTGAAGCCATGTTTTTGCACGAATACAACCCGCTGGAACACCGCCGGAATCACG
TGGTATGGCGACCGAGAGGGTCTTGGCAGCACAGGAGGAGCTTGTGGATACGGT
GATGCAGTGGCAAAGCACCCGTACAACCTGTATGATTTTCAGCCGGAGGACCTTCAT
TGTACCAAGATGGAAAGGGTTGTGGGACATGTTATAGGCTCGTATGTGACCATCC
GATGTGCACGAAAAGCCGATCAAGGTGATGATATCGGATGAGTGTCCCGGCTG
CACGAAGGAAGCGGTCCATTTTGATCTTAGCGGTAAGGCCTTTGGTGCATTGGCC
AAACATGGCAAGGCCGATCAATTACGTAACCTTGGAGAGCTAAAGGTTAGATAC
AAACGTGCATGCTGCAAACACCCTAAGAGTAAAATAGCTATTCATGTGACGCCC
GAGCAAATCCGTAACATGTCGTTCCGCGTTAAATATGCAAACGGTGACGGAAA
CTTTGCCTGCGTGGAGATCCAACCTGCCGGAGGAAAGTACCTGAAGATGGAGGA
AATGAGATCGGCCGTTTGGAACTTAACCCCGGCTGTGCATTGAAAGGTCCGTTT
AACGTCCGGCTTACCTCCGCGTGACCAAAAACGTGCTCGTTGCCAAAGCCGTTA
TCCCGGAAAATGGAATCCCGGTGCTATCTACCACTCCCTCGTTAACTTCGCCGTT
CCTAAGAAATCGGTTACAAGAAATCCGTTACAAGAAATCGGTTACAAGAAA
TCCGTTACAAGAAACCCGTTACAAGAAACACAAATGA

Nucleotide

>EsEXPB-04

GAGACATGGCATT TTTTTCAGGCAAAAAAATTTGCTTTATCGTTGCTCTCTTTGCA
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TCACGTGGTATGGCGACCGAGAGGGTCTTGGCAGCACAGGTAATTAATTAACC
ATTAATTGTTCCATTAATACAAATAATTTTTTTTTTTTGTAAATTTACATAGGGCC

GGTTCTTACAACATATACAATATACAGGAGGAGCTTGTGGATACGGTGATGCAGT
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GATGGAAAGGGTTGTGGGACATGTTATAGGGTATTTGATTATATTTGAAAACATA
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TTGTTAATGCGCTTCGTCACACAAACCGGTTAGGTTTCGGTTTGATAAGGTTTATTT
TAGATAGGAAATATAAATACCAATCTTTATGGGTATCGATCTTAAGCCAATTATTA
TAAATTTTTCATACATTAACGTTTTCTGGTTAACTGATAAAAAAGTTCCGTGATGA
TGCAGTGCATGCTGCAAACACCCTAAGAGTAAAATAGCTATTCATGTGACGCCC
GAGCAAATCCGTAACATGTGCTTCGCCGTTAAATATGCAAACGGTGACGGAAA
CTTTGCCTGCGTGGAGATCCAACCTGCCGGAGGAAAGTACCTGAAGATGGAGGA
AATGAGATCGGCCGTTTGGAACTTAACCCCGGCTGTGCATTGAAAGGTCCGTT
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CCTAAGAAATCGGTTACAAGAAATCCGTTACAAGAAATCGGTTACAAGAAA
TCCGTTACAAGAAACCCGTTACAAGAAACACAAATGATTAATTCCTTCAAACG
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TCA