

IDENTIFICATION

Species: *Eutrema salsugineum*

Locus: Thhalv10026076m

Gene Model: Thhalv10026076m

Description: EsEXLB-01

Family: Expansin Like Beta

3D structure:



GENOME DATABASES

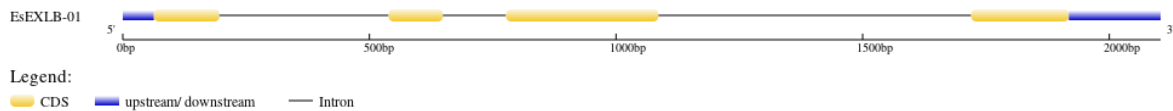
Phytozome: https://phytozome-next.jgi.doe.gov/info/Esalsugineum_v1_0

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

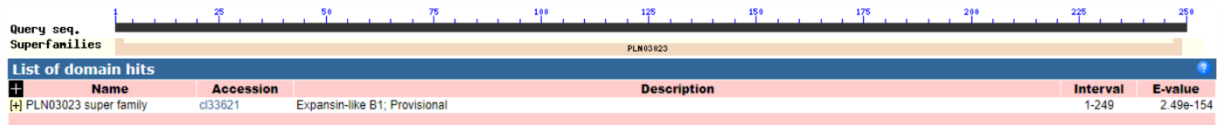
EXTERNAL RESOURCES

-

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>EsEXLB-01

MKRSHVLHLLL VQVIFLLPLLCLSDDYVSSRATFYGSPDCKANPRGACGYGEFGRDI
NNGEVSGVSSRLWNNGTGCGACYQVRCKIPPHCNEEGVYVVATDYGGAGGDFIFSL
EAYGRMARPGTEDQLYSFGVVDVEYKRVPCRYGGSNLVYKVHEKSYNPHYLAVLIL
YVGGVNDILAVEVWQEDCKEWRMRVFGAVHDLNPPRGTLRLFLVYGSAGIN
WVQSPNALPADWTAGATYNSNILLT*

CDS (coding sequence)

>EsEXLB-01

ATGAAGAGATCTCACGTTTTGCATCTTCTGCTTGTTCAAGTCATTTTCCTTTTGCCT
CTCCTTTGTTTATCTGATGACTATGTTAGCTCTAGAGCTACTTTTTATGGCAGCCC
CGATTGCAAAGCAAATCCTCGAGGAGCATGTGGGTATGGAGAATTCGGAAGAGA
TATCAATAATGGTGAAGTGAGTGGTGTTCATCCCGACTATGGAACAATGGA
ACTGGCTGTGGTGTGTTATCAGGTGAGGTGCAAATAACCTCCACACTGCAACGAGG
AAGGAGTATACGTGGTGGCTACGGACTACGGAGGAGCTGGTGGTACTTCATATT
TAGCCTTGAGGCGTACGGACGTATGGCAAGACCAGGCACAGAGGATCAGCTCTA
TTCCTTTGGTGTGGTCGACGTCGAGTACAAGAGAGTCCCTTGCCGGTACGGAGGG
TCCAATCTGGTGTATAAAGTCCATGAAAAAGCTACAATCCTCATTATCTTGCCG
TCCTTATCTTGTACGTTGGTGGTGTCAATGACATCCTCGCCGTTGAAGTCTGGCAG
GAGGATTGCAAAGAGTGGCGACGTATGAGAAGAGTGTTTGGAGCTGTACACGAC
TTGGAGAATCCACCAAGAGGCACTCTCTTTGAGGTTCTTAGTCTACGGAAGCG
CCGGAATCAATTGGGTCCAATCTCCGAACGCTCTTCCCGCCGATTGGACCGCCG
AGCCACTTACAACCTCAACATTCTACTTACTTGA

Nucleotide

>EsEXLB-01

CACTAATCTATTTTCGCAAATCACTTGTAAAATAGTCTCTTACAATAGTTATAGA
TAAAATATGAAGAGATCTCACGTTTTGCATCTTCTGCTTGTTCAAGTCATTTTCC
TTTTGCCTCTCCTTTGTTTATCTGATGACTATGTTAGCTCTAGAGCTACTTTTTATG
GCAGCCCCGATTGCAAAGCAAATCCTCGTACGTATTTGAATTTTTTGTGTCATATA
TCAAGTACATTAATTATGTCATTTTTAGTATTATTTAGCATGATTGGTAAAGCTAC
ATTAACAGGAACATCTCAACATATAGAGTCAATATCATTATCACGTTAACTATTT
AATCTATGTATAACAATATCATTATCTACGTATAAGTACATGTAGATGAACACGA
TTCCATTAAGTGTCCGTATCTTTGATTGAGTATGACATTACGTTAATAGTGAGA

TTTTTCCAAGAATCCGTTGGTATGGATAAAAATGCATAGAACTTTCTAATATGAAA
AAGGATGTAATAAATTTATTACTGGTTATGTATGCAGGAGGAGCATGTGGGTATG
GAGAATTCGGAAGAGATATCAATAATGGTGAAGTGAGTGGTGTTCATCCCGACT
ATGGAACAATGGAACCTGGCTGTGGTGCTTGTATCAGGTTTGTTTTTTACATATAT
TTTATCTAGTCCAATATTTTATCAATAACATTATGCTATATACTATAATTTCTCGTT
CGATTATCATTACTAAACGAATATCATCAATTATTATCGATTATAAAAAAAGGTG
AGGTGCAAAAATACCTCCACACTGCAACGAGGAAGGAGTATACGTGGTGGCTACG
GACTACGGAGGAGCTGGTGGTGACTTCATATTTAGCCTTGAGGCGTACGGACGTA
TGGCAAGACCAGGCACAGAGGATCAGCTCTATTCCTTTGGTGTGGTTCGACGTCGA
GTACAAGAGAGTCCCTTGCCGGTACGGAGGGTCCAATCTGGTGTATAAGGTCCAT
GAAAAAAGCTACAATCCTCATTATCTTGCCGTCCTTATCTTGTACGTTGGTGGTGT
CAATGACATCCTCGCCGTTGAAGTCTGGCAGGTAAATTTTCATCAAAAAGATTTCA
ACAAACAAATATTTGTATGTCTGTTTTTGAGGATCAAAATAGTTTTATTATAATCT
ATAAGTTTTTTGAACCTAGACTTTTTGGCTTTTTCAAAAAAACTACATACCTATGCCA
AATTTATTTGGCTATTCGTGGTAATTACATCATTTCTACGTCGCCATTTAATTAGT
AGTGCAAGTTAATCCGGCTGGTCATTGTGCGATTTACTAATGACCACTAAAGACAT
GTTTATCAATTTATCATTAGTGGTGACGACGCACTGATATGTTACATAATCTTATC
TAATTGCATGGATTAGCTAGAGTTAGTGAAGATCCTAGCTATTGTCAAAGATGAA
ACCCATCATTAAATCTTTCTTAAAAATCAACACAGTGCCAATATCTCTACGTAGGA
AATATTTTCATACAAAATGAAAAAATAAATTGTAATGTTTTGAATTTCTTGTTCCA
GGACTCCTTTTAGCTCTAGTTTCAACGCTTTTTCTTAAATTAACACAATGTATTCT
ACAACACTCATCATTAAAGACAATATATTTCTTAAAGATTAATAACATAGTTGTAA
GCAAAAACGGTTCGATGTTTTTTGAGTAAATAAAAACATGAATATATGATTCAG
GAGGATTGCAAAGAGTGCGGACGTATGAGAAGAGTGTTTGGAGCTGTACACGAC
TTGGAGAATCCACCAAGAGGCACTCTCTCTTTGAGGTTCTTAGTCTACGGAAGCG
CCGGAATCAATTGGGTCCAATCTCCGAACGCTCTTCCCGCCGATTGGACCGCCGG
AGCCACTTACAACCTCAACATTCTACTTACTTGATCCCCTAACATTTTGCATCTTT
CTCTCTATCTATTGTGTGGTTTCTCTATACATATGTAATAATGGAGATATATTTAAA
TAACGCCCTCTAGAACCATATAATAATTATCATAGTATATTCTTATAGTTATATTT
CTTGTGTCTATTTAAGAATATTGTAATGATTTGTAAGGTTTTGATTAGTAAT