

IDENTIFICATION

Species: *Eutrema salsugineum*

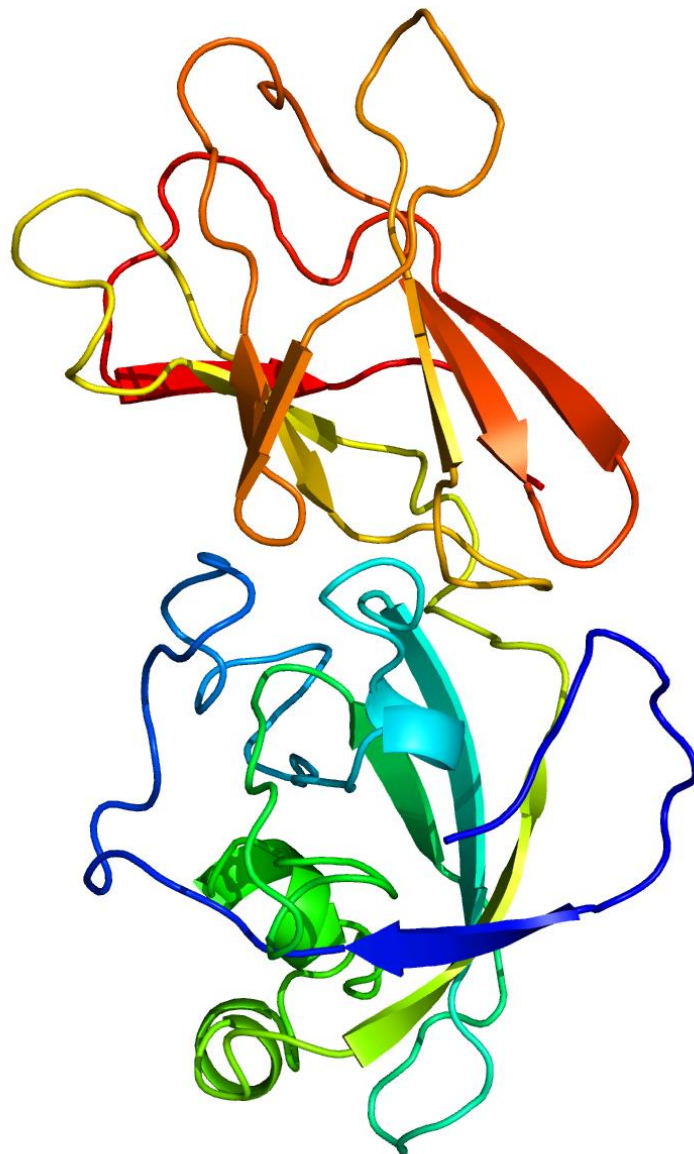
Locus: Thhalv10025976m

Gene Model: Thhalv10025976m

Description: EsEXLA-01

Family: Expansin Like Alpha

3D structure:



GENOME DATABASES

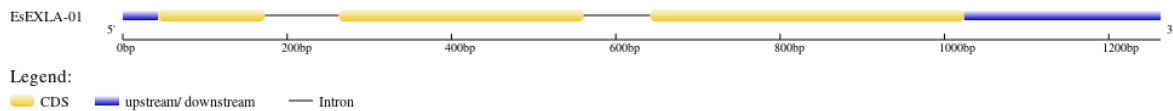
Phytozome: https://phytozome-next.jgi.doe.gov/info/Esalsugineum_v1_0

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

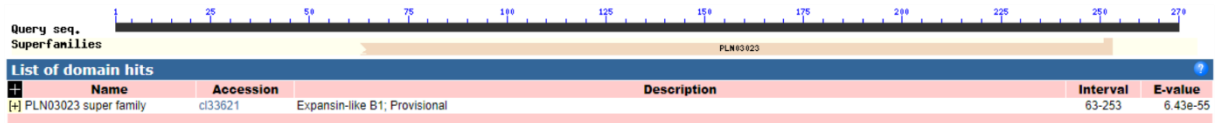
EXTERNAL RESOURCES

-

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>EsEXLA-01

MGSCFLFFVVA VVFISSSSVHACDRCLHRSKASYFSSASSLSSGACAYGSLATGFFA
GHIAAAVPSIFKDGAGCGACFQVRCVDPALCTTKGTTVMVTDLNIKSNHTDLVLSSR
AFRALAKPVLGADRNLRRGIVDIQYQRVPCDYGNKKMMNVRVEETSKSPNYLAIK
LLYQGGQTEVVAIDIAQVGSSRWYMTTRSHGAVWATDKVPTGALQFRFMVTGGYD
GKMLWSPSVLPANWEPGKTYDAGVQITDIAQEGCDPCDAHIWK*

CDS (coding sequence)

>EsEXLA-01

ATGGGAAGCTGTTTTCTCTTCTTCGTCGTCGCAGTCGTCCTTCATCTCCTCCTCCTCT
TCCGTTACGCTTGCGACCGTTGTCTCCACCGCTCTAAGGCTTCTTATTTCTCCTCT
GCTTCTTCTCTCCTCCGGAGCTTGTGCCTATGGTTCTCTAGCTACTGGTTTCTTC
GCCGGTCACATCGCCGCCCGCTGCCTTCCATCTTCAAAGACGGCGCCGGCTGCG
GAGCTTGCTTCCAGGTGCGTTGCGTCGACCCTGCTCTCTGCACCACCAAAGGAAC
CACCGTCATGGTCACAGACCTCAACATCAAGAGCAACCACACCGATCTCGTCCTC
AGCTCCAGAGCCTTTCAGGGCTTTGGCCAAGCCTGTTCTCGGCGCCGACAGAAACC
TTCTCAGACGAGGCATTGTCGACATTCAATACCAAAGAGTTCCTTGCGATTATGG
AAACAAGAAGATGATGAATGTGAGAGTGGAAGAAACAAGCAAAAGCCCAAATT
ACTTGGCGATAAAGCTCTTGTACCAAGGTGGCCAAACCGAAGTCGTTGCCATCGA
CATTGCTCAGGTGGGTTCCTCGCGTTGGACCTACATGACCAGATCTCACGGTGCC
GTCTGGGCCACCGACAAAGTACCCACCGGAGCTCTGCAGTTCAGGTTTCATGGTTA
CCGGTGGCTACGACGGCAAATGCTCTGGTCTCCGAGTGTTCTTCCCGCCAACTG
GGAACCTGGAAAGACCTACGACGCCGGCGTTCAGATCACCGACATTGCTCAGGA
AGGTTGTGATCCATGCGACGCTCACATCTGGAAATAA

Nucleotide

>EsEXLA-01

CTCTCTCTTAATAAACTTATAAAAAGAAAAACATAAACAAAAAATGGGAAGCTG
TTTTCTTCTTCGTCGTCGCAGTCGTCCTTCATCTCCTCCTCCTCTTCCGTTACGC
TTGCGACCGTTGTCTCCACCGCTCTAAGGCTTCTTATTTCTCCTCTGCTTCTTCTCT
CTCCTGTACTCTCTCTCTCTGTATTCAATCGTATGTGTTTTGTCTTCTTTTTCTC
ATATTTTTTTTTTTGACTTGTTAATGCCTTTGCAGCCGGAGCTTGTGCCTATGGT
TCTCTAGCTACTGGTTTCTTCGCCGGTCACATCGCCGCCCGCTGCCTTCCATCTT
CAAAGACGGCGCCGGCTGCGGAGCTTGCTTCCAGGTGCGTTGCGTCGACCCTGCT

CTCTGCACCACCAAAGGAACCACCGTCATGGTCACAGACCTCAACATCAAGAGC
AACCACACCGATCTCGTCCTCAGCTCCAGAGCCTTCAGGGCTTTGGCCAAGCCTG
TTCTCGGGCGCCGACAGAAACCTTCTCAGACGAGGCATTGTTCGACATTCAATACCA
AAGGTACACTCTTTTTTTTTTTGTTTTGTTTTGTAGTAGTAGTAGATTTCTTTGTCTA
GTGAGTAATAAAGGCAGTTGAAAACAGAGTTCCTTGCGATTATGGAAACAAGAA
GATGATGAATGTGAGAGTGGAAGAAACAAGCAAAGCCCAAATTACTTGGCGAT
AAAGCTCTTGTACCAAGGTGGCCAAACCGAAGTCGTTGCCATCGACATTGCTCAG
GTGGGTTCCCTCGCGTTGGACCTACATGACCAGATCTCACGGTGCCGTCTGGGCCA
CCGACAAAGTACCCACCGGAGCTCTGCAGTTCAGGTTTCATGGTTACCGGTGGCTA
CGACGGCAAATGCTCTGGTCTCCGAGTGTTCTTCCCGCCAACTGGGAACCTGGA
AAGACCTACGACGCCGGCGTTCAGATCACCGACATTGCTCAGGAAGGTTGTGATC
CATGCGACGCTCACATCTGGAAATAACTTACTCACTTACTTACTCGCCAACAATTC
TCTTTTCTCTCTTTTTCTTTTTCTTTTACAATGACAAAGCAGAGCCTCTTTCCTTATT
TATGGCTTTCATCATTGATTAAGTAACTGAAACAAAGTGTTAAACTAAGAAAGGTTTT
AAGGGATATATGTACAAAAGAGGTCTCTCTATATATATATATATGTACACCACCATT
CTTTTCTATCTGTAACCTTGCATCTTAGTTGACATTACTTT