

IDENTIFICATION

Species: *Eutrema salsugineum*

Locus: Thhalv10015496m

Gene Model: Thhalv10015496m

Description: EsEXPA-03

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>

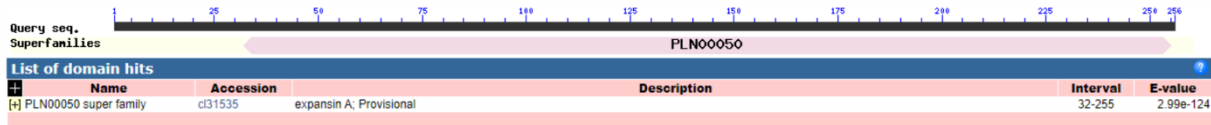
EXTERNAL RESOURCES

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GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>EsEXPA-03

MNLTEYSQIFILSLCTLNFCFFVINSDDNGEWESGHATFYGGADASGTMGGACGYGD
LYSQGYGLQTAALSTALFRNGQKCGACFELRCEDDPQWCLPGSIIVSATNFCPPNFAL
ANDNGGWCNPPLEHFDLAEP AFLQIAQYRAGIVPVAFRRVPCEKSGGIRFTINGNSYF
DLVLITNVGGAGDVRAVSLKGSKTGQWQSMSRNWQNWQSN TYLRGQSLSFQVTA
GDGRTVVS YD VVPQDWQFGQTFEGGQF*

CDS (coding sequence)

>EsEXPA-03

ATGAATCTCACGGAATATTCCCAAATATTTATCCTTTCACTATGCACCCTCAACTT
CTGCTTCTTTGTTATAAACTCCGACGACAACGGCGAATGGGAAAGTGGCCACGCC
ACTTTCTACGGCGGAGCTGATGCATCCGGCACTATGGGAGGTGCATGTGGGTACG
GTGACTTGTACAGCCAAGGCTACGGACTACAAACCGCGGCGCTGAGCACGGCTTT
GTTCAGAAACGGTCAGAAGTGTGGGGCCTGTTTTGAGCTACGGTGTGAGGATGAT
CCTCAGTGGTGCCTCCCTGGTTCCATCATCGTCTCGGCTACAAACTTTTGTCTCC
AAACTTTGCCTTAGCCAATGATAATGGTGGTTGGTGCAATCCTCCCCTTGAACATT
TTGACTTGGCCGAGCCTGCCTTCTCCAAATCGCTCAGTATCGAGCTGGGATCGTT
CCTGTCGCATTTAGGAGGGTTCCATGTGAGAAATCTGGAGGGATAAGGTTTACGA
TAAACGGGAATTCGTACTTCGACCTCGTGCTGATCACAACCGTGGGTGGTGCTGG
AGATGTTAGAGCCGTTTCTTTGAAAGGCTCAAAGACTGGTCAGTGGCAATCCATG
TCCAGAAACTGGGGACAGAATTGGCAAAGCAACTTACCTCAGAGGTCAAAGC
CTCTCCTTTCAAGTCACTGCTGGTGTGGTTCGGACTGTTGTGAGCTACGATGTTGT
GCCTCAGGATTGGCAGTTCGGTCAAACCTTTGAAGGAGGACAGTTCTAG

Nucleotide

>EsEXPA-03

ATGAATCTCACGGAATATTCCCAAATATTTATCCTTTCACTATGCACCCTCAACTT
CTGCTTCTTTGTTATAAACTCCGACGACAACGGCGAATGGGAAAGTGGCCACGCC
ACTTTCTACGGCGGAGCTGATGCATCCGGCACTATGGGTA CTCAAACATAAACT
TTTCGTTTCGCAAACACTAGACATCATCTCTAAATAATTACACATGTACATGGATA
TTTTGACATATATCTTAAAAACGTTAAAAGTGTTGACGTAAGGTTTTTGTAGGAG
GTGCATGTGGGTACGGTGACTTGTACAGCCAAGGCTACGGACTACAAACCGCGG
CGCTGAGCACGGCTTTGTTTCAGAAACGGTCAGAAGTGTGGGGCCTGTTTTGAGCT
ACGGTGTGAGGATGATCCTCAGTGGTGCCTCCCTGGTTCCATCATCGTCTCGGCTA

CAAAC TTTT GTCCTCCAAACTTTGCCTTAGCCAATGATAATGGTGGTTGGTGCAAT
CCTCCCCTTGAACATTTTGACTTGGCCGAGCCTGCCTTCCTCCAAATCGCTCAGTA
TCGAGCTGGGATCGTTCCTGTCGCATTTAGGAGGTAAAAAAAAAACATTTGGAGC
ATACTTAGGGATTAGCAATTCTAAATACGATTTTTTCGTATGTCCACCCTAGCGCA
AAAGTAGAAGCATTTTTTCATAAGAAAACATCTTCGCTTTTGATAAGTCTTGACCT
AATTAATGTACCATTTTTGTTCATCTGACAATGACAGGGTTCCATGTGAGAAATCT
GGAGGGATAAGGTTTACGATAAACGGGAATTCGTA CTTCGACCTCGTGCTGATCA
CAAACGTGGGTGGTGCTGGAGATGTTAGAGCCGTTTCTTTGAAAGGCTCAAAGAC
TGGTCAGTGGCAATCCATGTCCAGAACTGGGGACAGAATTGGCAAAGCAACAC
TTACCTCAGAGGTCAAAGCCTCTCCTTTCAAGTCACTGCTGGTGATGGTCGGACT
GTTGTGAGCTACGATGTTGTGCCTCAGGATTGGCAGTTCGGTCAAAC TTTTGAAG
GAGGACAGTTCTAG