

## IDENTIFICATION

**Species:** *Eutrema salsugineum*

**Locus:** Thhalv10017120m

**Gene Model:** Thhalv10017120m

**Description:** EsEXPA-19

**Family:** Alpha Expansin

**3D structure:**



## GENOME DATABASES

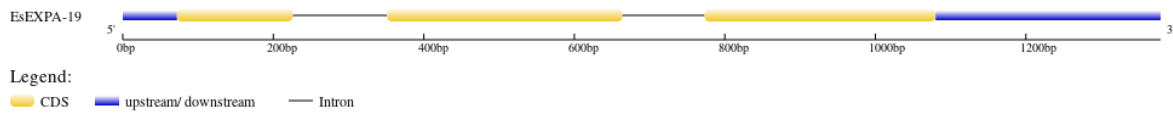
Phytozome: [https://phytozome-next.jgi.doe.gov/info/Esalsugineum\\_v1\\_0](https://phytozome-next.jgi.doe.gov/info/Esalsugineum_v1_0)

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

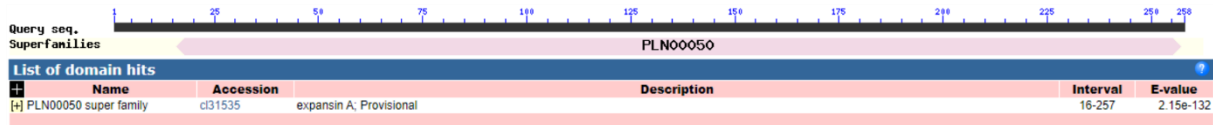
## EXTERNAL RESOURCES

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## GENE STRUCTURE



## DOMAIN ARCHITECTURE



## SEQUENCES

### Peptide

>EsEXPA-19

MFITSYSKYSVISTLSIFSLLFFLQRTHGDDGGWQGGHATFYGGGDASGTMGGACGY  
GNLYSQGYGTNTAALSTALFNGLTCGACYEMKCNDDPRWCLSSTITVTATNFCPPN  
LGLSNDNGGWCNPPLQHFDLAEP AFLQIAQYRAGIVPVSFRRVACMKKGGIRFTING  
HSYFNLVLISNVGGAGDVHAVSIKGSKTGSWQAMSRNWGQNWQSN SYLNDQSLSF  
QVTTSDGRTVVSNDVAPSNWQFGQTFQGGQF\*

### CDS (coding sequence)

>EsEXPA-19

ATGTTTATTACATCATACTCCAAATATTCTGTAATCTCAACACTATCCATATTCAG  
CTTATTATTCTTCCTCCAAAGAACCCATGGAGACGACGGAGGTTGGCAAGGTGGC  
CACGCCACCTTCTACGGTGGCGGCGACGCTTCAGGCACCATGGGAGGAGCTTGTG  
GCTATGGAAATCTGTATAGCCAAGGTTACGGGACGAACACGGCGGCTTTAAGCA  
CGGCTCTATTCAACAACGGACTCACGTGCGGCGCGTGCTACGAGATGAAGTGCAA  
TGATGACCCAAGATGGTGTCTCTCGTCAACTATCACCGTCACAGCCACCAACTTTT  
GCCACCAAACCTTGGTCTCTCCAACGATAATGGTGGATGGTGCAATCCTCCTCT  
CCAGCACTTCGACCTCGCCGAGCCAGCTTTCCTCCAGATCGCTCAGTATCGTGCC  
GGCATTGTCCCCGTCTCTTCCGAAGAGTAGCGTGTATGAAGAAAGGAGGGATAA  
GGTTTACGATAAACGGACATTCATACTTTAATTTGGTTCTGATATCGAACGTAGG  
AGGAGCAGGAGACGTCCACGCAGTGTTCGATCAAAGGCTCAAAAACAGGGTCGTG  
GCAAGCAATGTCTAGGAAGTGGGACAGAACTGGCAGAGCAACTCTTATCTCAA  
CGACCAAAGCCTCTCGTTCCAGGTTACTACCAGCGATGGTTCGCACCGTCGTTAGC  
AATGACGTGGCTCCTTCTAACTGGCAGTTCGGACAAACCTTCCAAGGCGGTCAAT  
TCTGA

### Nucleotide

>EsEXPA-19

CGATTCTTTCTCACCAAATCAAATCAGATACTCAAACCGAATTAACCTAACCCCT  
CAAAAACAAAAGAAAAATGTTTATTACATCATACTCCAAATATTCTGTAATCTC  
AACACTATCCATATTCAGCTTATTATTCTTCCTCCAAAGAACCCATGGAGACGAC  
GGAGGTTGGCAAGGTGGCCACGCCACCTTCTACGGTGGCGGCGACGCTTCAGGC  
ACCATGGGTATGACCAAAAAAAAAAAAAACAATAAATCCTTATGTTAATAGCTTAGC  
TAATTGAATCCATTTATACAAATACATGCGTATATGTTAGCTAGCTAACACGTGA

CATACACACAAAAAATGTTTCAGGAGGAGCTTGTGGCTATGGAAATCTGTATAGCC  
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TCACGTGCGGCGCGTGCTACGAGATGAAGTGCAATGATGACCCAAGATGGTGTCT  
CTCGTCAACTATCACCGTCACAGCCACCAACTTTTGCCACCAAACCTTGGTCTCT  
CCAACGATAATGGTGGATGGTGCATCCTCCTCTCCAGCACTTCGACCTCGCCGA  
GCCAGCTTTCCTCCAGATCGCTCAGTATCGTGCCGGCATTGTCCCCGTCTCTTCC  
GAAGGTTTCGTTTTTTACTTTTTCTTGATACTTGGAACGCAAGAAAGCAATAAACA  
ACAAAAGTGATTAACTAACTAATGAGTTATGTGTTGTTTGGTTGTGTAATTTGC  
AGAGTAGCGTGTATGAAGAAAGGAGGGATAAGGTTTACGATAAACGGACATTCA  
TACTTTAATTTGGTTCTGATATCGAACGTAGGAGGAGCAGGAGACGTCCACGCAG  
TGTCGATCAAAGGCTCAAAAACAGGGTCGTGGCAAGCAATGTCTAGGAACTGGG  
GACAGAACTGGCAGAGCAACTCTTATCTCAACGACCAAAGCCTCTCGTTCCAGGT  
TACTACCAGCGATGGTCGCACCGTCGTTAGCAATGACGTGGCTCCTTCTAACTGG  
CAGTTCGGACAAACCTTCCAAGGCGGTCAATTCTGAGTCCATCCTCCTCTCTCTCT  
CTCTCTCTGTTTTGGGTGATGACGTGGCTGCGTATTGCTGAGGTGGCTCGTAAACA  
CCCGCCATTAGCTTAGCCTTTTTCCTTTTTTTTTTCTTCTTTTTTCTTATTTACGAAT  
TAATGCTTCAAAGTTCAATGATTGCCTACAAAGAACAAGGTTTTTTTTTTTTTTGTG  
GTTTATTGAATTTAGCCTTTTGGCATGTACTTTTTGGTTTTTATTTTTGTAATCCAA  
AATCGTTTAGCCAGTGGCATAATAAGAATTATAAAATCGAATTTACATAACC