

IDENTIFICATION

Species: *Eutrema salsugineum*

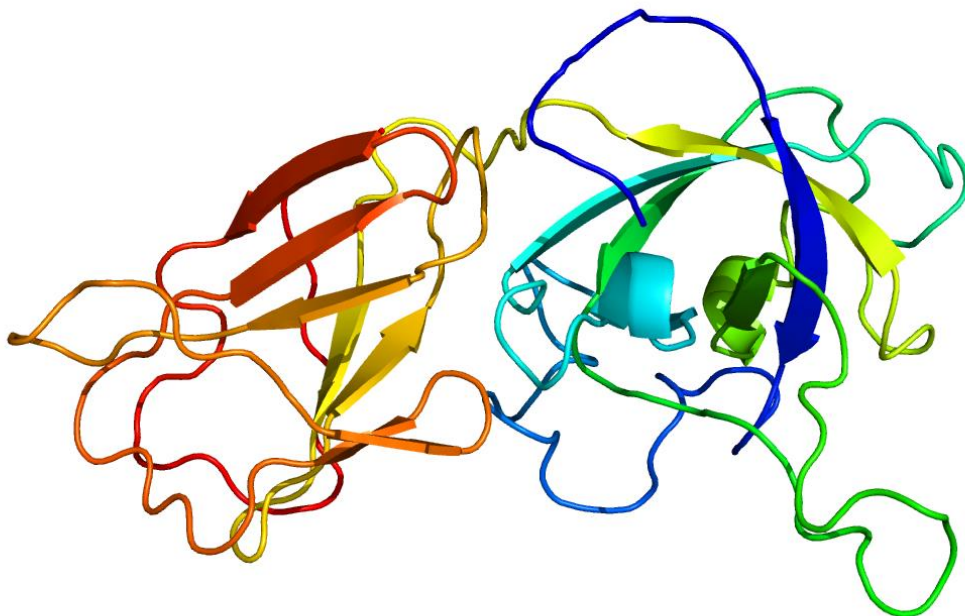
Locus: Thhalv10010989m

Gene Model: Thhalv10010989m

Description: EsEXPA-28

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>

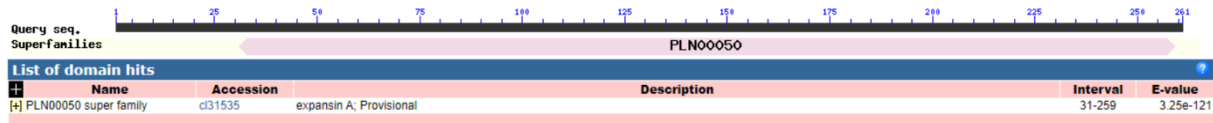
EXTERNAL RESOURCES

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GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>EsEXPA-28

MAINPSVLLTIFTLFLLLSLTNAGIPGVYSGSSWQTAHATFYGGDDASGTMGGACGY
GNLYSQGYGTNTAALSTALFNGLTCGACFEIKCVNDPKWCHSGSPSVFVTATNFCP
PNLAQPSDNGGWCNPPRAHFDLAMPVFLKIAQYRAGIVPISYRRVACRKSGGIRFTIN
GHRYFNLVLITNVAGAGDIVRASVKGSKSGSWMSLTRNWGQNWQSNQNDVLVGQSL
FRVTASDRRTSTSWNIVPSNWQFGQTFVGKNFR*

CDS (coding sequence)

>EsEXPA-28

ATGGCAATTAATCCATCGGTTCTCTTAACCATATCACTCTCTTTCTCCTCTTGAGC
CTCACCAACGCCGGAATCCCCGGCGTCTACTCCGGTAGCTCTTGCAAACCGCTC
ACGCCACTTTCTACGGTGGAGATGACGCTTCCGGAACCATGGGCGGTGCGTGCGG
TTACGGAAACCTGTACAGCCAAGGGTATGGCACAAACACAGCGGCGCTAAGCAC
GGCACTGTTCAACAGTGGCTTAACCTGCGGGGCATGCTTTGAAATCAAATGTGTC
AATGATCCTAAATGGTGTCACTCAGGCAGCCCTTCCGTCTTCGTGACCGCAACCA
ACTTTTGTCCTCCAACTTAGCTCAGCCTAGCGACAACGGTGGCTGGTGCAACCC
ACCACGCGCTCACTTCGACTTAGCCATGCCCGTTTTCTCAAGATCGCTCAATATC
GCGCCGGCATTGTCCCATCTCTTACCGCAGGGTGGCATGTAGGAAGAGTGGAGG
GATAAGGTTACGATCAACGGTCACCGTACTTCAACTTGGTGCTGATCACGAAC
GTGGCGGGAGCAGGAGACATCGTGAGAGCGAGCGTGAAAGGGTCAAAGAGTGG
TTCTTGATGAGTTTGACTAGGAACTGGGGACAGAACTGGCAGTCTAATGATGTT
CTTGTTGGTCAGTCACTTTCCCTTCCGTGTCACAGCCAGTGACCGTAGAACCTCTAC
TTCATGGAACATCGTACCTTCTAACTGGCAGTTTGGACAAACCTTTGTTCGGAAAG
AATTCAGG

Nucleotide

>EsEXPA-28

ATGGCAATTAATCCATCGGTTCTCTTAACCATATCACTCTCTTTCTCCTCTTGAGC
CTCACCAACGCCGGAATCCCCGGCGTCTACTCCGGTAGCTCTTGCAAACCGCTC
ACGCCACTTTCTACGGTGGAGATGACGCTTCCGGAACCATGGGTCAGTCCACTCT
CTTCAGTCTTCACACACACACATTTCCAAAAACCATATATAAAAACAAAAACAA
AAAACAGAGCACTCTGTTTTCTTTTGTGTTGGTCGAAACAGAGCACTCTGTTTCAT
TTTCTCATTTTTGTTTTGATTAAGTGTGTCAGGCGGTGCGTGCGGTTACGGAAAC
CTGTACAGCCAAGGGTATGGCACAAACACAGCGGCGCTAAGCACGGCACTGTTT

AACAGTGGCTTAACCTGCGGGGCATGCTTTGAAATCAAATGTGTCAATGATCCTA
AATGGTGTCACTCAGGCAGCCCTTCCGTCTTCGTGACCGCAACCAACTTTTGCCT
CCAAACTTAGCTCAGCCTAGCGACAACGGTGGCTGGTGCAACCCACCACGCGCTC
ACTTCGACTTAGCCATGCCCCGTTTTCTCAAGATCGCTCAATATCGCGCCGGCATT
GTCCCATCTCTTACCGCAGGTATCTATATATACTTCACATCTACGCTTAAAAGTG
TTATTTGGATTATTCGAGTGATTGAAATTGATAAGCTTGAGAAATTTTATAGGGTG
GCATGTAGGAAGAGTGGAGGGATAAGGTTACGATCAACGGTCACCGTTACTTC
AACTTGGTGCTGATCACGAACGTGGCGGGAGCAGGAGACATCGTGAGAGCGAGC
GTGAAAGGGTCAAAGAGTGGTTCTTGGATGAGTTTGACTAGGAACTGGGGACAG
AACTGGCAGTCTAATGATGTTCTTGTGGTCAGTCACTTTCCTTCCGTGTCACAGC
CAGTGACCGTAGAACCTCTACTTCATGGAACATCGTACCTTCTAACTGGCAGTTT
GGACAAACCTTTGTCGGAAAGAATTCAGG