

IDENTIFICATION

Species: *Lactuca sativa*

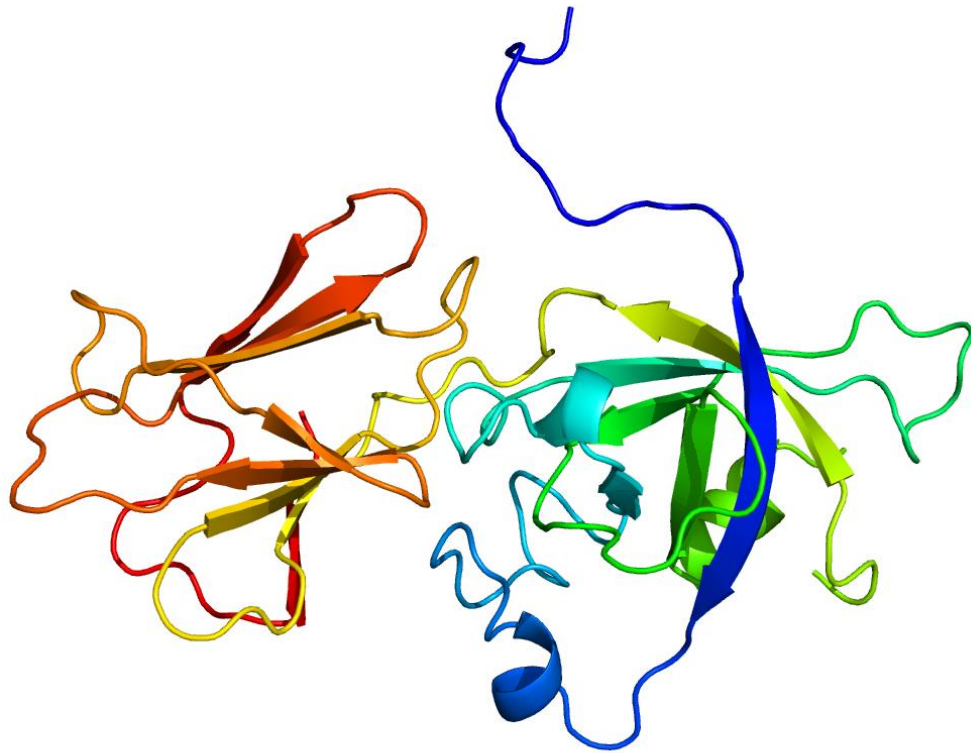
Locus: Lsat_1_v5_gn_2_71700

Gene Model: Lsat_1_v5_gn_2_71700.1

Description: LsEXPA-07

Family: Alpha Expansin

3D structure:



GENOME DATABASES

Phytozome: https://phytozome-next.jgi.doe.gov/info/Lsativa_V8

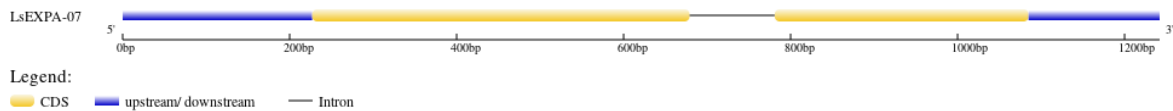
KEGG: <https://www.genome.jp/entry/T05352>

EXTERNAL RESOURCES

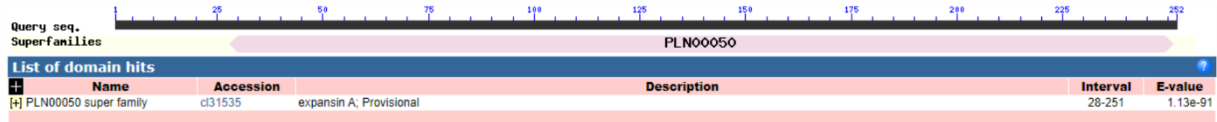
<https://lgr.genomecenter.ucdavis.edu/>

<https://www.lettucegdb.com/>

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>LsEXPA-07

MVLSFTLLFLVFAHYPYSTSSYPSSTEWRSARATYYAPADPRDAIGGACGYGDVEKA
GYGKATAGLSTVLFQKGQICGACFEVRCVEDLQWCIPGTSIIVTATNFCAPNYGFPAD
GGGKCNPPNPHFVLPPIEFKIAIWKASNMPPIQYRRIKCRKEGGIRFTIDGAGIFLSVMIS
NVAGAGDLAAVKIKGSRTGWLPMNRNWGQNWHINADMKNQPLSF EVTSSDGLT VT
SYNVAPKEWNFGQSFEGKQF*

CDS (coding sequence)

>LsEXPA-07

ATGGTGTTCATTCACACTGCTTTTTCTAGTTTTTGGCTCACTATCCCTACTCCACC
TCCTCCTACCCATCTTCTACAGAGTGGAGATCTGCAAGGGCAACGTA CTATGCAC
CCGCTGATCCGCGGGACGCCATCGGCGGCGCGTGTGGTTACGGCGACGTGGAGA
AAGCAGGGTATGGGAAGGCGACGGCGGGGCTCAGTACTGTGTTGTTCCAGAAAG
GACAGATCTGTGGTGCTTGTGTTGAGGTCAGGTGTGTAGAGGATCTCCAATGGTG
TATTCCGGGACTTCTATTATCGTGACAGCGACTAATTTCTGTGCTCCGAATTACG
GGTTTCCGGCAGACGGCGGTGGCAAGTGTAACCCTCCGAATCCCCATTTGTTTT
ACCGATTGAGATTTTTGAGAAGATTGCGATTTGGAAAGCTTCTAACATGCCAATT
CAGTATCGCAGGATCAAGTGCAGAAAGGAAGGAGGAATTAGGTTTACCATTGAT
GGAGCTGGAATCTTCTTATCGGTAATGATCAGCAATGTTGCCGGTGCCGGAGACT
TAGCTGCGGTGAAGATTAAGGTTACGAACCGGGTGGCTTCCGATGAACAGAA
ATTGGGGACAAAATTGGCATATAAATGCAGACATGAAAAATCAACCTCTTCTTT
CGAGGTCACTAGTAGTGATGGGTTAACTGTTACTTCTTACAATGTTGCTCCAAA
GAATGGAATTTTGGTCAGAGTTTTGAGGGCAAACAGTTCTAA

Nucleotide

>LsEXPA-07

ATCTAATCTATCAATGGTCCATGTTTTTATGCAGGAATGTTGTCGACCCAAGAGA
CGTGTACTTTTCCTTTTGCAAGTATCTCATGTTTATCGTGGACATGGCGGAATAAA
GCTGCCCACTAAACCTGCAAAGCACTCTACTTCCAACAATGCGACTACATACAAC
ACGCCATATCTTCCCCTTTTGGTCTTCTCTTCCCTCCACAGTTTTTCGATCTCTCTA
ACAATGGTGTTCATTCACACTGCTTTTTCTAGTTTTTGGCTCACTATCCCTACTC
CACCTCCTCCTACCCATCTTCTACAGAGTGGAGATCTGCAAGGGCAACGTA CTAT

GCACCCGCTGATCCGCGGGACGCCATCGGCGGGCGCGTGTGGTTACGGCGACGTG
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AAAGGACAGATCTGTGGTGCTTGTGTTTGGAGGTCAGGTGTGTAGAGGATCTCCAAT
GGTGTATTCCGGGGACTTCTATTATCGTGACAGCGACTAATTTCTGTGCTCCGAAT
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TTTTACCGATTGAGATTTTTGAGAAGATTGCGATTTGGAAAGCTTCTAACATGCCA
ATTCAGTATCGCAGGTAGTGTTC AATTGTTCACTCTGATACTTCCTTCCTTTCC
CCTCAAAGTTTGAATAACGAAAAGGTGAAATTAGGGTTTGATGCATATCATTGTT
GCAGGATCAAGTGCAGAAAGGAAGGAGGAATTAGGTTTACCATTGATGGAGCTG
GAATCTTCTTATCGGTAATGATCAGCAATGTTGCCGGTGCCGGAGACTTAGCTGC
GGTGAAGATTAAAGGTTACGAACCGGGTGGCTTCCGATGAACAGAAATTGGGG
ACAAAATTGGCATATAAATGCAGACATGAAAAATCAACCTCTTCTTTCGAGGTC
ACTAGTAGTGATGGGTTAACTGTTACTTCTTACAATGTTGCTCCAAAAGAATGGA
ATTTTGGTCAGAGTTTTGAGGGCAAACAGTTCTAATCTTGAATCTTGAATCTTGAA
TCTTGAATAGTTTTTTAATGGGACATTCCCTTTTATAGAGCCTGGTTTTTLAGTTGTA
TAAAATAATCTTTAGATTTAAGAAATATTATTATTGACAAGATCAGTTCTAAAAA
TACAGAATTGAAGGGAGATCTAAA