

## IDENTIFICATION

**Species:** *Lactuca sativa*

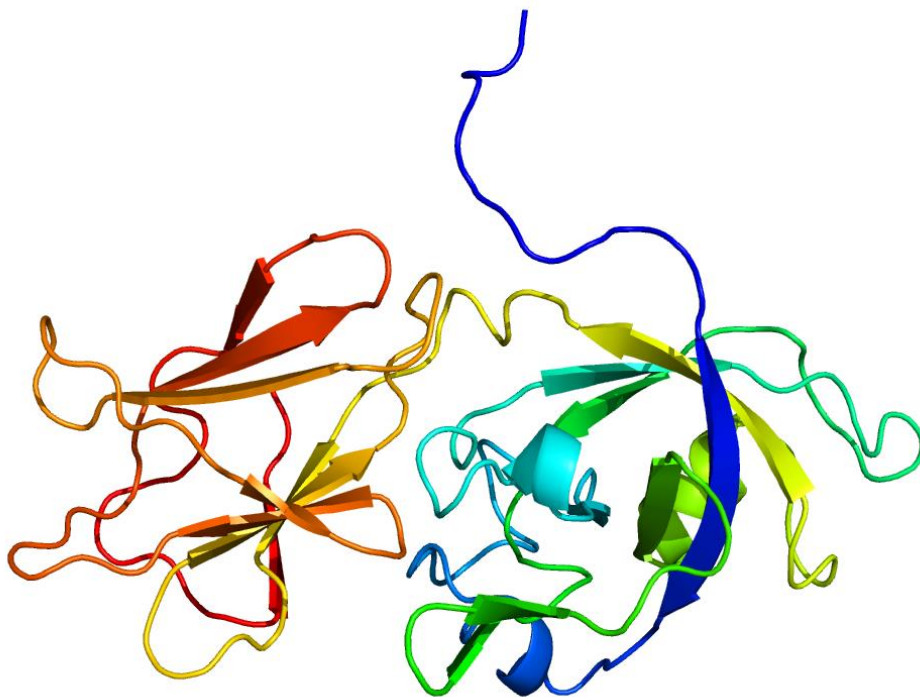
**Locus:** Lsat\_1\_v5\_gn\_2\_71700

**Gene Model:** Lsat\_1\_v5\_gn\_2\_71700.2

**Description:** LsEXPA-06

**Family:** Alpha Expansin

**3D structure:**



## GENOME DATABASES

Phytozome: [https://phytozome-next.jgi.doe.gov/info/Lsativa\\_V8](https://phytozome-next.jgi.doe.gov/info/Lsativa_V8)

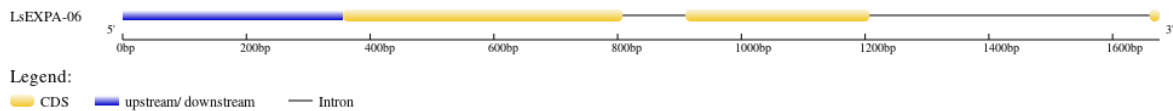
KEGG: <https://www.genome.jp/entry/T05352>

## EXTERNAL RESOURCES

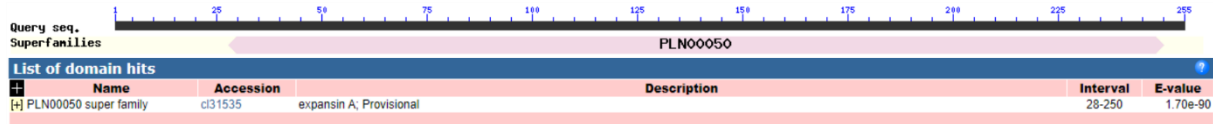
<https://lgr.genomecenter.ucdavis.edu/>

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

## GENE STRUCTURE



## DOMAIN ARCHITECTURE



## SEQUENCES

### Peptide

>LsEXPA-06

MVLSFTLLFLVFAHYPYSTSSYPSSTEWRSARATYYAPADPRDAIGGACGYGDVEKA  
GYGKATAGLSTVLFQKGQICGACFEVRCVEDLQWCIPGTSIIVTATNFCAPNYGFPAD  
GGGKCNPPNPHFVLPPIEFKIAIWKASNMPIQYRRIKCRKEGGIRFTIDGAGIFLSVMIS  
NVAGAGDLAAVKIKGSRTGWLPMNRNWGQNWHINADMKNQPLSF EVTSSDGLT VT  
SYNVAPKEWNFGQSFEGKHRKRL\*

### CDS (coding sequence)

>LsEXPA-06

ATGGTGTTCATTACACTGCTTTTTCTAGTTTTTGCTCACTATCCCTACTCCACC  
TCCTCCTACCCATCTTCTACAGAGTGGAGATCTGCAAGGGCAACGTA CTATGCAC  
CCGCTGATCCGCGGGACGCCATCGGCGGCGCGTGTGGTTACGGCGACGTGGAGA  
AAGCAGGGTATGGGAAGGCGACGGCGGGGCTCAGTACTGTGTTGTTCCAGAAAG  
GACAGATCTGTGGTGCTTGTGTTGAGGTCAGGTGTGTAGAGGATCTCCAATGGTG  
TATCCGGGACTTCTATTATCGTGACAGCGACTAATTTCTGTGCTCCGAATTACG  
GGTTTCCGGCAGACGGCGGTGGCAAGTGTAACCCTCCGAATCCCCATTTTGT  
ACCGATTGAGATTTTGGAGAAGATTGCGATTTGGAAAGCTTCTAACATGCCAATT  
CAGTATCGCAGGATCAAGTGCAGAAAGGAAGGAGGAATTAGGTTTACCATTGAT  
GGAGCTGGAATCTTCTTATCGGTAATGATCAGCAATGTTGCCGGTGCCGGAGACT  
TAGCTGCGGTGAAGATTAAGGTTACGAACCGGGTGGCTTCCGATGAACAGAA  
ATTGGGGACAAAATTGGCATATAAATGCAGACATGAAAAATCAACCTCTTCTTT  
CGAGGTCACTAGTAGTGATGGGTTAACTGTTACTTCTTACAATGTTGCTCCAAA  
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### Nucleotide

>LsEXPA-06

CAATTACTAACTTTGAGTGATCCTTAATCAAATATATATTTTGTCTCCTAACAA  
CTATTTCTTCTACCAACAAAATCCACCATCTATAATGTATCCATCAAAGTAAATA  
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TGCGACTACATAACAACGCCATATCTTCCCCTTTTGGTCTTTCTCTTCCCTCACA

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ATACTTCCTTCCCTTTCCCTCAAAGTTTGAATAACGAAAAGGTGAAATTAGGGTTT  
GATGCATATCATTGTTGCAGGATCAAGTGCAGAAAGGAAGGAGGAATTAGGTTT  
ACCATTGATGGAGCTGGAATCTTCTTATCGGTAATGATCAGCAATGTTGCCGGTG  
CCGGAGACTTAGCTGCGGTGAAGATTAAGGTTACACGAACCGGGTGGCTTCCGAT  
GAACAGAAATTGGGGACAAAATTGGCATATAAATGCAGACATGAAAAATCAACC  
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ATTATAAAATTTTATTTTCATTTTTTCTTATTATAGCAAAAAACAAGAAAACG  
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