

## IDENTIFICATION

**Species:** *Lactuca sativa*

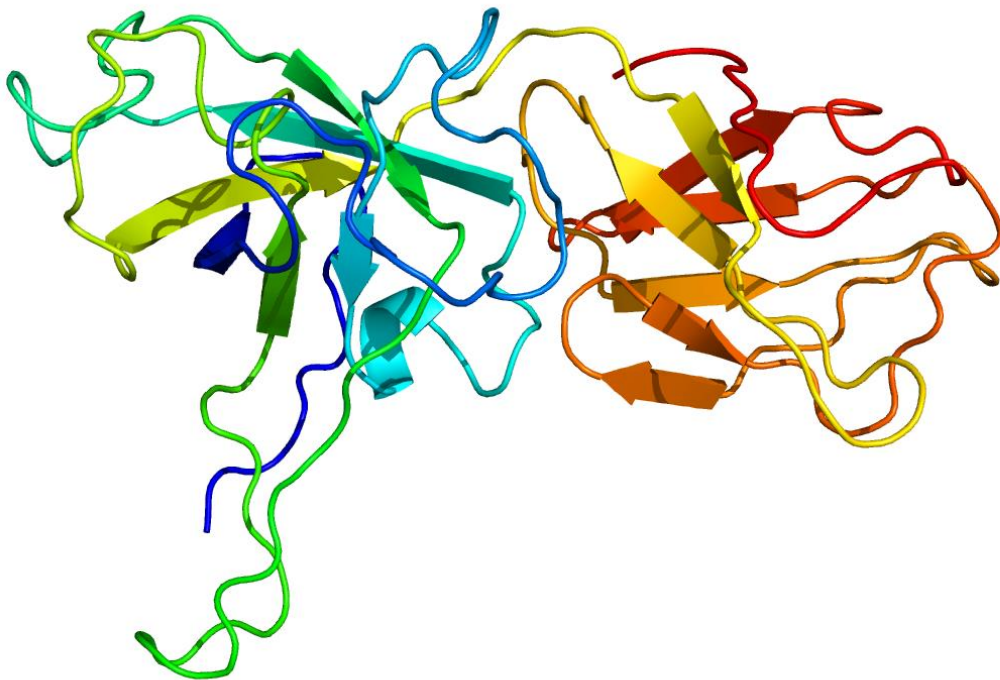
**Locus:** Lsat\_1\_v5\_gn\_9\_23601

**Gene Model:** Lsat\_1\_v5\_gn\_9\_23601.1

**Description:** LsEXPA-30

**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)

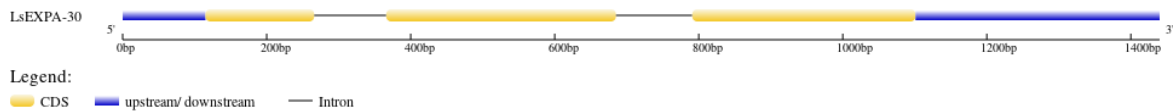
KEGG: <https://www.genome.jp/entry/T05352>

## EXTERNAL RESOURCES

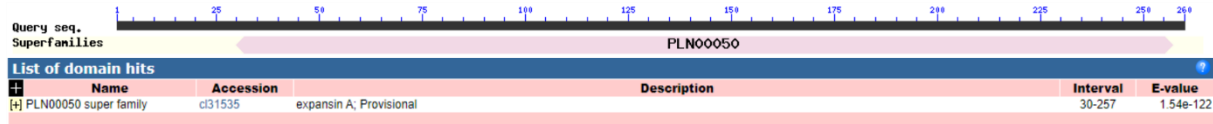
<https://lgr.genomecenter.ucdavis.edu/>

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

## GENE STRUCTURE



## DOMAIN ARCHITECTURE



## SEQUENCES

### Peptide

>LsEXPA-30

MGLAGGILFIIVTISVFSATHARIPGNYAGGSWQGAHATFYGGSDASGTMGGACGYG  
NLYSQGYGVNTAALSTALFNKGFSCGACFEIKCSQDPRWCHPGSPSIFITATNFCPPNF  
ALPNDNGGWCNPPRTHFDLAMPNFLKIAEYRAGIVPVS YRRVPCRKAGGIRFTINGH  
RYFNLILISNVAGAGDVQKVWVKGTKTNWMSMSRNWQNWQSNVAVLVGQALSFR  
VTGSDRRTSTSWNIAPASWQFGQTFTGKNFRV\*

### CDS (coding sequence)

>LsEXPA-30

ATGGGTCTCGCCGGCGGCATTCTCTTCATCATCGTCACCATCTCGGTTTTCTCAGC  
GACCCACGCCAGAATCCCTGGAAACTACGCCGGCGGCTCGTGGCAAGGTGCTCAT  
GCTACCTTCTATGGTGGCAGTGACGCCTCTGGCACTATGGGAGGTGCTTGTGGTT  
ATGGAAACCTGTACAGCCAAGGCTACGGCGTTAACACGGCGGGCGCTGAGCACGG  
CGTTGTTCAACAAAGGGTTTAGCTGCGGTGCGTGCTTCGAAATCAAGTGCAGCCA  
AGATCCGAGGTGGTGCCATCCCGGCAGCCCCCTCCATCTTCATCACCGCCACTAAC  
TTCTGCCCTCCGAACTTCGCTCTCCCTAACGACAATGGTGGATGGTGTAAACCCTCC  
TCGTACCCACTTCGACCTCGCCATGCCATGTTCCCTCAAGATCGCCGAATACCGC  
GCCGGAATCGTCCCCGTTTCTTATCGCCGAGTGCCATGCCGAAAGCTGGTGGGA  
TCAGGTTACCATCAACGGCCACCGTACTTCAACTTGATTTTAATCAGCAACGTC  
GCGGGTGCAGGGGATGTCCAGAAGGTCTGGGTCAAAGGGACGAAAATAATTGG  
ATGAGCATGAGTCGTAAC TGGGGTCAA AATTGGCAGTCAAACGCCGTCCTCGTCG  
GTCAAGCACTCTCCTTCAGGGTCACCGGGAGTGACCGGCGAACCTCCACCTCATG  
GAACATCGCTCCGGCGAGTTGGCAGTTTGGTCAAACCTTCACCGGAAAGAATTTC  
CGAGTGTA

### Nucleotide

>LsEXPA-30

TAAATACCAGCATAACTACCTCCCATTCTTCACATTCCCACCATTAACCTCCCTC  
ACCCTCTCTCTCCGAACCCA ACTGAAGAGCTCAGATCTGCTCTCTTGTGCCGGACT  
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AGCGACCCACGCCAGAATCCCTGGAAACTACGCCGGCGGCTCGTGGCAAGGTGC  
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TTCTCTCACATTTATACTGTTTGTATGCACTTAGTCTAGAAGCTCCTAGATTCCGCC  
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CAAAGGGTTTAGCTGCGGTGCGTGCTTCGAAATCAAGTGCAGCCAAGATCCGAG  
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CGAACTTCGCTCTCCCTAACGACAATGGTGGATGGTGTAACCCTCCTCGTACCCA  
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GTCCCCGTTTCTTATCGCCGGTAAATTTACACATATCCATTCTGTCTTCTAAAA  
CACCTGCATTGCGTGATATTTCTGAGGAAATGACGAAACTGACCTTGGTGTCTGT  
GATGTATTACTACAGAGTGCCATGCCGGAAAGCTGGTGGGATCAGGTTACCATC  
AACGGCCACCGTTACTTCAACTTGATTTTAATCAGCAACGTCGCGGGTGCAGGGG  
ATGTCCAGAAGGTCTGGGTCAAAGGGACGAAAATAATTGGATGAGCATGAGTC  
GTAAC TGGGGTCAA AATTGGCAGTCAAACGCCGTCCTCGTCGGTCAAGCACTCTC  
CTTCAGGGTCACCGGGAGTGACCGGCCGAACCTCCACCTCATGGAACATCGCTCCG  
GCGAGTTGGCAGTTTGGTCAAACCTTACC GGAAAGAATTTCCGAGTGTA AATC  
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