

## IDENTIFICATION

**Species:** *Lactuca sativa*

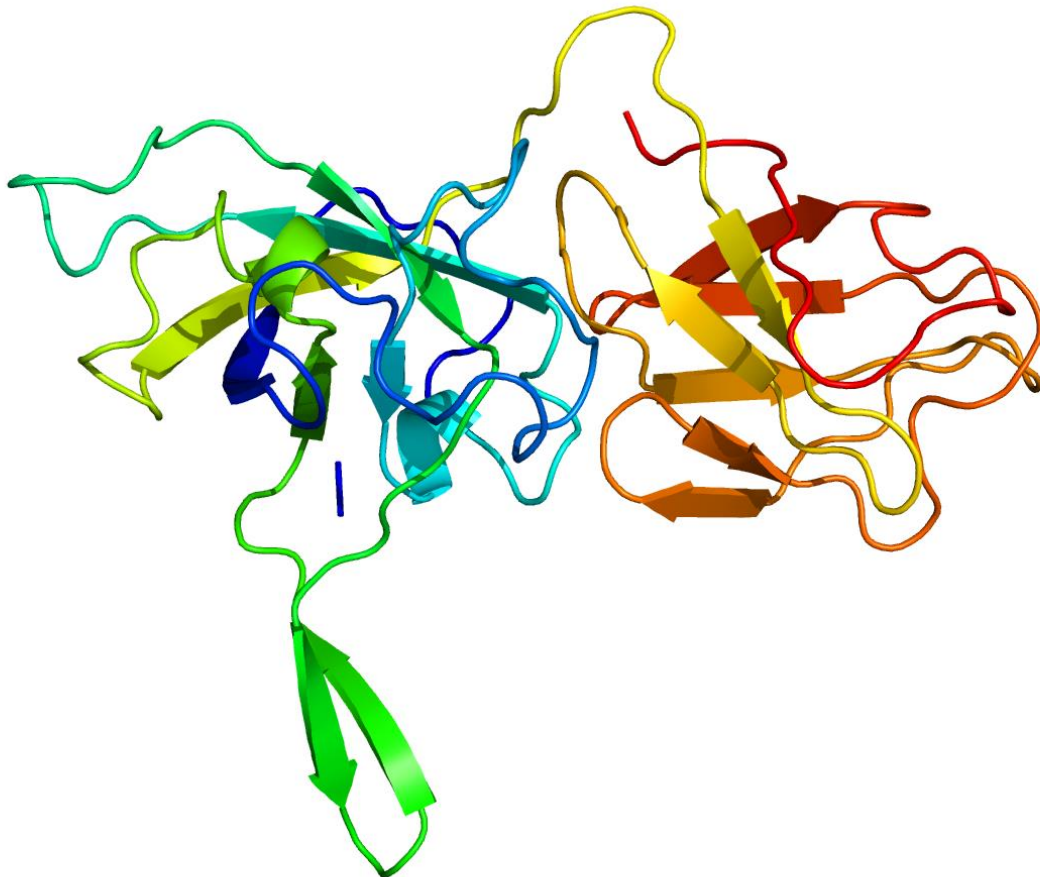
**Locus:** Lsat\_1\_v5\_gn\_9\_37760

**Gene Model:** Lsat\_1\_v5\_gn\_9\_37760.3

**Description:** LsEXPA-33

**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)

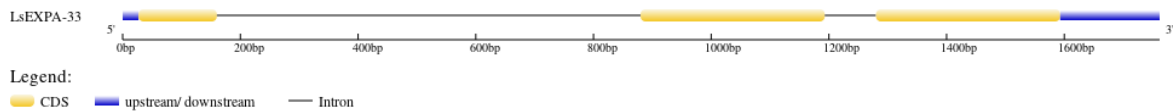
KEGG: <https://www.genome.jp/entry/T05352>

## EXTERNAL RESOURCES

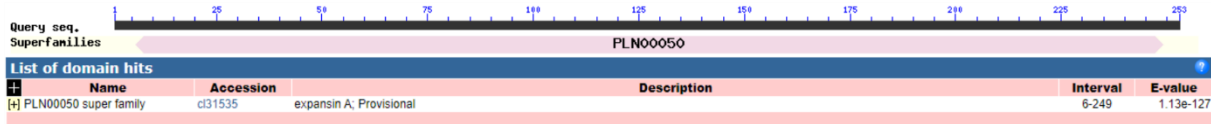
<https://lgr.genomecenter.ucdavis.edu/>

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

## GENE STRUCTURE



## DOMAIN ARCHITECTURE



## SEQUENCES

### Peptide

>LsEXPA-33

MQIMAILFLLTIMLLSLHTIHANKGGWQKAHATFYGGEDASGTMGGACGYGNLYSD  
GYGTNTAALSTTLFNGQSCGSCYQLRCIDDPKWCLHGIITITATNYCPPNYALANDN  
GGWCNPLRHFDSLQPAFLKIAQYRAGIVPVAYRRVPCVKRGGMRFTINGHSYFNLV  
LITNVGGAGDIHGVSIGSKTGWQRMTRNWGQNWQSNYSYLDGQRLSFRVTAGDGR  
TVTSYNVVPAGWQFGQTFQGGQYENF\*

### CDS (coding sequence)

>LsEXPA-33

ATGCAAATCATGGCTATTCTCTTCCTTTTAACCATCATGCTCTTGTCTCTCCACACC  
ATCCATGCCAATAAAGGGGGTTGGCAAAGGCTCATGCAACTTTCTACGGTGGTG  
AGGATGCTTCTGGTACCATGGGTGGTGCATGCGGGTACGGCAATCTTTACAGCGA  
CGGCTACGGCACAAATACGGCGGGCGTTGAGCACCACCCTCTTCAACAACGGCCA  
GAGCTGCGGTTCTGCTACCAACTGCGGTGTATCGACGACCCAAAATGGTGTCTT  
CATGGAATCATCACCATCACCGCCACCAACTATTGCCACCAAATTACGCCCTTG  
CTAATGACAACGGCGGGTGGTGCAACCCACCGCTCCGCCACTTCGATCTGTCACA  
GCCTGCTTTCTTAAAGATCGCACAGTATCGCGCCGGAATAGTCCCTGTTGCGTAC  
AGAAGGGTACCATGTGTAAAGAGAGAGGGATGAGGTTACCATTAATGGTCAC  
TCTTACTTTAACTTGGTTTTGATAACCAACGTCGGAGGTGCAGGAGATATTCATG  
GGGTTTCAATCAAAGGGTTCGAAAACAGGGTGGCAAAGGATGACCAGAACTGGG  
GTCAA AATTGGCAAAGCAACTCGTATCTTGATGGTCAACGCCTCTCTTTTAGGGT  
AACGGCAGGTGACGGAAGAACAGTCACCAGCTATAACGTGGTGCCTGCTGGTTG  
GCAGTTTGGGCAGACGTTTCAAGGTGGCCAATATGAAAATTTTTGA

### Nucleotide

>LsEXPA-33

ACCATCTCTCCATTGTAAATTTGTTTCATGCAAATCATGGCTATTCTCTTCCTTTTA  
ACCATCATGCTCTTGTCTCTCCACACCATCCATGCCAATAAAGGGGGTTGGCAA  
AGGCTCATGCAACTTTCTACGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT  
TTCCTGTATCTGCATTTACATTGTACATATGATTTTGTGTTTATTAGAACCCTAAG  
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TCAAGATCATGAAGGACAAACTCATTGAGGTCATTGGAGACAAATTAAGATGGG

CACTTGTTATTTGATGTGTAAATTATGCTTCATGCCACATTTTTGTTTATAATTAAT  
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GAATGATTTTTTTTTCGTCTTACCTACTAGAAAAAACTTATTTTTATTAATTTAAACTT  
TAAACCATTTTATACGTACATTTTATTTCTCCATTTGTGGGGACCTTATTTCTACTC  
ATGTTACTATATGAAATATGGATATATAATCCATATTTATTGTGAGACACGGTTGT  
ATTGTTGCATGGGTGGCAACCAACCTCCTAGGGTTTAGCAATTAGCTGGCTTAGT  
GGACTCATGACTCACTTTTCTGTGACCAAATTTAATACGCAGGTGGTGCATGCGG  
GTACGGCAATCTTTACAGCGACGGCTACGGCACAAATACGGCGGCGTTGAGCAC  
CACCTCTTCAACAACGGCCAGAGCTGCGGTTCTGCTACCAACTGCGGTGTATC  
GACGACCCAAAATGGTGTCTTCATGGAATCATCACCATCACCGCCACCAACTATT  
GCCACCAAATTACGCCCTTGCTAATGACAACGGCGGGTGGTGAACCCACCGCT  
CCGCCACTTCGATCTGTACAGCCTGCTTTCTTAAAGATCGCACAGTATCGCGCCG  
GAATAGTCCCTGTTGCGTACAGAAGGTACAATAACACACCAGTAACTGTGCATAA  
CGTAAAATAATCGAGTCTTTTTTTATATATTTTTTATAATTTGATAAGCGTATTTCA  
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GTTAAAATAATTGAAAGTGGGAGAATATATGTTTCAAGTGTTG