

## IDENTIFICATION

**Species:** *Lactuca sativa*

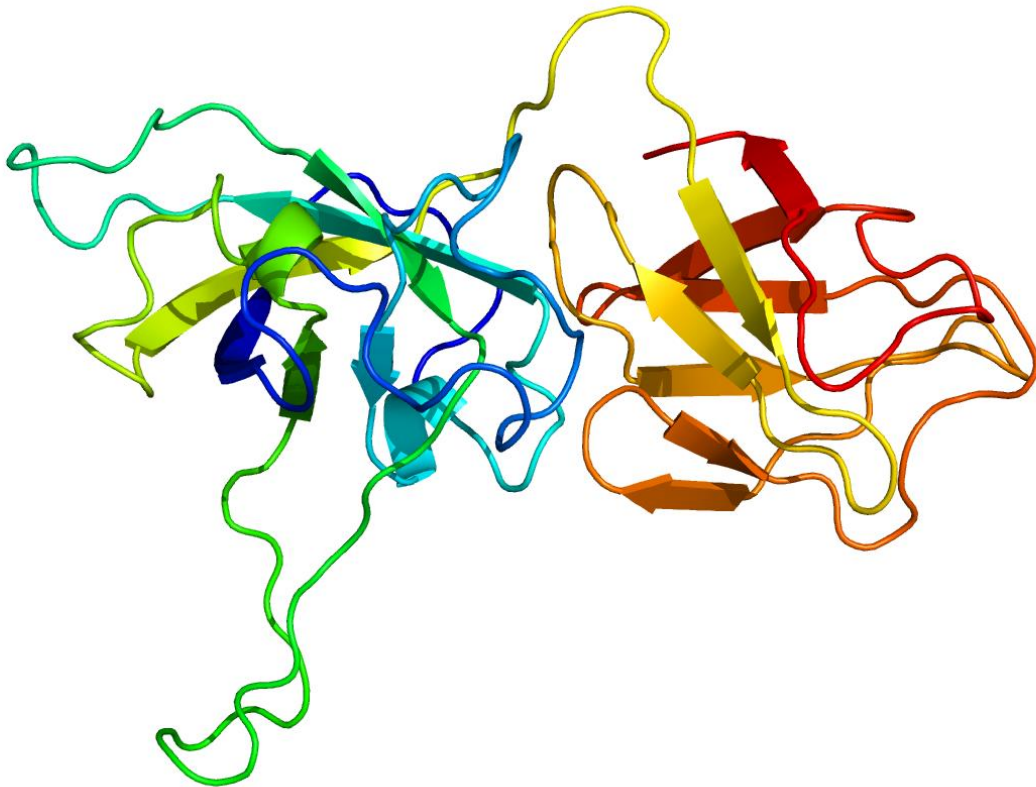
**Locus:** Lsat\_1\_v5\_gn\_4\_109320

**Gene Model:** Lsat\_1\_v5\_gn\_4\_109320.2

**Description:** LsEXPA-15

**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

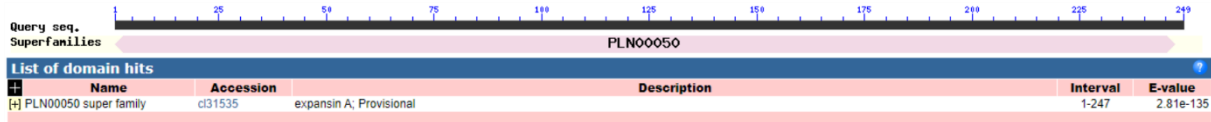
<https://lgr.genomecenter.ucdavis.edu/>

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

## GENE STRUCTURE



## DOMAIN ARCHITECTURE



## SEQUENCES

### Peptide

>LsEXPA-15

MAPIALLVVGILSFVSMVHGNNGGWIEAHATFYGGGDASGTMGGACGYGNLYSQG  
YGTNTAALSTALFNNGMSCGACFEIKCAGEKKWCRPGSIVVTATNFCPPNNALPNA  
GGWCNPPLHHFDLSQPIFQQIAQYKAGIVPVHYKRVPCVKKGGIRFTVNGHSYFNLV  
LITNVGGAGDVKAVAIKGSRTGWVPMSRNWQNWQSNSNLDGQALSFKVTTSDGH  
TVICNNAVPAGWSFGQTFGGQFT\*

### CDS (coding sequence)

>LsEXPA-15

ATGGCTCCAATTGCGCTTTTAGTGGTGGGTATTCTCTCATTCGTCTCGATGGTTCA  
TGGCAACAATGGAGTTGGATTGAAGCTCATGCTACGTTCTATGGAGGCGGCGAC  
GCTTCTGGCACAATGGGTGGAGCTTGTGGATATGGAACTTATACAGCCAAGGGT  
ATGGTACAAACACAGCAGCACTAAGTACAGCTCTATTCAACAATGGAATGAGTTG  
TGGAGCTTGTTTCGAAATCAAATGTGCAGGTGAAAAAAATGGTGTCGACCTGGA  
TCTATCGTCGTCACCGCGACTAATTTCTGTCTCCGAACAACGCCTTACCTAACAA  
CGCCGGTGGATGGTGTAACCCCTCCGCTACATCATTTCGACCTCTCTCAGCCTATTT  
TCCAACAAATCGCTCAATATAAAGCCGAATTGTTCTGTTCATTATAAGAGGGT  
ACCTTGTGTGAAGAAGGGAGGGATCAGGTTACCCGTGAATGGACATTCGTA CTTC  
AATTTGGTGTGATAACGAACGTCGGAGGAGCAGGCGACGTGAAAGCGGTTGCG  
ATCAAAGGTTCAAGAACAGGGTGGGTTCCCATGTGCGAGAAATTGGGGTCAAAT  
TGGCAGAGCAACTCGAATCTTGATGGGCAAGCTTTATCTTTCAAGGTTACCTACTA  
GCGATGGCCACACAGTCATCTGCAACAACGCCGTCCCCGCCGGGTGGTCTTTTGG  
TCAGACATTCACCGGAGGACAATCACTTAG

### Nucleotide

>LsEXPA-15

TCATCACCACCATCCCCTTCGTTCTCTTCCATGTATTTCTCGAAAGCTATAACTTTT  
ATCCATTATTTCAATTTCCCTTTTTAGTTTTAACAATCTTCCAACCTTAAAAAGTTCA  
TCTTTCATAACATTTTCTTAATTTATACAGAAAACATGGCTCCAATTGCGCTTTT  
AGTGGTGGGTATTCTCTCATTCGTCTCGATGGTTCATGGCAACAATGGAGGTTGG  
ATTGAAGCTCATGCTACGTTCTATGGAGGCGGCGACGCTTCTGGCACAATGGGTA  
AAACTCTAAAACCCTAAAATCCGACACTTATTTCCCGATTTAAGAAAATGGATCA

AACTATATGGTTTTGGGGATGTTAATTTGCAGGTGGAGCTTGTGGATATGGAAAC  
TTATACAGCCAAGGGTATGGTACAAACACAGCAGCACTAAGTACAGCTCTATTCA  
ACAATGGAATGAGTTGTGGAGCTTGTTTCGAAATCAAATGTGCAGGTGAAAAAA  
AATGGTGTTCGACCTGGATCTATCGTCGTCACCGCGACTAATTTCTGTCCTCCGAAC  
AACGCCTTACCTAACAACGCCGGTGGATGGTGTAAACCCTCCGCTACATCATTTTCG  
ACCTCTCTCAGCCTATTTTCCAACAAATCGCTCAATATAAAGCCGGAATTGTTCTT  
GTTTATTATAAGAGGTGTGTAATCGTGTAAATGTAGTCTTAATTTGTTCTCTAATTG  
CATGCAAAATCATGAAGGAATTAATAAATCGCGAATTTTGACAGGGTACCTTGTG  
TGAAGAAGGGAGGGATCAGGTTACCGTGAATGGACATTCGTACTTCAATTTGGT  
GTTGATAACGAACGTCGGAGGAGCAGGCGACGTGAAAGCGGTTGCGATCAAAGG  
TTCAAGAACAGGGTGGGTTCCCATGTTCGAGAAATTGGGGTCAAATTTGGCAGAG  
CAACTCGAATCTTGATGGGCAAGCTTTATCTTTCAAGGTTACCACTAGCGATGGC  
CACACAGTCATCTGCAACAACGCCGTCCCCGCCGGGTGGTCTTTTGGTCAGACAT  
TCACCGGAGGACAATTCACTTAGACATTTTCGTCGAACAGATGGCAAGCCTACAAA  
AGAGCTCGTATTAGAGAGGCTC