

## IDENTIFICATION

**Species:** *Lactuca sativa*

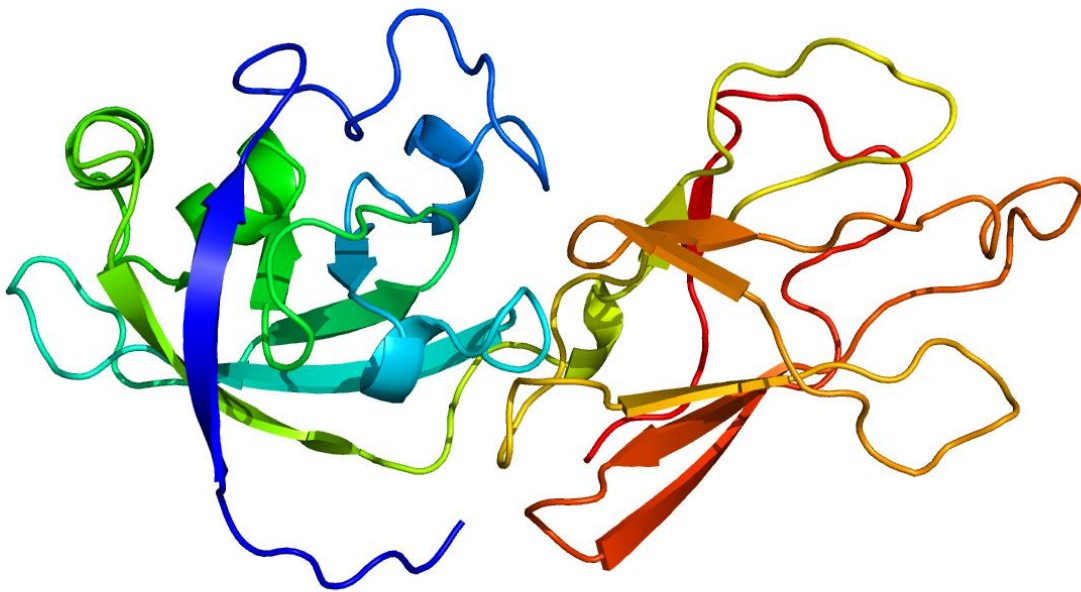
**Locus:** Lsat\_1\_v5\_gn\_6\_60620

**Gene Model:** Lsat\_1\_v5\_gn\_6\_60620.1

**Description:** LsEXLB-01

**Family:** Expansin Like Beta

**3D structure:**



## GENOME DATABASES

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

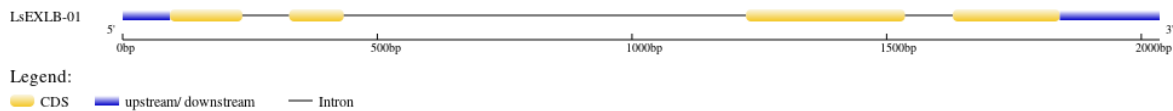
KEGG: <https://www.genome.jp/entry/T05352>

## EXTERNAL RESOURCES

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

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

## GENE STRUCTURE



## DOMAIN ARCHITECTURE

Query seq. Superfamilies

List of domain hits

Name	Accession	Description	Interval	E-value
PLN03023 super family	cl33621	Expansin-like B1; Provisional	11-256	8.08e-152

## SEQUENCES

### Peptide

>LsEXLB-01

MGLTLDNCFSLMFVIFILLPSLCFSQDYVSSRATYYGSPDCLGTPGACGYKAYGS  
TINGGEVSGVSRLFKNGTGCGACYQVRCKSPKHCSSENGVKVVVTDHGEGDNTDFILS  
TRAYNKLALPGLAEALFSYGVDVEYKRIPCQYSGYNLMFKVHEHSRFPDYLSLIPIY  
QAGVSEITAVEIWQEDCQEWVCMRRAYGAVWDMPNPPRGQPEGAINVRIQVTGSSG  
SKWVQLKNLIPSAWKVGAAYDTSIQLD\*

### CDS (coding sequence)

>LsEXLB-01

ATGGGTTTAACTAGACAACCTGTTTCTCTCTTATGTTTGTCAATTTTTATCCTTCTT  
CTGCCCTTCACTTTGCTTCAGTCAAGACTATTATGTCTCCTCTAGGGCAACTTATTA  
CGGTAGTCCTGATTGCTTAGGGACTCCAACCTGGTGCTTGTGGGTACAAAGCTTAT  
GGAAGCACCATCAATGGTGGTGAGGTGAGTGGCGTCTCTAGGCTCTTCAAGAATG  
GCACTGGTTGTGGAGCATGCTATCAGGTTTCGATGCAAGTCTCCGAAGCATTGCAG  
TGAAAACGGGGTGAAAGTGGTGGTGACAGACCATGGTGAAGGAGACAACACGG  
ACTTCATCCTGAGTACCCGTGCCTACAACAACTCGCTCTTCCAGGACTAGCAGA  
AGCATTATTCTCATATGGGGTGGTAGATGTTGAATACAAGAGGATTCCCTTGCCAG  
TATTCAGGCTATAATCTCATGTTCAAAGTTCATGAGCACAGTAGATTCCCTGACTA  
CCTTTCTCTCATCCCTATATATCAAGCAGGTGTCAGTGAAATCACAGCCGTTGAA  
ATATGGCAGGAGGATTGTCAGGAATGGGTGTGTATGAGAAGGGCATATGGAGCA  
GTGTGGGACATGCCTAACCCACCAAGGGGACAACCAGAGGGAGCTATAAACGTA  
AGGATCCAAGTGACAGGGAGTTCGGGTCAAAGTGGGTCCAGCTTAAGAATTTG  
ATTCCTAGCGCGTGGAAGGTTGGGGCTGCTTATGACACTTCTATACAGCTTGATT  
AA

### Nucleotide

>LsEXLB-01

GATCTCATCTATAAATATCGTTTCTTACACCCACTTCTAGTATCTGATCACAGAC  
TTTGTCACTTTCTGTGGGAAAAGAAAACCTCATAAGACATGGGTTTAACTAGAC  
AACTGTTTCTCTCTTATGTTTGTCAATTTTTATCCTTCTTCTGCCTTCACTTTGCTTCA  
GTCAAGACTATTATGTCTCCTCTAGGGCAACTTATTACGGTAGTCCTGATTGCTTA  
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AATGCCTAAAAGGCTTTTTAAAAAGACAAACCATGATCTGTAAAGACATGAAAG  
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ATCAAACCTTATTA AAAACTTTGAACCATTTTCCTTTGACAGTTTTAGTTGAAAACAA  
AATTTCAAACCAAGAAAACATCATATAGTATGCAAGAATTAACGACCGATTAC  
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TCAAAGTTCATGAGCACAGTAGATTCCCTGACTACCTTTCTCTCATCCCTATATAT  
CAAGCAGGTGTCAGTGAAATCACAGCCGTTGAAATATGGCAGGTAAAGACTTTAT  
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AAGTTATTTCTGATAATTGTCTTGCTTGAATAAATGATACTCGGTT