IDENTIFICATION

Species: *Lactuca sativa*

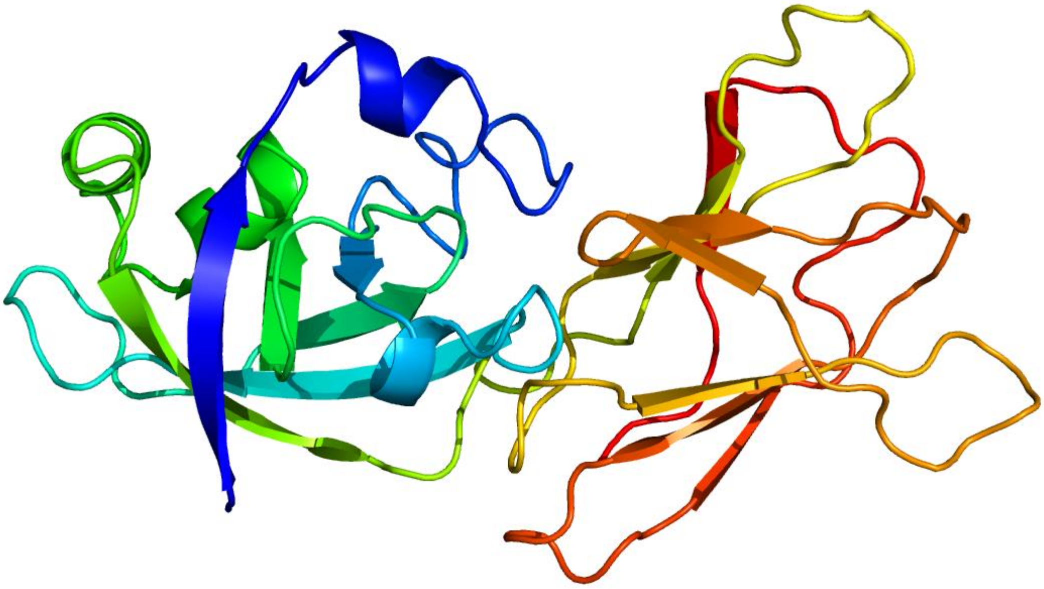
Locus: Lsat_1_v5_gn_3_47800

Gene Model: Lsat_1_v5_gn_3_47800.1

Description: LsEXLA-01

Family: Expansin Like Alpha

3D structure:



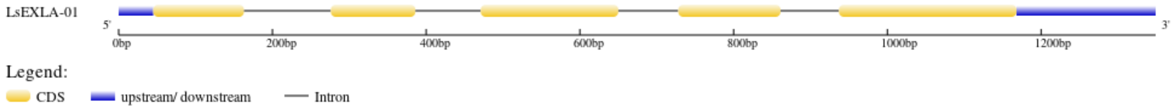
GENOME DATABASES

Phytozome: https://phytozome-next.jgi.doe.gov/info/Lsativa_V8
KEGG: https://www.genome.jp/entry/T05352

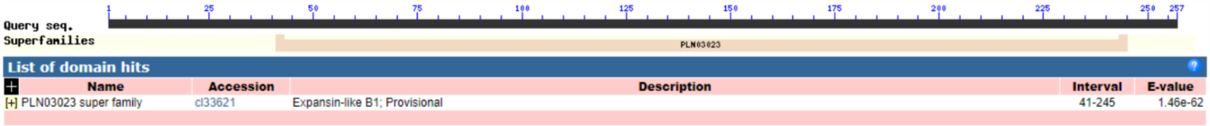
EXTERNAL RESOURCES

https://lgr.genomecenter.ucdavis.edu/
https://www.lettucegdb.com/

GENE STRUCTURE



DOMAIN ARCHITECTURE



List of domain hits

Name	Accession	Description	Interval	E-value
[+] PLN03023 super family	cl33621	Expansin-like B1; Provisional	41-245	1.46e-62

SEQUENCES

Peptide

>LsEXLA-01

MAIFLYFLFTLPVIASTNACDRCLHQTKALLFSNASALSYGACGYGSSAPSFYNGHLA
AAVPNIYKFGSGCGACFQVRCMDAKLCSKVGTQVIVTDLNSNTQTDLVLSSRALMA
MANKGMEQKLLKLGAANVEYKRVPCDYKGKNLALRVEESSRKPHYLAIKFLFQGG
QTEIVSVDVAQVGLSNWGFLSRKSGAIWETSRVPAGALQFRLAVTSGYDRKAIWAKS
VLPADWNVGVVYDSGVQIDDVAEEGCGRCD*

CDS (coding sequence)

>LsEXLA-01

ATGGCGATCTTTCTCTACTTTCTCTTTACTCTTCCCGTAATTGCCTCTACAAATGCT
TGTGATAGATGTCTGCATCAAACTAAAGCACTTCTCTTCTCCAATGCATCTGCTCT
TTCATATGGAGCATGTGGGTATGGTTCATCTGCTCCAAGCTTCTACAATGGCCATC
TTGCTGCTGCTGTTCCCAACATCTACAAATTCGGGTCGGGTTGTGGTGCTTGTTTC
CAGGTCAGATGCATGGATGCTAAGTTGTGCTCAAAAGTTGGAACTCAAGTGATAG
TGACTGATCTGAATAGCAACACACAGACAGATTTGGTGTTGAGCAGCAGAGCTTT
AATGGCTATGGCGAATAAGGGTATGGAGCAAAAGCTATTGAAACTTGGTGCTGC
CAACGTGGAATATAAAAGAGTACCTTGTGATTACAAAGGCAAAAATCTGGCATT
GAGGGTGGAAGAATCAAGCCGGAAGCCCCATTATCTTGCCATCAAGTTCTTATTT
CAAGGTGGCCAAACTGAGATCGTATCCGTTGATGTTGCCCAGGTTGGATTGTCGA
ATTGGGGTTTTTTGAGCAGAAAGTCAGGGGCAATTTGGGAAACGAGTAGAGTTCC
GGCAGGGGCGTTGCAGTTCCGGTTGGCGGTGACGTCTGGATATGATCGGAAGGC
GATTTGGGCCAAGAGTGTGCTCCCGGCCGACTGGAATGTTGGAGTTGTGTATGAT
TCCGGCGTACAAATTGACGACGTTGCTGAAGAAGGTTGTGGTCGATGTGATTAG

Nucleotide

>LsEXLA-01

TTATACTTACACAGATACACATATCACACCTACATAGTAAAAACAATGGCGATCT
TTCTCTACTTTCTCTTTACTCTTCCCGTAATTGCCTCTACAAATGCTTGTGATAGAT
GTCTGCATCAAACTAAAGCACTTCTCTTCTCCAATGCATCTGCTCTTTCATGTACC
ATTTCTCTATTCTTTTTTGTTTTGGAAAATTTTGATTTTGAGATTGACCATGTTATT
ATTTCTTGATTTAATTTACTGGGTAATAACTATTTTCGAAAAAAAATGTAGATGGA
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TGTTCCCAACATCTACAAATTCGGGTCGGGTTGTGGTGCTTGTTTCCAGGTACAAA
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TTGGAACTCAAGTGATAGTGACTGATCTGAATAGCAACACACAGACAGATTTGGT
GTTGAGCAGCAGAGCTTTAATGGCTATGGCGAATAAGGGTATGGAGCAAAAGCT
ATTGAAACTTGGTGCTGCCAACGTGGAATATAAAAGGTATATCGAATCAAAATAA
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TAGAGTACCTTGTGATTACAAAGGCAAAAATCTGGCATTGAGGGTGGAAGAATC
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GAGATCGTATCCGTTGATGTTGCCCAGGTAAATCTTTGTTGTTGTTGTTACGATAA
TCCAACGTAATTGTTGTCGAAAACTTACAGGACACGTTGTGTTTCAGGTTGGATT
GTCGAATTGGGGTTTTTTGAGCAGAAAGTCAGGGGCAATTTGGGAAACGAGTAG
AGTTCCGGCAGGGGCGTTGCAGTTCCGGTTGGCGGTGACGTCTGGATATGATCGG
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ATGATTCCGGCGTACAAATTGACGACGTTGCTGAAGAAGGTTGTGGTCGATGTGA
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