

IDENTIFICATION

Species: *Lactuca sativa*

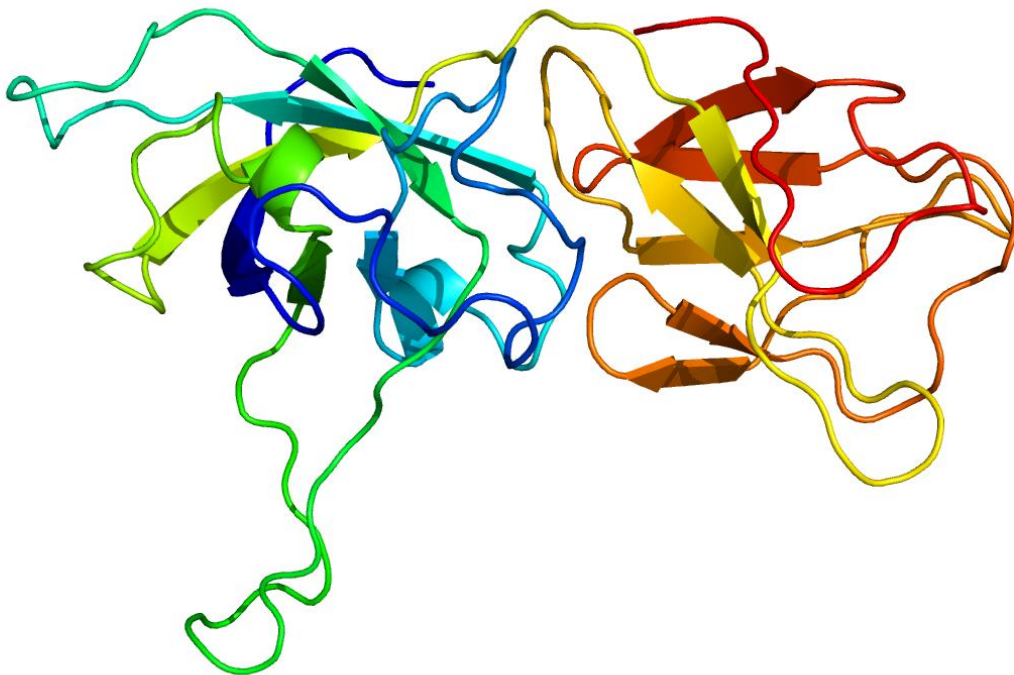
Locus: Lsat_1_v5_gn_4_109320

Gene Model: Lsat_1_v5_gn_4_109320.1

Description: LsEXPA-14

Family: Alpha Expansin

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

Query seq. Superfamilies

PLN00050

Name	Accession	Description	Interval	E-value
PLN00050 super family	cl31535	expansin A; Provisional	41-287	6.81e-137

SEQUENCES

Peptide

>LsEXPA-14

MYFSKAITFIHYFISLFSFNNLPTLKSSSFITFFLIYTENMAPIALLVVGILSFVSMVHGN
NGGWIEAHATFYGGGDASGTMGGACGYGNLYSQGYGTNTAALSTALFNNGMSCGA
CFEIKCAGEKKWCRPGSIVVTATNFCPPNNALPNNAGGWCNPLLHHFDLSQPIFQQIA
QYKAGIVPVHYKRVPCVKKGGIRFTVNGHSYFNLVLITNVGGAGDVKAVAIKGSRT
GWVPMSRNWQNWQSNLNLDGQALSFKVTTSDGHTVICNNAVPAWWSFGQFTFTGG
QFT*

CDS (coding sequence)

>LsEXPA-14

ATGTATTTCTCGAAAGCTATAACTTTTATCCATTATTTTCATTTCCCTTTTTAGTTTT
ACAATCTTCCAACCTTAAAAAGTTCATCTTTCATAACATTTTTCTTAATTTATAC
AGAAAACATGGCTCCAATTGCGCTTTTAGTGGTGGGTATTCTCTCATTTCGTCTCGA
TGGTTCATGGCAACAATGGAGGTTGGATTGAAGCTCATGCTACGTTCTATGGAGG
CGGCGACGCTTCTGGCACAATGGGTGGAGCTTGTGGATATGGAACTTATACAGC
CAAGGGTATGGTACAAACACAGCAGCACTAAGTACAGCTCTATTCAACAATGGA
ATGAGTTGTGGAGCTTGTTCGAAATCAAATGTGCAGGTGAAAAAAAAATGGTGTC
GACCTGGATCTATCGTCGTCACCGCGACTAATTTCTGTCCTCCGAACAACGCCTTA
CCTAACAACGCCGGTGGATGGTGTAAACCCTCCGCTACATCATTTCGACCTCTCTCA
GCCTATTTTCCAACAATCGCTCAATATAAAGCCGGAATTGTTCTGTTTATTATA
AGAGGGTACCTTGTGTGAAGAAGGGAGGGATCAGGTTACCGTGAATGGACATT
CGTACTTCAATTTGGTGTGATAACGAACGTCGGAGGAGCAGGCGACGTGAAAG
CGGTTGCGATCAAAGGTTCAAGAACAGGGTGGGTCCCATGTCGAGAAATTGGG
GTCAA AATTGGCAGAGCAACTCGAATCTTGATGGGCAAGCTTTATCTTTCAAGGT
TACCACTAGCGATGGCCACACAGTCATCTGCAACAACGCCGTCCCCGCCGGGTGG
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Nucleotide

>LsEXPA-14

ATGTATTTCTCGAAAGCTATAACTTTTATCCATTATTTTCATTTCCCTTTTTAGTTTT
ACAATCTTCCAACCTTAAAAAGTTCATCTTTCATAACATTTTTCTTAATTTATAC
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CTCAATATAAAGCCGGAATTGTTCCCTGTTTCATTATAAGAGGTGTGTAATCGTGTA
ATGTAGTCTTAATTTGTTCTCTAATTGCATGCAAAATCATGAAGGAATTAAAAAA
TCGCGAATTTTGACAGGGTACCTTGTGTGAAGAAGGGAGGGATCAGGTTACCCGT
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CGTATCCTG