

IDENTIFICATION

Species: *Lactuca sativa*

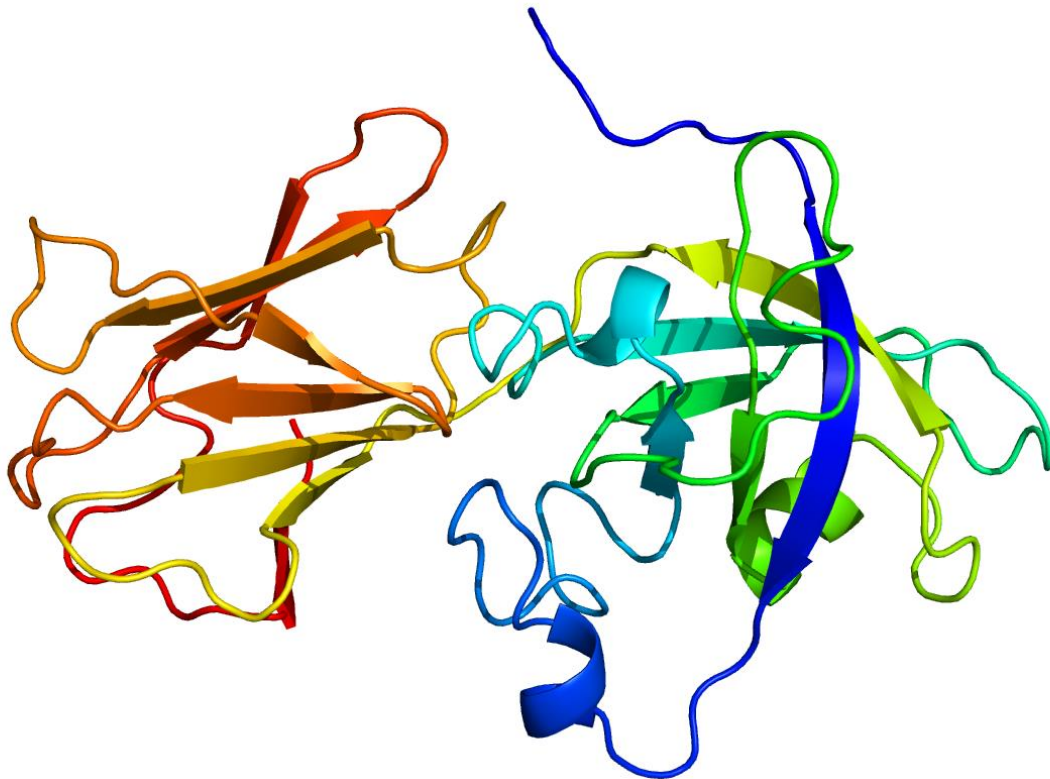
Locus: Lsat_1_v5_gn_4_11020

Gene Model: Lsat_1_v5_gn_4_11020.1

Description: LsEXPA-12

Family: Alpha Expansin

3D structure:



GENOME DATABASES

Phytozome: https://phytozome-next.jgi.doe.gov/info/Lsativa_V8

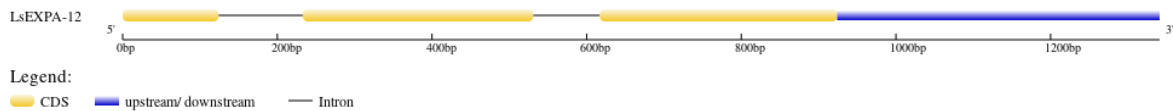
KEGG: <https://www.genome.jp/entry/T05352>

EXTERNAL RESOURCES

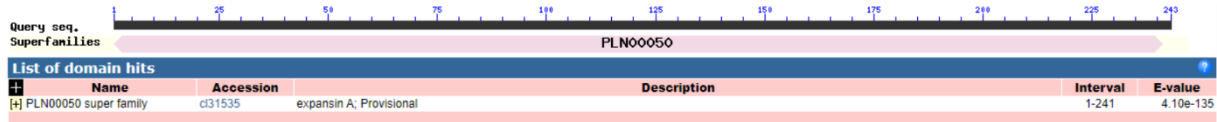
<https://lgr.genomecenter.ucdavis.edu/>

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

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>LsEXPA-12

MAILGFLVVGFLSIASSVNGDGGWVNAHATFYGGGDASGTMGGACGYGNLYSQGY
GTNTAALSTALFNGLSCGSCFEIKCVNDHQWCLPGSIKVTATNFCPPNSDGGWCNP
PNQHFDLSQPIFQHIAQYKAGIVPVAYRRIPCVRGGIRFQINGHSYFNLVLITNVGGA
GDVHVSVAIKGSKTGWQQMSRNWGQNWQSNNYLNQSLSFKVTTS DGKTVVSNV
VPAGWSFGQTFAGAQR*

CDS (coding sequence)

>LsEXPA-12

ATGGCTATTTTGGGTTTTTTAGTTGTGGGTTTTCTCTCAATTGCGTCCTCCGTCAAT
GGCGACGGTGGTTGGGTCAATGCACATGCCACCTTCTACGGCGGTGGTGATGCCT
CCGGCACAATGGGTGGTGCTTGTGGGTATGGGAATCTGTATAGTCAAGGGTATGG
TACAAACACAGCAGCGTTAAGTACTGCTTTGTTCAACAATGGTTTGAGCTGTGGC
TCGTGCTTTGAAATCAAGTGCGTGAATGACCATCAATGGTGTGTTGCCGGGGTCTA
TTAAGGTCACCGCCACCAACTTCTGCCACCGAACTCCGACGGTGGGTGGTGCAA
CCCTCCTAACCAACACTTCGATCTCTCTCAGCCTATCTTCCAACATATTGCTCAAT
ACAAAGCCGGAATCGTCCCTGTTGCTTACAGAAGGATACCATGCGTTAGAAGGG
GTGGGATTAGGTTCAAATCAATGGACATTCGTATTTCAATTTGGTGTGATTACA
AATGTGGGTGGCGCCGGTGATGTTCAATTCGGTGGCAATTAAGGGTCAAAGACTG
GGTGGCAACAAATGTCAAGAACTGGGGGCAAATTTGGCAATCCAACAATTATC
TCAACGGGCAGAGTCTGTCTTTAAGGTCACCACAAGTGATGGTAAAACCGTGGT
GTCTAACAAATGTTGTTCCCTGCTGGCTGGTCTTTCGGGCAGACCTTCGCTGGTGCC
AATTCAGATGA

Nucleotide

>LsEXPA-12

ATGGCTATTTTGGGTTTTTTAGTTGTGGGTTTTCTCTCAATTGCGTCCTCCGTCAAT
GGCGACGGTGGTTGGGTCAATGCACATGCCACCTTCTACGGCGGTGGTGATGCCT
CCGGCACAATGGGTATGTAATATGTTTTTCTTCATCTTCTAATCTTCAAATCTTTA
CTCTCCTTATCTCTATCTCTATTTCTTCGATTAATTGACTGAGATTTGGTGTAT
TTTGATAGGTGGTGCTTGTGGGTATGGGAATCTGTATAGTCAAGGGTATGGTACA
AACACAGCAGCGTTAAGTACTGCTTTGTTCAACAATGGTTTGAGCTGTGGCTCGT

GCTTTGAAATCAAGTGCGTGAATGACCATCAATGGTGTTTGCCGGGGTCTATTAA
GGTCACCGCCACCAACTTCTGCCACCGAACTCCGACGGTGGGTGGTGCAACCCT
CCTAACCAACACTTCGATCTCTCTCAGCCTATCTTCCAACATATTGCTCAATACAA
AGCCGGAATCGTCCCTGTTGCTTACAGAAGGTGAGAAATTACGAAAACACCCTCA
CACCAACTCACAAGGGTATTATGGTAACTTCACTTAACGTATTTTTCTTTGTTTT
TGTAGGATACCATGCGTTAGAAGGGGTGGGATTAGGTTCCAAATCAATGGACATT
CGTATTTCAATTTGGTGTTGATTACAAATGTGGGTGGCGCCGGTGATGTTTCATTCTG
GTGGCAATTAAGGGTCAAAGACTGGGTGGCAACAAATGTCAAGAACTGGGGG
CAAATTTGGCAATCCAACAATTATCTCAACGGGCAGAGTCTGTCTTTTAAGGTCA
CCACAAGTGATGGTAAAACCGTGGTGTCTAACAATGTTGTTCCCTGCTGGCTGGTC
TTTCGGGCAGACCTTCGCTGGTGCCCAATTCAGATGAAAAGACGTTTTTCACCCTT
GTTTGGGAAATTGGTTTTAGTGGTCACCTTGGTGTTACTATTGTATCTTTTAGCAA
CTACAATAGCTACTACTACTACTGCTATAATGACTAAGGGCTTATTTTGATAG
GGTCATTTTAGTCATTTTGTTTTTTTAGGGTGCCCATCTAGTTTTTAGTTAGGGTG
CCCTAGGGTTTTGTTTTGGGTTTTGGGGTTGGTTTTCTTTCTTTTTTTGTGTTTTAGGGC
AGTGGTGGACTATTACCACCCGCCATAGTCGTAATTGACGTTTTTGCCCTTGGTAT
TGGGCCATTAGAAATCTTTTTTATTTTTGCATTGTATTGGGTTTTGTGAGGTGTTA
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TGCATT