

IDENTIFICATION

Species: *Lactuca sativa*

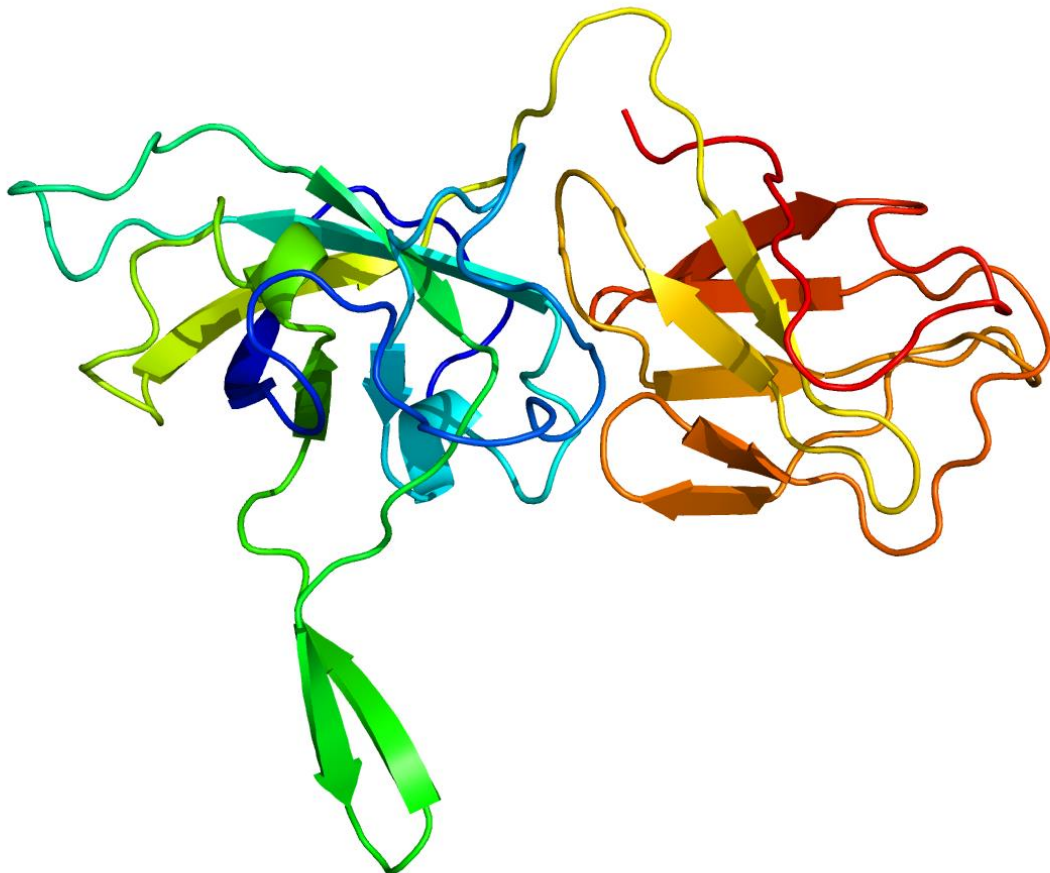
Locus: Lsat_1_v5_gn_9_37760

Gene Model: Lsat_1_v5_gn_9_37760.1

Description: LsEXPA-32

Family: Alpha Expansin

3D structure:



GENOME DATABASES

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

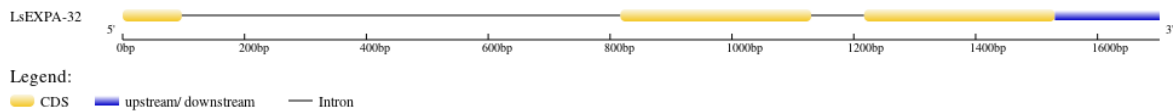
KEGG: <https://www.genome.jp/entry/T05352>

EXTERNAL RESOURCES

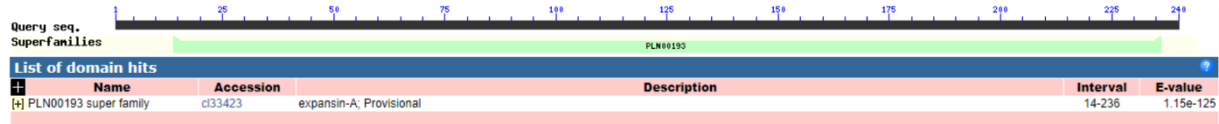
<https://lgr.genomecenter.ucdavis.edu/>

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

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>LsEXPA-32

MLLSLHTIHANKGGWQKAHATFYGGEDASGTMGGACGYGNLYSDGYGTNTAALST
TLFNNGQSCGSCYQLRCIDDPKWCLHGIITITATNYCPPNYALANDNGGWCNPPLRH
FDLSQPAFLKIAQYRAGIVPVAYRRVPCVKRGGMRFTINGHSYFNLVLTNVGGAGDI
HGVSIIKGSKTGWQRMTRNWGQNWQSNYSYLDGQRLSFRVTAGDGRTVTSYNVVPAG
WQFGQTFQGGQYENF*

CDS (coding sequence)

>LsEXPA-32

ATGCTCTTGTCTCTCCACACCATCCATGCCAATAAAGGGGGTGGCAAAGGCTC
ATGCAACTTTCTACGGTGGTGAGGATGCTTCTGGTACCATGGGTGGTGCATGCGG
GTACGGCAATCTTTACAGCGACGGCTACGGCACAATAACGGCGGCGTTGAGCAC
CACCTCTTCAACAACGGCCAGAGCTGCGGTTCTGCTACCAACTGCGGTGTATC
GACGACCCAAAATGGTGTCTTCATGGAATCATCACCATCACCGCCACCAACTATT
GCCACCAAATTACGCCCTTGCTAATGACAACGGCGGGTGGTGAACCCACCGCT
CCGCCACTTCGATCTGTACAGCCTGCTTTCTTAAAGATCGCACAGTATCGCGCCG
GAATAGTCCCTGTTGCGTACAGAAGGGTACCATGTGTAAAGAGAGGGATGA
GGTTCACCATTAATGGTCACTCTTACTTTAACTTGGTTTTGATAACCAACGTCGGA
GGTGCAGGAGATATTCATGGGGTTTCAATCAAAGGGTTCGAAAACAGGGTGGCAA
AGGATGACCAGAACTGGGGTCAAATTGGCAAAGCAACTCGTATCTTGATGGT
CAACGCCTCTTTTTAGGGTAACGGCAGGTGACGGAAGAACAGTCACCAGCTATA
ACGTGGTGCCTGCTGGTTGGCAGTTTGGGCAGACGTTTCAAGGTGGCCAATATGA
AAATTTTTGA

Nucleotide

>LsEXPA-32

ATGCTCTTGTCTCTCCACACCATCCATGCCAATAAAGGGGGTGGCAAAGGCTC
ATGCAACTTTCTACGGTGGTGAGGATGCTTCTGGTACCATGGGTACGTTTTCTGT
ATCTGCATTTACATTGTACATATGATTTTGTGTTTATTAGAACCCTAAGGGCTTTT
TTAATCGACTTTTAAATTGACAAATTAATGCTTACATACCCTTTGAATAATCAAGAT
CATGAAGGACAACTCATTGAGGTCATTGGAGACAAATTAAGATGGGCACTTGT
ATTTGATGTGTAAATTATGCTTCATGCCACATTTTTGTTTATAATTAATATATAAT

CTATGGTCCAGAGTTTCATTTTGTATTATATCGATTTATATTTTTTCATTGATTACAA
TTATAACGTCTAAGATACTTAAAATTACACAATTGTTGTGAAAGTACGAATTA
TAGATTAAGATTGCATCAAAGTATATGATCTTTCAATATGAATTTAGGATCTTCC
CTAATTTGATTGGCTTTGAAACACTTAATGGTAATGGTAAGTTCAGTTGAATGATT
TTTTTTCGTCTTACCTACTAGAAAAAACTTATTTTATTAATTTAAACTTTAAACCAT
TTTATACGTACATTTTATTTCTCCATTTGTGGGGACCTTATTTCTACTCATGTTACT
ATATGAAATATGGATATATAATCCATATTTATTGTGAGACACGGTTGTATTGTTGC
ATGGGTGGCAACCAACCTCCTAGGGTTTAGCAATTAGCTGGCTTAGTGGACTCAT
GACTCACTTTTCTGTGACCAAATTTAATACGCAGGTGGTGCATGCGGGTACGGCA
ATCTTTACAGCGACGGCTACGGCACAAATACGGCGGGCGTTGAGCACCACCCTCTT
CAACAACGGCCAGAGCTGCGGTTCCCTGCTACCAACTGCGGTGTATCGACGACCCA
AAATGGTGTCTTCATGGAATCATCACCATCACCGCCACCAACTATTGCCACCAA
ATTACGCCCTTGCTAATGACAACGGCGGGTGGTGCAACCCACCGCTCCGCCACTT
CGATCTGTCACAGCCTGCTTTCTTAAAGATCGCACAGTATCGCGCCGGAATAGTC
CCTGTTGCGTACAGAAGGTACAATAACACACCAGTAACTGTGCATAACGTAAAAT
AATCGAGTCTTTTTTTATATATTTTTATAATTTGATAAGCGTATTTTCAGGGTACCA
TGTGTAAGAGAGAGGGATGAGGTTACCATTAATGGTCACTCTTACTTTAACT
TGGTTTTGATAACCAACGTCGGAGGTGCAGGAGATATTCATGGGGTTTCAATCAA
AGGGTCGAAAACAGGGTGGCAAAGGATGACCAGAAACTGGGGTCAAATTTGGCA
AAGCAACTCGTATCTTGATGGTCAACGCCTCTCTTTTAGGGTAACGGCAGGTGAC
GGAAGAACAGTCACCAGCTATAACGTGGTGCCTGCTGGTTGGCAGTTTGGGCAGA
CGTTTCAAGGTGGCCAATATGAAAATTTTTGAACCAACAAAACCTATAATTGAAAT
CCCATTAAGATTAATAAATAAAGAGGGGATTTATGTGTTACTAGTGATGTTGAAAA
AAAGCATTGAATCTTGTTTGTATTATATATAATTGTATACTAAAAGTTGTTAAAAT
AATTGAAAGTGGGAGAATATATGTTTCAAGTGTGTGTTA