

IDENTIFICATION

Species: *Lactuca sativa*

Locus: Lsat_1_v5_gn_9_13940

Gene Model: Lsat_1_v5_gn_9_13940.1

Description: LsEXPA-29

Family: Alpha Expansin

3D structure:



GENOME DATABASES

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

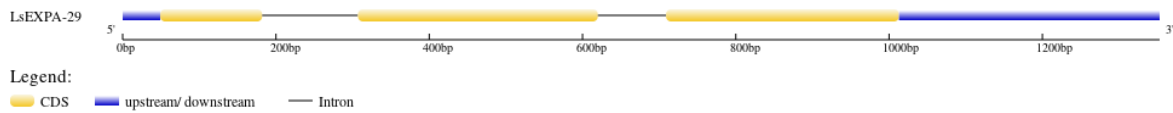
KEGG: <https://www.genome.jp/entry/T05352>

EXTERNAL RESOURCES

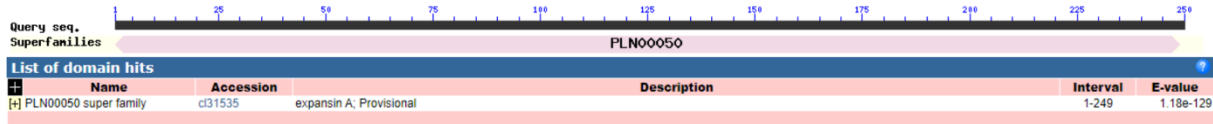
<https://lgr.genomecenter.ucdavis.edu/>

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

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>LsEXPA-29

MSFMTTSLVLLTALLHTATANYGGWQSAHATFYGGGDASGTMGGACGYGDLYS
QGYGTNTAALSTALFNGLSCGGCYEMMCVNDPQWCLPGSVIITATNFCPPNFDLPS
NNGGWCNPPLQHFDMAQPAFLQIAKYKAGIVPVSFRRVPCIKRGGIRFTMHGHSYFN
LVLISNVGGAGDVHEVSIKGSKTGWQAMSRNWGQNWQSNLYLNGQSLFRVTTSD
GKTTISYNVVGSGWQFGQTFQGDQF*

CDS (coding sequence)

>LsEXPA-29

ATGTCTTTTATGACAACCTCGCTGGTTTTCTTGCTGACCACCGCCCTCCTCCACAC
CGCCACCGCCA ACTATGGTGGCTGGCAGAGCGCCACGCTACCTTTTATGGTGGC
GGCGATGCTCCGGAACAATGGGTGGAGCATGTGGTTATGGGGATTTGTATAGCC
AAGGATACGGAACAAACACCGCAGCATTGAGCACTGCACTTTTTAACAACGGATT
AAGCTGCGGAGGGTGTACGAGATGATGTGTGTCAACGATCCGCAGTGGTGCCTC
CCTGGCTCCGTCATCATCACCGCCACCAATTTCTGCCCGCCTAACTTCGACTTGCC
CAGCAACAATGGCGGATGGTGCAACCCGCCACTCCAGCATTTTGACATGGCTCAA
CCTGCTTTCTTGCAAATAGCTAAATACAAGGCAGGCATCGTTCCTCGTATCTTTCAG
AAGGGTTCCTTGCAATAAAAGAGGAGGAATAAGGTTCACTATGCATGGCCACTC
GTACTTCAACTTGGTTTTGATCAGCAACGTCGGAGGTGCAGGGGACGTGCATGAG
GTCTCGATCAAAGGGTCGAAAACAGGGTGGCAGGCTATGTCGAGAACTGGGGT
CAAACCTGGCAAAGCAATTCGTATCTTAATGGTCAAAGTCTCTCTTTTAGAGTCA
CAACTAGTGACGGAAAGACGACGATAAGTTATAATGTGGTGGGTTCTGGTTGGCA
GTTCGGCCAGACTTTCCAAGGGGACCAATTTTAA

Nucleotide

>LsEXPA-29

TCTCTCTCTCTCTCTCTCTCTCTCTTACACACCACCATCTTTGAAACATGTCTTT
TATGACAACCTCGCTGGTTTTCTTGCTGACCACCGCCCTCCTCCACACCGCCACCG
CCA ACTATGGTGGCTGGCAGAGCGCCACGCTACCTTTTATGGTGGCGGCGATGC
TTCCGGAACAATGGGTACATTTAATTCTGAACTTCTATGAACATATTACATCATGT
TTAATTAATTTGTA ACTATTA AACATTTAGTTTGATCGAAACCATCAAGATACATA
GTTTCTTAAGCTATTACATTTATGCAGGTGGAGCATGTGGTTATGGGGATTTGTAT

AGCCAAGGATACGGAACAAACACCGCAGCATTGAGCACTGCACTTTTTAACAAC
GGATTAAGCTGCGGAGGGTGTACGAGATGATGTGTGTCAACGATCCGCAGTGGT
GCCTCCCTGGCTCCGTCATCATCACCGCCACCAATTTCTGCCCGCCTAACTTCGAC
TTGCCCAGCAACAATGGCGGATGGTGCAACCCGCCACTCCAGCATTTTGACATGG
CTCAACCTGCTTTCTTGCAAATAGCTAAATACAAGGCAGGCATCGTTCCCGTATCT
TTCAGAAGGTAAAGGATAACTTCTATCATTTACTAATAATTGTAAATTTACTTGTT
TACCCTTATATTGAACATTTGACCAAGTTTTTATCATAACAGGGTTCCTTGCATAAA
AAGAGGAGGAATAAGGTTCACTATGCATGGCCACTCGTACTTCAACTTGGTTTTG
ATCAGCAACGTCGGAGGTGCAGGGGACGTGCATGAGGTCTCGATCAAAGGGTCG
AAAACAGGGTGGCAGGCTATGTGCGAGAACTGGGGTCAAACACTGGCAAAGCAAT
TCGTATCTTAATGGTCAAAGTCTCTCTTTTAGAGTCACAACACTAGTGACGGAAAGA
CGACGATAAGTTATAATGTGGTGGGTTCTGGTTGGCAGTTCGGCCAGACTTTCCA
AGGGGACCAATTTTAATATTTCAAAGTGGAGGGGGGTTTCAATTTGATATTTTCTTT
AAGAAATGCCCACTTTTCGATTAAATTCGTTAGAAAACATGACGAATATTCATATA
AGAATAGCAGCAAAGAATATGTGTCATGTTTTTTGAAGCCTCCCGCATTTTTTTTG
GCATTTGGCTATACGGACCCCATATATTTGTATAATATAATTTTTATGCTTTATG
TTTCTATTTTTGGTTCGGTCTGTGAAGCTGAGGTGTTGAATAGCATCCGCGAAACGT
TGTATTGAACTGCCTTAATAAATGTTAGGTTGTGATATGATTGTATTTAGATTTGA
ACCTTTATCTTTATTTTATAA