

IDENTIFICATION

Species: *Lactuca sativa*

Locus: Lsat_1_v5_gn_6_78860

Gene Model: Lsat_1_v5_gn_6_78860.1

Description: LsEXPA-21

Family: Alpha Expansin

3D structure:



GENOME DATABASES

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

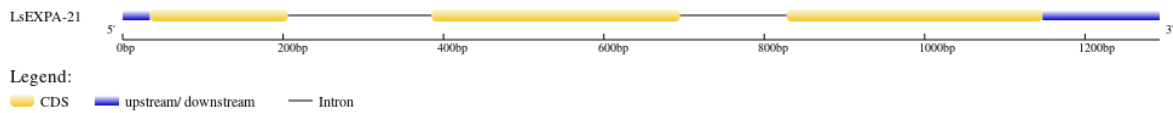
KEGG: <https://www.genome.jp/entry/T05352>

EXTERNAL RESOURCES

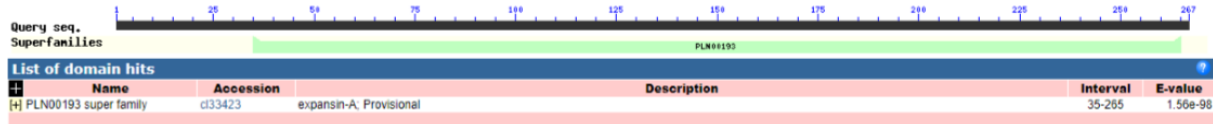
<https://lgr.genomecenter.ucdavis.edu/>

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

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>LsEXPA-21

MASLHHPRRFFFILNIITLAFSWFVKPSEAVYHGYVPSPWTLAHATFYGDSEASETMG
GACGYGNLITNGYGTDTAALSTTIFNDGYACGQCYQIRCVQSPWCYKGYTTVTATN
LCPNWSQDSNNGGWCNPPRTHFDMAKPAFMKIAQWKAGIVPVMYRRVPCNAIRK
GGIRFSFQNGYWLLVYVMNVAGAGDIKQMWVKGTKGWMSMSHNWGAASYQAF
ATLKGQALSFRITSYTTKQTITAYNVAPANWNLGLTYQGNVNFH*

CDS (coding sequence)

>LsEXPA-21

ATGGCTTCACTTCATCATCCACGGAGGTTTTTCTTCATCCTTAACATCATCACACT
TGCCTTCTCCTGGTTTGTGAAACCTAGCGAAGCTGTTTACCATGGCTACGTACCGA
GTCCATGGACCCTTGCCCATGCGACATTTTATGGGGATGAGAGTGCATCTGAAAC
CATGGGTGGTGTCTGTGGATATGGAACTTGATAACTAATGGATACGGAACGGAT
ACAGCTGCTTTGAGCACAACCATCTTTAACGATGGTTATGCCTGTGGTCAATGTTA
CCAAATACGGTGTGTCCAATCTCCATGGTGCTACAAAGGATACACCACGGTACT
GCCACCAACCTCTGCCCCTAACTGGTCACAGGATTCAAACAATGGTGGATGGT
GTAACCCTCCCAGAACCCACTTCGACATGGCCAAGCCTGCGTTCATGAAAATTGC
TCAGTGGAAGGCAGGCATTGTCCCTGTCATGTACCGCAGGGTACCATGCAATGCT
ATTAGGAAAGGTGGCATCAGATTCTCTTTTCAAGGCAATGGGTACTGGCTGTTGG
TGTATGTGATGAATGTTGCTGGTGTGGAGACATCAAACAGATGTGGGTGAAAGG
GACGAAGACAGGTTGGATGAGCATGAGTCATAACTGGGGTGCCTCGTACCAAGC
TTTTGCTACTCTTAAGGGACAAGCCCTCTCTTTTAGAATAACTTCATACACCACCA
AACAGACTATCACTGCCTACAATGTCGCCCTGCTAACTGGAAGTCTAGGGTTGAC
ATATCAAGGCAACGTCAACTTCCATTGA

Nucleotide

>LsEXPA-21

CTTGTACAAAAAAGTTCACAACTTCAAAGTCACCATGGCTTCACTTCATCATCCA
CGGAGGTTTTTCTTCATCCTTAACATCATCACACTTGCCTTCTCCTGGTTTGTGAA
ACCTAGCGAAGCTGTTTACCATGGCTACGTACCGAGTCCATGGACCCTTGCCCAT
GCGACATTTTATGGGGATGAGAGTGCATCTGAAACCATGGGTAAATATCATGGCT
TAAAGCTAGTATCTTCTAGCTATCAAATATCCGTTTTAATTACTCTCAAGTGAATA

TAACATTTTTGGATATATATATTTTCAGGTGGTGCTTGTGGATATGGAAACTTGATA
ACTAATGGATACGGAACGGATACAGNTATATATATATATATATATATTTTTTCAGGTG
GTGCTTGTGGATATGGAAACTTGATAACTAATGGATACGGAACGGATACAGCTGC
TTTGAGCACAACCATCTTTAACGATGGTTATGCCTGTGGTCAATGTTACCAAATAC
GGTGTGTCCAATCTCCATGGTGCTACAAAGGATACACCACCGTTACTGCCACCAA
CCTCTGCCCGCCTAACTGGTCACAGGATTCAAACAATGGTGGATGGTGTAAACCCT
CCCAGAACCCTTTCGACATGGCCAAGCCTGCGTTCATGAAAATTGCTCAGTGGA
AGGCAGGCATTGTCCCTGTCATGTACCGCAGGTAAATTTCTGTTCCCATACTAGC
AAGCATCAAGCTTTTCTACTTTATAACTTTTGATGCACAAAGATGAACAAATTAA
TTTAATTTGATATGTATTCTATGGGCATGCTAATTACATTTTTTTGGTATTTTAGGGT
ACCATGCAATGCTATTAGGAAAGGTGGCATCAGATTCTCTTTTCAAGGCAATGGG
TACTGGCTGTTGGTGTATGTGATGAATGTTGCTGGTGGTGGAGACATCAAACAGA
TGTGGGTGAAAGGGACGAAGACAGGTTGGATGAGCATGAGTCATAACTGGGGTG
CGTCGTACCAAGCTTTTGCTACTCTTAAGGGACAAGCCCTCTTTTTAGAATAACT
TCATACACCACCAAACAGACTATCACTGCCTACAATGTCGCCCCTGCTAACTGGA
ACTTAGGGTTGACATATCAAGGCAACGTCAACTTCCATTGATTACCGGCCGTGTT
TACAGTATTCAAACACCTCTTAATGTTGCATCTCTTCAAACGCATTTGAAACCGTT
TGATTGAGTTGAAGCTAGTACATCTGCTTCTAAGTTATATTGCATCCAGTTAGTGT
TTTTCAAATTGTAATTTCCG