

IDENTIFICATION

Species: *Lactuca sativa*

Locus: Lsat_1_v5_gn_6_78920

Gene Model: Lsat_1_v5_gn_6_78920.1

Description: LsEXPA-22

Family: Alpha Expansin

3D structure:



GENOME DATABASES

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

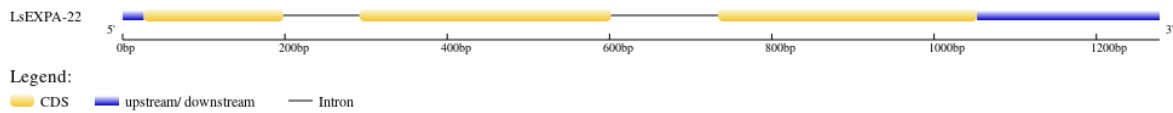
KEGG: <https://www.genome.jp/entry/T05352>

EXTERNAL RESOURCES

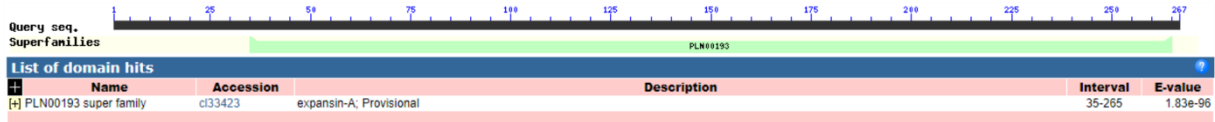
<https://lgr.genomecenter.ucdavis.edu/>

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

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>LsEXPA-22

MASLHHPPRFFFILSIITLAFSWFVKPSEAVYHGYVPSWTLAHATFYGDSEASETMG
GACGYGNLITNGYGTDTAALSTTIFSEGYACGQCYQIRCVQSPWCYKGYTTVTATNL
CPPNWSQDSNNGGWCNPPRTHFDMAKPAFMKIAQWKAGIVPVMYRRVPCNAIRKG
GIRFSFQNGYWLLVYVMNVAGAGDIKQMWVKGTKTGWMSMSHNWGASYQAF
TLKGQALSFRLLSYTTKQTITAYNVAPANWNLGLTYRANVNFH*

CDS (coding sequence)

>LsEXPA-22

ATGGCTTCACTTCATCATCCACCAAGGTTTTTCTTCATCCTTAGCATCATCACACT
TGCCTTCTCCTGGTTTGTGAAACCTAGCGAAGCTGTCTACCATGGCTACGTACCGA
GTCCATGGACCCTTGCCCATGCGACATTTTATGGGGATGAGAGTGCATCTGAAAC
CATGGGTGGTGCTTGTGGATATGGAACTTGATAACTAATGGATACGGAACGGAT
ACAGCTGCTTTGAGCACAACCATCTTTAGCGAAGGTTACGCCTGTGGTCAATGTT
ACCAAATACGGTGTGTCCAATCTCCATGGTGCTACAAAGGATACACCACCGTTAC
TGCCACCAACCTCTGCCCGCCTAACTGGTCACAGGATTCAAACAACGGAGGATGG
TGTAATCCTCCAGAACCCTTCGACATGGCCAAGCCTGCGTTCATGAAAATTG
CTCAGTGAAGGCAGGCATTGTCCCTGTCTGTACCGCAGGGTACCATGCAATGC
TATTAGGAAAGGAGGCATCAGATTCTCTTTTCAAGGAAATGGGTATTGGCTGTTG
GTTTATGTGATGAATGTTGCTGGTGCTGGAGATATCAAACAGATGTGGGTGAAAG
GGACAAAGACAGGTTGGATGAGCATGAGTCATAACTGGGGTGCCTCGTACCAAG
CTTTTGCTACTCTTAAGGGACAAGCCCTCTCCTTCAGATTAACCTTCATACACCACA
AAACAGACCATCACTGCTTACAATGTCGCCCTGCTAACTGGAACCTTAGGGTTGA
CATATCGAGCCAACGTCAACTTCCATTGA

Nucleotide

>LsEXPA-22

AAAAAGTTCACAACCTTCAAAGTCACCATGGCTTCACTTCATCATCCACCAAGGTT
TTTCTTCATCCTTAGCATCATCACACTTGCCTTCTCCTGGTTTGTGAAACCTAGCG
AAGCTGTCTACCATGGCTACGTACCGAGTCCATGGACCCTTGCCCATGCGACATT
TTATGGGGATGAGAGTGCATCTGAAACCATGGGTAAATATCATGGCTTAAAGCTA
GTATCTTCTAGCTATCATATAACCGTTTTACTATCAAGTGAATATAACATTTTTGG

ATATATATATTTTCAGGTGGTGCTTGTGGATATGGAACTTGATAACTAATGGATA
CGGAACGGATACAGCTGCTTTGAGCACAACCATCTTTAGCGAAGGTTACGCCTGT
GGTCAATGTTACCAAATACGGTGTGTCCAATCTCCATGGTGCTACAAAGGATACA
CCACCGTACTGCCACCAACCTCTGCCCGCCTAACTGGTCACAGGATTCAAACAA
CGGAGGATGGTGTAATCCTCCCAGAACCCACTTCGACATGGCCAAGCCTGCGTTC
ATGAAAATTGCTCAGTGAAGGCAGGCATTGTCCCTGTCATGTACCGCAGGTGAA
TTTCTGCTCCCATACTAGCAAGCATCAAGCTTTTCTACTTTATAACTTTTGATGCA
CAAAGATGAACAAATTAACCTTAATTTGATATGTATTCTACGGGCATGCTAATTAC
ATTTTTTGTGCTTTAGGGTACCATGCAATGCTATTAGGAAAGGAGGCATCAGATT
CTCTTTTCAAGGAAATGGGTATTGGCTGTTGGTTTATGTGATGAATGTTGCTGGTG
CTGGAGATATCAAACAGATGTGGGTGAAAGGGACAAAGACAGGTTGGATGAGCA
TGAGTCATAACTGGGGTGCGTCGTACCAAGCTTTTGCTACTCTTAAGGGACAAGC
CCTCTCCTTCAGATTAACCTTCATACACCACAAAACAGACCATCACTGCTTACAAT
GTCGCCCCTGCTAACTGGAACCTTAGGGTTGACATATCGAGCCAACGTCAACTTCC
ATTGATCTACTGGACGTGTTTACAGTATTCAAACACCTTTTAATGTTCTGTCTCTT
CAAACGCATTTGAAACCGTTTGATTGAGTTGAAGCTAGTATATCTGCTTCTAAGTT
ATATTGTATCCAGTTAGTGTTTTTCAAACCTGTAATTTCCGTCCATCCTATTA
TAAACATTCTAATGGGTTAGAGATGGAGTTAACCTAGCTGTGTATTTAACTAGT
ATAAAT