

IDENTIFICATION

Species: *Lactuca sativa*

Locus: Lsat_1_v5_gn_6_8220

Gene Model: Lsat_1_v5_gn_6_8220.1

Description: LsEXPA-20

Family: Alpha Expansin

3D structure:



GENOME DATABASES

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

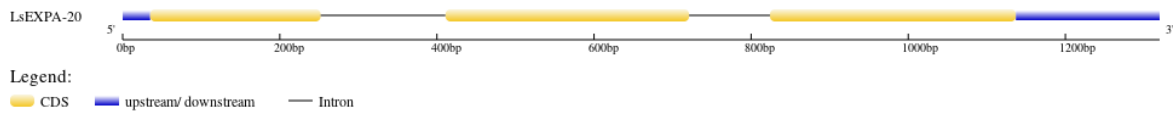
KEGG: <https://www.genome.jp/entry/T05352>

EXTERNAL RESOURCES

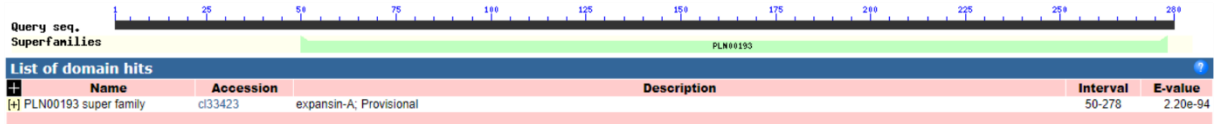
<https://lgr.genomecenter.ucdavis.edu/>

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

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>LsEXPA-20

MAPVHPLWGLCVFVASIMIILSTLDSVTAATYTSRVPRTRVPRTAPVVYTPSPWTLA
HATFYGDESAASTMGGACGYGNIVTNGYGTDAALSSTIFTDGYACGQCYQIKCVQS
PWCSKGVATITATNLCPPNWSKDSNAGGWCNPPRTHFDMAKPAFMKIAQWKAGIVP
VQYRRVPCSRAGGIRFSFQNGYWLLTYVMNVGGAGDIGQMWVKGTKTAWISMHS
NWGASYQAFATLKGQALSFKITSYTTKQIVCANNVAPANWNLGLTYQASVNFH*

CDS (coding sequence)

>LsEXPA-20

ATGGCTCCGGTTCATCCACTATGGGGATTATGTGTCTTTGTTGCGAGCATCATGAT
AATCTTATCCACTTTGGATTCTGTAACCGCAGCTACATATACTTCACGAGTTCCAC
GTACAACACGAGTTCCGCGTACTGCACCAGTTGTTTATACACCGAGCCCTTGGAC
CCTCGCCCACGCTACGTTTTATGGGGACGAGTCTGCGGCTTCAACCATGGGGGGT
GCTTGTGGATATGGAAACATTGTGACCAACGGGTATGGAAGTATACAGCAGCAT
TGAGCTCTACAATCTTTACAGATGGATATGCATGTGGGCAGTGTTATCAGATTAA
GTGTGTCCAATCTCCATGGTGTTCCAAAGGTGTTGCTACGATCACAGCAACAAC
CTCTGCCCACTGGTCCAAAGACTCTAACGCTGGTGGATGGTGTAAACCC
CAAGAACTCATTTCGACATGGCTAAGCCCGCCTTCATGAAGATCGCACAAATGGAA
GGCAGGCATTGTCCCTGTCCAATACCGCAGGGTACCATGTAGTCGGGCAGGGGGT
ATCAGGTTCTCTTTCCAAGGAAATGGTACTGGCTGTTGACGTATGTGATGAACG
TTGGTGGTGTGGTGTATTTGGCCAGATGTGGGTTAAAGGGACCAAGACTGCATG
GATCAGTATGAGCCACAACCTGGGGAGCCTCATAACCAAGCATTTGCCACGCTTAA
GGTCAAGCTCTCTTTCAAGATCACCTCCTACACAACCAACAGACCATTGTGT
GTAACAATGTCGCCCCGGCTAACTGGAAGTTAGGTTTGACGTACCAGGCAAGCGT
CAATTTTCATTAA

Nucleotide

>LsEXPA-20

CTTTTGGATCAGCCCGAGTCAAGAAACAGAACACAATGGCTCCGGTTCATCCACT
ATGGGGATTATGTGTCTTTGTTGCGAGCATCATGATAATCTTATCCACTTTGGATT
CTGTAACCGCAGCTACATATACTTCACGAGTTCCACGTACAACACGAGTTCCGCG
TACTGCACCAGTTGTTTATACACCGAGCCCTTGGACCCTCGCCCACGCTACGTTTT

ATGGGGACGAGTCTGCGGCTTCAACCATGGGTACGAGTTTGCCTACGCATGTATT
TTGGTGAAAGATAAATGCACCTACAAGGGCCCACTGATTACGTGGGCCCTCATCT
GGTGTGTCTGAATCCAAAAGTTTTTACAATTTGAAGGTGCAAATGTTGATTGTTTT
TTTTTTGTTGAAATTTTGTATAGGGGGTGCTTGTGGATATGGAAACATTGTGACCA
ACGGGTATGGAACTGATACAGCAGCATTGAGCTCTACAATCTTTACAGATGGATA
TGCATGTGGGCAGTGTTATCAGATTAAGTGTGTCCAATCTCCATGGTGTTCAAA
GGTGTGCTACGATCACAGCAACAAACCTCTGCCACCCAACCTGGTCCAAAGACT
CTAACGCTGGTGGATGGTGTAAACCCCAAGAACTCATTTCGACATGGCTAAGCC
CGCCTTCATGAAGATCGCACAAATGGAAGGCAGGCATTGTCCCTGTCCAATACCGC
AGGTATATATATTGTATTCCACAAATCATCAATACATTGCATGTTGATACCTTAAT
TCTATATACAGATAACAATGAAGGTCTTAATTTGTTTGTGTTGTTGTAGGGTACCA
TGTAGTCGGGCAGGGGGTATCAGGTTCTCTTTCCAAGGAAATGGTACTGGCTGT
TGACGTATGTGATGAACGTTGGTGGTGCTGGTGATATTGGCCAGATGTGGGTAA
AGGGACCAAGACTGCATGGATCAGTATGAGCCACAACCTGGGGAGCCTCATACCA
AGCATTTGCCACGCTTAAAGGTCAAGCTCTCTCTTTCAAGATCACCTCCTACACAA
CCAAACAGACCATTGTGTGTAACAATGTCGCCCCGGCTAACTGGAACCTTAGGTTT
GACGTACCAGGCAAGCGTCAATTTTCATTAATTAATGTAAATGTTACAGGTTTCA
AACACCTCGTCTAACATGTATTATGTTGGTTTTTTGAGAGTTGCTACCTTATATATT
CGAAATGAAGGATTATTGGTTTGGTTCGGATAATTTATCGACTTTATTTCATTGCAA
CATTCGTGGTTTAATTTGTACAATGCAAAGTATATTAATTAATAGC