

IDENTIFICATION

Species: *Lactuca sativa*

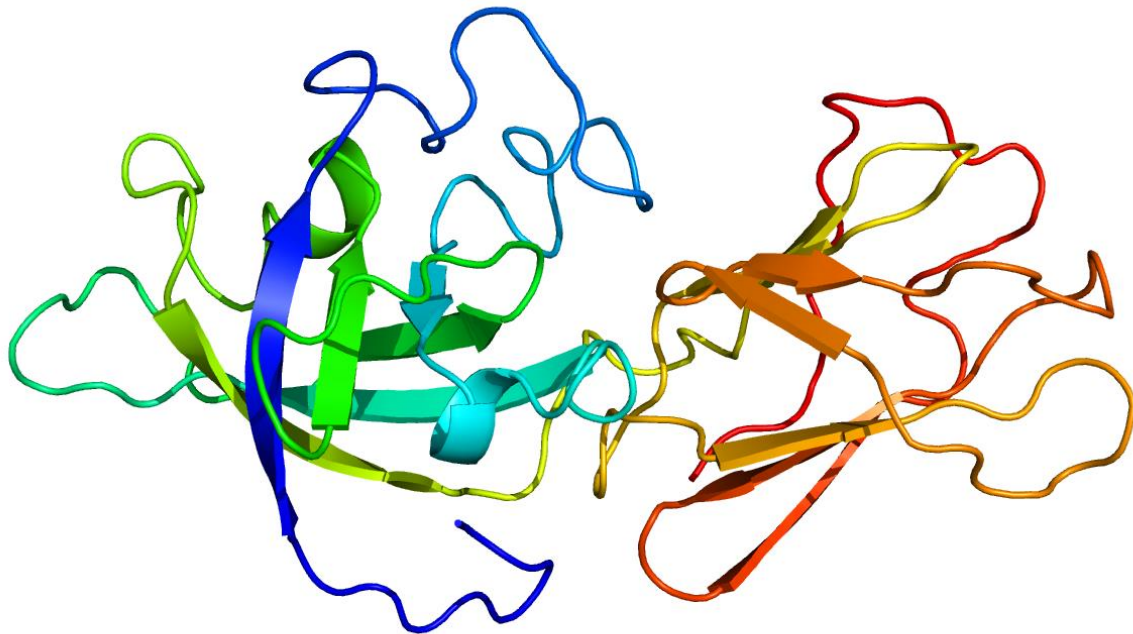
Locus: Lsat_1_v5_gn_8_29600

Gene Model: Lsat_1_v5_gn_8_29600.1

Description: LsEXPA-25

Family: Alpha Expansin

3D structure:



GENOME DATABASES

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

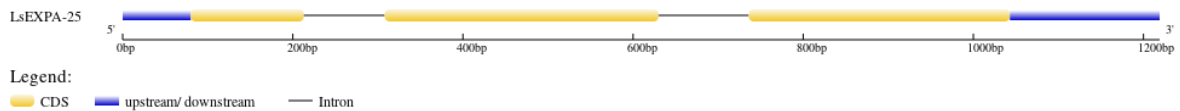
KEGG: <https://www.genome.jp/entry/T05352>

EXTERNAL RESOURCES

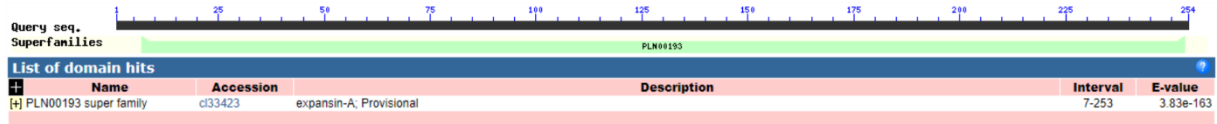
<https://lgr.genomecenter.ucdavis.edu/>

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

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>LsEXPA-25

MAKLCFLLLTVIYSLFLHVHALTPSRWTKAHATFYGEADASGTMGGACGYGNLYST
GYGTRTAALSTALFNDGAACGQCQYKIICDVKTDPKWCKKGVSVTITATNFCPPNYAQ
ANDAGGWCNPPLQHFDMAQPAWEKIGIYRGGIIPVIYQRVPCKKHGGVRFAINGRDY
FELVLITNVGNAGAIRSVKVKGSKTGWMPMSRNWGANWQSN SYLNGQSMSFMVTT
TDGITKTFTNIVPSSWTFGQTFSSRLQF*

CDS (coding sequence)

>LsEXPA-25

ATGGCGAAACTTTGCTTTCTCTTGCTAACTGTTATCTACTCTCTATTCCTCCATGTC
CATGCACTTACCCCTTCGAGATGGACAAAAGCCCATGCAACCTTTTATGGAGAAG
CCGATGCTTCCGGAACAATGGGTGGTGCTTGCGGATATGGTAACCTGTACTCCAC
CGGATACGGAACAAGAACGGCGGGCGTTGAGTACTGCTCTTTTCAACGACGGCGCT
GCTTGCGGCCAGTGTTACAAGATCATATGCGATGTCAAGACGGACCCAAAGTGGT
GCAAGAAAGGAGTGTCGGTGACAATCACCGCCACCAACTTTTGCCCACTAACTA
CGCTCAGGCCAACGACGCCGGAGGGTGGTGCAACCCACCGCTACAGCATTTCGA
CATGGCTCAGCCTGCTTGGGAGAAGATCGGGATTTACAGAGGTGGAATCATCCCC
GTTATCTACAAAGAGTACCATGTAAGAAACACGGCGGAGTTAGATTTCGCGATA
AACGGGAGAGATTACTTCGAGCTTGTTTTGATAACGAATGTCGGAAATGCCGGAG
CTATTAGGTCGGTGAAGGTGAAGGGATCAAAAACCGGGTGGATGCCGATGTCGA
GGAATTGGGGAGCTAACTGGCAATCGAATTCATACCTCAACGGCCAATCTATGTC
GTTCATGGTGACAACCACCGATGGTATCACCAAACTTTCACAAACATTGTCCCT
TCAAGCTGGACATTTGGTCAAACCTTTCTCAAGCCGTTTACAGTTCTGA

Nucleotide

>LsEXPA-25

CTTATTTAAGCAGCTCTTATTCTAATCCTCTAAACCCATCTTCTTCCTCATTGCTT
CATCTCATCTCTGCACATCAAAAATGGCGAAACTTTGCTTTCTCTTGCTAACTGTT
ATCTACTCTCTATTCCTCCATGTCCATGCACTTACCCCTTCGAGATGGACAAAAGC
CCATGCAACCTTTTATGGAGAAGCCGATGCTTCCGGAACAATGGGTATATAATTA
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TGATCTTAACTTGTTTCTATATATGCAGGTGGTGCTTGCGGATATGGTAACCTGTA

CTCCACCGGATACGGAACAAGAACGGCGGCGTGTGAGTACTGCTCTTTTCAACGAC
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AGTGGTGCAAGAAAGGAGTGTCGGTGACAATCACCGCCACCAACTTTTGCCACC
AAACTACGCTCAGGCCAACGACGCCGGAGGGTGGTGCAACCCACCGCTACAGCA
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AAACTTACAAACTCCATCTTCTGGCATTGACTGATTGTTTTTAATCTAATTACTT
GTTTGTGATCAGAGTACCATGTAAGAAACACGGCGGAGTTAGATTCGCGATAAA
CGGGAGAGATTACTTCGAGCTTGTTTTGATAACGAATGTCGGAATGCCGGAGCT
ATTAGGTCGGTGAAGGTGAAGGGATCAAAAACCGGGTGGATGCCGATGTCGAGG
AATTGGGGAGCTAACTGGCAATCGAATTCATACCTCAACGGCCAATCTATGTCGT
TCATGGTGACAACCACCGATGGTATCACCAAACTTTCACAAACATTGTCCCTTC
AAGCTGGACATTTGGTCAAACCTTCTCAAGCCGTTTACAGTTCTGAAAGAAAGAG
ATGAGAAGACCGTGTGCTTCAGTGTTTATTATGATTTGGAATTTTTTAAGGGGGC
AGCGGCGTGCTTTCTCTTTTTATAGAAGCAGCCC GCCGGGTTTTCTTTTTCCGGGC
GTTTTCTTTTTATATAATATTATTATATAATAAGTATATGGATATGGATTTGAG