

IDENTIFICATION

Species: *Lactuca sativa*

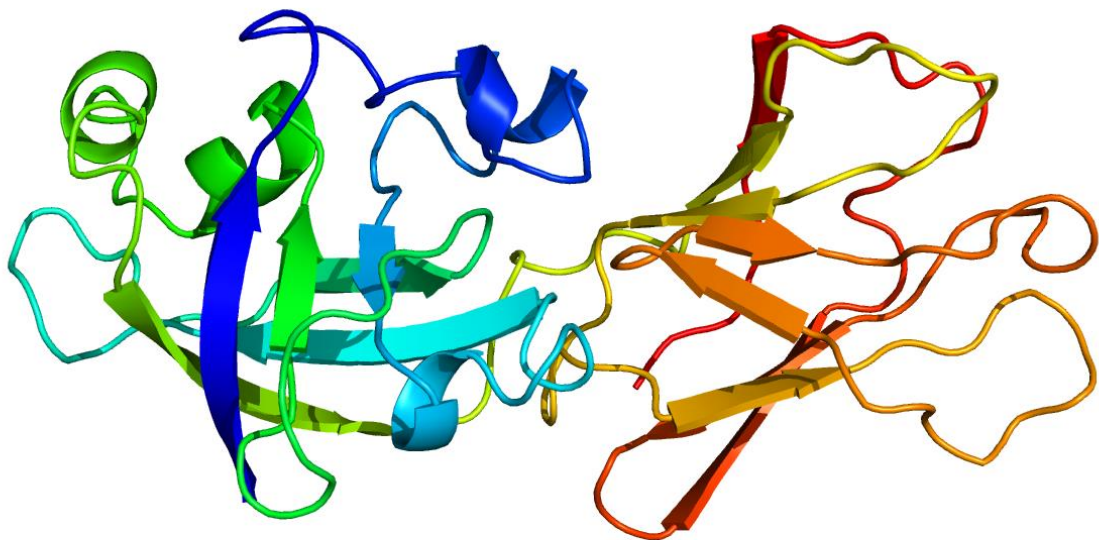
Locus: Lsat_1_v5_gn_8_99280

Gene Model: Lsat_1_v5_gn_8_99280.5

Description: LsEXPB-07

Family: Beta Expansin

3D structure:



GENOME DATABASES

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

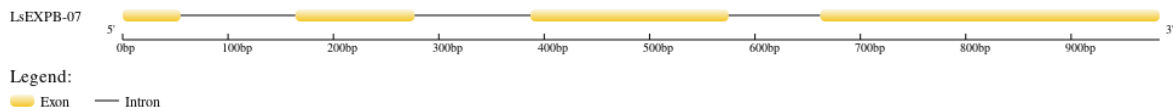
KEGG: <https://www.genome.jp/entry/T05352>

EXTERNAL RESOURCES

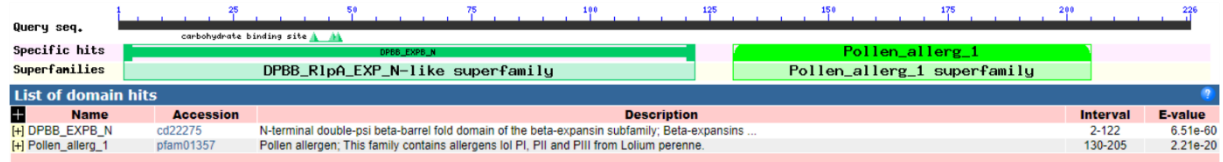
<https://lgr.genomecenter.ucdavis.edu/>

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

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>LsEXPB-07

MFSAGLATWYGDETGAGSGGACGWKDDVKNPPLSSMIAAGNANIFLSGRGCGHCF
QIVCHQPPYCSGKPITVTISDECPGCSDAPFHFDMSGFAFGAMANPGQDHNLRQLGKL
MVQYQRVPCSYRNTNIAFKVDEGSTKYWFAAAIEYADGNNGDFKS VEMAPSGSTNFV
SMDNLWGTIWKININPSFQAPYSFRLTSSGGETIIASDVIPQNFVVGGQKYLSHVNF*

CDS (coding sequence)

>LsEXPB-07

ATGTTTTTCGGCTGGTTTGGCAACATGGTATGGGGATGAAACTGGTGCCGGAAGCG
GAGGAGCTTGTGGATGGAAGGATGATGTGAAGAATCCCCCGTTATCATCAATGAT
AGCAGCAGGAAACGCCAACATCTTTTTATCAGGCAGAGGATGTGGACATTGTTTT
CAAATAGTGTGCATCAACCACCATACTGCTCAGGTAAACCAATCACTGTAACCA
TTAGCGATGAGTGTCTTGGATGTAGCGATGCACCTTTCCATTTTGATATGAGTGG
GTTTGCTTTTGGTGCAATGGCTAATCCTGGCCAAGATCACAATCTACGACAACCTT
GGCAAACCTTATGGTGCAATATCAAAGGGTGCCATGCAGTTATAGAAATACCAAC
ATTGCATTCAAAGTTGATGAGGGTAGTACCAAATATTGGTTCGCCGCAGCAATAG
AGTATGCAGATGGGAATGGTGATTTTAAATCTGTGGAGATGGCACCAAGTGGAA
GTACGAATTTTGTTCATGGATAACTTATGGGGTACAATTTGGAAAATAAACAT
TAATCCATCATTCCAAGCTCCATATTCTTTCCGGCTGACATCTAGTGGTGGGGAGA
CCATTATAGCAAGCGATGTGATTCCTCAAATTTTGTAGTTGGGCAAAAGTACTT
ATCACATGTAAATTTTAA

Nucleotide

>LsEXPB-07

ATGTTTTTCGGCTGGTTTGGCAACATGGTATGGGGATGAAACTGGTGCCGGAAGCG
GTAATGCAATGAAAGTTTCACGTTAAAATGTTATAAATATCTTTTTCATAATTCTA
TTAGTTTGTCAATTCCTACTCTTATTGATTTCTGTTTTGCGATAATTAGTAGGAGG
AGCTTGTGGATGGAAGGATGATGTGAAGAATCCCCCGTTATCATCAATGATAGCA
GCAGGAAACGCCAACATCTTTTTATCAGGCAGAGGATGTGGACATTGTTTTCAAG
TATGTACAGTTGGTTATTTTCATCTAAGTCTTGTTCGTTTTGTTCCTTTGATCACTT

AACATGAAACAAAATGCTTAGTCTTGATGAAGAATTGCAAATGTATACGCAGATA
GTGTGTCATCAACCACCATACTGCTCAGGTAAACCAATCACTGTAACCATTAGCG
ATGAGTGTCTGGATGTAGCGATGCACCTTCCATTTTGATATGAGTGGGTTTGCT
TTTGGTGCAATGGCTAATCCTGGCCAAGATCACAATCTACGACAACCTGGCAAAC
TTATGGTGCAATATCAAAGGTGAGTATATACTCAATGAATTATATAAGTTATTAT
ATGATTAATTACATTTTTTATTGTTGAAACAAGCCATGTGTTCGTGTGATAGGGTGC
CATGCAGTTATAGAAATACCAACATTGCATTCAAAGTTGATGAGGGTAGTACCAA
ATATTGGTTCGCCGCAGCAATAGAGTATGCAGATGGGAATGGTGATTTTAAATCT
GTGGAGATGGCACCAAGTGGAAGTACGAATTTTGTTCATGGATAACTTATGGG
GTACAATTTGGAAAATAAACATTAATCCATCATTCCAAGCTCCATATTCTTTCCGG
CTGACATCTAGTGGTGGGGAGACCATTATAGCAAGCGATGTGATTCCTCAAATTT
TTGTAGTTGGGCAAAGTACTTATCACATGTAAATTTTAA