

IDENTIFICATION

Species: *Lactuca sativa*

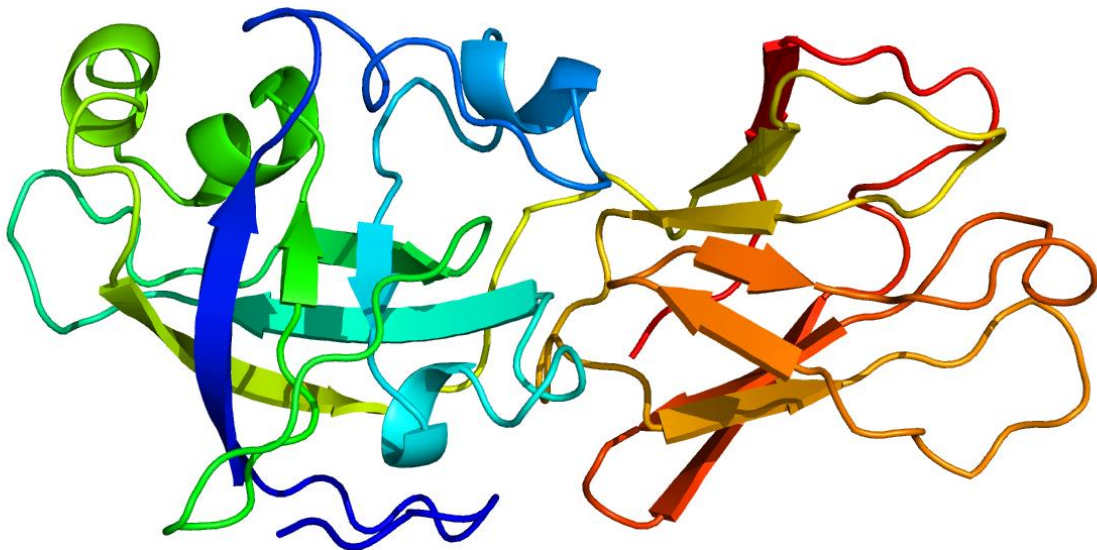
Locus: Lsat_1_v5_gn_7_78660

Gene Model: Lsat_1_v5_gn_7_78660.1

Description: LsEXPB-03

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

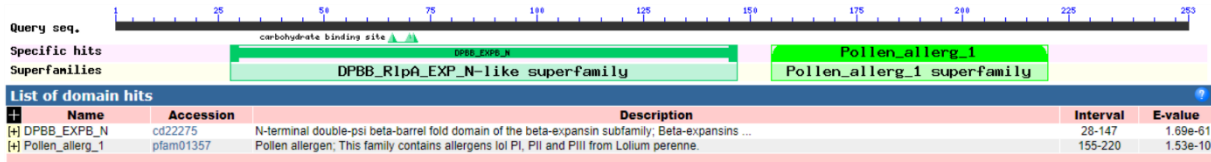
<https://lgr.genomecenter.ucdavis.edu/>

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

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>LsEXPB-03

MMSLFINSSSCSNQTLPAKTSNLTGFKPALASWYGDRHGAGSGGACGWANDVKSAP
FSAMIAAGNANLFLEGKGCCTCYQVLCTQEPYCSKNPITVTITDECPGECNKVPFAFD
LSGTAFGAMSSPGQADNLRNLGQVNIQYRRVACNYGSTKIAFKIDPKVNPYWFAMA
VEFCEGDGGLDAVEVAANGSQEFRCMENIWGAVVAVSIDPSFRGPFSFRLFSRKNEG
VVALKAIPYSFVPGQTYSHVNFVR*

CDS (coding sequence)

>LsEXPB-03

ATGATGTCCTTTGTTTCATAAACTCCTCTTCATGTTCTAACCAAACACTCCCTGCTAA
AACTAGCAATCTTACCGGTTTTAAACCAGCTTTAGCATCGTGGTATGGAGATCGA
CATGGTGCTGGAAGTGGAGGAGCTTGTGGATGGGCTAATGATGTGAAATCAGCTC
CATTCTCAGCCATGATAGCAGCAGGAAACGCCAACTTGTTTTTGGGAAGGAAAAGG
GTGTGGGACTTGTTATCAGGTCTTATGCACTCAAGAGCCATATTGCTCCAAGAAT
CCTATTACTGTAACCATAACCGATGAGTGCCCTGGTGAATGTAACAAAGTCCCAT
TCGCTTTTGATTTAAGCGGAACTGCTTTTGGTGCAATGTCAAGTCCAGGACAAGC
TGATAATCTGCGTAATCTTGGCCAAGTTAACATTCAATATCGAAGGGTAGCATGC
AACTATGGTAGCACAAAAATTGCGTTCAAGATAGATCCAAAGGTGAACCCATACT
GGTTCGCTATGGCAGTAGAGTTTTGTGAGGGAGATGGTGGTCTTGACGCAGTAGA
GGTAGCAGCAAATGGTTCACAGGAGTTTAGATGCATGGAGAACATATGGGGCGC
AGTTTGGGCAGTTAGCATTGACCCATCATTTCTGTGGTCCATTTTCATTCAGGCTAT
TCTCTAGAAAGAACGAAGGGGTTGTTGCGTTGAAGGCGATTCCATATAGTTTTGT
ACCTGGACAACTTATTACTCGCATGTCAATTTTAGAGTCTAG

Nucleotide

>LsEXPB-03

ATGATGTCCTTTGTTTCATAAACTCCTCTTCATGTTCTAACCAAACACTCCCTGCTAA
AACTAGCAATCTTACCGGTTTTAAACCAGCTTTAGCATCGTGGTATGGAGATCGA
CATGGTGCTGGAAGTGGTAATGCATCGCAACAGATTTTTATTATTATCTAATGA
GAGCTTATTATACATAAATAAATCGTTGGACTTATTTGAAGTGCACATACACAAA

CAAGTGTTATATGTACACATATTTATTTTAATCATTTCAATCACATTAGTTATTATT
AATAAGAAATTTTCCATTACATCTCGTTATTATCAATCGAGCCTCTACAACCTCAT
TTTCATGATTACGCAGGAGGAGCTTGTGGATGGGCTAATGATGTGAAATCAGCTC
CATTCTCAGCCATGATAGCAGCAGGAAACGCCAACTTGTTTTTGGAAGGAAAAGG
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CAGACTAATTCAAGCAATATTGTAATTACATTTAATATCTCAGGTCTTATGCACTC
AAGAGCCATATTGCTCCAAGAATCCTATTACTGTAACCATAACCGATGAGTGCCC
TGGTGAATGTAACAAAGTTCCATTTCGCTTTTGATTTAAGCGGAACTGCTTTTGGTG
CAATGTCAAGTCCAGGACAAGCTGATAATCTGCGTAATCTTGCCAAGTTAACAT
TCAATATCGAAGGTGCATAAAATAAGCAAAACCTTTGATCAACCTAATGTTTTGT
ACTAATATCTTACATTTCAATTTGGCTTTGTTTACATATCTAGGGTAGCATGCAAC
TATGGTAGCACAAAATTGCGTTCAAGATAGATCCAAAGGTGAACCCATACTGGT
TCGCTATGGCAGTAGAGTTTTGTGAGGGAGATGGTGGTCTTGACGCAGTAGAGGT
AGCAGCAAATGGTTCACAGGAGTTTAGATGCATGGAGAACATATGGGGCGCAGT
TTGGGCAGTTAGCATTGACCCATCATTTCGTGGTCCATTTTCATTCAGGCTATTCT
CTAGAAAGAACGAAGGGGTTGTTGCGTTGAAGGCGATTCCATATAGTTTTGTACC
TGGACAACTTATTACTCGCATGTCAATTTTAGAGTCTAG