

IDENTIFICATION

Species: *Lactuca sativa*

Locus: Lsat_1_v5_gn_8_51000

Gene Model: Lsat_1_v5_gn_8_51000.1

Description: LsEXPA-27

Family: Alpha Expansin

3D structure:



GENOME DATABASES

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

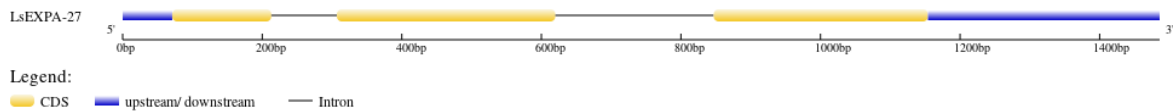
KEGG: <https://www.genome.jp/entry/T05352>

EXTERNAL RESOURCES

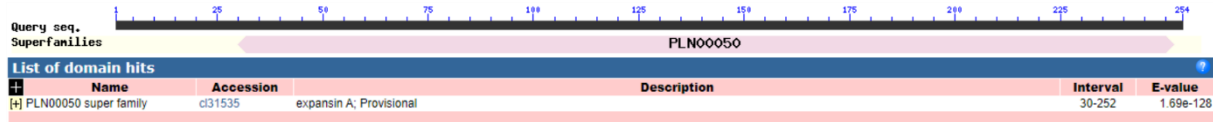
<https://lgr.genomecenter.ucdavis.edu/>

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

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>LsEXPA-27

MALLAIFFLGFLAILSPVHGRGGRGGGAGWKNAHATFYGGGDASGTMGGACGYGN
LYSQGYGTNTAALSTAMFNGLSCGSCFAIKCVNDKWLCPATIVVTATNFCPPNNA
LPNNNGGWCNPPNHFDLSQPIFQHIAQFKAGIVPVAYKRVPCRRRGGIRFQINGHSY
FNLVLITNVGGAGDVHAVAVKGSRTGWQQMSRNWQNWQSN SYLNGQSLSFKVT
TSDGRTVVSYNVAPARWSFGQTFSGAQFH*

CDS (coding sequence)

>LsEXPA-27

ATGGCACTTTTAGCTATTTTCTTTCTGGGTTTTCTCGCAATCCTCTCCCCTGTTTAC
GGCAGAGGCGGCCGCGGGCGGAGCTGGCTGGAAAACGCCCATGCAACCTTC
TACGGCGGCGGCGATGCATCTGGAACAATGGGTGGAGCTTGTGGATATGGGAAT
TTATACAGTCAAGGGTATGGTACAAACACAGCAGCGCTAAGTACAGCTATGTTCA
ACAATGGTTTAAGCTGTGGCTCTTGCTTTGCGATTAAATGCGTAAACGACGCTAA
ATGGTGTTTGCCGGCGACCATTGTCGTCACCGCCACCAACTTCTGCCCACCGAAC
AACGCCTTACCTAACAACAACGGCGGGTGGTGCAACCCTCCAAATCACCCTTCG
ACCTTTCTCAGCCTATCTTTCAACACATTGCCCAATTCAAAGCCGGAATCGTCCCT
GTTGCTTACAAAAGGGTACCATGTTCGGAGAAGGGGTGGAATTAGGTTTCAGATA
AATGGGCACTCGTACTTCAATCTGGTGTGATTACAAACGTGGGTGGCGCCGGTG
ACGTTTATGCGGTGGCGGTCAAAGGGTCAAGGACAGGGTGGCAGCAAATGTCTC
GGAAGTGGGGGCAAATTGGCAATCCAACCTTACCTCAACGGGCAGTCTTTGTC
TTTTAAGGTCACCACAAGTGATGGTCAACTGTTGTTTCATACAATGTTGCCCTG
CCCGTTGGTCTTTCGGTCAGACCTTCAGTGGTGCCAGTTTCACTGA

Nucleotide

>LsEXPA-27

GTAAATTCTCTTATTTATATCCTCTGCCACCACTCCCAAATTCTCTACATCACCATT
TCAATTCAAATCCATGGCACTTTTAGCTATTTTCTTTCTGGGTTTTCTCGCAATCC
TCTCCCCTGTTACGGCAGAGGCGGCCGCGGGCGGAGCTGGCTGGAAAACG
CCCATGCAACCTTCTACGGCGGCGGCGATGCATCTGGAACAATGGGTACTTTCTA
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TAAATTTATCGACTGAATTGTGAGCAGGTGGAGCTTGTGGATATGGGAATTTATA

CAGTCAAGGGTATGGTACAAACACAGCAGCGCTAAGTACAGCTATGTTCAACAA
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TGTTTGCCGGCGACCATTGTCGTCACCGCCACCAACTTCTGCCACCGAACAACG
CCTTACCTAACAAACGCGGGTGGTGCAACCCTCCAAATCACCCTTCGACCT
TTCTCAGCCTATCTTTCAACACATTGCCCAATTCAAAGCCGGAATCGTCCCTGTTG
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GTTTGCGTCAATGTAATAACGTTTAAGTTCTTCATTTGTAATTTTGGCTTTTCTCAA
ATTACCAAATACCCTCAGGGGTAAATATGGTAAATACGTTTGCTAAACATTTGGG
ATCTGTTTTGTAGGGTACCATGTCGGAGAAGGGGTGGAATTAGGTTTCAGATAAA
TGGGCACTCGTACTTCAATCTGGTGTGATTACAAACGTGGGTGGCGCCGGTGAC
GTTTATGCGGTGGCGGTCAAAGGGTCAAGGACAGGGTGGCAGCAAATGTCTCGG
AACTGGGGGCAAATTTGGCAATCCAACCTTACCTCAACGGGCAGTCTTTGTCTT
TTAAGGTCACCACAAGTGATGGTCGAACTGTTGTTTCATACAATGTTGCCCTGCC
CGTTGGTCCTTCGGTCAGACCTTCAGTGGTGCCAGTTTCACTGAAAAGACATAT
CTACCCTCCATACCTAATACGGTAGCGGCATATAAATTATTATTTAGTTACTGCTA
CAATTTATGACTCAGAGAGGCTTATTTTGGAAAAGGTCAATTTGGTCAATTTGGTT
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GCAACGGAGGGCAGTGGTGGACTTTAACCACCCGCTAGTAGTACTGTAGTGGTAG
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