

IDENTIFICATION

Species: *Lactuca sativa*

Locus: Lsat_1_v5_gn_9_59761

Gene Model: Lsat_1_v5_gn_9_59761.1

Description: LsEXPA-34

Family: Alpha Expansin

3D structure:



GENOME DATABASES

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

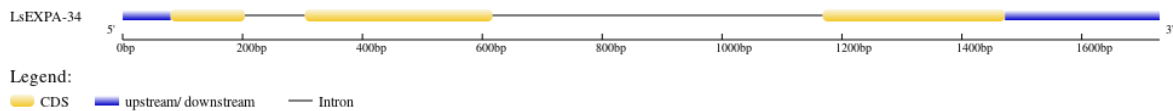
KEGG: <https://www.genome.jp/entry/T05352>

EXTERNAL RESOURCES

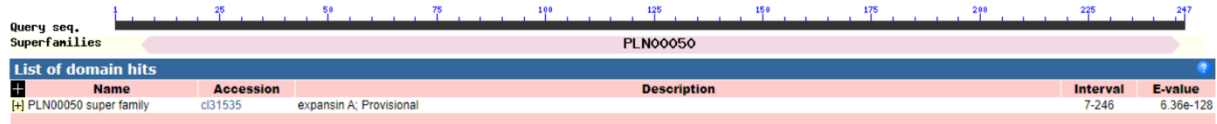
<https://lgr.genomecenter.ucdavis.edu/>

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

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>LsEXPA-34

MTSSQITILALLISFFFTLVYGNWQNGHATFYGGGDASGTMGGACGYGNLYSQGYGT
NTAALSTALFNGLSCGSCYEMRCNDDPRWCLPGSIIVTATNF CPPNPAQSN DNGGW
CNPPLQHFDLAEP AFLQIAQYRAGIVPVAFQRVPCM KKG VRF TINGHSYFNLVLVT
NVGGAGDVH AVSIKSKTGWQPMSRNW GQNWQSN SYLNGQSLSFQVTTSDGRTITS
YNVASSGWQFGQTFQGGQF*

CDS (coding sequence)

>LsEXPA-34

ATGACTTCTTCACAAATAACAATTCTTGCTCTCCTTATTTCCCTTCTTCTTCACTCTT
GTTTATGGAAATTGGCAAATGGTCATGCCACCTTTTATGGAGGAGGAGACGCTT
CGGGCACAATGGGGGGTGCTTGTGGTTATGGGAATTTATATAGCCAAGGATATGG
GACCAATACTGCAGCATTGAGCACTGCTCTTTTAAACAATGGTTTGAGTTGTGGAT
CTTGTTATGAAATGAGATGTAATGATGACCCTAGGTGGTGCTTACCTGGTAGCAT
AATTGTGACTGCGACCAATTTTGTCCACCGAACCCTGCTCAATCTAACGATAAT
GGTGGTTGGTGCAACCCCTCTCCAACACTTTGATTTGGCTGAGCCTGCTTTCTT
GCAAATAGCGCAATATCGAGCTGGTATTGTGCCTGTTGCATTCCAAAGGGTGCCT
TGCATGAAGAAGGGAGGAGTGAGATTTACAATCAACGGTCACTCATACTTCAACT
TGGTATTAGTTACAAACGTGGGAGGTGCAGGAGATGTACACGCAGTCTCAATCAA
AGGATCGAAGACAGGGTGGCAACCGATGTCACGGAAC TGGGGGCAAAACTGGCA
AAGCAACTCATATCTTAACGGACAAAGTCTTTCTTTTCAAGTCACAACTAGCGAT
GGAAGAACCATCACTAGCTACAACGTCGCATCGTCTGGTTGGCAATTTGGTCAGA
CATTTC AAGGGGGGCAATTTTAA

Nucleotide

>LsEXPA-34

TTTCCCTCCCTACACTTCAATCCCCCTATATAACTATATCTTCATTTGCTCAATTC
TCAAACCCCAAGACTCTTCCAATGACTTCTTACAAATAACAATTCTTGCTCTC
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CTTTTATGGAGGAGGAGACGCTTCGGGCACAATGGGTATATTTACATACATATCT
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AAGGATATGGGACCAATACTGCAGCATTGAGCACTGCTCTTTTTAACAATGGTTT
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CCTGGTAGCATAATTGTGACTGCGACCAATTTTTGTCCACCGAACCCCTGCTCAATC
TAACGATAATGGTGGTTGGTGCAACCCCTCTCCAACACTTTGATTTGGCTGAG
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AAAGAAAAATAGGAACAAAAGATTGGAAGTTCATTTAGTGAAAAAAAACAACGT
ATAAATATCTTTTCTCAATCGTGTGATTGACTTGTTTGCAATGTTTTTATATAGGG
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CAACTTGGTATTAGTTACAAACGTGGGAGGTGCAGGAGATGTACACGCAGTCTCA
ATCAAAGGATCGAAGACAGGGTGGCAACCGATGTCACGGAACCTGGGGGCAAAAC
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