

IDENTIFICATION

Species: *Lactuca sativa*

Locus: Lsat_1_v5_gn_8_15340

Gene Model: Lsat_1_v5_gn_8_15340.1

Description: LsEXPA-24

Family: Alpha Expansin

3D structure:



GENOME DATABASES

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

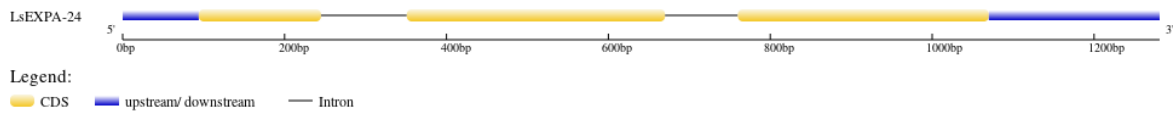
KEGG: <https://www.genome.jp/entry/T05352>

EXTERNAL RESOURCES

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

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

GENE STRUCTURE



DOMAIN ARCHITECTURE

Query seq. Superfamilies

PLN00050

Name	Accession	Description	Interval	E-value
PLN00050 super family	cl31535	expansin A, Provisional	30-257	1.63e-119

SEQUENCES

Peptide

>LsEXPA-24

MELSRVYCFMLMTAFFTTVVNARIPGVYTGQWESAHATFYGGSDASGTMGGACG
YGNLYSQGYGVNTAALSTALFNNGFRCGACFEIKCTNDPQWCHPGSPSIFITATNFCP
PNFAQPSDNGGWCNPPRPHFDLAMPFLKIAEYRAGIVPVNYRRVACRKQGGIRFTI
NGFRYFNLILISNVAGAGDITMAWVKGSNTDWMSLSRNWQNWQSNALIGQSLSF
RVRSSDGRSSASMNIVPSNWQFGQTFGKNFRV*

CDS (coding sequence)

>LsEXPA-24

ATGGAGCTCAGTCGTGTTTACTGCTTTTTAATGTTAACTGCATTCTTCACAACCGT
CGTCAATGCTCGTATCCCCGGAGTTTACACCGGAGGCCAGTGGGAATCCGCCCAC
GCCACCTTCTACGGTGGTAGTGACGCATCTGGCACCATGGGTGGAGCATGTGGGT
ATGGGAATTTATACAGTCAAGGGTACGGCGTGAACACGGCGGCGCTAAGCACGG
CGCTGTTCAACAATGGGTTTCAGATGCGGCGCTTGTGTTTGGAGATAAAGTGTACGAA
CGACCCTCAATGGTGTACCCCCGGCAGCCCTTCAATTTTCATCACCGCCACCAATT
TCTGCCCTCCTAACTTCGCTCAACCCAGTGACAATGGTGGATGGTGTAAACCCACC
TCGCCCTCATTTTCGATCTCGCCATGCCCATGTTCTCAAATTTGCAGAGTATCGTG
CCGGAATTGTCCCCGTTAACTACCGCCGGGTGGCGTGCCGGAAACAAGGTGGGAT
AAGGTTACCATTAATGGATTCCGGTACTTCAACTTGATTTTGATCAGCAACGTCG
CCGGTGCCGGAGATATCACGATGGCATGGGTTAAAGGTTCGAACACCGATTGGAT
GAGTCTAAGCAGAAATTGGGGTCAAATTTGGCAATCAAACGCTCAGCTGATTGG
ACAATCGCTTTCTTTAGGGTTAGAAGCAGTGATGGTTCGATCTTCAGCCTCCATGA
ACATAGTACCTTCGAACTGGCAATTTGGGCAAATTTTACCGGGAAGAATTTCCG
GGTTTGA

Nucleotide

>LsEXPA-24

ATTTTTTTTTCTTCCATAAGTACCCCCTTAACATTCTTCATCCTCTTCACGCTTTAC
AACTTCCTATCTTCATCACTCTGTTTCTTCTTCAAAAATGGAGCTCAGTCGTGTTT
ACTGCTTTTTAATGTTAACTGCATTCTTCACAACCGTCGTCAATGCTCGTATCCCC
GGAGTTTACACCGGAGGCCAGTGGGAATCCGCCCACGCCACCTTCTACGGTGGTA
GTGACGCATCTGGCACCATGGGTAAGTTCCCCGTTCCCGATTCCCAATTACAAA

TTAGTTCAGAAGAAACAAAGCAATTGAATCTCGAATTGCAAGAAAACCCTTTTAA
CATTTTTTCATTTTTTCAGGTGGAGCATGTGGGTATGGGAATTTATACAGTCAAGGGT
ACGGCGTGAACACGGCGGCGCTAAGCACGGCGCTGTTCAACAATGGGTTCAGAT
GCGGCGCTTGTTTTGAGATAAAGTGTACGAACGACCCTCAATGGTGTACCCCGG
CAGCCCTTCAATTTTCATCACCGCCACCAATTTCTGCCCTCCTAACTTCGCTCAAC
CCAGTGACAATGGTGGATGGTGTAAACCCACCTCGCCCTCATTTTCGATCTCGCCAT
GCCCATGTTCTTCAAATTTGCAGAGTATCGTGCCGGAATTGTCCCGTTAACTAC
CGCCGGTGAGTCAATATTTAACTTCATCACTCCCATTTCCCATAGGTGTACAGATTG
TCAAATTTGTTGTAAGACTGGTAACGATTTTCTTTTTAGGGTGGCGTGCCGGAAAC
AAGGTGGGATAAGGTTCACCATTAATGGATTCCGGTACTTCAACTTGATTTTTGAT
CAGCAACGTCGCCGGTGCCGGAGATATCACGATGGCATGGGTAAAGGTTTCGAA
CACCGATTGGATGAGTCTAAGCAGAAATTGGGGTCAAATTTGGCAATCAAACGC
TCAGCTGATTGGACAATCGCTTTCTTTTAGGGTTAGAAGCAGTGATGGTTCGATCTT
CAGCCTCCATGAACATAGTACCTTCGAACTGGCAATTTGGGCAAACCTTTTACCGG
GAAGAATTTCCGGGTTTGAATTTGGATTCGGGTTTGGATTGGCGGGTCAAATTTG
TCCATTTTTAGTTTTATTTTTAAGAAATAGTATTATTTTGGGGGGAAAATACGAGA
GTGCTTTTTGTTGACTTTTTGACTATGAAGAAGTGCTTTTATGATCCTTTGTATTTT
GTAATGAAGCTGAAGTGGCTATGCCTAATTCTAGGGGCCC GCAGCTTTAATTTTC
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