IDENTIFICATION

Species: *Linum usitatissimum*

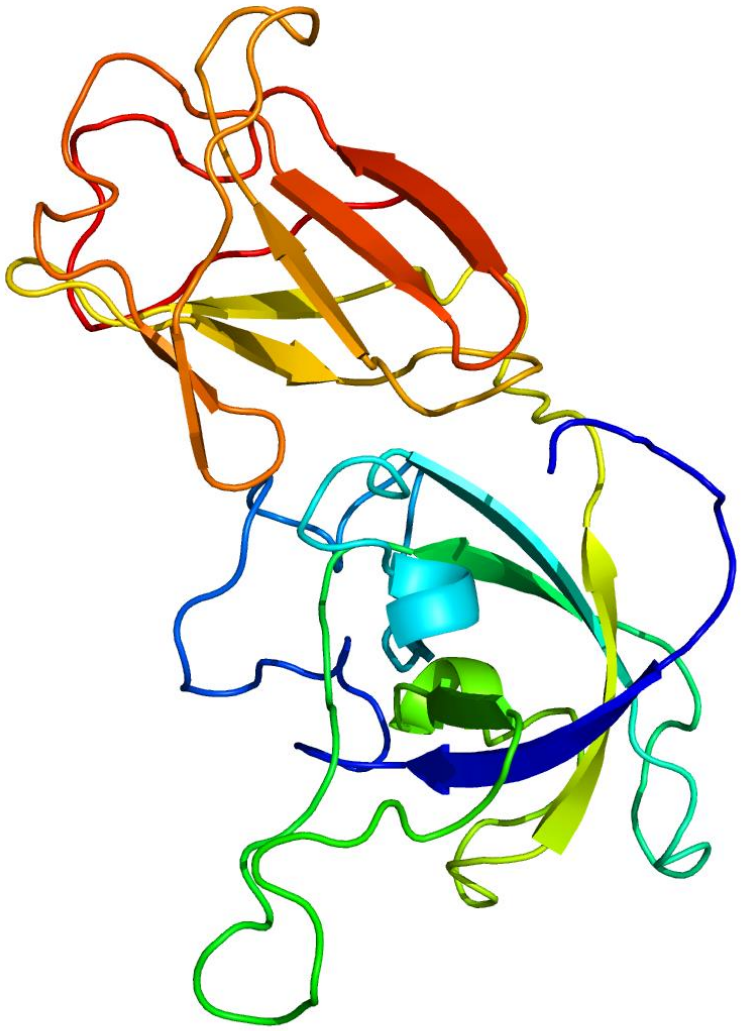
Locus: Lus10026614

Gene Model: Lus10026614

Description: LusEXPA-28

Family: Alpha Expansin

3D structure:



GENOME DATABASES

Phytozome: https://phytozome-next.jgi.doe.gov/info/Lusitatissimum_v1_0
KEGG: https://www.genome.jp/entry/D12016

EXTERNAL RESOURCES

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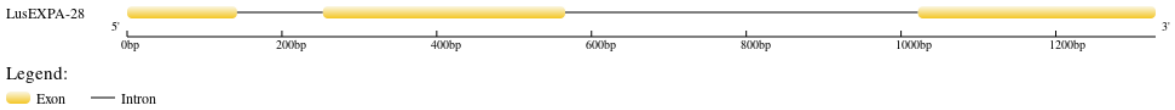
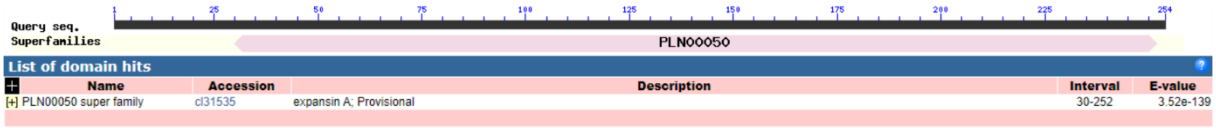
GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>LusEXPA-28

MGLRLFLLSVSALAMAATAAGYGGGEGGGWVNAHATFYGGGDASGTMGGACGYG
NPYSQGYGTNTAALSTALFNNGLACGSCYEIKCVNDGKWCLPGSILITATNFCPPNNA
LPNNAGGWCNPPQHHFDLSQPVFQHIAQYKAGIVPVAYRRVACRRRGGIRFTINGHS
YFNLVLITNVGGAGDVHSVSIKGSKTGWQAMSRNWGQNWQSNNYLNGQALSFKVT
TSDGRTVISNNVTPSGWSFGQTFAGAQFR*

CDS (coding sequence)

>LusEXPA-28

ATGGGTCTTAGGCTTTTCCTCCTCTCTGTTTCAGCTCTGGCAATGGCGGCCACTGC
CGCCGGCTACGGCGGCGGAGAAGGCGGAGGATGGGTCAACGCTCACGCCACTTT
CTACGGCGGCGGCGATGCTTCTGGCACAATGGGCGGAGCTTGTGGGTATGGGAAT
CCGTACAGCCAGGGATACGGGACGAACACTGCAGCTTTGAGCACGGCGCTGTTC
AACAATGGACTTGCTTGTGGCTCTTGCTACGAGATTAAGTGTGTCAACGACGGGA
AATGGTGCTTGCCCGGCTCGATTCTCATCACGGCGACAAACTTCTGCCCGCCGAA
TAATGCTCTGCCCAACAACGCCGGCGGGTGGTGCAACCCTCCTCAGCATCACTTT
GACCTCTCTCAGCCTGTATTCCAGCACATTGCTCAGTACAAGGCCGGAATCGTCC
CTGTCGCCTACCGCCGGGTTGCATGCAGGAGAAGAGGAGGCATCAGGTTCACAA
TCAATGGCCACTCATACTTCAATCTGGTCTTGATCACCAACGTTGGTGGAGCTGGT
GATGTCCACTCCGTGTCGATTAAGGGGTCGAAAACCGGATGGCAAGCCATGTCTA
GGAACTGGGGGCAGAATTGGCAGAGCAACAACTACCTCAATGGCCAAGCCTTGT
CCTTCAAGGTCACAACCAGCGATGGCCGCACCGTCATCTCCAACAATGTCACCCC
TTCCGGGTGGTCCTTTGGCCAGACCTTCGCTGGCGCACAATTCCGTTGA

Nucleotide

>LusEXPA-28

ATGGGTCTTAGGCTTTTCCTCCTCTCTGTTTCAGCTCTGGCAATGGCGGCCACTGC
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CTACGGCGGCGGCGATGCTTCTGGCACAATGGGTCTGCATTACGCCTTAAAACCC
ATTCCCAATTTCAAGTTTTCAACTCATTTCGTTTAAGAAGACGACAGCTTTTTGGC
TGGTTTTGAGAAATTTATGATTTTTTTTTCAGGCGGAGCTTGTGGGTATGGGAATC
CGTACAGCCAGGGATACGGGACGAACACTGCAGCTTTGAGCACGGCGCTGTTCA

ACAATGGACTTGCTTGTGGCTCTTGCTACGAGATTAAGTGTGTCAACGACGGGAA
ATGGTGCTTGCCCGGCTCGATTCTCATCACGGCGACAAACTTCTGCCCGCCGAAT
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ACCTCTCTCAGCCTGTATTCCAGCACATTGCTCAGTACAAGGCCGGAATCGTCCCT
GTCGCCTACCGCCGGTAAGAAATTATAACCAGTTATCCAAAAGTTTTCCAGTTAG
TCTAAATATGAAATAACCAAATTACCCCCTCCAACTGACCAAATTTCCTCTACTA
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GTTTGTCTGGTTTGGTTTAGTAATGTTGAAACCAATATGTCCATAAAGAACCTTAC
TTATCCTTGAAATTGGAAACTATTACCCTTGGTGACTATGAACCATTGTTTAGACT
TTAACCCATCTTTGGTTTAATGATGTTGAGACCAATATGTATGTCCACAAATAAAC
CTACTTTTTCCAATATGGACACTTTTACCCCTGGGGAACCATTCATTTACATGGCT
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GCCTTGTCCTTCAAGGTCACAACCAGCGATGGCCGCACCGTCATCTCCAACAATG
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