

## IDENTIFICATION

**Species:** *Linum usitatissimum*

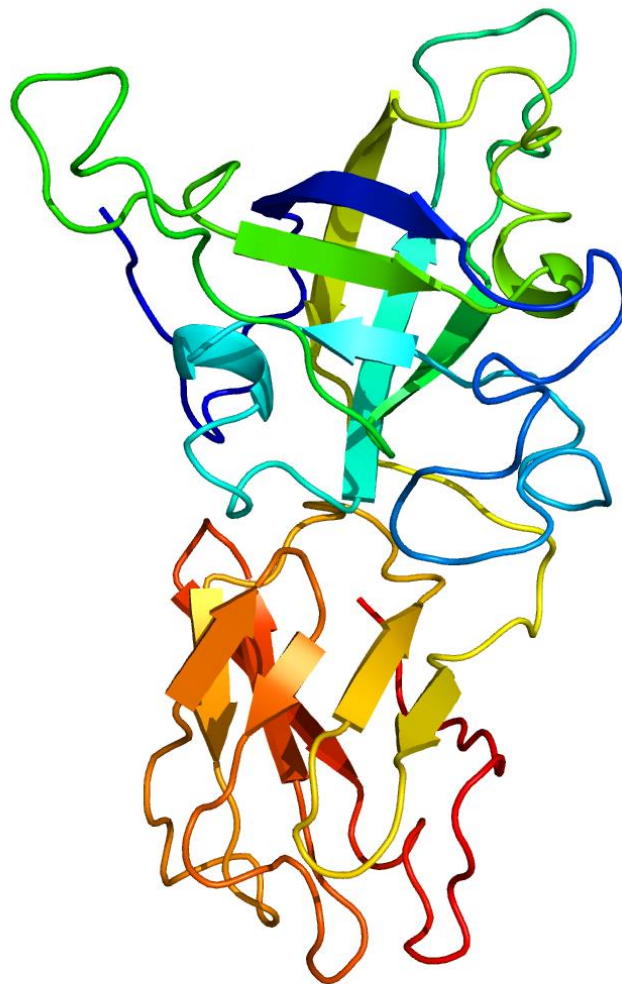
**Locus:** Lus10037164

**Gene Model:** Lus10037164

**Description:** LusEXPA-23

**Family:** Alpha Expansin

**3D structure:**



## GENOME DATABASES

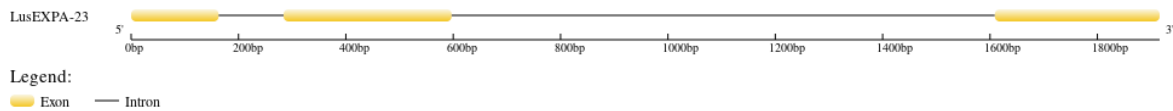
Phytozome: [https://phytozome-next.jgi.doe.gov/info/Lusitatissimum\\_v1\\_0](https://phytozome-next.jgi.doe.gov/info/Lusitatissimum_v1_0)

KEGG: <https://www.genome.jp/entry/D12016>

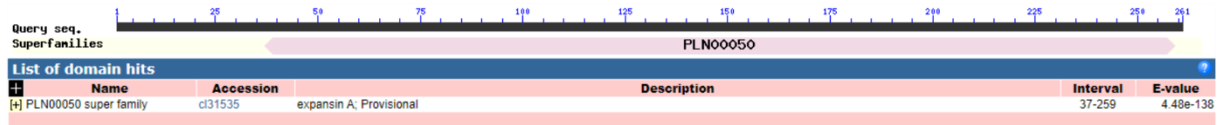
## EXTERNAL RESOURCES

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## GENE STRUCTURE



## DOMAIN ARCHITECTURE



## SEQUENCES

### Peptide

>LusEXPA-23

MGLAPFLAIMALTAAMASSVHGYGGRGGGRGGGGGNWVNAHATFYGGGDASGTM  
GGACGYGNLYSQGYGTNTAALSTALFNGLACGSCYEIKCVNDRRWCLPGSILITAT  
NFCPPNSALPNNAGGWCNPPQHFDLSQPVFQHIAQYKAGIVPVA YRRVACRRRGGI  
RFTINGHSYFNLVLTNVGGAGDVHSVAIKGSRTGWQTMSRNWQNWQSNKLDG  
QALSFKVTTSDGRSVVSYNVAPSRWSFGQTFAGAQFR\*

### CDS (coding sequence)

>LusEXPA-23

ATGGGTCTTGCCCCATTCCTTGCAATAATGGCTCTGACGGCCGCAATGGCGTCTTC  
TGTCCACGGCTACGGTGGCAGAGGTGGCGGCAGAGGAGGCGGCGGGCAACTG  
GGTTAACGCTCATGCAACTTTCTACGGCGGCGGTGATGCATCAGGAACAATGGGT  
GGGGCTTGTGGTTACGGGAACCTGTACAGTCAAGGCTATGGAACGAACACAGCT  
GCGTTGAGCACGGCTCTGTTCAACAATGGACTTGCGTGTGGGTCCTGCTACGAGA  
TTAAGTGCGTGAACGACCGGAGATGGTGCCTTCCCGGCTCAATTCTCATCACCGC  
CACTAATTTCTGCCCGCCGAACAGTGC GTTGCCCAACAACGCCGGCGGGTGGTGT  
AACCTCCTCAGCACCCTTTGACCTCTCTCAGCCTGTCTTCCAGCACATTGCTCA  
GTACAAGGCTGGAATCGTTCGGTTGCTTACAGAAGGGTGGCCTGCAGGAGAAG  
AGGAGGAATAAGGTTACAATCAACGGCCACTCCTACTTCAACCTAGTCCTGATC  
ACCAATGTCGGCGGGGCCGGTGACGTGCATTCGGTGGCAATCAAAGGATCAAGA  
ACAGGATGGCAAACAATGTCGAGGA ACTGGGGTCAA AATTGGCAAAGCAACAGC  
AAGCTCGACGGTCAAGCTTTGTCTTCAAAGTTACAACCAGTGATGGCCGCTCTG  
TTGTGTCCTACAACGTCGCCCTTCCCGTTGGTCGTTTCGGCCAGACTTTTGCCGGC  
GCTCAGTTCGGTTGA

### Nucleotide

>LusEXPA-23

ATGGGTCTTGCCCCATTCCTTGCAATAATGGCTCTGACGGCCGCAATGGCGTCTTC  
TGTCCACGGCTACGGTGGCAGAGGTGGCGGCAGAGGAGGCGGCGGGCAACTG  
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CCCATCTTTTCATGTGGACTATTGTACCCTTGTTAATTCGTTGAAAATTGGACTAG  
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CAATTTATGAATATTTTTTTAAAGCGTAATACTGAGTTAAAATATATAACAACAC  
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CTCAAGGCCGAAATTGCCTTGAGCTGTGACTCTCCCGGGCTCCCCTTGTATCCGCC  
CCTGTTTACCGTGCTCTATCACCAAACCAATTCCATTTAAACAAACTAAGGATGA  
AAATCATAATTGTCATTATGATATCCTGTGCAATTTGATTCGGTCAAATATAATAA  
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CGTTCGGCCAGACTTTTGCCGGCGCTCAGTTCGGTTGA