

IDENTIFICATION

Species: *Arabidopsis lyrata*

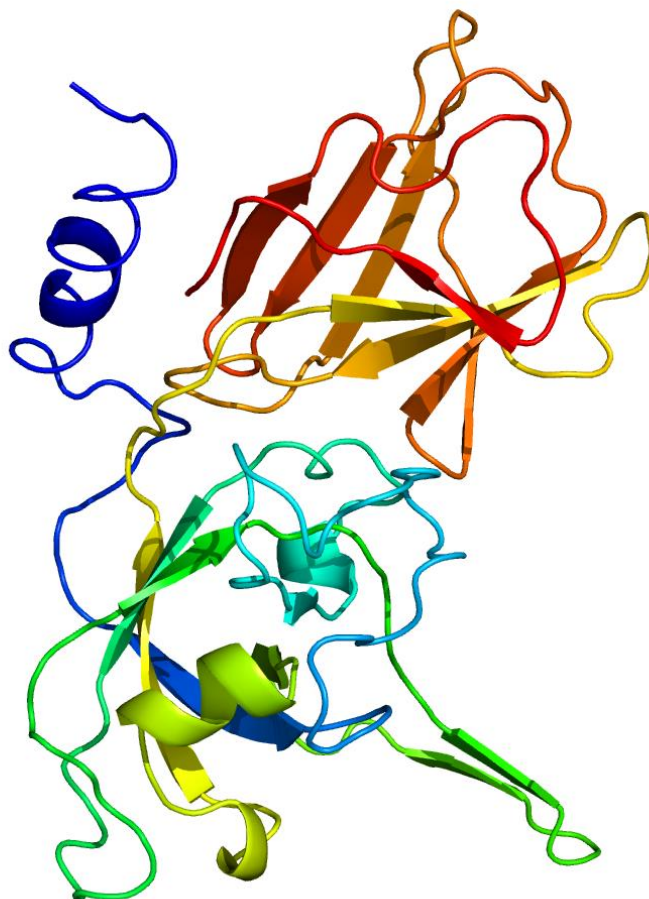
Locus: AL6G51710

Gene Model: AL6G51710.t1

Description: ALEXPA-17

Family: Alpha Expansin

3D structure:



GENOME DATABASES

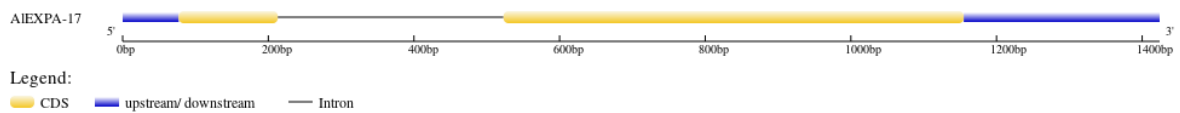
Phytozome: https://phytozome-next.jgi.doe.gov/info/Alyrata_v2_1

Kegg: <https://www.genome.jp/entry/T01578>

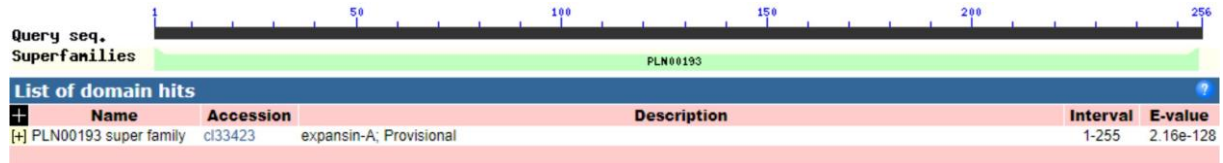
EXTERNAL RESOURCES

https://plants.ensembl.org/Arabidopsis_lyrata/Info/Index

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>AIEXPA-17

MTKIFSLLVAMIFSIMFFMKISSVSAGWLQAHATFYGGSDASGTMGGACGYGNLYTD
GYKTNTAALSTALFNDGKSCGGCYQILCDATKVPQWCLKGKSITITATNFCPPNFAQ
ASDDGGWCNPPRPHFDMAQPAFLTIAKYKAGIVPILYKRVGCRRSGGMRFTMNGRN
YFELVLISNVAGAGEISKVWIKGSKSNKWETMSRNWGANYQSNTYLNQSLSFVKVQ
LSDGRIKAALNVVPSNWQFGQSFKSNINF*

CDS (coding sequence)

>AIEXPA-17

ATGACGAAGATTTTCTCTCTATTGGTCGCAATGATCTTTTCCATAATGTTCTTCAT
GAAGATCAGCTCAGTTTCTGCTGGTTGGTTGCAAGCTCATGCGACCTTTTATGGCG
GAAGTGATGCTTCTGGTACAATGGGTGGAGCTTGTGGTTATGGAAACCTATACAC
AGACGGTTACAAGACAAACACAGCGGCGCTAAGCACGGCACTGTTCAACGACGG
CAAGTCATGCGGTGGATGTTACCAAATCTTGTGTGATGCAACCAAAGTACCACAA
TGGTGTCTTAAAGGAAAATCAATCACAAATCACAGCCACAACTTCTGTCCACCAA
ACTTTGCTCAGGCAAGCGACGATGGAGGATGGTGCAACCCACCAAGACCTCACTT
TGACATGGCTCAGCCTGCGTTTCTAACCATCGCTAAGTACAAAGCTGGTATCGTT
CCATTCTCTACAAAAGGGTTGGATGTAGAAGAAGCGGAGGGATGAGATTTACG
ATGAACGGTAGAACTATTTTCGAGCTTGTTCATCTCAAACGTAGCAGGAGCTG
GTGAGATCTCTAAAGTTTGGATTAAGGCTCTAAGAGCAACAAATGGGAGACAA
TGTCAGAAATTGGGGAGCTAATTATCAGAGCAACACTTACCTTAATGGACAATC
TCTCTTTTCAAAGTTCAACTCAGTGATGGAAGAATCAAAGCAGCTCTCAACGTT
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Nucleotide

>AIEXPA-17

TGCATCCAACACTACAACAATCATCAACTTCTTCTCTAATCAAAGTTAAACACC
TAAGACATTGAAAGAAAAACAAATGACGAAGATTTTCTCTCTATTGGTCGCAATG
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CACAAACTAGAGATGGAAATTTGGTTTTTAGGGTTTATTCGATTTGGAGATATTTA
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CTCTCATAGTTTTCTTCTTCAGGTGGAGCTTGTGGTTATGGAAACCTATACACAGA
CGGTTACAAGACAAACACAGCGGCGCTAAGCACGGCACTGTTCAACGACGGCAA
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TTGCTCAGGCAAGCGACGATGGAGGATGGTGCAACCCACCAAGACCTCACTTTGA
CATGGCTCAGCCTGCGTTTTCTAACCATCGCTAAGTACAAAGCTGGTATCGTTCCC
ATTCTCTACAAAAGGGTTGGATGTAGAAGAAGCGGAGGGGATGAGATTTACGATG
AACGGTAGAAACTATTTTCGAGCTTGTTCATCTCAAACGTAGCAGGAGCTGGTG
AGATCTCTAAAGTTTGGATTAAGGCTCTAAGAGCAACAAATGGGAGACAATGT
CAAGAAATTGGGGAGCTAATTATCAGAGCAACACTTACCTTAATGGACAATCTCT
CTCTTTCAAAGTTCAACTCAGTGATGGAAGAATCAAAGCAGCTCTCAACGTTGTT
CCTTCGAATTGGCAGTTTGGTCAGAGCTTCAAGAGCAACATCAACTTCTGATCTC
AGTAATGATTGGGTTTTATGGTTTTTATCCATCTTTTGTATTTACTTTTCATTGGGTAT
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