

IDENTIFICATION

Species: *Arabidopsis lyrata*

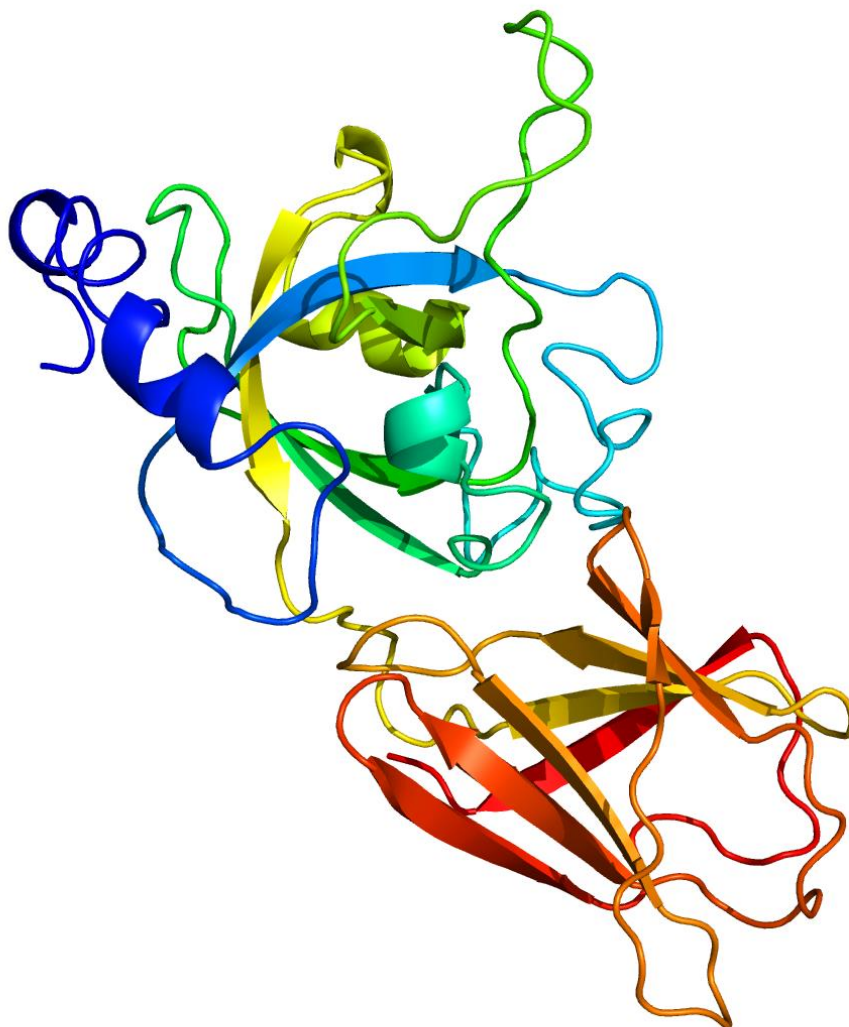
Locus: AL4G38480

Gene Model: AL4G38480.t1

Description: ALEXPA-11

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>

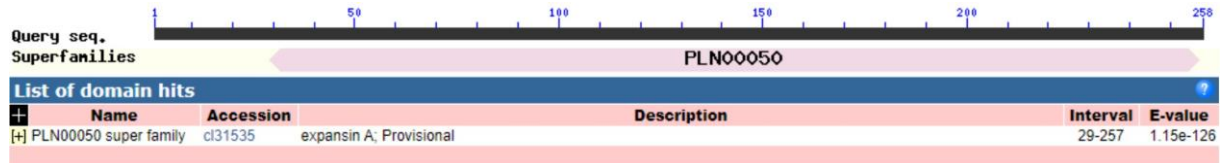
EXTERNAL RESOURCES

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

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>AIEXPA-11

MSITSASKYSIISIISLLSLSFFLQGTHGDDGGWQGGHATFYGGEDASGTMGGACGYG
NLYGQGYGTNTAALSTALFNGLTCGACYEMKCNDDPRWCLGSTITVTATNFCPPN
PGLSNDNGGWCNPPLQHFDLAEPAFLQIAQYRAGIVPVSFRRVPCMKKGGIRFTINGH
SYFNLVLISNVGGAGDVHAVSIKGSKTQSWQAMSRNWGQNWQSNSYMNDQSLSFQ
VTSDGRTLVSNDVAPSNWQFGQTYQGGQF*

CDS (coding sequence)

>AIEXPA-11

ATGTCTATCACATCAGCCTCCAAATATTCAATAATCTCAATTATATCTTTACTCAG
CTTATCATTCTTCCTCCAAGGAATCATGGAGACGACGGAGGTTGGCAAGGTGGC
CACGCTACGTTCTACGGCGGCGAAGATGCTTCCGGCACCATGGGCGGAGCTTGTG
GCTATGGAAATTTGTATGGCCAAGGTTACGGGACGAACACGGCGGCTTTAAGTAC
GGCTTTGTTCAACAACGGACTCACGTGTGGCGGTGCTATGAGATGAAGTGTAAC
GATGACCCGAGGTGGTGTCTCGGGTCTACCATCACCGTCACAGCCACTAACTTTT
GCCACCAAACCCTGGCCTCTCCAACGATAATGGAGGTTGGTGCAATCCTCCTCT
TCAACATTTTCGACCTAGCCGAGCCAGCTTTTCTCCAGATCGCTCAGTATCGTGCCG
GCATTGTTCCCTGTTTCTTTCCGAAGAGTACCATGTATGAAGAAAGGAGGAATAAG
GTTACAGATCAACGGACATTCATACTTCAACCTCGTCCTGATCTCGAACGTAGGA
GGAGCAGGAGACGTACACGCTGTCTCGATCAAAGGCTCAAAAACACAGTCGTGG
CAAGCAATGTCTAGAAATTGGGGACAAAACCTGGCAGAGCAATTCTTACATGAAC
GACCAAAGCCTTTCTTCCAGGTCACCACCAGCGATGGTTCGCACACTCGTTAGCA
ATGACGTGGCTCCTTCTAATTGGCAATTCGGACAAACCTACCAAGGCGGTCAATT
CTGA

Nucleotide

>AIEXPA-11

AATCTCACGATTCTCACCAAATCATATCCGATATCACAACCGAAATAACTAACCC
CTTAAAAAAAATGTCTATCACATCAGCCTCCAAATATTCAATAATCTCAATTA
TATCTTTACTCAGCTTATCATTCTTCCTCCAAGGAATCATGGAGACGACGGAGGT

TGGCAAGGTGGCCACGCTACGTTCTACGGCGGCGAAGATGCTTCCGGCACCATGG
GTACGTATGACCAATAACAATAAAGAAAAAAGCGTATGTTAGCTAAATTATATCT
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GTGGCTATGGAAATTTGTATGGCCAAGGTTACGGGACGAACACGGGCGGCTTTAAG
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TCTTCAACATTTTCGACCTAGCCGAGCCAGCTTTTCTCCAGATCGCTCAGTATCGTG
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GGACGCTAAATGATAAGATTGCGACAAAACCTCTTCATAGTTTTTAACAATTTTGG
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CTAAGGAAACAAAACAAACTATTTTACATGTAATTGATGTAAAGATTAATCACCA
ATCTATATTTACCAATATAATTGACTTAGAGACATGACTTTTGTAGCTACCATTGT
TAAAACCTAAAACCTAATTAACAAATACATTAGGATATTTTGTGCCATTATTAATT
TTTACTAGTGATGTTTGCCGTGTAGAAAAGCCTAGGCAAGAGCTTTTATAAGTCT
ATGTTCTTAATTAACCTAATGGCTTATGTCCGGTGTTTTTACGTGATTATTACAGAG
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CAACCTCGTCCTGATCTCGAACGTAGGAGGAGCAGGAGACGTACACGCTGTCTCG
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AACTGGCAGAGCAATTCTTACATGAACGACCAAAGCCTTTCCTTCCAGGTCACCA
CCAGCGATGGTCGCACACTCGTTAGCAATGACGTGGCTCCTTCTAATTGGCAATT
CGGACAAACCTACCAAGGCGGTCAATTCTGATCAGACCATCATCATCCACATCTC
TCTGTTTTGGGTGCTGACGTGGCTGCGTATTGCTGAGGTGGCTCGTAAGCACCCG
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