

IDENTIFICATION

Species: *Arabidopsis lyrata*

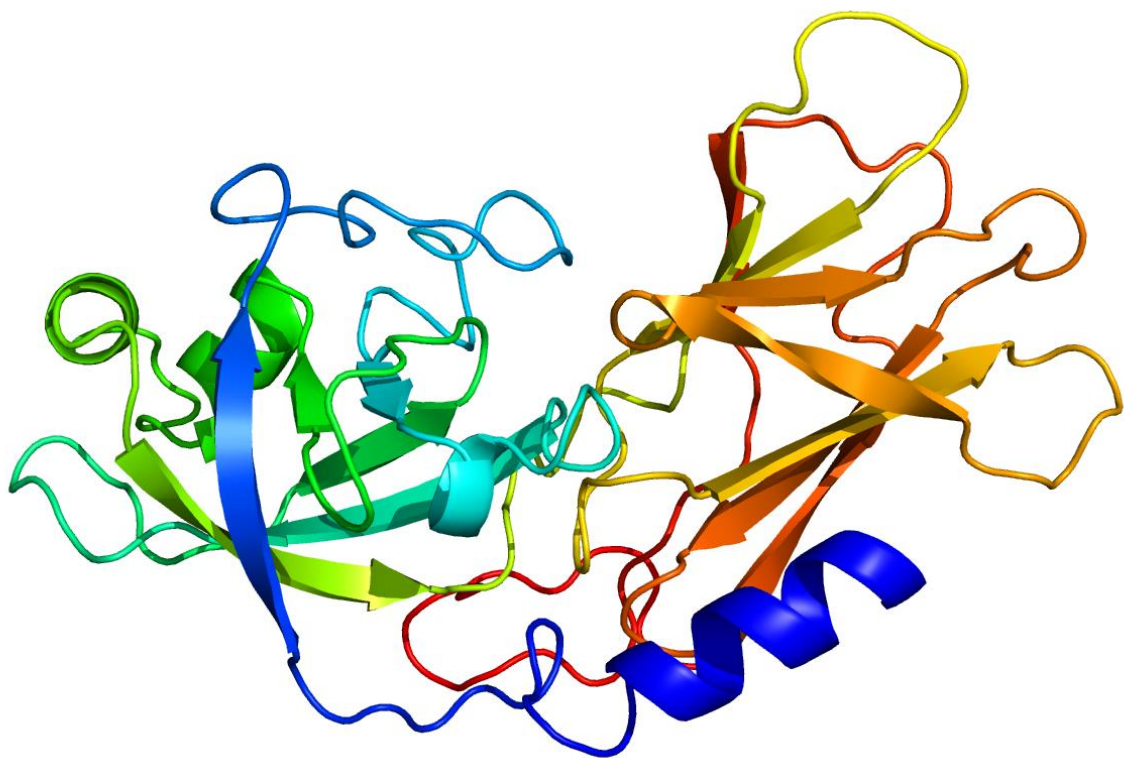
Locus: AL5G24680

Gene Model: AL5G24680.t1

Description: ALEXLA-02

Family: Expansin Like Alpha

3D structure:



GENOME DATABASES

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

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

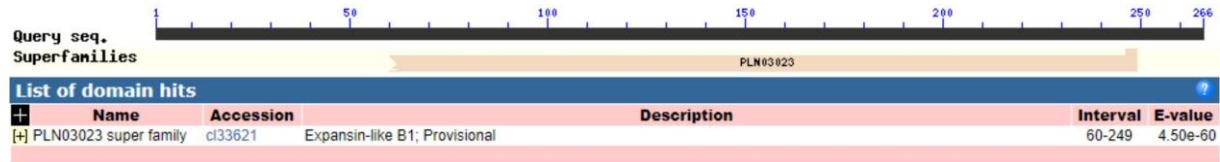
EXTERNAL RESOURCES

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

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>ALEXLA-02

MGSFLYLIVVIFLFSVVNACDRCLHRSKAAYFSSASALSSGACSYGSMATSFFAGHIA
AAIPSIYKDGAGCGACFQVRCKNPKLCSSKGTIVMVTDLNKSNTDLVLSRAFRAM
AKPVVGADKDLLKQGIVDIEYQRPVPCDYGNKLNLRVEEASKKPNYLEIKLLYQGG
QTEVVSIDIAQVGSSPNWGYMTRSHGAVWVTDKVPVTPGALQFRFIVTGGYDGMKIWS
QNVLPNWEAGKTYDAGVQITDIAQEGCDPCDAHIWN*

CDS (coding sequence)

>ALEXLA-02

ATGGGAAGCTTTCTCTATCTCATTGTAGTCATCTTCCTCTTCTCATCATCTGTAAAC
GCTTGTGATCGATGTCTTCACCGTTCTAAAGCAGCTTATTTCTCCTCTGCTTCTGCT
CTCTCTTCTGGAGCTTGTCTTATGGCTCTATGGCTACGAGTTTCTTCGCCGGACA
CATAGCCGCAGCAATACCTTCGATCTACAAAGACGGCGCTGGATGCGGAGCTTGC
TTTCAAGTCAGATGCAAGAACCCTAAGCTGTGTAGCAGCAAAGGAACCATTGTGA
TGGTCACAGACTTGAACAAGAGCAACCAAAACCGATCTTGTCTTAGTAGCAGAGC
ATTTAGAGCTATGGCTAAACCTGTTGTTGGTGCTGACAAAGATCTTCTCAAACAA
GGAATCGTCGACATTGAATACCAAAGAGTTCCTTGCATTATGGGAACAAGAATC
TAAACGTGAGAGTCGAAGAAGCAAGTAAAAAGCCAAACTACTTAGAGATAAAGC
TTTTATAACCAAGGAGGACAAACCGAAGTAGTATCAATCGACATTGCTCAGGTCGG
TTCATCGCCAAATTGGGGTTACATGACCAGAAGCCACGGCGCGGTATGGGTGACT
GACAAAGTACCAACCGGCGCTTTCAGTTCAGATTCATAGTAACCGGCGGCTACG
ACGGTAAAATGATTTGGTACAGAATGTTCTTCCATCCAATTGGGAAGCTGGTAA
GACTTACGACGCCGGCGTTCAAATCACAGACATTGCTCAAGAAGGTTGTGATCCA
TGCGATGCTCACATCTGGAATAA

Nucleotide

>ALEXLA-02

CTTTTCATGTTATTCACATATCTCTCTAATTTGATCATATATATTATTTATTGTTTT
CTCTTGAAAGAAACAAAATGGGAAGCTTTCTCTATCTCATTGTAGTCATCTTCCT
CTTCTCATCATCTGTAAACGCTTGTGATCGATGTCTTCACCGTTCTAAAGCAGCTT

ATTTCTCCTCTGCTTCTGCTCTCTCTTGTAAGCATTACACATCTTCTCTGATCATTAC
TTCTTTTTAACTGTATCTGTTTGTTCCTTTTCTCATGTTTTGTTAATGGGTTTTTGCA
GCTGGAGCTTGTTCTTATGGCTCTATGGCTACGAGTTTCTTCGCCGGACACATAGC
CGCAGCAATACCTTCGATCTACAAAGACGGCGCTGGATGCGGAGCTTGCTTTCAA
GTCAGATGCAAGAACCCTAAGCTGTGTAGCAGCAAAGGAACCATTGTGATGGTC
ACAGACTTGAACAAGAGCAACCAAACCGATCTTGTCTTAGTAGCAGAGCATTTA
GAGCTATGGCTAAACCTGTTGTTGGTGCTGACAAAGATCTTCTCAAACAAGGAAT
CGTCGACATTGAATACCAAAGGTATGATTCTCAAACACCTTAACTCTTTGGTTTT
CATATAATCACATGACTTTAATTTGCTAATGAAAAACAGAGTTCCTTGCGATTA
TGGGAACAAGAATCTAAACGTGAGAGTCGAAGAAGCAAGTAAAAAGCCAAACTA
CTTAGAGATAAAGCTTTTATACCAAGGAGGACAAACCGAAGTAGTATCAATCGA
CATTGCTCAGGTCGGTTCATCGCCAAATTGGGGTTACATGACCAGAAGCCACGGC
GCGGTATGGGTGACTGACAAAGTACCAACCGGCGCTCTTCAGTTCAGATTCATAG
TAACCGGCGGCTACGACGGTAAAATGATTTGGTCACAGAATGTTCTTCCATCCAA
TTGGGAAGCTGGTAAGACTTACGACGCCGGCGTTCAAATCACAGACATTGCTCAA
GAAGGTTGTGATCCATGCGATGCTCACATCTGGAACCTAACTCATTCCAATTCTCCT
TATTTAGGCAAACAACAACACCCTTATAGGTTTATTATATATGAAATGTGTAAC
AGAGTTAAAGAACATAATGTGAATGCTTAGTCTAATGATTCTATAATGATTAAC
AAGAGAACCAATC