

IDENTIFICATION

Species: *Arabidopsis lyrata*

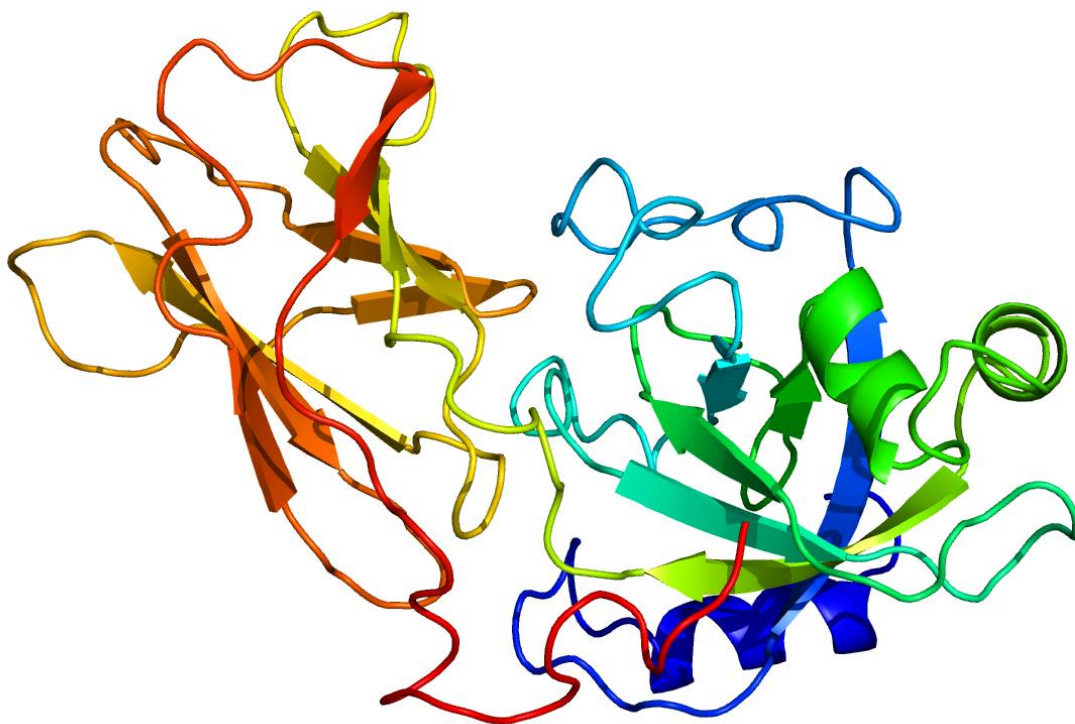
Locus: AL7G10270

Gene Model: AL7G10270.t1

Description: AEXLA-03

Family: Expansin Like Alpha

3D structure:



GENOME DATABASES

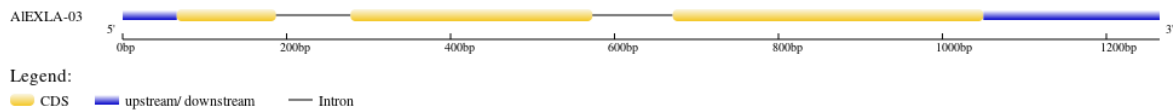
Phytozome: https://phytozome-next.jgi.doe.gov/info/Alyrata_v2_1

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

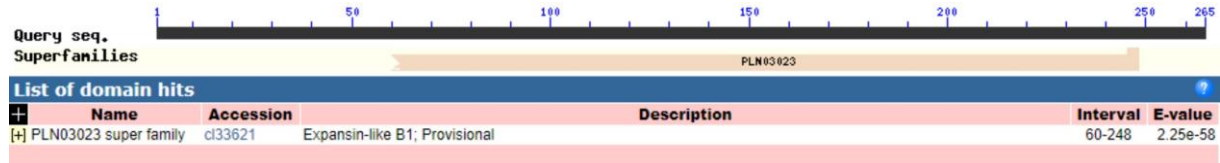
EXTERNAL RESOURCES

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

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>ALEXLA-03

MEGFLFLLSVVFLFSSAAACDRCLHRSKAA YFSSASALSSGACAYGSMATGFFAGHI
AAALPSIYKDGSGCGACFQVRCTNPTLCSSKGTVM L TDLNKS NQTDLILSSRA FRA
MAKPVVGSDRDLLKEGLVDIEYRRVPCDYGNK KMNV RVEESSINPNYLAIKLLYQG
GQTEVVAIDIAHV GSSHWSY MTRSHGAVWVTDK VPTGALQFRFVVTAGYDGKMV
WSQRVLPANWEAGMTYDAGVQITDIAQEGCDPCDDHTWN*

CDS (coding sequence)

>ALEXLA-03

ATGGAAGGCTTTCTCTTCCTCCTCTCAGTCGTCTTCCTCTTCTCCTCATCTGCAGCC
GCCTGCGACCGATGTCTTCACCGTTCTAAGGCTGCTTATTTCTCCTCCGCTCTGC
TCTCTCCTCCGGAGCTTGTGCCTATGGCTCTATGGCTACGGGTTTCTTCGCCGGAC
ACATTGCCGCGGCTCTGCCTTCCATCTACAAAGACGGCTCCGGCTGCGGAGCTTG
CTTCCAGGTCAGATGTACGAACCCGACCCTTTGCAGCAGCAAAGGAACAACGGT
GATGCTCACAGACCTGAACAAGAGCAACCAAACCGATCTTATCCTTAGCAGCAG
AGCCTTTAGGGCCATGGCCAAGCCTGTTGTTGGCTCCGACAGAGATCTTCTCAA
GAAGGCCTTGTCGACATTGAATACAGGAGAGTTCCTTGCGATTACGGGAACAAG
AAGATGAACGTGAGAGTTGAAGAGTCAAGTATAAATCCAACTACTTGGCGATA
AAGCTCTTGTACCAAGGAGGCCAAACCGAAGTGGTAGCCATTGACATTGCTCACG
TTGGTTCGTCACACTGGAGTTACATGACCAGAAGCCACGGAGCCGTGTGGGTTAC
TGACAAAGTACCAACCGGAGCTCTGCAGTTCAGGTTTCGTGGTGACCGCAGGCTAC
GACGGCAAATGGTCTGGTCGCAGAGGGTCCTTCCAGCTAACTGGGAAGCTGGG
ATGACCTATGACGCCGGCGTTCAGATCACCGACATTGCTCAGGAAGGTTGTGATC
CATGCGACGATCACACCTGGA ACTGA

Nucleotide

>ALEXLA-03

CCTCTCCTCACTTTTCGTCGCATCCCCATTAATAATAGTATTGTTTTGTTGGTTTC
TTCAAGAAAATGGAAGGCTTTCTCTTCCTCCTCTCAGTCGTCTTCCTCTTCTCCTCA
TCTGCAGCCGCTGCGACCGATGTCTTCACCGTTCTAAGGCTGCTTATTTCTCCTC

CGCCTCTGCTCTCTCCTGTAAGCTTTCCATCTCCTTTCATTA CTTCACTCTTTTGTG
TCTCTTTTCTCATCTTTTAATTTGTACTTACGGGTTTTTTTCTTTAATTCAGCCGGAG
CTTGTGCCTATGGCTCTATGGCTACGGGTTTCTTCGCCGGACACATTGCCGCGGCT
CTGCCTTCCATCTACAAAGACGGCTCCGGCTGCGGAGCTTGCTTCCAGGTCAGAT
GTACGAACCCGACCCTTTGCAGCAGCAAAGGAACAACGGTGATGCTCACAGACC
TGAACAAGAGCAACCAAACCGATCTTATCCTTAGCAGCAGAGCCTTTAGGGCCAT
GGCCAAGCCTGTTGTTGGCTCCGACAGAGATCTTCTCAAAGAAGGCCTTGTCGAC
ATTGAATACAGGAGGTTTCGATTCCCAAAGA AACTCTTACTATCTATGATATATGC
TAGCTTTTCTTCTCATTTTCCTTCAAGTAGTAATAAGAATAATTGAAAATGAAACA
GAGTTCCTTGCGATTACGGGAACAAGAAGATGAACGTGAGAGTTGAAGAGTCAA
GTATAAATCCAACTACTTGGCGATAAAGCTCTTGTACCAAGGAGGCCAAACCGA
AGTGGTAGCCATTGACATTGCTCACGTTGGTTCGTCACACTGGAGTTACATGACC
AGAAGCCACGGAGCCGTGTGGGTTACTGACAAAGTACCAACCGGAGCTCTGCAG
TTCAGGTTTCGTGGTGACCGCAGGCTACGACGGCAA AATGGTCTGGTTCGCAGAGG
GTCCTTCCAGCTAACTGGGAAGCTGGGATGACCTATGACGCCGGCGTTCAGATCA
CCGACATTGCTCAGGAAGGTTGTGATCCATGCGACGATCACACCTGGA ACTGACT
CACTCCA ACTCTCTACTTTCTCTCTATGTATGCGTACGTAACAGACTTGTTTATTTG
ACGAGAGGAAGAATCAACGGGAATGCATAATCTGACGATTCCATAAGAATGAAG
AGAGCTAAGAATGTAAAGGGATATATGCATGTGTATGTACAAAAGGTCTATATAT
ATGTACACCATTCTTTCTATCTGTAACCTTGC GACTTAAAATGACAT