

IDENTIFICATION

Species: *Arabidopsis lyrata*

Locus: AL7G51180

Gene Model: AL7G51180.t1

Description: ALEXPA-20

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>

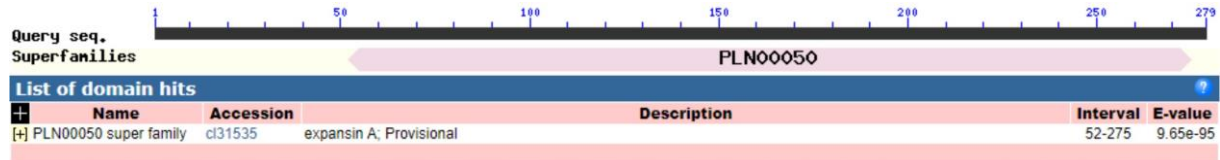
EXTERNAL RESOURCES

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

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>AIEXPA-20

MKLLGKMIYVECFMIIMATWFVSMSYGHARAMMVSVDVAEAPVIDDVVGSPTNGLDTS
WYDARATFYGDIHGGETQQGACGYGDLFRQYGLATAALSTALFNEGYTCGACYEI
MCANNPQWCLPGSIKITATNFCPPNYTKTVGVWCNPPQKHFDLSLPMFLKIAQYKAG
VVPVRYRRVACAKTGGVKFETKGNPYFLMILPYNVGGAGDIKFVQVKGKNTGWIT
MKKNWGQNWTTGVKLTGQGISLRVTTSDGITKDFINLMPKNWGFQTFDGKINF*

CDS (coding sequence)

>AIEXPA-20

ATGAAACTCTTAGGAAAAATGATATATGTAGAATGTTTTATGATAATAATGGCGA
CATGGTTCGTGTCCATGAGTTATGGTCATCGAGCGATGATGGTTAGTGATGTAGC
CGAAGCACCCGTGATTGACGATGTAGTAGGAAGCCCAACCAACGGACTCGACAC
TTCTTGGTATGACGCACGAGCAACATTTACGGTGATATCCATGGTGGAGAACT
CAACAGGGAGCTTGTGGATATGGTGATCTATTCAGACAAGGCTATGGTCTAGCCA
CAGCGGCATTGAGCACAGCACTCTTCAATGAAGGGTACACATGTGGGGGCTTGTTA
CGAGATCATGTGTGCGAACAATCCACAATGGTGTGGCCCGGATCCATTAAGATC
ACTGCTACAAATTTCTGTCCACCAAATTACACCAAACCGTCGGCGTTTGGTGCA
ACCCACCCCAAAGCATTGATCTCTCCTTACCAATGTTCCCTCAAGATCGCCCAG
TACAAAGCTGGGGTTGTTCCAGTTAGATACAGACGTGTTGCTTGTGCAAAAACCTG
GTGGTGTCAAGTTTGAACCAAAGGAAACCCTTATTTCTTAATGATATTGCCATA
CAATGTAGGAGGAGCTGGAGATATTAAGTTCGTGCAAGTTAAAGGAAACAAAC
CGGGTGGATAACAATGAAAAAGAATTGGGGACAGAATTGGACCACTGGTGTAA
GTAACTGGTCAGGGTATATCGTTAAGGGTTACAACGAGTGATGGGATTACAAA
GATTTTATTAATTTGATGCCAAAAAATTGGGGATTTGGACAGACTTTTATGATGAA
AGATTAATTTTAG

Nucleotide

>AIEXPA-20

ATGAAACTCTTAGGAAAAATGATATATGTAGAATGTTTTATGATAATAATGGCGA
CATGGTTCGTGTCCATGAGTTATGGTCATCGAGCGATGATGGTTAGTGATGTAGC

CGAAGCACCCGTGATTGACGATGTAGTAGGAAGCCCAACCAACGGACTCGACAC
TTCTTGGTATGACGCACGAGCAACATTTTACGGTGATATCCATGGTGGAGAACT
CAACGTAAGTGAAAATACTAATATTTTTCTTGATTAATCCAATTATTGAATTCTTG
TTTTGTTTTCAAACATCGTATACGCTGCGATTGTTTTAAATACTTACTTTTGCGT
TGCGTTTGCATTGACATTTACTAAAAGAACTACGAGTGTTTTTCTATAT
AAAAAGTACGAGTATATGATAACATGTTATTATAAATAATCTTAAAACATTCATT
TTTATTTTATTTTATTCAATATAGAGGGAGCTTGTGGATATGGTGATCTATTCAG
ACAAGGCTATGGTCTAGCCACAGCGGCATTGAGCACAGCACTCTTCAATGAAGG
GTACACATGTGGGGCTTGTACGAGATCATGTGTGCGAACAATCCACAATGGTGT
TTGCCCGGATCCATTAAGATCACTGCTACAAATTTCTGTCCACCAAATTACACCA
AAACCGTCGGCGTTTGGTGCAACCCACCCCAAAGCATTTTGATCTCTCCTTACC
AATGTTCCCTCAAGATCGCCCAGTACAAAGCTGGGGTTGTTCCAGTTAGATACAGA
CGTGTGCTTGTGCAAAAACCTGGTGGTGTCAAGTTTGAAACCAAAGGAAACCCTT
ATTTCTTAATGATATTGCCATACAATGTAGGAGGAGCTGGAGATATTAAGTTCGT
GCAAGTTAAAGGAAACAAAACCGGGTGGATAACAATGAAAAAGAATTGGGGAC
AGAATTGGACCACTGGTGTAAAGTTAACTGGTCAGGGTATATCGTTAAGGGTTAC
AACGAGTGATGGGATTACAAAAGATTTTATTAATTTGATGCCAAAAAATTGGGGA
TTTGGACAGACTTTTGATGGAAAGATTAATTTTAG