

IDENTIFICATION

Species: *Arabidopsis lyrata*

Locus: AL2G28670

Gene Model: AL2G28670.t1

Description: ALEXPA-05

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>

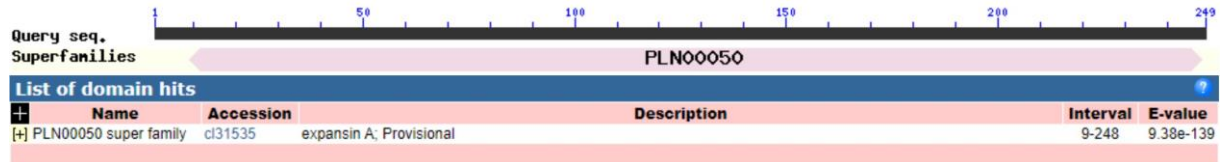
EXTERNAL RESOURCES

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

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>AIEXPA-05

MALVTFLFIATLGAMTSHVNGYAGGGWVNAHATFYGGGDASGTMGGACGYGNLY
SQGYGTNTAALSTALFNGLSCGACFEIRCQNDGKWCLPGSIVVTATNFCPPNNALP
NNAGGWCNPPQQHFDSLQPVFQRIAQYRAGIVPVA YRRVPCVRRGGIRFTINGHSYF
NLVLITNVGGAGDVHSMVKGSRTGWQAMSRNWGQNWQSN SYLNGQSLSFKVT
SDGRTIVSNNVANAGWSFGQTF TGAQ*

CDS (coding sequence)

>AIEXPA-05

ATGGCTCTTGTCACCTTCTTGTTTATAGCTACCCTTGGAGCAATGACATCACATGT
CAACGGCTACGCCGGAGGAGGTTGGGTCAACGCACACGCCACATTCTACGGTGG
TGGTGATGCTTCCGGCACAATGGGAGGTGCTTGTGGTTACGGAAACCTTTATAGC
CAAGGCTATGGAACCAACACCGCAGCTCTAAGCACGGCTCTGTTCAACAATGGTT
TAAGTTGTGGTGCTTGCTTCGAGATAAGATGCCAAAACGATGGAAAATGGTGTCT
CCCTGGCTCAATTGTCGTCACAGCCACAACTTTTGCCCGCCTAACACGCGTTA
CCGAACAACGCAGGAGGTTGGTGTAACCCTCCTCAGCAACATTTTGATCTCTCTC
AGCCCGTATTTCAACGTATCGCTCAATACAGAGCCGGCATTGTTCCCGTCGCTTAC
CGAAGAGTGCCATGCGTGAGAAGAGGAGGAATAAGGTTTACGATAAACGGACAC
TCTTACTTCAACTTAGTTCTTATTACTAACGTCGGAGGAGCCGGAGATGTTCACTC
AGTGATGGTTAAGGGTTCAAGAACAGGATGGCAAGCTATGTCAAGAACTGGGG
ACAGA ACTGGCAGAGTAACTCTTACCTAACGGACAATCTCTCTCATTCAAAGTC
ACCACAAGCGATGGTCGAACCATTGTCTCTAACAACGTCGCTAACGCAGGCTGGT
CTTTTGGCCAGACCTTCACCGGAGCACAGTAA

Nucleotide

>AIEXPA-05

TCCAATTCTAAACCAAACAACATATTCTCACAATCATCTCTTCTTTTATTCTCTTTA
AGAAAGGAAGAGAGATCAAAGCTTCCAAGTAATCATTTTCTTTCTCTCTCACATA
TACATTCACTAGTTTTAGCTTCACAAAATGTGATCTAACTTCATTTACCTATGTGC
AGGTTTACACAAAACGAAAAAAGAACCATGGCTCTTGTCACCTTCTTGTTTATAG

CTACCCTTGGAGCAATGACATCACATGTCAACGGCTACGCCGGAGGAGGTTGGGT
CAACGCACACGCCACATTCTACGGTGGTGGTGATGCTTCCGGCACAATGGGTATA
TTTCCTTAAACCTTTTCTCTCACAAGACTATAAAGCTTTCAAGATTTTGCTTTTACC
ACAATTCTTAAGATATTCTATGAAATTTTGGATTGCAGGAGGTGCTTGTGGTTACG
GAAACCTTTATAGCCAAGGCTATGGAACCAACACCGCAGCTCTAAGCACGGCTCT
GTTCAACAATGGTTTAAGTTGTGGTGCTTGCTTCGAGATAAGATGCCAAAACGAT
GGAAAATGGTGTCTCCCTGGCTCAATTGTCGTCACAGCCACAAACTTTTGCCCGC
CTAACACGCGTTACCGAACACGCAGGAGGTTGGTGTAACCCTCCTCAGCAACA
TTTTGATCTCTCTCAGCCCGTATTTCAACGTATCGCTCAATACAGAGCCGGCATTG
TTCCCGTCGCTTACCGAAGGTAAAACCTAAAAAACAGAGCTGCTCTGTTTTTCTCC
CAAAACAGAGTATAGTTAATTATTGGAATCTTACTCGGTTTTTTTTTTTTTTTTGT
TGTGGTGTGTTAACAGAGTGCCATGCGTGAGAAGAGGAGGAATAAGGTTTACG
ATAAACGGACACTCTTACTTCAACTTAGTTCCTTATTACTAACGTCGGAGGAGCCG
GAGATGTTCACTCAGTGATGGTTAAGGGTTCAAGAACAGGATGGCAAGCTATGTC
AAGAACTGGGGACAGAACTGGCAGAGTAACTCTTACCTAAACGGACAATCTCT
CTCATTCAAAGTCACCACAAGCGATGGTCGAACCATTGTCTCTAACACGTCGCT
AACGCAGGCTGGTCTTTTGGCCAGACCTTACC GGAGCACAGTAAGAGTGATTCTG
GTGAAATCTCATCTCATTGAACGTGTGGTCTATGTAGTAGAAGCAGTAAGCAAAA
AGCTTAGAGAGGGGGCATGATAGTAATTTGGTCCTTTCTTTCAATTGAAGTTTACC
TAAAAGAAGTGGTGCTTCGAGTGCTTGATTTTGCACGAGGCCTTGATGGTGTAC
CTTTTAGGAACCTTTTCTTATCTTTCTTCATTTTTATTGGTAAGGTTTTATGTTATA
CTGATGCAGAGGTGGTCTTAAGTTTAAGTACCACCCGCTAGTAGTAGTAGTAGTA
GTCTCTCATGTACTCATTTGTATCCCTTCTCGAAGCGAGAGGGAGAGTTTTAGATT
GTATTAAGCTCGTTAAAGTCATCATGTATGTTGTAAATTTTTCAATTTCTACAAGT
AATGAATGTTGGGGATTTGT