

IDENTIFICATION

Species: *Arabidopsis lyrata*

Locus: AL3G53860

Gene Model: AL3G53860.t1

Description: ALEXPB-01

Family: Beta Expansin

3D structure:



GENOME DATABASES

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

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

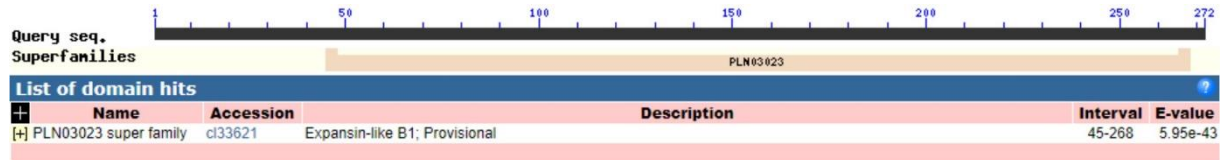
EXTERNAL RESOURCES

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

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>AIEXPB-01

MQLFPVILPTLCLFLHLLGGGSGSTPSLTHSSQQVAVTRWLPATATWYGSPEGDGSSG
GACGYGSLVDVKPFKARVGAVSPILFKGGEGCGACYKVRCLDKTICKRAVTIIVTD
QSPSGPSAKANHTHFDLSGAAFHMAIPGHNGVIRNRGLLNIRYGRACKYKGNIA
FHVNAGSTDYWLSLLIEYEDGEDIGSMHIRQAGSKEWISMKHIWGANWCIVEGPLK
GPFVSVKLTTLSNKTLSAADVIPS NWVPKATYTSRLNFPVL*

CDS (coding sequence)

>AIEXPB-01

ATGCAGCTCTTTCCGGTCATCCTACCGACACTATGCCTCTTCCTCCACCTTCTAGG
AGGCGGCTCTGGCTCTACTCCATCGTTGACTCACTCCAGTCAACAAGTGGCAGTC
ACCCGTTGGCTTCCCGCAACTGCCACCTGGTACGGAAGTCCCGAGGGCGACGGCA
GCAGTGGAGGAGCTTGTGGTTACGGGTCCTAGTGGACGTGAAGCCGTTTAAGGC
AAGAGTTGGAGCGGTGAGTCCGATTCTGTTCAAGGGTGGTGAAGGCTGCGGTGC
ATGTTACAAAGTCAGGTGTCTCGACAAGACCATTTGCTCTAAGAGAGCAGTCACC
ATTATTGTCACCGACCAGTCACCGTCGGGACCATCTGCTAAAGCAAACCACTC
ACTTCGACCTTAGCGGTGCCGCCTTTGGACATATGGCTATTCCCGGCCATAACGG
TGTCATCCGCAACCGTGGCTTATTAACATCCGCTACGGCCGAACGGCATGCAAA
TACAAAGGGAAGAACATAGCCTTCCATGTGAATGCAGGATCAACAGATTATTGGT
TATCTCTTCTCATTGAGTATGAAGACGGTGAAGGAGACATTGGCTCTATGCACAT
TCGTCAAGCGGGTCTAAGGAGTGGATATCAATGAAGCACATATGGGGAGCAAA
CTGGTGCATTGTGAAGGACCACTCAAGGGACCATTCTCTGTGAAGCTTACAAC
TTGTCCAACAACAAGACTCTCTGCCGCCGACGTCATCCCCAGTAACTGGGTTC
CCAAAGCTACTTACACCTCCCGCCTCAACTTCTCCCCTGTTCTCTAA

Nucleotide

>AIEXPB-01

AACTAACCAACAATTCTTCCACTCTCACTTCTCCACTTTTTTTTTTGGTTTTTTTTTG
GCTTGTCTCTCCGGTCAAAATGCAGCTCTTTCCGGTCATCCTACCGACACTATGCC
TCTTCCTCCACCTTCTAGGAGGCGGCTCTGGCTCTACTCCATCGTTGACTCACTCC

AGTCAACAAGTGGCAGTCACCCGTTGGCTTCCCGCAACTGCCACCTGGTACGGAA
GTCCCGAGGGCGACGGCAGCAGTGGTAAACATTTCTTTACATAATATCCACAACA
ATTGATTTACTTTTTACAGTAACAAAGTCAAAAGTTTACTGCGAAATCAATAACA
ATGCAAGGGCTTATTAATGAAACCGCAGGAGGAGCTTGTGGTTACGGGTCACTAG
TGGACGTGAAGCCGTTTAAGGCAAGAGTTGGAGCGGTGAGTCCGATTCTGTTCAA
GGGTGGTGAAGGCTGCGGTGCATGTTACAAAGTCAGGTGTCTCGACAAGACCATT
TGCTCTAAGAGAGCAGTCACCATTATTGTCACCGACCAGTCACCGTCGGGACCAT
CTGCTAAAGCAAACCACACTCACTTCGACCTTAGCGGTGCCGCCTTTGGACATAT
GGCTATTCCCGGCCATAACGGTGTTCATCCGCAACCGTGGCTTATTAACATCCGC
TACGGCCGGTACCTCTTGGCGCTCTAAATAACCAACTTATTATTTTATTTAACGAA
CAAATGAGTAAATGGTTTTTTCTTACATTGGGAGGACTAAACAAACA ACTAAAGA
AGCTTTAACGGCGTTCTTGTCTTTTATTGATGGTCCCGTATTTTGACCTTTGACTAC
ACAACACACACCTATGGATCTCTGACACACACCTACACTTGTTTGTTTTTGT
TAAAACAGAACGGCATGCAAATACAAAGGGAAGAACATAGCCTTCCATGTGAAT
GCAGGATCAACAGATTATTGGTTATCTCTTCTCATTGAGTATGAAGACGGTGAAG
GAGACATTGGCTCTATGCACATTCGTCAAGTAATATTTCTCATTACTCTCTCCTAC
ATTTTCTTTAAAATGTTTACTTAATTTTACTTCTTTTGTGTGTTGAATTATGAAGGC
GGGTCTAAGGAGTGGATATCAATGAAGCACATATGGGGAGCAA ACTGGTGCAT
TGTCGAAGGACCACTCAAGGGACCATTCTCTGTGAAGCTTACA ACTTTGTCCAAC
AACAAGACACTCTCTGCCGCCGACGTCATCCCCAGTAACTGGGTTCCCAAAGCTA
CTTACACCTCCCGCCTCAACTTCTCCCCTGTTCTCTAATTAACCACTCTTCGTTTTT
TTTTGTTGTGGGAGAGAGTAACACGGAGAGGACAATGAGTGAGCCATCTCCAAA
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CATTTTCATTTTTTTTCTTGTCCATAGGGATGTGTGTATCAATCATCTATAATCTT
GTTTGTGGGACATTACTATATATAAGAAGAGAATTTACAAAAGATGTAATAATGT
GCAAAATCTCAT