

IDENTIFICATION

Species: *Arabidopsis lyrata*

Locus: AL2G12650

Gene Model: AL2G12650.t1

Description: ALEXPA-04

Family: Alpha Expansin

3D structure:



GENOME DATABASES

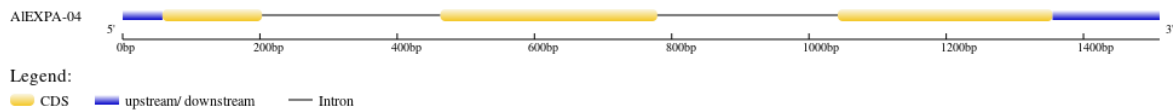
Phytozome: https://phytozome-next.jgi.doe.gov/info/Alyrata_v2_1

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

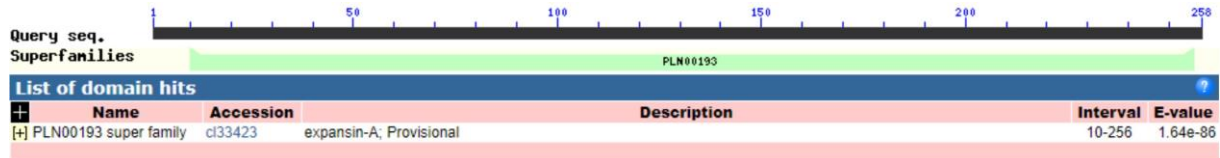
EXTERNAL RESOURCES

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

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>ALEXPA-04

MDQNLRYRKCLVILSMMALIGTSMAAYAGTPWRTASATFYGDETGSATMGGACGYG
NMWDSGYGVATTALSTALFNDGYACGQCFQIRCVSSPNCYYGSPATVVTATNICPPN
YGQASNNGGWCNPPQVHFDLAKPAFMKIANWKAGIIPLSYRRVACKRTGGIRFKFEG
NGYWLLVYVMNVGGAGDIKTMAVKGSRTGWINMSHNWGASYQAFSSLYGQSLSF
RLTSYTTRQTIYAYNAAPASWSAGKTYQSKANFS*

CDS (coding sequence)

>ALEXPA-04

ATGGATCAA AATTTGTATCGCAAGTGCTTGGTTATTTTATCAATGATGGCACTGAT
CGGCACATCAATGGCGGCATATGCGGGGACCCCATGGCGTACGGCCTCAGCCACT
TTTTACGGTGATGAGACCGGCAGCGCAACTATGGGTGGGGCTTGTGGCTATGGTA
ACATGTGGGACAGCGGCTACGGCGTAGCCACGACTGCTCTGAGCACAGCTCTGTT
CAACGACGGTTATGCATGCGGTCAATGTTTCCAGATAAGGTGTGTGTCATCGCCT
AACTGCTACTACGGTTCACCAGCCACCGTGGTGACTGCCACCAACATATGTCCAC
CAAATTATGGCCAAGCTTCCAACAATGGTGGATGGTGTAAATCCACCACAAGTCCA
TTTTGATTTGGCTAAACCAGCTTTCATGAAGATCGCTAATTGGAAGGCTGGTATC
ATCCCCCTCTCATACCGCAGAGTGGCATGTAAGAGAACCGGAGGAATAAGGTTTA
AATTTGAAGGAAATGGGTATTGGCTACTTGTGTACGTGATGAACGTAGGTGGTGC
AGGTGACATCAAGACCATGGCCGTGAAAGGTAGCCGCACAGGCTGGATCAACAT
GAGCCATAATTGGGGAGCTTCGTACCAAGCCTTTTCTTCTCTCTACGGTCAGTCTC
TCTCGTTCCGGCTCACCTCTTACACCACTCGTCAGACCAATTTACGCTTATAATGCT
GCTCCGGCTAGCTGGAGCGCCGGCAAGACCTACCAGAGCAAGGCTAATTTTAGCT
GA

Nucleotide

>ALEXPA-04

AGACTTGGCTTTACAGAGAGAAAATAAGAGTAGGAGCCCTCAAGAAAACAGAGT
AAAAATGGATCAA AATTTGTATCGCAAGTGCTTGGTTATTTTATCAATGATGGCA
CTGATCGGCACATCAATGGCGGCATATGCGGGGACCCCATGGCGTACGGCCTCAG

CCACTTTTTACGGTGATGAGACCGGCAGCGCAACTATGGGTAAAGTCCATATACT
TCTACATTCTATTGTATGTAGAAGTAGAACACAACTATATATGACTCGATTGCA
TATAAATTATTTAAAACGATTGTTTGTGGTTGCATTTCTATGTTTTAATATACTA
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TAAATACATAAATCTTTATTTTCGAAGATCGTTAAAATGTATTGACAATTTTTAAC
ATGACCATGTATACCGATCAGGTGGGGCTTGTGGCTATGGTAACATGTGGGACAG
CGGCTACGGCGTAGCCACGACTGCTCTGAGCACAGCTCTGTTCAACGACGGTTAT
GCATGCGGTCAATGTTTCCAGATAAGGTGTGTGTCATCGCCTAACTGCTACTACG
GTTCAACCAGCCACCGTGGTGACTGCCACCAACATATGTCCACCAAATTATGGCCA
AGCTTCCAACAATGGTGGATGGTGTAAATCCACCACAAGTCCATTTTGATTTGGCT
AAACCAGCTTTCATGAAGATCGCTAATTGGAAGGCTGGTATCATCCCCCTCTCAT
ACCGCAGGTAATATCCACTAGACCAATATATATAGATAAGTACATAGTAATTTAAA
TAGTGTATATACTATTACAATTTTTACTTTTTTTGGAAGGGATGTGTATATACTAAC
GTTGTATATACTATTACGATTGAAAACGTAAAGAAATTCTTTATATAACCATTGTG
AAATTCAATATATTTATAATCAAATATATTTAAATGAGATCTTGTCCGAATGCAC
ATTTTGCACATGCTAAAATACGATGATTTTGTTTATATATATATGCAGAGTGGCAT
GTAAGAGAACCGGAGGAATAAGGTTTAAATTTGAAGGAAATGGGTATTGGCTAC
TTGTGTACGTGATGAACGTAGGTGGTGCAGGTGACATCAAGACCATGGCCGTGAA
AGGTAGCCGCACAGGCTGGATCAACATGAGCCATAAATTGGGGAGCTTCGTACCA
AGCCTTTTCTTCTCTCTACGGTCAGTCTCTCTCGTTCCGGCTCACCTCTTACACCAC
TCGTCAGACCATTTACGCTTATAATGCTGCTCCGGCTAGCTGGAGCGCCGGCAAG
ACCTACCAGAGCAAGGCTAATTTTAGCTGATTTAGGTCATATTCAATTCCGAAAA
CCCGGTTATTTGAATTTACGGTTTTGCTACTTGTCTTGAGGCTGATCGATCCAGA
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