

IDENTIFICATION

Species: *Arabidopsis thaliana*

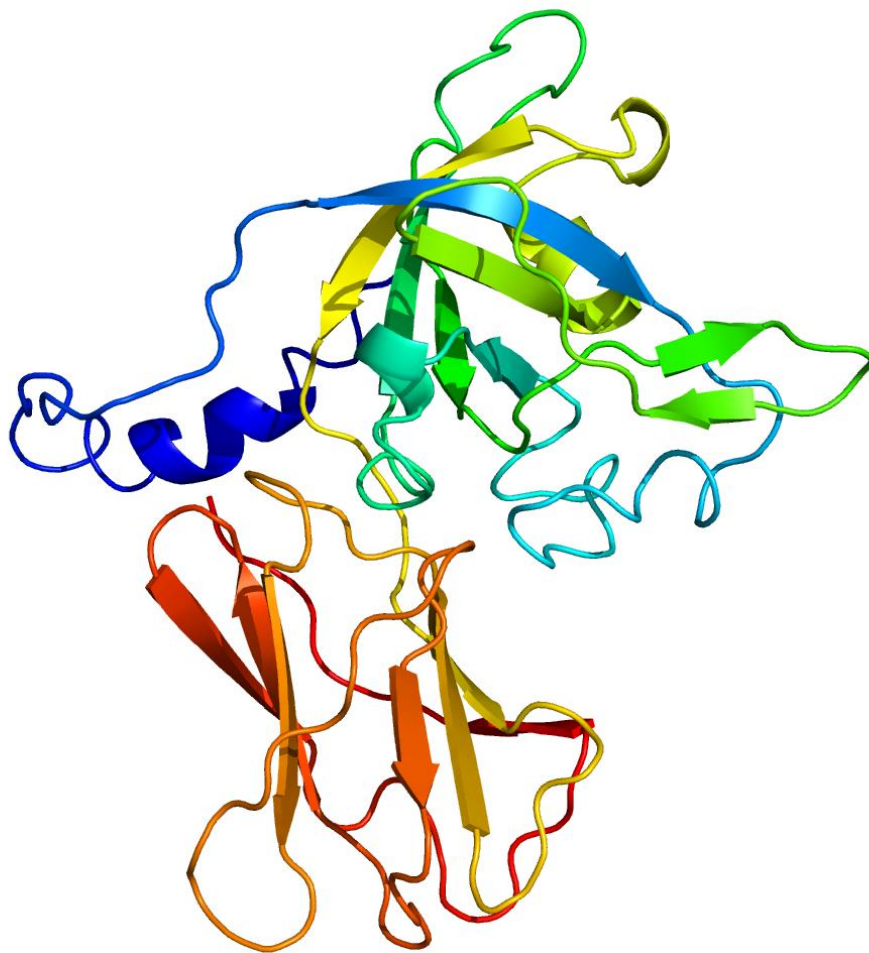
Locus: AT3G55500

Gene Model: AT3G55500.1

Description: AtEXPA-21

Family: Alpha Expansin

3D structure:



GENOME DATABASES

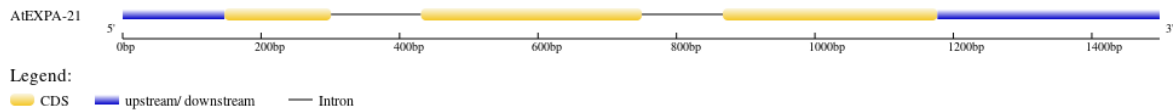
TAIR: <https://www.arabidopsis.org/>

KEGG: <https://www.genome.jp/entry/T00041>

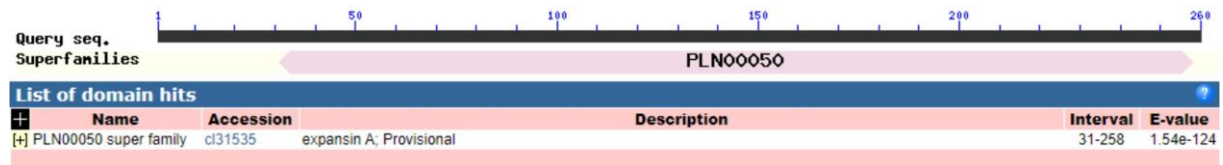
EXTERNAL RESOURCES

<https://www.gabipd.org/database/cgi-bin/GreenCards.pl.cgi?Mode=Show&QueryKey=197c0ef939ecd1d29302d8a4a92c1bc3&x.Overview=1&Start=1>

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>AtEXPA-21

MAINPLILLTIFPLFLLLSFTDAGIPRVFSGGSWQTAHATFYGGNDASGTMGGACGYG
NLYSQGYGTNTAALSTSLFNSGQSCGACFEIKCVNDPKWCHPGNPSVFTATNFCPP
NLAQPSDNGGWCNPPRSHFDLAMPVFLKIAEYRAGIVPISYRRVACRKS GGIRFTING
HRYFNLV LITNVAGAGDIARTSVKGSKTGWMSLTRNWGQNWQSNV LVGQSL SFR
VTSSDRRTSTSWNIAPSNWQFGQTFVGKNFRV

CDS (coding sequence)

>AtEXPA-21

ATGGCAATCAATCCATTGATTCTCTTAACCATATCCCCTCCTTCTCTTGAG
CTTACCGACGCCGGAATCCCTAGAGTCTTCTCAGGTGGTTCTTGGCAAACCGCT
CACGCCACTTTCTACGGTGGAAACGATGCTTCGGGAACAATGGGTGGCGCGTGTG
GATACGGGAATCTGTATAGCCAAGGATACGGAACAAACACGGCGGCGCTGAGCA
CATCGTTGTTTAAACAGTGGTCAAAGCTGCGGGCGCATGCTTCGAAATCAAATGTGT
CAATGATCCCAAATGGTGTCAACCGGTAATCCTTCTGTCTTCGTAACCGCAACC
AACTTTTGCCCTCCAACTTAGCCAGCCTAGCGACAATGGTGGCTGGTGCAACC
CGCCACGCTCTCATTTTCGACCTCGCCATGCCCGTTTTCTCAAGATCGCTGAGTAT
CGTGCCGGCATTGTCCCATCTTACCGCAGGGTGGCATGTAGGAAGAGTGGAG
GGATAAGGTTACGATCAACGGTCACCGTACTTCAACTGGTGCTGATTACGAA
CGTGGCCGGAGCAGGAGACATCGCGAGGACGAGTGTGAAAGGTTCAAAGACTGG
TTGGATGAGTTTAACTAGGAACTGGGGACAGAACTGGCAGTCTAATGCTGTTCTC
GTTGGTCAGTCACTTTCCTTCCGTGTTACATCCAGCGATCGTAGAACCTCTACTTC
ATGGAACATCGCTCCTTCGAACTGGCAGTTTGGACAAACCTTTGTTCGGAAAGAAT
TTCAGGGTCTAA

Nucleotide

>AtEXPA-21

TATTTCTCTAACTTTGGAGTTCTCTCCACCAATATAAATAGCGATCTTCACAAGTG
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GCTTTCTCCAATTCAATTA AAAATACTTACCAAATGGCAATCAATCCATTGATTC
TCTTAACCATATTCCCCTCTTCTTCTGAGCTTCACCGACGCCGGAATCCCT
AGAGTCTTCTCAGGTGGTTCCTTGGCAAACCGCTCACGCCACTTTCTACGGTGGAA
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TGCCCTCCAACTTAGCCCAGCCTAGCGACAATGGTGGCTGGTGCAACCCGCCAC
GCTCTCATTTTCGACCTCGCCATGCCCGTTTTCTCAAGATCGCTGAGTATCGTGCC
GGCATTGTCCCATCTCTTACCGCAGGTATACTTAAACATCCCTATATGTAGCCTA
CGATTTGAGAAATGATTCGTATATAAAAGAAGTTGCAAATGCAATGAATCAAAAT
GCTAAGATTACGAAATGTGGGTATTTGTATAGGGTGGCATGTAGGAAGAGTGGA
GGGATAAGGTTACGATCAACGGTCACCGTTACTTCAACTTGGTGCTGATTACGA
ACGTGGCCGGAGCAGGAGACATCGCGAGGACGAGTGTGAAAGGTTCAAAGACTG
GTTGGATGAGTTTAACTAGGAACTGGGGACAGAACTGGCAGTCTAATGCTGTTCT
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