

IDENTIFICATION

Species: *Arabidopsis thaliana*

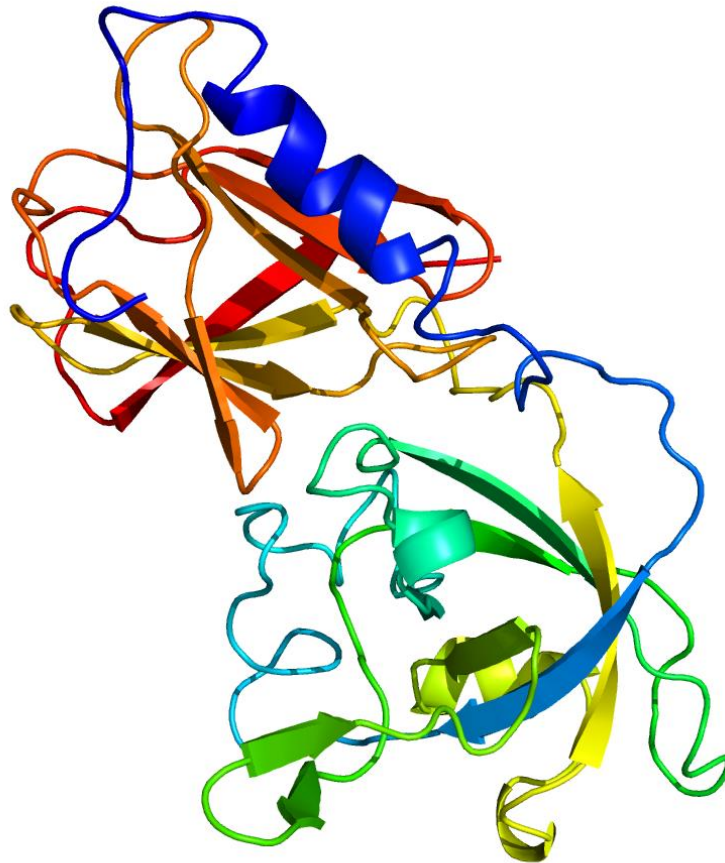
Locus: AT1G26770

Gene Model: AT1G26770.2

Description: AtEXPA-05

Family: Alpha Expansin

3D structure:



GENOME DATABASES

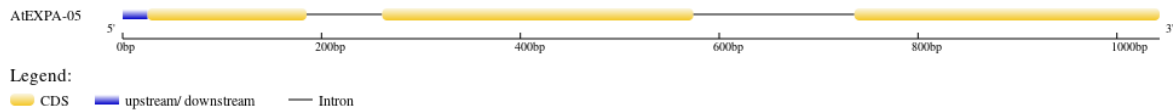
TAIR: <https://www.arabidopsis.org/>

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

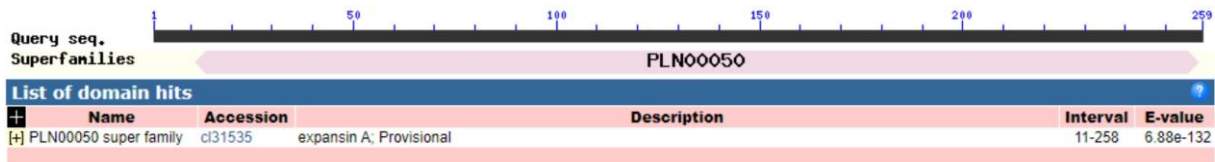
EXTERNAL RESOURCES

<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-05

MCRLLTQDVNMGHLGFLVMIMVGVMASVSGYGGGWINAHATFYGGGDASGTMG
GACGYGNLYSQGYGTSTAALSTALFNNGLSGSCFEIRCENDGKWCLPGSIVVTATN
FCPPNNALANNNGWCNPPLEHFDLAQPVFQRIAQYRAGIVPVSYRRVPCRRRGGIR
FTINGHSYFNLVLITNVGGAGDVHSAAIKGSRTVWQAMSRNWGQNWQNSYLNQ
ALSFKVTTSDGRTVVSFNAAPAGWSYGQTFAGGQFR

CDS (coding hits sequence)

>AtEXPA-05

ATGTGCAGGTTGTTAACACAAGACGTAACATGGGTCATCTTGGGTTCTTAGTTA
TGATTATGGTAGGAGTCATGGCTTCTTCTGTGAGCGGCTACGGTGGCGGTTGGAT
CAACGCTCACGCCACTTTTTACGGTGGTGGTGTATGCTTCCGGCACAATGGGTGGT
GCTTGTGGATATGGTAATCTATATAGCCAAGGCTACGGGACGAGCACGGCGGCTC
TAAGCACAGCTCTTCAACAATGGACTTAGCTGTGGTTCTTGCTTTGAGATAAG
ATGTGAAAACGATGGTAAATGGTGTTCCTGGCTCAATCGTTGTAACCGCTACA
AACTTCTGCCC GCCAAATAACGCGTTAGCGAACAATAATGGCGGTTGGTGTAAATC
CTCCTCTTGAACACTTTGACCTTGCTCAGCCTGTTTTTCAACGCATTGCTCAGTAC
AGAGCTGGAATCGTCCCTGTTTCCTACAGAAGGGTTCCTTGCAGGAGAAGAGGAG
GAATAAGATTCACGATAAACGGCCACTCATACTTCAACCTTGTGCTGATCACAAA
CGTCGGTGGTGCCGGAGACGTTCACTCGGCGGCGATCAAGGGTTCAAGAACAGT
GTGGCAAGCTATGTCAAGGAAGTGGGGGCAAATTGGCAAAGCAACTTTACCT
CAACGGTCAAGCACTTTCCTTTAAGGTCACCACCAGCGACGGCCGCACAGTTGTC
TCCTTCAACGCCGCTCCTGCCGGCTGGTCTTATGGCCAGACTTTTGCCGGTGGACA
GTTCCGTTAA

Nucleotide

>AtEXPA-05

ATAAGTAATTGATTTTATATCACCCATGTGCAGGTTGTTAACACAAGACGTAAAC
ATGGGTCATCTTGGGTTCTTAGTTATGATTATGGTAGGAGTCATGGCTTCTTCTGT
GAGCGGCTACGGTGGCGGTTGGATCAACGCTCACGCCACTTTTTACGGTGGTGGT
GATGCTTCCGGCACAATGGGTAAAAACCGTTATTTACATAACTCATTCCCTTACAA
ATTATCATATTTACTAATCTTCAATGTTACTTCTTTGTAGGTGGTGCTTGTGGATAT
GGTAATCTATATAGCCAAGGCTACGGGACGAGCACGGCGGCTCTAAGCACAGCT
CTCTTCAACAATGGACTTAGCTGTGGTTCTTGCTTTGAGATAAGATGTGAAAACG
ATGGTAAATGGTGTTTACCTGGCTCAATCGTTGTAACCGCTACAACTTCTGCCCCG
CCAAATAACGCGTTAGCGAACAATAATGGCGGTTGGTGTAATCCTCCTCTTGAAC
ACTTTGACCTTGCTCAGCCTGTTTTTCAACGCATTGCTCAGTACAGAGCTGGAATC
GTCCCTGTTTCCTACAGAAGGTAACATTTTATTCAGCTTCTCTGTTTCAAACAGA
GGATATCAAATTTCTCTAGATGCTCTGTTTTTTTCTTAAAACAGAGTATATGCTAA
GTTTAATAACAGAGTTCTTGAAGAAAAAAGATCCAAAATATAAACTTTTCGATAC
TTTGGTGTTTTGTAGGGTTCCTTGCAGGAGAAGAGGAGGAATAAGATTCACGATA
AACGGCCACTCATACTTCAACCTTGTGCTGATCACAAACGTCGGTGGTGCCGGAG
ACGTTCACTCGGCGGCGATCAAGGGTTCAGAACAGTGTGGCAAGCTATGTCAA
GGAAGTGGGGGCAAAATTGGCAAAGCAACTCTTACCTCAACGGTCAAGCACTTTC
CTTTAAGGTCACCACCAGCGACGGCCGCACAGTTGTCTCCTTCAACGCCGCTCCT
GCCGGCTGGTCTTATGGCCAGACTTTTGCCGGTGGACAGTTC CGTTAA