

IDENTIFICATION

Species: *Arabidopsis thaliana*

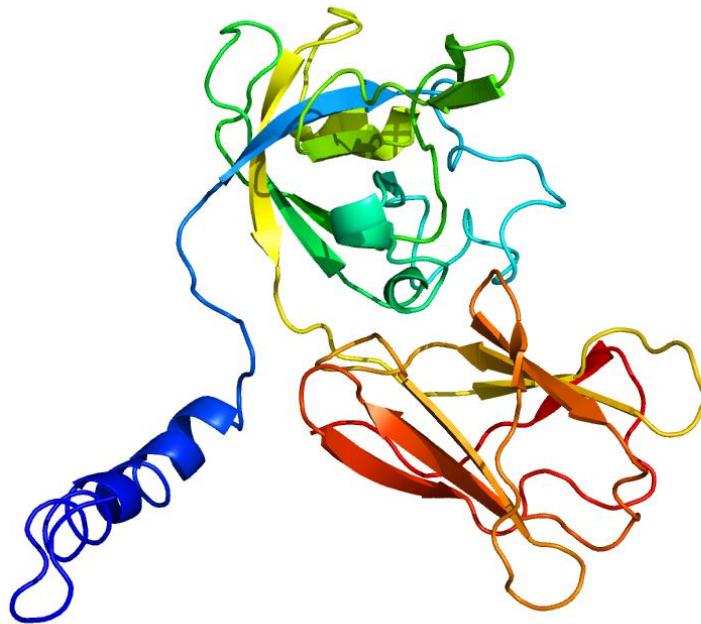
Locus: AT1G12560

Gene Model: AT1G12560.1

Description: AtEXPA-01

Family: Alpha Expansin

3D structure:



GENOME DATABASES

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

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

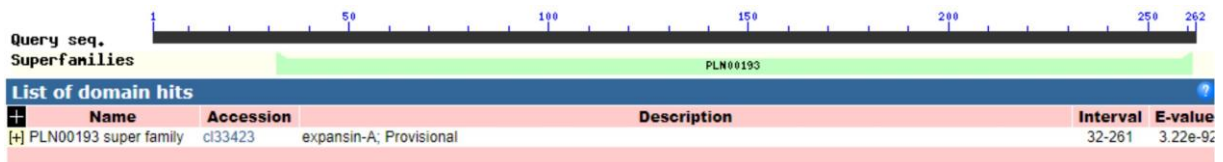
EXTERNAL RESOURCES

<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-01

MGPISSWSFNKFFSIVFVVFAISGEFVAGYYRPGPWRYAHATFYGDETGGGETMGGACGYGNLFSNGYGLSTAALSTTLFNDGYGCGQCFQITCSKSPHCYSGKSTVVTATNLCPPNWWYQDSNAGGWCNPPRTHFDMAKPAFMKLAYWRAGIIPVAYRRVPCQRSGGMR FQFQGNYSWLLIFVMNVGGAGDIKSMVKGSR TNWISMSHNWGASYQAFSSLYGQSLSFRVTSYTTGETIYAWNVPANWSSGGKTYKSTANFR

CDS (coding sequence)

>AtEXPA-01

ATGGGTCCAATCTCAAGTTCTTGAGCTTTAACAAATCTTCTCAATAGTTTTTCGT
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AGATATGCTCACGCCACTTTCTACGGTGACGAGACCGGTGGTGAAACCATGGGTG
GTGCATGTGGGTACGGAAACCTTTTTAACAGCGGCTACGGACTGTCCACGGCGGC
GCTAAGCACGACATTGTTCAATGATGGTTACGGATGCGGCCAATGTTTTTCAGATA
ACATGTTTCGAAATCACCGCATTGTTACTCTGGAAAATCAACAGTGGTCCACAGCCA
CCAATCTTTGCCCTCCTAATTGGTACCAAGACTCCAACGCTGGTGGTTGGTGCAAT
CCTCCTAGAACCCATTTTCGATATGGCTAAACCAGCTTTCATGAAACTCGCTTACTG
GAGGGCCGGTATCATCCCAGTTGCATACCGAAGAGTGCCATGCCAAAGGAGTGG
AGGTATGAGGTTTCAATTCCAAGTAATTCTTATTGGCTTCTTATCTTCGTCATGA
ACGTTGGTGGCGCCGGAGACATCAAGAGCATGGCCGTTAAAGGTAGCCGGACGA
ATTGGATAAGCATGAGCCACAATTGGGGAGCCTTTACCAAGCTTTTTCTCTCTC
TATGGTCAATCTCTCTTTCCGGGTCCTTCTTACACCACCGGTGAAACCATCTA
TGCTTGGAACGTTGCTCCGGCTAACTGGAGCGGCGGTAAGACTTACAAGAGCACC
GCTAATTTCCGTTAA

Nucleotide

>AtEXPA-01

ATCAAAAACAAACCAAAAACAAACCCTAAGAATAAAGAAAAAGAGGCTAGAA
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CCTAATTGGTACCAAGACTCCAACGCTGGTGGTTGGTGCATCCTCCTAGAACCC
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CATCCAGTTGCATACCGAAGGTATATATACTACACTTAGTTATTCAACTTCAT
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TGCCAAAGGAGTGGAGGTATGAGGTTTCAATTCCAAGGTAATTCTTATTGGCTTC
TTATCTTCGTCATGAACGTTGGTGGCGCCGGAGACATCAAGAGCATGGCCGTTAA
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AGCTTTTTCTCTCTCTATGGTCAATCTCTCTCTTTCCGGGTCACTTCTTACACCAC
CGGTGAAACCATCTATGCTTGGAACGTTGCTCCGGCTAACTGGAGCGGCGGTAAAG
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AAAACGGAGTTTTCTCTTCTCCTTCTTTTTTTGTTAAGAGTTTCGGTGGCCTTTTGT
TGTGGTGGCCCGGCTTTATGTTATACATCTACATGTATGTATAATGTATGTATGTA
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TCGCTTGCTTTTGTTTAGAAGACAAA