

IDENTIFICATION

Species: *Arabidopsis thaliana*

Locus: AT5G56320

Gene Model: AT5G56320.1

Description: AtEXPA-32

Family: Alpha Expansin

3D structure:



GENOME DATABASES

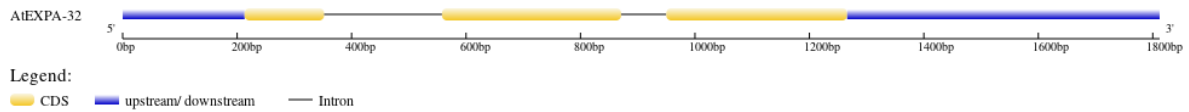
TAIR: <https://www.arabidopsis.org/>

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

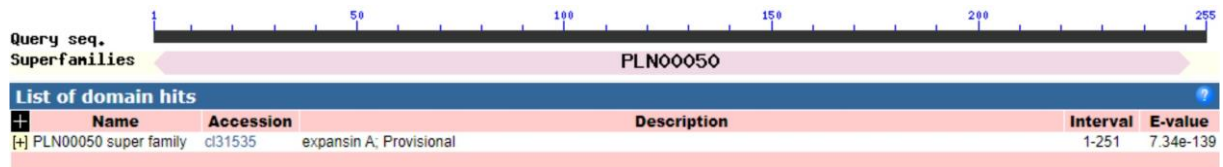
EXTERNAL RESOURCES

<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-32

MEFFGKMIISLSLMMMIMWKSVDGYSSGWVNARATFYGGADASGTMGGACGYGN
LYSQYGTNTAALSTALFNGGQSCGACFQIKCVDDPKWCIGGTITVTGTNFCPPNFA
QANNAGGWCNPPQHFDLAQPIFLRIAQYKAGVVPVQYRRVACRRKGGIRFTINGHS
YFNLVLITNVAGAGDVISVSIKGTNTRWQSMSRNWQNWQSNAKLDGQALSFKVTT
SDGRTVISN NATPRNWSFGQTYTGKQFRAQR

CDS (coding sequence)

>AtEXPA-32

ATGGAGTTTTTTGGTAAAATGATAATTTTCATTGAGTCTTATGATGATGATAATGTG
GAAGAGCGTGGATGGTTACAGTAGTGGTTGGGTC AATGCTCGAGCCACATTCTAT
GGAGGAGCTGATGCTTCTGGCACCATGGGCGGCGCGTGTGGTTACGGAACTTAT
ACAGTCAAGGATACGGCACTAACACGGCGGCTCTAAGCACGGCTCTATTCAACG
GCGGCCAAAGCTGTGGTGCTTGTTCAGATAAAATGCGTAGACGACCCAAAATG
GTGTATCGGTGGAACAATCACCGTCACCGGAACAACTTTTGTCCACCCAACTTT
GCTCAAGCCAACAACGCCGGAGGTTGGTGT AATCCTCCTCAACACCACTTCGATT
TAGCTCAGCCCATCTTCTCCGTATTGCTCAATACAAAGCCGGCGTCTGCCCTGTC
CAATACCGGAGAGTGGCTTGCCGGAGAAAAGGAGGAATAAGATTCACGATCAAC
GGTCATTCATACTTCAACCTCGTACTTATAACCAACGTCGCCGGCGCCGGAGATG
TTATCTCCGTCTCCATTAAAGGAACCAATACACGTTGGCAAAGCATGTCAAGAAA
CTGGGGACAGAATTGGCAAAGCAATGCAAACTTGATGGTCAAGCTTTGTCTTTT
AAAGTAACA ACTAGTGATGGCCGTACAGTTATATCTAACAATGCTACACCACGTA
ACTGGAGCTTCGGACAGACTTATACCGGAAAACAGTTCCGGGCTCAGAGGTGA

Nucleotide

>AtEXPA-32

ACAACAACATTGAAACCCATTTCTTCGCCTTTAACCTTACTTGAATTTTTGTGTGG
GTCCTTTTTTTTTCTTTCTCCAAGCCATTGTAAGCTCCAATCTTCCACATTCTATCT
CTTCTTCCTCATTTTCTTCCATACATACACACATATATATTTCTGTTACCATTTAAG
TGATCATAAAGTTTTCTTGTGTAGGAATAAAAAGGCAGAGAAAATGGAGTTTTTT
GGTAAAATGATAATTTCAATTGAGTCTTATGATGATGATAATGTGGAAGAGCGTGG
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GGCGCGTGTGGTTACGGAACTTATACAGTCAAGGATACGGCACTAACACGGCG
GCTCTAAGCACGGCTCTATTCAACGGCGGCCAAAGCTGTGGTGCTTGTTTTCAGA
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TAATCCTCCTCAACACCCTTCGATTTAGCTCAGCCCATCTTCCTCCGTATTGCTC
AATACAAAGCCGGCGTCCCTGTCCAATACCGGAGGTACGTTTCCCGATCTCG
GTTTAGCTCGGTTTGGTAATTGGTACGTGTGGTTTGATTTATGCTCTGTTTTTAAA
TCAGAGTGGCTTGCCGGAGAAAAGGAGGAATAAGATTCACGATCAACGGTCATT
CATACTTCAACCTCGTACTTATAACCAACGTCGCCGGCGCCGGAGATGTTATCTC
CGTCTCCATTAAGGAACCAATACACGTTGGCAAAGCATGTCAAGAACTGGGG
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ACAAC TAGTGATGGCCGTACAGTTATATCTAACAATGCTACACCACGTAACCTGGA
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