

IDENTIFICATION

Species: *Arabidopsis thaliana*

Locus: AT3G45960

Gene Model: AT3G45960.2

Description: AtEXLA-02

Family: Expansin Like Alpha

3D structure:



GENOME DATABASES

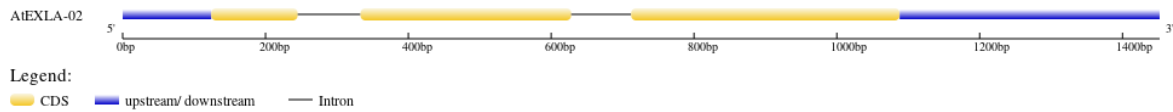
TAIR: <https://www.arabidopsis.org/>

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

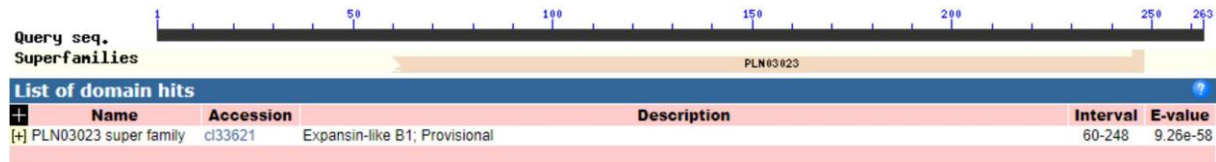
EXTERNAL RESOURCES

<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

>AtEXLA-02

MRSFLYLIVVIFLFSVVNACDRCLHRSKASYFSSASALSSGACAYGPMATSFAGHIA
AAIPSIYKDGAGCGACFQVRCKNPKLCLNSKGTIVMVTDLNLSNQTDLVLSSRAFRAM
AKPVVGVVDKYLKQGVVDVEYQRVPCNYGKRNLNVRVEEASKKPNYLAIKLLYQGG
QTEVVGIDIAPVGSQWSYMSRSHGAVWATDKVPTGALQFKFTVTGGYDGKTVWS
KRVLPANWNSGRIYDAGVQITDIAQEGCDTCGHIWN

CDS (coding sequence)

>AtEXLA-02

ATGAGAAGCTTTCTCTACCTCATCGTAGTCATCTTCCTCTTCTTTCATCCGTTAAC
GCTTGTGATCGATGTCTACACCGTTCTAAAGCATCTTATTTCTCCTCTGCTTCTGCT
CTCTCTTCCGGGGCTTGTGCCTATGGCCCTATGGCTACGAGCTTCTTTGCCGGCCA
CATTGCGGCCGCTATACCTTCCATTTACAAAGATGGTGCTGGCTGTGGAGCTTGCT
TTCAAGTCAGATGCAAGAACCCCAAGTTGTGTAACAGTAAAGGAACCATTGTGAT
GGTCACAGACTTGAACACGAGCAACCAAAGTATCTTGTCTTAGTAGTAGAGCT
TTAGGGCTATGGCTAAGCCTGTTGTTGGTGTGACAAATACCTTCTCAAACAAG
GCATCGTCGACGTTGAATACCAAAGAGTTCCTTGCAATTACGGTAAAAGGAATTT
GAACGTGAGAGTGGAAGAAGCAAGCAAAAAGCCAAATTAATTGGCGATAAAGCT
ATTGTACCAAGGAGGTCAAACCGAAGTGGTAGGTATCGACATTGCTCCAGTAGGT
TCGTCACAATGGAGTTACATGAGTAGAAGCCACGGAGCCGTTTGGGCGACCGAT
AAAGTACCAACGGGAGCTCTACAGTTCAAGTTCACGGTGACAGGCGGCTACGAT
GGCAAACGGTTTGGTCAAAGAGGGTTCTTCCGGCGAATTGGAAGTCTGGGAGG
ATTTATGATGCCGGCGTTCAGATCACCGACATTGCTCAAGAAGGTTGTGATACAT
GCGGTCACATATGGAAGTGA

Nucleotide

>AtEXLA-02

TCATCATTCATCATACTATATTATATAATCCATTCTTTGTCCTCTCTTCTCTTTACA
TGTA AATTACATATCTCTCTAATTTGCTCACTAGATATTATTTCTTTCCTCTTGAA
AAGTCCAAAAATGAGAAGCTTTCTCTACCTCATCGTAGTCATCTTCCCTCTTCTCT
CATCCGTTAACGCTTGTGATCGATGTCTACACCGTTCTAAAGCATCTTATTTCTCC
TCTGCTTCTGCTCTCTCTTGTAAACATTCCCATCTTCTTCTAACTACTTCCGTTTAA
CTACTAGTTTGTCTTTTTTCTCATGTCTTGTATGTTTATGGGTATTTTCTAGCCGGGC
TTGTGCCTATGGCCCTATGGCTACGAGCTTCTTTGCCGGCCACATTGCGGCCGCTA
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AAGAACCCCAAGTTGTGTAACAGTAAAGGAACCATTGTGATGGTCACAGACTTG
AACACGAGCAACCAAAGTATCTTGTCTTAGTAGTAGAGCTTTTAGGGCTATGG
CTAAGCCTGTTGTTGGTGTGACAAATACCTTCTCAAACAAGGCATCGTCGACGT
TGAATACCAAAGGTTTCGATGCTTGAAACACTTGACTTATTGGTTTTTTTTATAGTCA
CTTGATGTACTAATAAGAAGGTTTGGGAAATGAAAAACAGAGTTCCTTGCAATTA
CGGTA AAGGAATTTGAACGTGAGAGTGGAAGAAGCAAGCAAAAAGCCAAATTA
CTTGGCGATAAAGCTATTGTACCAAGGAGGTCAAACCGAAGTGGTAGGTATCGA
CATTGCTCCAGTAGGTTTCGTCACAATGGAGTTACATGAGTAGAAGCCACGGAGCC
GTTTGGGCGACCGATAAAGTACCAACGGGAGCTCTACAGTTCAAGTTCACGGTGA
CAGGCGGCTACGATGGCAAACGGTTTGGTCAAAGAGGGTCTTCCGGCGAATTG
GAACTCTGGGAGGATTTATGATGCCGGCGTTCAGATCACCGACATTGCTCAAGAA
GGTTGTGATACATGCGGTCACATATGGAAGTACTCATTACAATTCTCCTTATTTA
GGCAAACAACAACAACACCCTTTATAGGATATATACATGTATGTGTAACAGA
GTTCAATTATTTAATGAGTTGAAGAATTCACAACAGGAGTGGCTTATATAATCTGG
ATTAACA AAGAACTAGAGAGTAAAGGTCATGCTAAAAGCTAGAGTCCATGTC
ACCAAAAAACAAGAAAAACA AAAAAATGTCATTATCATTGCAAGCAAGAATC
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