IDENTIFICATION

Species: *Chenopodium quinoa*

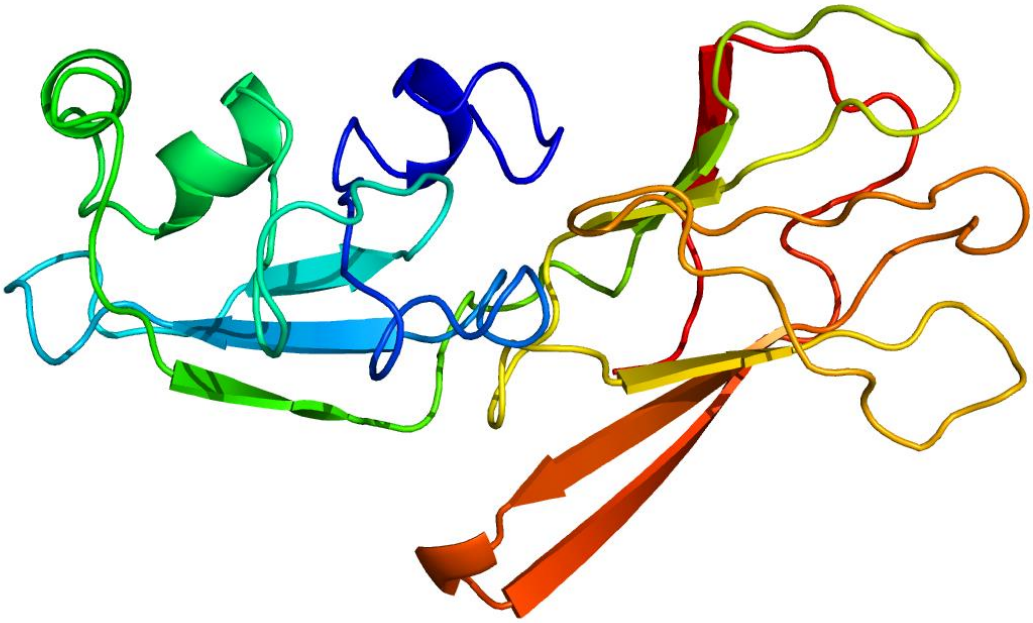
Locus: AUR62018845

Gene Model: AUR62018845

Description: CqEXLB-02

Family: Expansin Like Beta

3D structure:



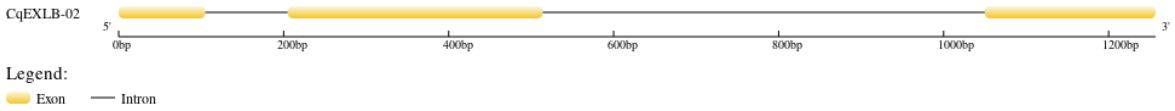
GENOME DATABASES

Phytozome: https://phytozome-next.jgi.doe.gov/info/Cquinoa_v1_0
KEGG: https://www.genome.jp/entry/T05764

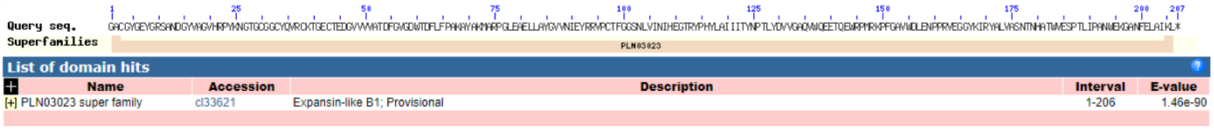
EXTERNAL RESOURCES

https://www.cbrc.kaust.edu.sa/chenopodiumdb/
http://quinoa.kazusa.or.jp/index.html

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>CqEXLB-02

GACGYGEYGRSANDGYVAGVHRPYKNGTGCGGCYQVRCKTGECTEDGVVVVATD
FGVGDWTDFLFPAKAYAKMARPGLEAELLAYGVVNIEYRRVPCTFGGSNLVINIHEG
TRYPHYLAIIITYNPTLYDVVGAQVWQEETQEWRPMRKPFGAVWDLENPPRVEGGY
KIRYALVASNTNHATWVESPTLIPANWEKGANFELAIKL*

CDS (coding sequence)

>CqEXLB-02

GGAGCATGTGGATATGGAGAATATGGAAGAAGTGCTAATGATGGTTATGTAGCT
GGTGTCCATAGACCTTACAAAAACGGCACTGGATGTGGTGGTTGCTACCAGGTAA
GGTGCAAGACAGGAGAATGCACAGAAGACGGGGTGGTGGTGGTGGCAACAGATT
TCGGGGTGGGTGATTGGACCGATTTCCTATTTCCGGCCAAGGCCTATGCTAAGAT
GGCCCGGCCCGGGTTAGAAGCCGAACTGCTCGCATACGGCGTCGTTAACATCGAA
TACCGTCGAGTCCCTTGCACCTTCGGTGGTTCAAACCTCGTAATTAATATACATGA
AGGCACAAGATACCCTCACTACTTGGCCATTATTATCACTTATAATCCTACTCTCT
ATGACGTTGTGGGTGCTCAAGTTTGGCAGGAGGAAACCCAAGAATGGAGGCCCA
TGAGAAAGCCATTTGGAGCAGTTTGGGACCTGGAAAATCCACCAAGAGTAGAAG
GAGGTTATAAAATAAGATACGCTCTTGTTGCCAGCAACACTAATCATGCCACCTG
GGTGGAATCACCTACTCTTATTCCTGCTAATTGGGAGAAAGGAGCTAATTTTGAG
CTTGCCATTAAACTCTAA

Nucleotide

>CqEXLB-02

GGAGCATGTGGATATGGAGAATATGGAAGAAGTGCTAATGATGGTTATGTAGCT
GGTGTCCATAGACCTTACAAAAACGGCACTGGATGTGGTGGTTGCTACCAGGTAC
TCCCTTCGTTCCATAATGTTCTATTTGAATTTTTTTTACGGTTTTTAATGCATGTAC
TTGATCAATATATAATTTCCCTATTTAAATAATTACTAGGTAAGGTGCAAGACAG
GAGAATGCACAGAAGACGGGGTGGTGGTGGTGGCAACAGATTTCGGGGTGGGTG
ATTGGACCGATTTCCTATTTCCGGCCAAGGCCTATGCTAAGATGGCCCGGCCCGG
GTTAGAAGCCGAACTGCTCGCATACGGCGTCGTTAACATCGAATACCGTCGAGTC
CCTTGCACCTTCGGTGGTTCAAACCTCGTAATTAATATACATGAAGGCACAAGAT
ACCCTCACTACTTGGCCATTATTATCACTTATAATCCTACTCTCTATGACGTTGTG

GGTGCTCAAGTTTGGCAGGTTTGTTTCCTCCACCCTTTTATCCATACACTTGGGGT
CATTTTAAATTTTAGGTCTCAAATCGACCCATGCACAACACGTGTACACGTGGAA
GGGTATGTCAACACGCGGGTATACATAGTGTCATAAAAAAATCACTTAATATTAT
TAGGTGCCTTAATAATTTATGAAATTACTACCTCCGTTACATATTATTTGCCAAGA
TTTGACATAAACTAGAGAAAAAAAATGTTTAATCATTGCAAATAATATGTAACGG
AAGTACTATATAAAAATACAAACACATTGAAATATTGGATATAATTGGATGAAAT
TGCAGGGTTATTTTAGATGGCATAATATCACATGTTGATAGGATATGAATCGAGC
TTTAAGGATTCAGGCACCGCACAGACGATCTGCGCTCATTCAATTACATTAAGTT
GCCTATAATTATATAATGATATCAGTTTTGGGCTCCAATTTTTGGTACAAGTAATT
TGTATATTGGGCTCAATTGGGCCTCTAACTATTTAAAAAAAAAATTGGAAATGCA
GGAGGAAACCCAAGAATGGAGGCCCATGAGAAAGCCATTTGGAGCAGTTTGGGA
CCTGGAAAATCCACCAAGAGTAGAAGGAGGTTATAAAATAAGATACGCTCTTGTT
GCCAGCAACACTAATCATGCCACCTGGGTGGAATCACCTACTCTTATTCCTGCTA
ATTGGGAGAAAGGAGCTAATTTTGAGCTTGCCATTAAACTCTAA