

## IDENTIFICATION

**Species:** *Chenopodium quinoa*

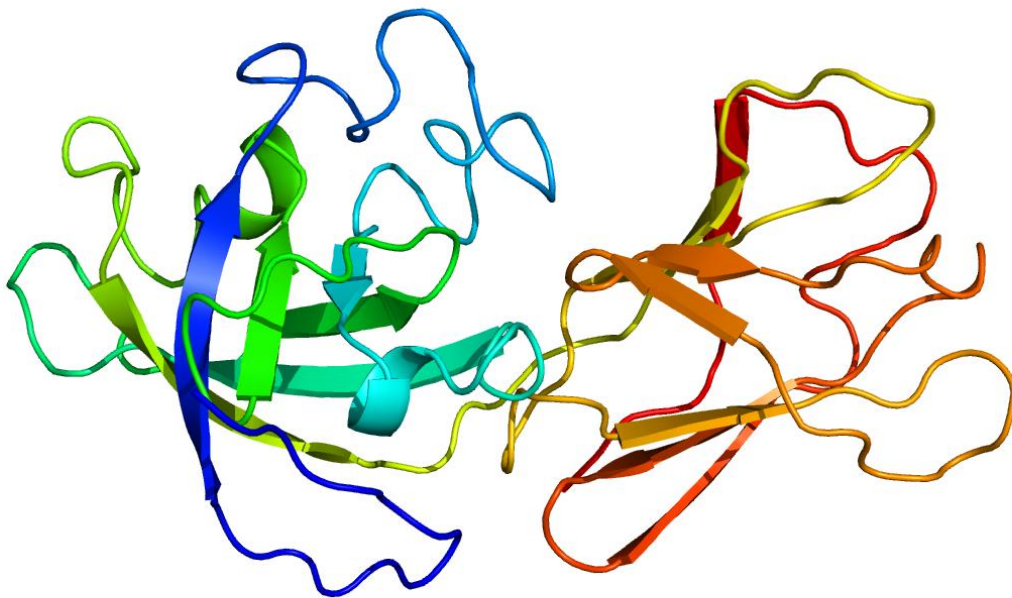
**Locus:** AUR62018603

**Gene Model:** AUR62018603

**Description:** CqEXPA-21

**Family:** Alpha Expansin

**3D structure:**



## GENOME DATABASES

Phytozome: [https://phytozome-next.jgi.doe.gov/info/Cquinoa\\_v1\\_0](https://phytozome-next.jgi.doe.gov/info/Cquinoa_v1_0)

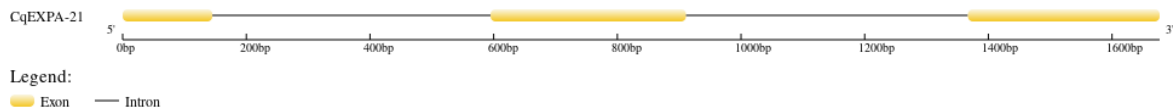
KEGG: <https://www.genome.jp/entry/T05764>

## EXTERNAL RESOURCES

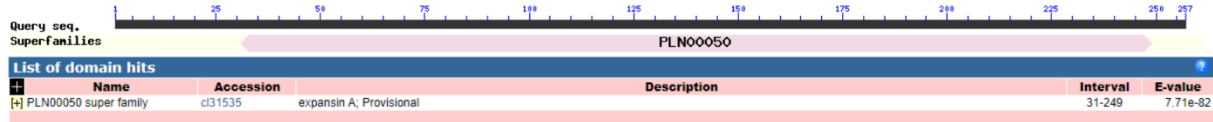
<https://www.cbrc.kaust.edu.sa/chenopodiumdb/>

<http://quinoa.kazusa.or.jp/index.html>

## GENE STRUCTURE



## DOMAIN ARCHITECTURE



## SEQUENCES

### Peptide

>CqEXPA-21

MTMRSTNADYGAYTPSTS YTPSTS YSPTEIWQSGHATFYGDESGSETMGGACGYGNL  
HDSGYGFETAALSTVLFNNGNACGTCYEIKCVESKWCFTNAPSIKITATNLCPPNWY  
QASDAGGWCNPPRSHFDLSKPMFMKIAEWTAGIVPVS YRKVSCGRTGGIRFQFQGNP  
YWLLVSVINVGDDISQMWVKGTETDWVSMRNWGFQAFSKLGGQPLSFKLQ  
NAAGQIVIAYNVCPTYWSNGLTYESNTNFY\*

### CDS (coding sequence)

>CqEXPA-21

ATGACGATGAGATCGACAAACGCGGATTACGGAGCGTACACGCCATCGACCTCC  
TACACGCCGTCGACCTCCTATTCACCAACAGAAATATGGCAATCAGGGCATGCTA  
CGTTTTATGGGGATGAAAGTGGCTCTGAGACCATGGGAGGAGCGTGTGGGTACG  
GAAACTTGCATGATAGCGGGTACGGATTCGAAACGGCAGCACTTAGCACGGTGT  
GTTCAACAATGGTAACGCTTGTGGAACGTGTTACGAAATCAAGTGTGTCGAGTCA  
AAATGGTGCTTCACCAATGCGCCTTCGATAAAGATCACAGCCACTAACCTCTGCC  
CTCCTAACTGGTACCAGGCTAGCGATGCCGGCGGGTGGTGCAACCCACCTCGCTC  
CCATTCGACTTGTCTAAGCCCATGTTTCATGAAGATTGCTGAATGGACTGCTGGC  
ATTGTTCCCGTTAGCTATAGAAAGGTATCATGTGGAAGGACAGGAGGAATTAGAT  
TTCAATTCCAAGGAATCCATATTGGCTCCTAGTGTCCGTGATAAACGTAGGAGG  
AGATGGAGATATATCCCAAATGTGGGTGAAAGGTACCGAACTGATTGGGTAG  
CATGAGCCGTAATTGGGGAGCTTCTTTCCAAGCATTCTCCAAATTAGGAGGCCAA  
CCTCTTTCTTTCAAGCTACAAAATGCAGCTGGACAAATTGTTATAGCTTATAATGT  
TTGCCCTACTTATTGGTCTAATGGGCTAACTTATGAATCCAATACCAATTTTTATT  
AA

### Nucleotide

>CqEXPA-21

ATGACGATGAGATCGACAAACGCGGATTACGGAGCGTACACGCCATCGACCTCC  
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CCTTAGCAATATTAATATAAATAAATGGGTGTTTTTTTAAAAAAAAAAAAAAAAATA  
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GAGTCAAATGGTGCTTACCAATGCGCCTTCGATAAAGATCACAGCCACTAACC  
TCTGCCCTCCTAACTGGTACCAGGCTAGCGATGCCGGCGGGTGGTGCAACCCACC  
TCGCTCCCATTTCGACTTGTCTAAGCCCATGTTTCATGAAGATTGCTGAATGGACTG  
CTGGCATTGTTCCCGTTAGCTATAGAAAGTATGTTTTCAATTCCTCCATTTTCATAT  
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AAATTAGGAGGCCAACCTCTTTCTTTCAAGCTACAAAATGCAGCTGGACAAATTG  
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AATACCAATTTTTATTAA