

## IDENTIFICATION

**Species:** *Chenopodium quinoa*

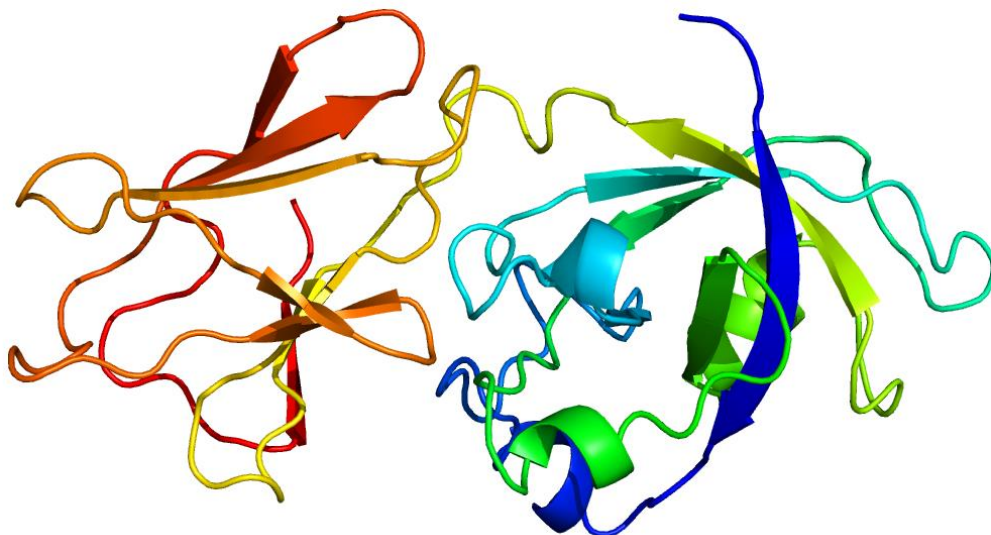
**Locus:** AUR62021586

**Gene Model:** AUR62021586

**Description:** CqEXPA-18

**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)

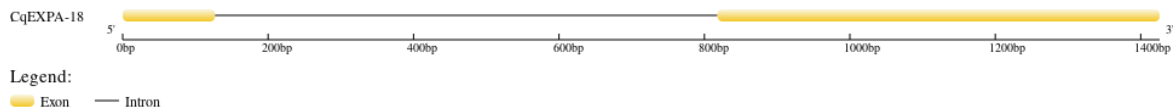
KEGG: <https://www.genome.jp/entry/T05764>

## EXTERNAL RESOURCES

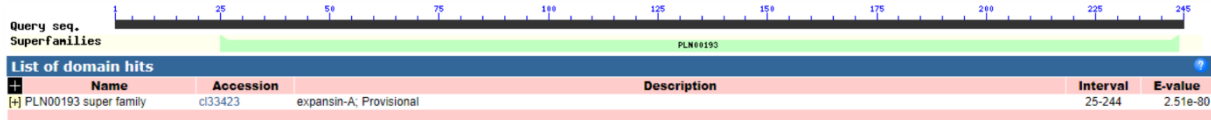
<https://www.cbrc.kaust.edu.sa/chenopodiumdb/>

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

## GENE STRUCTURE



## DOMAIN ARCHITECTURE



## SEQUENCES

### Peptide

>CqEXPA-18

MSFSQNAFGFLAIMALVTMVHCQDWTDAHATFYGDAKGGDTEKGACVYRTLQGY  
GLQTTALSTALYLDGATCGACYEIKCTNSEWCKDGAGTIKVTSTNLCPPSIGPEAWC  
NPPLQHFDLTQPMFVTIAKYKAGIVPVQYTRVPCTKQGGVKFLINGNPNFILVLIFNV  
GGVGDVKEMKIKGSGDWAQMSRNWGMNWQIGGSGWINQELSFQVTTSDGKTLEFE  
GVVPSNWQFSETFEGKSNF\*

### CDS (coding sequence)

>CqEXPA-18

ATGTCTTTTTCTCAAATGCTTTTGGATTTCTTGCTATCATGGCCTTAGTTACCATG  
GTACATTGTCAAGATTGGACAGATGCTCATGCAACGTTTTATGGTGATGCTAAGG  
GTGGTGATACCGAGAAGGGTGCTTGTGTTTATAGAACACTTACGCAAGGATATGG  
ACTGCAAACAACAGCTCTTAGCACAGCACTTTATCTAGATGGTGCAACTTGTGGA  
GCATGTTATGAAATCAAATGTACCAACTCAGAATGGTGCAAAGACGGTGCTGGC  
ACGATCAAAGTCACGTCCACCAACTTGTGTCCACCCTCAATTGGTCCTGAGGCAT  
GGTGTAATCCTCCGTTGCAACACTTTGACTTGACACAACCCATGTTTGTTACAATT  
GCTAAGTACAAAGCCGGTATTGTACCTGTACAATACACGAGAGTACCTTGTACTA  
AGCAAGGAGGAGTCAAGTTTCTTATTAATGGAAACCCTAATTTTATTTTGGTACT  
AATCTTTAATGTTGGAGGTGTCGGAGATGTTAAAGAAATGAAAATCAAGGGCTCG  
GGTGATTGGGCTCAAATGTCGCGAAATTGGGGTATGAACTGGCAAATTGGTGGTT  
CGGGTTGGATCAACCAAGAGTTATCATTCCAAGTGACTIONTAGTGATGGAAAAAC  
CCTAGAGTTTGAAGGTGTTGTGCCATCAAATTGGCAATTTAGTGAGACATTTGAA  
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### Nucleotide

>CqEXPA-18

ATGTCTTTTTCTCAAATGCTTTTGGATTTCTTGCTATCATGGCCTTAGTTACCATG  
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CTTTTCCTAACATAATTTTTGGTTGTTGGTGCCATGCAGAGGGTGCTTGTGTTTAT  
AGAACACTTACGCAAGGATATGGACTGCAAACAACAGCTCTTAGCACAGCACTTT  
ATCTAGATGGTGCAACTTGTGGAGCATGTTATGAAATCAAATGTACCAACTCAGA  
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CCCTCAATTGGTCCTGAGGCATGGTGTAAATCCTCCGTTGCAACACTTTGACTTGAC  
ACAACCCATGTTTGTTACAATTGCTAAGTACAAAGCCGGTATTGTACCTGTACAA  
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ACCCTAATTTTATTTTGGTACTAATCTTTAATGTTGGAGGTGTCGGAGATGTTAAA  
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GCAATTTAGTGAGACATTTGAAGGAAAGTCTAATTTTTAA