

## IDENTIFICATION

**Species:** *Chenopodium quinoa*

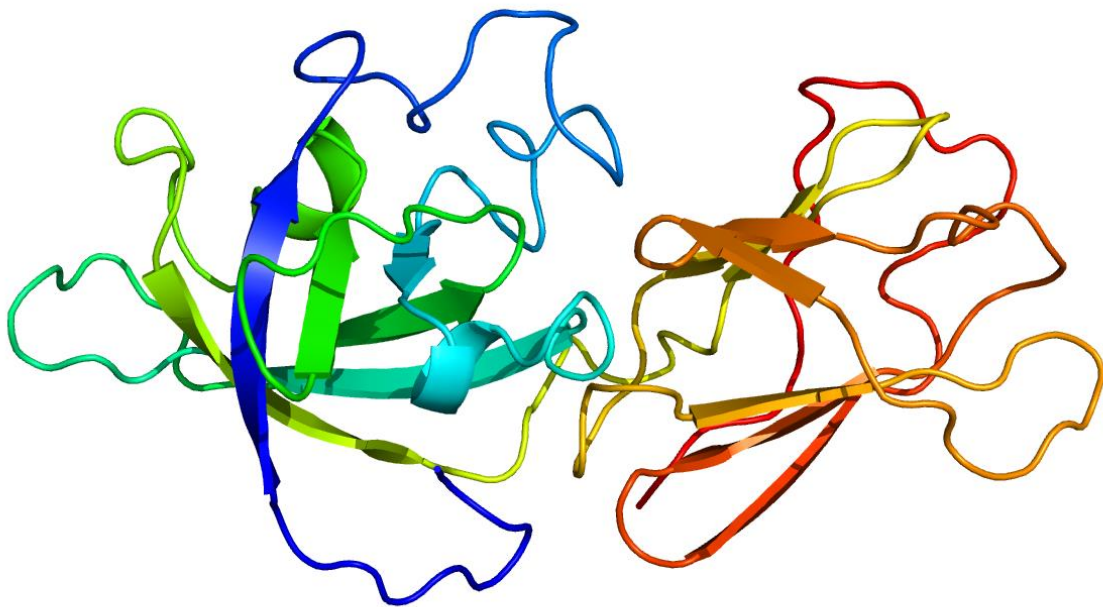
**Locus:** AUR62018280

**Gene Model:** AUR62018280

**Description:** CqEXPA-27

**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

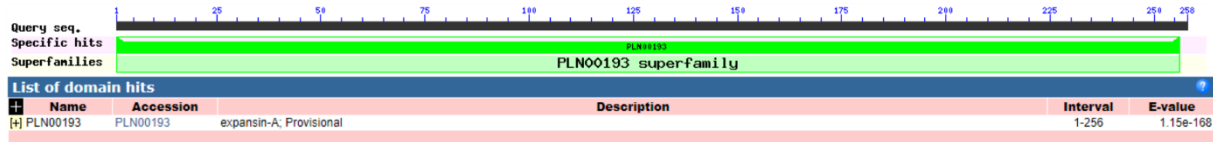
<https://www.cbrc.kaust.edu.sa/chenopodiumdb/>

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

## GENE STRUCTURE



## DOMAIN ARCHITECTURE



## SEQUENCES

### Peptide

>CqEXPA-27

MNKATSVVATIFLGVCFLNINVD AFRASGWQKAHATFYGGSDASGTMGGACGYGN  
LYTSGYGTRTAALSTALFNNGASCGQCYKIMCDYKTD P QWCRKGVSVTITATNFCPP  
NPAQPND DGGWCNPPLQHFDMAQPAWEKIGIYRGGIIPVMFQRVPCKKHGGVRF TIN  
GRDYFELVTISNVAAAGSIQSASIKGSKTNWMAMSRNWGANWQSLAYLDGQSL SFR  
ITTTD GQTRVFNNVVPANWQFGQTYSSRVQFH\*

### CDS (coding sequence)

>CqEXPA-27

ATGAACAAAGCAACCTCAGTTGTAGCAACAATTTTTCTAGGAGTATGTTTCCTAA  
ATATTAATGTTGATGCCTTTAGGGCTTCTGGATGGCAAAGGCTCATGCCACTTTC  
TACGGCGGCAGTGATGCATCCGGGACTATGGGAGGGGCTTGTGGGTACGGTAAC  
TTATACTAGTGGATATGGGACTAGAACCGCGGCTCTAAGTACTGCTTTGTTCA  
ACAACGGGGCATCATGTGGACAATGCTACAAGATCATGTGTGACTACAAGACGG  
ATCCCAGTGGTGCAGGAAGGGAGTTTCGGTCACTATTACCGCGACTAATTTCTG  
CCCTCCAACCCTGCTCAGCCTAACGATGATGGAGGTTGGTGTAAACCCTCCTCTG  
CAACACTTTGACATGGCCCAACCTGCTTGGGAGAAGATTGGCATTACAGGGGTG  
GAATCATTCCTGTCATGTTTCAAAGGGTTCCTTGCAAGAAACATGGAGGAGTAAG  
ATTTACTATTAATGGAAGGGACTACTTTGAGCTTGT TACAATAAGCAATGTAGCC  
GCAGCAGGATCAATACAATCTGCTTCGATCAAGGGATCGAAAACCAACTGGATG  
GCAATGTCTAGAAATTGGGGGGCTAACTGGCAGTCATTGGCTTACCTCGATGGAC  
AATCTCTATCTTTCAGAATTACTACCACTGATGGCCAAACCCGAGTTTTTAACAAT  
GTTGTTCCAGCTAATTGGCAATTTGGCCAAACATATTCGAGTCGTGTACAATTCCA  
TTAA

### Nucleotide

>CqEXPA-27

AAGTGAAAAAAAAAAAAAAAAATGAACAAAGCAACCTCAGTTGTAGCAACAATTT  
TCTAGGAGTATGTTTCCTAAATATTAATGTTGATGCCTTTAGGGCTTCTGGATGGC  
AAAAGGCTCATGCCACTTTCTACGGCGGCAGTGATGCATCCGGGACTATGGGTAC  
GTGTTTTTGTATTGTTTTTGAAGTGTAATAACTATAACATATATATGTTTGATTCAT

CGAATCGAAGAGACATAGGACTGAATCTTTTTGTTGTTATGCAGGAGGGGCTTGT  
GGGTACGGTAACTTATACTAGTGGATATGGGACTAGAACC GCGGCTCTAAGTA  
CTGCTTTGTTCAACAACGGGGCATCATGTGGACAATGCTACAAGATCATGTGTGA  
CTACAAGACGGATCCCCAGTGGTGCAGGAAGGGAGTTTCGGTCACTATTACCGCG  
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ACCCTCCTCTGCAACACTTTGACATGGCCCAACCTGCTTGGGAGAAGATTGGCAT  
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CCTTCAATACTCGATCAGTACATATTTGTTAGTGTTAATTCATTAGTATTACATTT  
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CAGGGTTCCTTGCAAGAAACATGGAGGAGTAAGATTTACTATTAATGGAAGGGA  
CTACTTTGAGCTTGTTACAATAAGCAATGTAGCCGCAGCAGGATCAATACAATCT  
GCTTCGATCAAGGGATCGAAAACCAACTGGATGGCAATGTCTAGAAATTGGGGG  
GCTAACTGGCAGTCATTGGCTTACCTCGATGGACAATCTCTATCTTTCAGAATTAC  
TACCACTGATGGCCAAACCCGAGTTTTTAACAATGTTGTTCCAGCTAATTGGCAA  
TTTGGCCAAACATATTCGAGTCGTGTACAATTCCATTAACATTATGGAGTGCACA  
TACACTTGCAGTACAGTTTGTGAGTTTCAACCAGATATTTCTTGATAGGCAGAGG  
CGTGCTCATAGCTTTTTTCGCCATTGAAGCAGCCCGCCAAATCTATCATTTGTAATA  
TATTAAGCAGCTTAATTA AAAATTCATTGAAAGGTTGATAATGGAAGTGGCAAACC  
ATGAACTCAAAGACTACTGCTAGTGAAGTGGGAATTTAAAGTAACCCATTATAT  
AGTCTTATACATATTAAGTTGGAAGATGTTTTAGTGCATCTAATAAGAAAGCATC  
CAATAAATTTTTTTGGTCCTCATCACCTTATACATATCTTTTGTAATTTGTTTTGGT  
TTAATTTGTGTGATTAGTGATAGTGGATTATTTAATTTTCTAAATTCAGGCTCTTG  
TTTTGGTTGTTTTTCAGACTATGGACTATAATTCAGATTATGTAATACTATGTACTA  
TATATAGTTCAGGCTCTTTGTGCTTTATGCTAC