

IDENTIFICATION

Species: *Chenopodium quinoa*

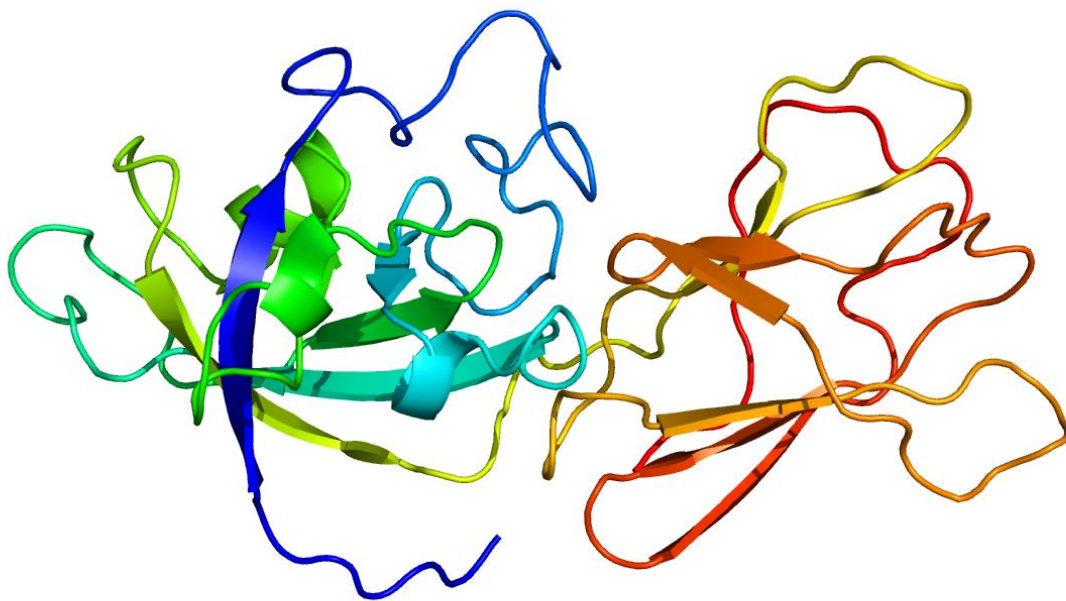
Locus: AUR62026939

Gene Model: AUR62026939

Description: CqEXPA-32

Family: Alpha Expansin

3D structure:



GENOME DATABASES

Phytozome: https://phytozome-next.jgi.doe.gov/info/Cquinoa_v1_0

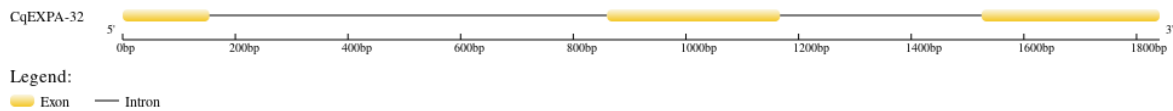
KEGG: <https://www.genome.jp/entry/T05764>

EXTERNAL RESOURCES

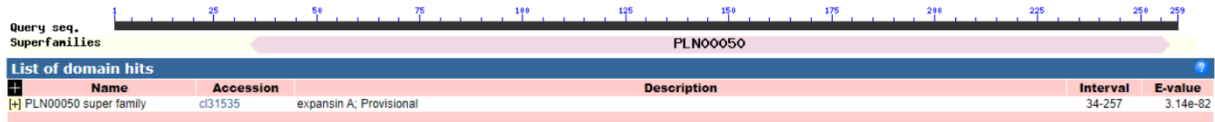
<https://www.cbrc.kaust.edu.sa/chenopodiumdb/>

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

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>CqEXPA-32

MKSSLLGILAVLFLVVFVSNVHAKRPNFRPGPWRIGRATFYGGSDGSGTFEGACGYG
DITTKEGKGGFGVQTA AISTALFNNGAACGSCYELSCEEPAKGCKAGASTITITGNW
CPDGGWCSPPQEHLDTQPAFLQIAEYKAGVVPKIKYRRVPCIRTTGGIRFISISPHSNPYY
LLVLIWNVAGAGDVESVMIKGDKGKPKPKMKRNWQNWESDDNYVGQSITFRVRT
SDGKKSTSWHVVPNTWQFGQTYEGKNFR*

CDS (coding sequence)

>CqEXPA-32

ATGAAGTCGTCTCTTCTTGGCATCATTTTGGCGGTGTTATTTCTTGTGGTATTTGTC
TCTAATGTTTCATGCCAAGAGGCCAAACTTCCGGCCTGGTCCGTGGAGAATCCGTA
GGGCTACCTTTTACGGTGGCTCAGATGGCTCGGGAACCTTTGAAGGAGCATGTGG
ATATGGAGATATAACAACCAAAGAAGGCAAAGGGGGGTTTGGGGTGCAAACCTGC
AGCTATAAGCACAGCATTGTTCAACAATGGAGCAGCTTGTGGCTCTTGCTATGAG
CTCAGTTGTGAAGAGCCTGCAAAGGGCTGCAAAGCTGGTGCATCTACCATCACCA
TTACCGGCAACAACCTGGTGCCCTGACGGAGGGTGGTGCAGCCCTCCGCAGGAGC
ATTTTGATCTCACTCAACCAGCCTTTCTTCAAATTGCCGAGTACAAGGCTGGCGTT
GTACCAATTAATAACCGCAGGGTTCATGCATAAGAACAGGAGGAATCCGTTTCA
GCATATCTCCGCATTCGAACCCGTA CTACTGCTGGTGTGATATGGAATGTCGC
AGGTGCAGGGGATGTAGAAAGCGTAATGATAAAGGGAGATAAGGGTAAGCCATT
TAAACCAATGAAGCGCAACTGGGGCCAAACTGGGAGAGCGATGACAATTACGT
AGGGCAGTCCATTACCTTCAGAGTCAGAACCAGCGATGGCAAGAAGTCTACTTCA
TGGCATGTTGTCCCAAACACTTGGCAGTTTGGTCAGACATACGAAGGCAAGAACT
TCAGATAA

Nucleotide

>CqEXPA-32

ATGAAGTCGTCTCTTCTTGGCATCATTTTGGCGGTGTTATTTCTTGTGGTATTTGTC
TCTAATGTTTCATGCCAAGAGGCCAAACTTCCGGCCTGGTCCGTGGAGAATCCGTA
GGGCTACCTTTTACGGTGGCTCAGATGGCTCGGGAACCTTTGGTAATTACTTCTCC
ATATTACTCTATCCATCTCTAAAAGTTTCTATTGAGCAATAATTGTATTAA
AAAAACAAAGCATAAAGA ACTTATAGAGATGGGAGCATTATTTTAGTCATGTCAC

CATTATTGTTATTGTTAATAAATTACATAGCTAGATTCCATTGAGTACATATGCAT
GTATGTTTCATAGATTACGCATGCATGGTGAATTTAAATAGCAATATGAGAATGAT
CAACCTTTTCCTAAGAAAATATATGTGTGGCGTGACTCTGTCTCTCTCTTTGAAAT
GGAAAATGAAAGTTAGCACCAATTCAATATAAAAATTATTTTTAATATTTCAAAT
AAAAGATTATAGTGCCTTATATACTCTGTATATTAAGGCTACGATTCTTAATAATG
CAAGTAATTTTTTTTTTTAAAAGGAACATAACTCACGTATGAGTTGACGTTATTTGT
CTCACATTAAATAAATAGAGAAAAAATTTATTATCACGCTACCACTCCCATTATA
AATTGGTTTTTTGGAAACAATCATATTGGACTTGTATGTGGTCAAACCTCTCCTCCAAT
ACAAGTTTATAATTTATATACGGCCCAACAAGATCTATTAGTCTTATTTAAAAGTT
CAATTCTAGGGGTGAATGCATCTGCATAGAGTATATGAAAGTGCACAAAGTTGAA
TAAAGTTGGATTTGAATGTAAACAGAAGGAGCATGTGGATATGGAGATATAACA
ACCAAAGAAGGCAAAGGGGGGTTTTGGGGTGCAAACCTGCAGCTATAAGCACAGCA
TTGTTCAACAATGGAGCAGCTTGTGGCTCTTGCTATGAGCTCAGTTGTGAAGAGC
CTGCAAAGGGCTGCAAAGCTGGTGCATCTACCATCACCATTACCGGCAACAACCTG
GTGCCCTGACGGAGGGTGGTGCAGCCCTCCGCAGGAGCATTTTGATCTCACTCAA
CCAGCCTTTCTTCAAATTGCCGAGTACAAGGCTGGCGTTGTACCAATTAATAACC
GCAGGTATGTAAATCATGAAGCACTCCATTTGTTCCGGAACATATGTCACACTAT
CCTAACTCCTCATAATGCTGCATTTTCTCTAAGTCAGCTAGTCATGAAGCAATGAG
CTAGGAAATGATTTACAGAACTTCAGAGAAATCAATCTGCTTGAGAACTTTCAA
CATGGATTTATTTGCCCCCAAAAATATATATATACTGTATTTAGTTAGTAAA
GCTGAAAAGTTGATACATGACTTGCCACAATTTTTTTTTTTTTTTTTTTTTTTTT
TTTTCCCCCCTTCATATCGCAAACTAACAGATCAGAGAATCAGAGTAACTGA
ATCGAATGTTTTATGCATGACATGCAGGGTTCCATGCATAAGAACAGGAGGAATC
CGTTTCAGCATATCTCCGCATTCGAACCCGTACTACCTGCTGGTGTGATATGGAA
TGTCGCAGGTGCAGGGGATGTAGAAAGCGTAATGATAAAGGGAGATAAGGGTAA
GCCATTTAAACCAATGAAGCGCAACTGGGGCCAAAACCTGGGAGAGCGATGACAA
TTACGTAGGGCAGTCCATTACCTTCAGAGTCAGAACCAGCGATGGCAAGAAGTCT
ACTTCATGGCATGTTGTCCCAAACACTTGGCAGTTTGGTCAGACATACGAAGGCA
AGAACTTCAGATAA