IDENTIFICATION

Species: *Chenopodium quinoa*

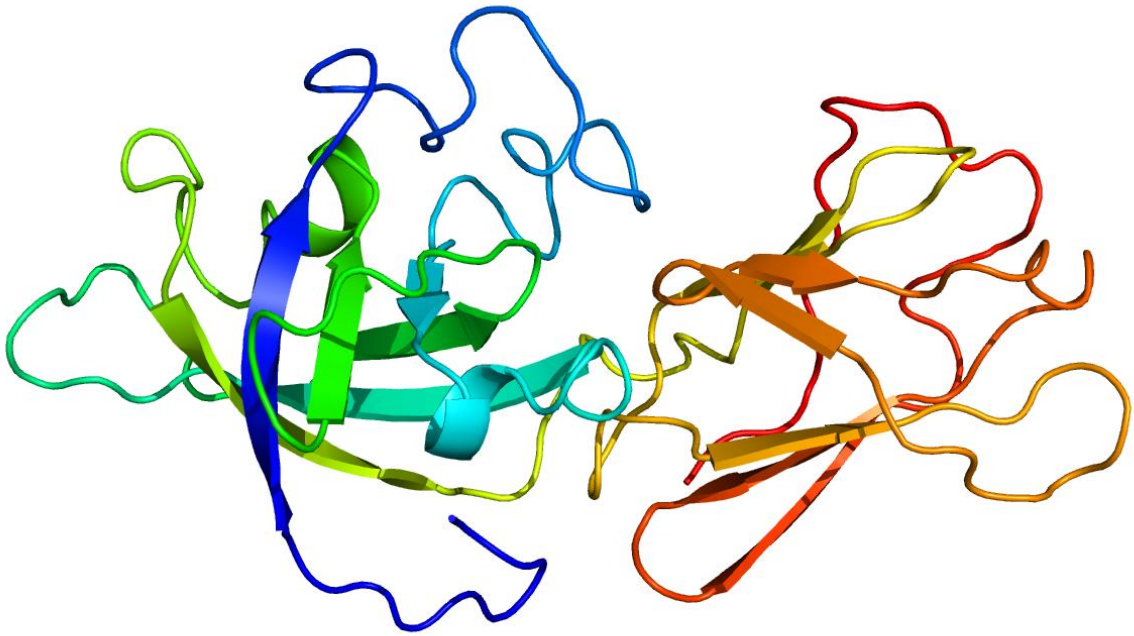
Locus: AUR62018283

Gene Model: AUR62018283

Description: CqEXPA-30

Family: Alpha Expansin

3D structure:



GENOME DATABASES

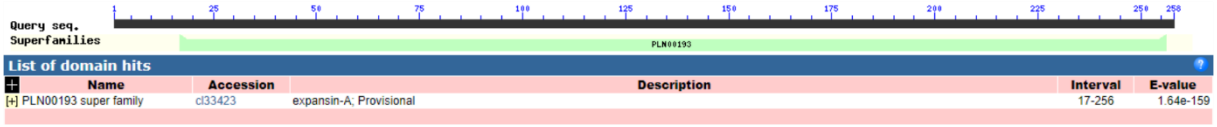
Phytozome: https://phytozome-next.jgi.doe.gov/info/Cquinoa_v1_0
KEGG: https://www.genome.jp/entry/T05764

EXTERNAL RESOURCES

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

GENE STRUCTURE

DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>CqEXPA-30

MNKPILLATLFLLGLYFLNVNVNAFVASGWQKASATFYGGSDASGTMGGACGYGN
LYSTGYGTSTAALSTVLFNDGAACGQCYRIMCDYKTDPTWCRKGVSVTITATNFCPP
NYALPSDAGGWCNPPRQHFDMSQPIWEKIGIYRGGIIPVIYQRVPCIKRGGVRFTINGR
DYFELVLITNVGGAGSIKSVSIKGSNTNWMAMSRNWGANWQSLAYLNGQSLSFRVT
STDGQTQTFNNIVPANWRYGQSFMSSIQFK*

CDS (coding sequence)

>CqEXPA-30

ATGAACAAACCCATCTTATTAGCTACACTTTTTCTACTAGGATTATATTTCCTAAA
CGTTAATGTTAATGCATTTGTGGCTTCTGGATGGCAAAAGGCTTCTGCCACTTTCT
ACGGCGGTAGTGATGCTTCTGGAACTATGGGAGGAGCTTGTGGGTACGGAAACTT
GTACTCCACTGGTTATGGGACTAGCACCGCGGCCTTAAGTACTGTATTGTTCAAC
GATGGTGCTGCATGTGGGCAATGCTACAGGATCATGTGTGACTATAAGACGGATC
CCACGTGGTGCCGGAAGGGAGTTTCAGTTACTATTACCGCGACTAACTTCTGCCC
TCCAAACTATGCATTGCCAAGTGATGCTGGAGGTTGGTGTAACCCTCCTCGCCAG
CACTTTGACATGTCGCAACCTATCTGGGAGAAGATTGGCATTTACAGAGGCGGAA
TCATTCCTGTCATCTACCAAAGGGTTCCCTGCATAAAGCGAGGAGGAGTGAGGTT
TACTATTAACGGAAGGGACTACTTTGAGCTTGTATTGATCACCAATGTAGGTGGA
GCAGGATCAATCAAATCAGTTTCAATTAAGGGATCGAATACTAACTGGATGGCGA
TGTCTAGAAACTGGGGGGCTAACTGGCAGTCATTGGCTTATCTTAATGGACAATC
ACTATCCTTCAGAGTCACTAGTACTGATGGCCAAACCCAAACATTTAACAACATT
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AA

Nucleotide

>CqEXPA-30

ATGAACAAACCCATCTTATTAGCTACACTTTTTCTACTAGGATTATATTTCCTAAA
CGTTAATGTTAATGCATTTGTGGCTTCTGGATGGCAAAAGGCTTCTGCCACTTTCT
ACGGCGGTAGTGATGCTTCTGGAACTATGGGTATGTTTTTAAATCTATGTTTCTAA
TCCCTCAATGTAGATATAATTCACTTTGGTTTATGTGATTATGTTTACTATGACAT
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GAGCTTGTGGGTACGGAAACTTGTACTCCACTGGTTATGGGACTAGCACCGCGGC
CTTAAGTACTGTATTGTTCAACGATGGTGCTGCATGTGGGCAATGCTACAGGATC
ATGTGTGACTATAAGACGGATCCCACGTGGTGCCGGAAGGGAGTTTCAGTTACTA
TTACCGCGACTAACTTCTGCCCTCCAAACTATGCATTGCCAAGTGATGCTGGAGG
TTGGTGTAACCCTCCTCGCCAGCACTTTGACATGTCGCAACCTATCTGGGAGAAG
ATTGGCATTTACAGAGGCGGAATCATTCCTGTCATCTACCAAAGGTAATTAATTT
AAGAACATGTGCTCATAGATTTAACACATAACTGCATGTATTTTATGGTATGTTTG
GGGCTATAAATATAGTTCTAATATTGAATACTCTCTCATTTTATTCAGGGTTCCCT
GCATAAAGCGAGGAGGAGTGAGGTTTACTATTAACGGAAGGGACTACTTTGAGC
TTGTATTGATCACCAATGTAGGTGGAGCAGGATCAATCAAATCAGTTTCAATTAA
GGGATCGAATACTAACTGGATGGCGATGTCTAGAAACTGGGGGGCTAACTGGCA
GTCATTGGCTTATCTTAATGGACAATCACTATCCTTCAGAGTCACTAGTACTGATG
GCCAAACCCAAACATTTAACAACATTGTTCCTGCTAATTGGAGATATGGACAGTC
ATTTATGAGTAGTATACAATTCAAGTAA