IDENTIFICATION

Species: *Anacardium occidentale*

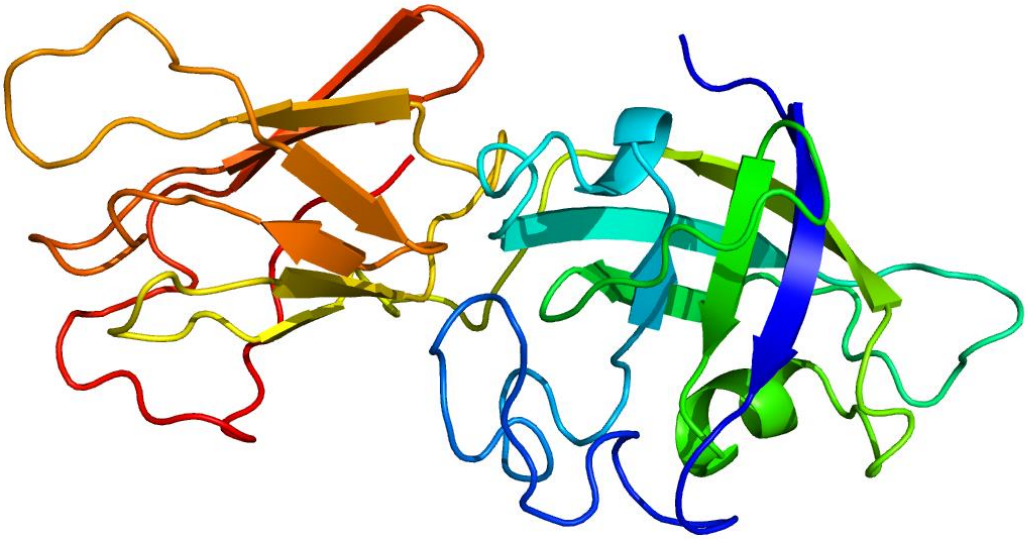
Locus: Anaoc.0002s1771

Gene Model: Anaoc.0002s1771.1.p

Description: AocEXPA-05

Family: Alpha Expansin

3D structure:



GENOME DATABASES

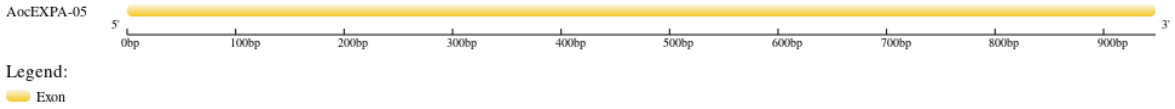
Phytozome: https://phytozome-next.jgi.doe.gov/info/Aoccidentale_v0_9

KEGG:-

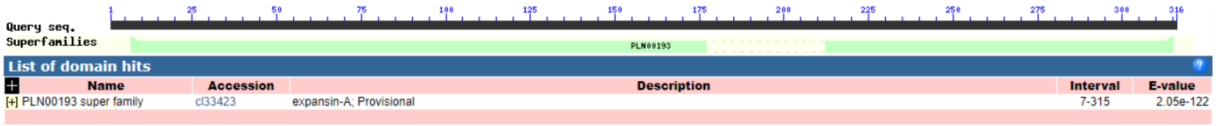
EXTERNAL RESOURCES

-

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>AocEXPA-05

MEGAFAFICVISISVIFNVASADWQKAHATFYGGSDASGTMGEFLIHAHLQFTISFFFC
FSLMASISSSGGACGYGNLYTDGYDTNTAALSTALFNDGKACGGCYQIVCDATQEPQ
WCHKGTHITITATNFCPPNYDLPSDNGGWCNPPLAHFDMAQPAFESIAIYSAGIVPVF
YRKYVEFHILVFIELPCIYDFLVYYICLNNKDVSSRLIRVGCKRSGGIRFTINGKDYFEL
VLISNVGGAGDISSVWIKGSKMSDWQVMSRNWGANWQSLSYLNGQSLSFKIQLSNG
RTRDALNVVPSDWQFGQSFKSNVQF*

CDS (coding sequence)

>AocEXPA-05

ATGGAAGGGGCCTTCGCATTCATTTGCGTCATTTCAATTTCAGTAATATTTAATGT
GGCATCTGCTGATTGGCAGAAAGCCCATGCAACTTTTTACGGCGGAAGTGATGCT
TCAGGAACAATGGGTGAGTTTCTAATTCATGCTCACTTACAATTTACAATTTCATT
TTTTTTTTGCTTTTCTCTAATGGCTTCAATTTCTTCATCAGGTGGTGCATGTGGTTA
TGGAAATCTGTATACAGATGGTTATGACACAAATACGGCAGCGTTGAGTACGGCT
TTGTTCAACGATGGCAAGGCATGCGGTGGCTGCTACCAGATAGTCTGCGACGCCA
CCCAGGAGCCTCAGTGGTGCCACAAAGGCACACATATCACCATTACTGCTACAAA
CTTCTGTCCTCCGAACTATGATCTCCCAAGTGACAATGGCGGTTGGTGCAATCCTC
CCCTGGCGCACTTTGACATGGCTCAGCCTGCTTTTGAGTCCATTGCCATTTACAGT
GCTGGAATCGTACCTGTTTTTTATAGGAAGTATGTTGAGTTCCACATTCTCGTCTT
CATAGAACTTCCTTGCATATACGACTTTCTAGTTTACTATATATGTTTGAATAACA
AGGACGTTTCTTCTCGTCTTATCAGAGTTGGATGCAAGAGAAGTGGAGGAATCAG
ATTCACCATCAATGGAAAGGATTACTTTGAGCTAGTGCTAATATCAAATGTAGGT
GGAGCTGGAGATATCTCAAGTGTCTGGATCAAAGGGTCCAAAATGAGTGATTGG
CAAGTTATGTCAAGGAACTGGGGTGCGAATTGGCAGAGTTTAAGCTACCTCAATG
GCCAGAGCTTGTCTTTCAAAATTCAACTAAGCAATGGAAGGACCCGCGACGCTCT
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TTCTAA

Nucleotide

>AocEXPA-05

ATGGAAGGGGCCTTCGCATTCATTTGCGTCATTTCAATTTCAGTAATATTTAATGT
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CTTCTGTCCTCCGAACTATGATCTCCCAAGTGACAATGGCGGTTGGTGCAATCCTC
CCCTGGCGCACTTTGACATGGCTCAGCCTGCTTTTGAGTCCATTGCCATTTACAGT
GCTGGAATCGTACCTGTTTTTTATAGGAAGTATGTTGAGTTCCACATTCTCGTCTT
CATAGAACTTCCTTGCATATACGACTTTCTAGTTTACTATATATGTTTGAATAACA
AGGACGTTTCTTCTCGTCTTATCAGAGTTGGATGCAAGAGAAGTGGAGGAATCAG
ATTCACCATCAATGGAAAGGATTACTTTGAGCTAGTGCTAATATCAAATGTAGGT
GGAGCTGGAGATATCTCAAGTGTCTGGATCAAAGGGTCCAAAATGAGTGATTGG
CAAGTTATGTCAAGGAACTGGGGTGCGAATTGGCAGAGTTTAAGCTACCTCAATG
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