

IDENTIFICATION

Species: *Ricinus communis*

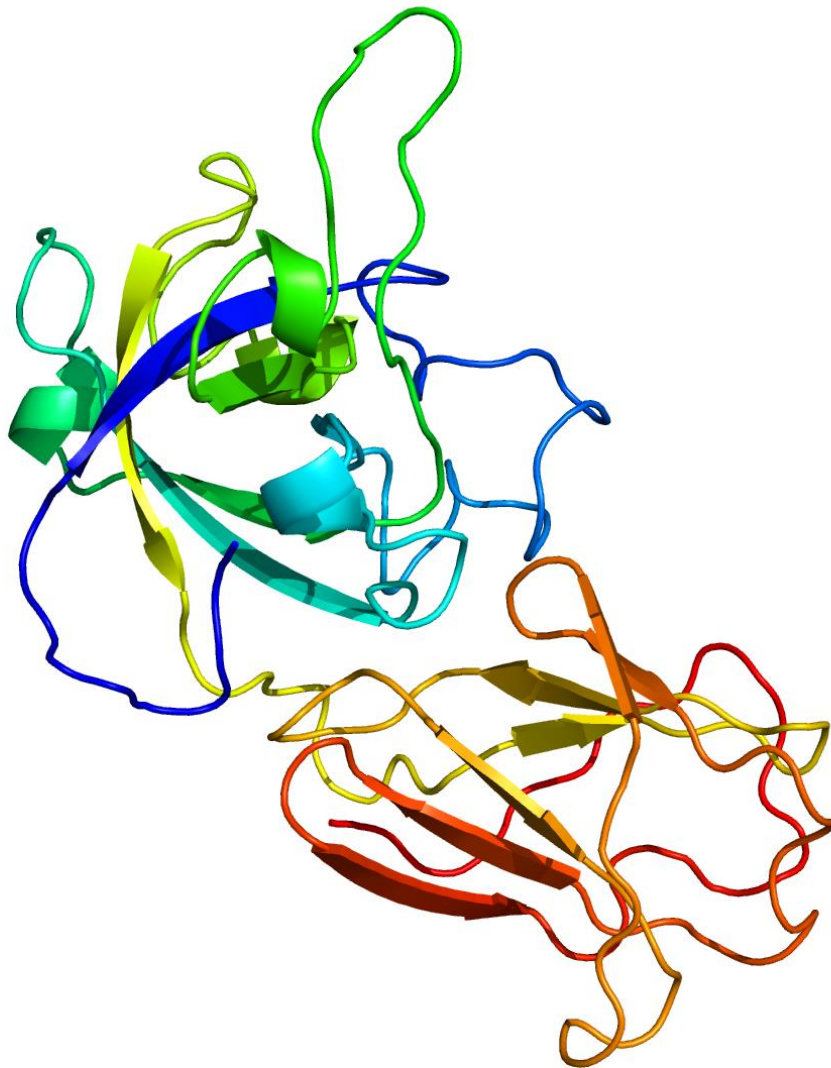
Locus: 30162.m001293

Gene Model: 30162.m001293

Description: RcEXPA-15

Family: Alpha Expansin

3D structure:



GENOME DATABASES

Phytozome: https://phytozome-next.jgi.doe.gov/info/Rcommunis_v0_1

KEGG: <https://www.genome.jp/entry/T01087>

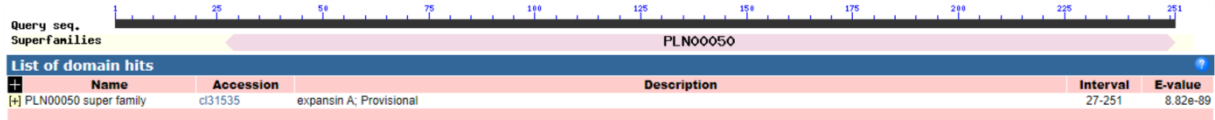
EXTERNAL RESOURCES

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GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>RcEXPA-15

MDALKAILLYFIMLQTCNISAIDEEEWKTATATCTKQKDGSIIIEGACGYGDLHKASY
GKYSAGLSRMLFNRGSTCGACFELRCVDHILWCLQGSPSVILTATNFCPPNYGLSAD
YGGWCNFPKEHFEMSEAAFAEIAERKADVVPVQYRRVNCDRKGGRLFTVSGNFHFY
QVLVTNVGLDGEVVAVKVKGSRGTGWIPMARNWGWQIWTNVDLIGQPLSFEVTTSSG
RTLTSYNVAPVNWKFGQSFEGKQF

CDS (coding sequence)

>RcEXPA-15

ATGGATGCTCTAAAAGCCATCCTTCTCTACTTTATCATGTTGCAAACCTGCAACAT
CAGTGCCATTGATGAGGAGGAATGGAAGACTGCTACTGCAACTTGCACCAAACA
AAAAGATGGGTCAATCATTATAGAAGGAGCTTGTGGGTATGGAGATCTTCACAA
AGCTTCCTATGGGAAGTACAGTGCTGGACTAAGTCGCATGTTGTTTAACAGAGGA
AGCACATGTGGAGCTTGCTTTGAGCTCAGATGTGTAGACCACATCCTGTGGTGCC
TGCAGGGTAGCCCCTCTGTCAATTCTCACTGCCACGAATTTCTGTCTCCTCAAATTAT
GGGCTTTCAGCAGACTATGGTGGCTGGTGCAATTTCCCCAAAGAACACTTTGAAA
TGTCGGAGGCAGCATTGCTGAAATTGCAGAAAGAAAAGCTGATGTTGTTCCAGT
TCAGTACAGGAGGGTAAACTGTGACAGGAAGGGCGGGCTGAGATTCACAGTCAG
TGGAATTTTCATTTCTATCAAGTACTTGTTACCAATGTAGGACTAGATGGTGAA
GTGGTTGCTGTGAAAGTGAAGGGGTCAAGAACAGGGTGGATACCTATGGCAAGA
AACTGGGGACAAATCTGGCAAACCAATGTTGACCTTATTGGACAACCTCTTTCTT
TTGAGGTTACCACTAGCAGCGGAAGAACACTCACATCTTACAATGTTGCACCAGT
AAACTGGAAATTTGGTCAATCATTGGAAGGCAAACAATTCTAG

Nucleotide

>RcEXPA-15

ATGGATGCTCTAAAAGCCATCCTTCTCTACTTTATCATGTTGCAAACCTGCAACAT
CAGTGCCATTGATGAGGAGGAATGGAAGACTGCTACTGCAACTTGCACCAAACA
AAAAGATGGGTCAATCATTATAGGTAATAGCTTCCATTGTTTCAATTAATAAT
GGAGCTTTTCTTTCTTTCTTTTTTTTTTCTTTCTTTAATGAACCAATAGATGTATA
AAGCCAATTATAGATAGATTAAGAGACACAGTTCAGTATCTCTGATTTTTGCTAG
TATTTTAAGCAGCATTGTTTTGTGTTGCAGAAGGAGCTTGTGGGTATGGAGATCTT
CACAAAGCTTCTATGGGAAGTACAGTGCTGGACTAAGTCGCATGTTGTTTAAACA
GAGGAAGCACATGTGGAGCTTGCTTTGAGCTCAGATGTGTAGACCACATCCTGTG

GTGCCTGCAGGGTAGCCCCTCTGTCATTCTCACTGCCACGAATTTCTGTCCTCCAA
ATTATGGGCTTTTCAGCAGACTATGGTGGCTGGTGCAATTTCCCAAAGAACA
TTTGAAATGTTCGGAGGCAGCATTTCGCTGAAATTGCAGAAAGAAAAGCTGATGTTGTT
CCAGTTCAGTACAGGAGGTAAAATCAATCAAATTAGAAATTATTGGCAAAATAA
CTAAAGTTACCACTTAGATACATGAGCAAACCTCTCTGTACCGATATTGTGCAGGG
TAAACTGTGACAGGAAGGGCGGGCTGAGATTCACAGTCAGTGGAAATTTTCATTT
CTATCAAGTACTTGTTACCAATGTAGGACTAGATGGTGAAGTGGTTGCTGTGAAA
GTGAAGGGGTCAAGAACAGGGTGGATACCTATGGCAAGAACTGGGGACAAATC
TGGCAAACCAATGTTGACCTTATTGGACAACCTCTTTCTTTTGAGGTTACCACTAG
CAGCGGAAGAACA
CTCACATCTTACAATGTTGCACCAGTAAACTGGAAATTTGGT
CAATCATTGGAAGGCAAACAATTCTAG