

IDENTIFICATION

Species: *Ricinus communis*

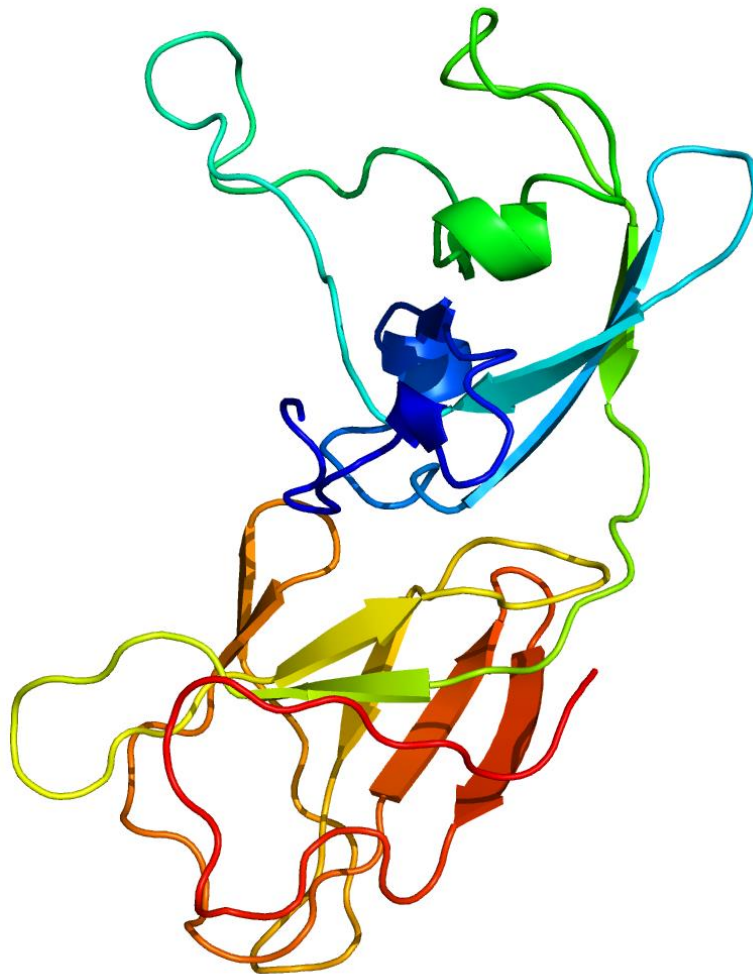
Locus: 27383.m000164

Gene Model: 27383.m000164

Description: RcEXPA-01

Family: Alpha Expansin

3D structure:



GENOME DATABASES

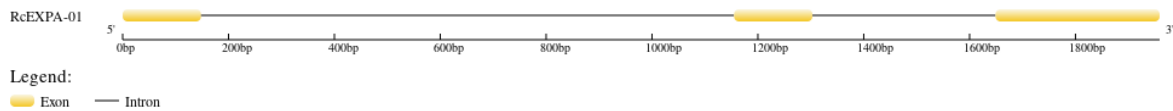
Phytozome: https://phytozome-next.jgi.doe.gov/info/Rcommunis_v0_1

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

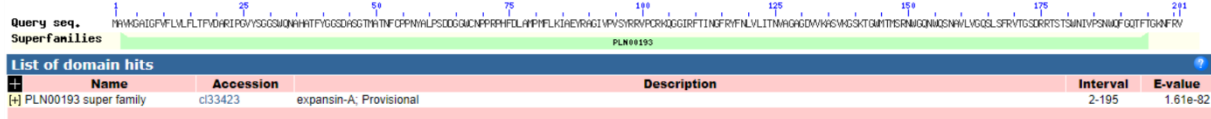
EXTERNAL RESOURCES

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GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>RcEXPA-01

MAVKGAIGFVFLVLFLLTFVDARIPGVYSGGSWQNAHATFYGGSDASGTMATNFCPP
NYALPSDDGGWCNPPRPHFDLAMPMFLKIAEYRAGIVPVSYRRVPCRKQGGIRFTIN
GFRYFNLVLTINVAGAGDVVKASVKGSKTGWMTMSRNWQNWQSNVAVLVGQSLS
FRVTGSDRRTSTSWNIVPSNWQFGQTFGTGKNFRV

CDS (coding sequence)

>RcEXPA-01

ATGGCGGTTAAGGGTGCAATTGGTTTTGTGTTTTTGGTGCTGTTTTTGACCTTTGTT
GATGCAAGAATTCCTGGTGTTTACAGTGGTGGATCATGGCAAACGCCCATGCTA
CTTTCTATGGCGGCAGTGATGCTTCTGGAACAATGGCCACAACTTTTGCCCCCT
AACTATGCTCTGCCTAGTGACGATGGTGGTTGGTGCAACCCTCCTCGCCCTCACTT
CGATCTCGCCATGCCCATGTTCCCTCAAGATCGCCGAGTACCGTGCCGGCAGTCGTC
CCTGTCTCTTATCGCCGGGTGCCGTGTAGAAAGCAAGGAGGAATCAGGTTACAA
TCAACGGCTTCCGTTACTTCAACTTGGTTTTGATCACCAACGTCGCAGGTGCAGG
AGATGTCGTGAAGGCTAGCGTGAAAGGGTCGAAGACTGGTTGGATGACCATGAG
CCGTAACCTGGGGTCAAACTGGCAATCAAATGCCGTTTTGGTTGGTCAGTCACTT
TCCTTCAGGGTCACAGGCAGTGATAGACGCACCTCCACTTCTTGGAATATCGTCC
CTTCAAATTGGCAATTTGGTCAAACCTTTCACCGGAAAGAATTCAGGGTCTAA

Nucleotide

>RcEXPA-01

ATGGCGGTTAAGGGTGCAATTGGTTTTGTGTTTTTGGTGCTGTTTTTGACCTTTGTT
GATGCAAGAATTCCTGGTGTTTACAGTGGTGGATCATGGCAAACGCCCATGCTA
CTTTCTATGGCGGCAGTGATGCTTCTGGAACAATGGGTACTTCCATTATTTACCT
ATTCATGCTGTTATGCTTTGAAATTCCTGTTTAGCTCATCATTATGAATACTGGGT
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CCCTAACTATGCTCTGCCTAGTGACGATGGTGGTTGGTGCAACCCTCCTCGCCCTC
ACTTCGATCTCGCCATGCCCATGTTCCCTCAAGATCGCCGAGTACCGTGCCGGCAT
CGTCCCTGTCTCTTATCGCCGGTAAAAGATTGAACTTTCTTGCTCTGTTTACTACT
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GCTCAAATAAGGAAAAGTATTAATGGGTATTTTGATAAGCAAAGTAAGGAATAT
ATTCAGATTATGTATTGATTTTTACCATTCTTTTTTTGGCAAAAAAATCTGGCCAC
CTTGAAATAAAAGTCAAATACACAGGTGATGATGAGTATGAATTAGTATCATTG
GCTAAACTTAGGGCCCTAATTGCTCCAATTTCTACTGTTAATTACCAAATGCCTA
TCTAAATATTTTTATTTTCTTTTTTAAAAATAGGGTGCCGTGTAGAAAGCAAGGA
GGAATCAGGTTCAACAATCAACGGCTTCCGTTACTTCAACTTGGTTTTGATCACCAA
CGTCGCAGGTGCAGGAGATGTCGTGAAGGCTAGCGTGAAAGGGTCGAAGACTGG
TTGGATGACCATGAGCCGTAACCTGGGGTCAAACCTGGCAATCAAATGCCGTTTTG
GTTGGTCAGTCACTTTCCTTCAGGGTCACAGGCAGTGATAGACGCACCTCCACTT
CTTGGAATATCGTCCCTTCAAATTGGCAATTTGGTCAAACCTTTCACCGGAAAGAA
TTTCAGGGTCTAA