

IDENTIFICATION

Species: *Ricinus communis*

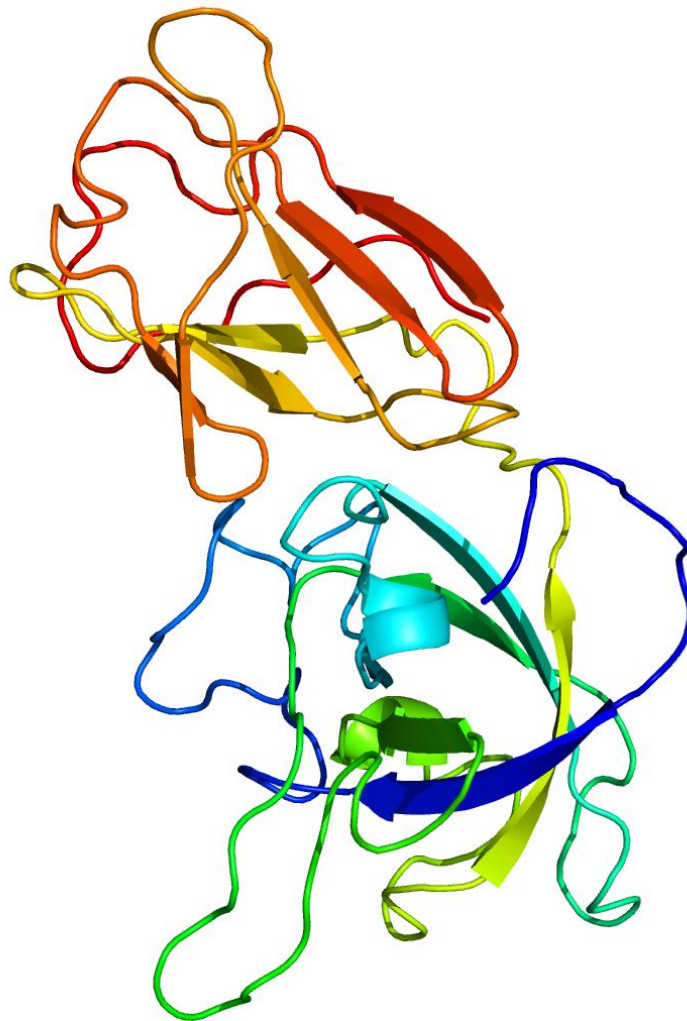
Locus: 29950.m001164

Gene Model: 29950.m001164

Description: RcEXPA-10

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>

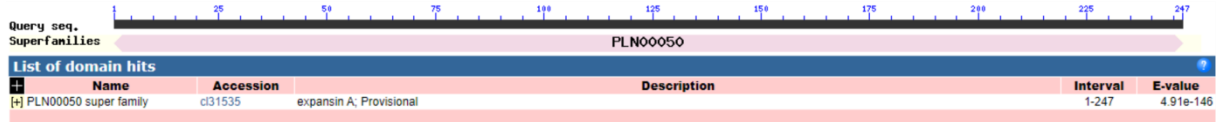
EXTERNAL RESOURCES

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GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>RcEXPA-10

MGFVGIYLLVFLAISKRIQGYGSGWSRAHATFYGGDASGTMGGACGYGNLYSQGY
GTSTAALSTALFNGLTCGACFEIKCVNDARWCLPGSIIVTATNFCPPNNVLP
SNAGGWCNPPLKHFDSLSPVVFQHIANKAGIVPVQYRRVACRKTGGIRFTINGHSYFNLV
LVTVN VGGAGDVVSISIKSRTGWQPMSRNWQNWQSN SYLNGQALSFKVTTSDGHTVIS
NNVAPPNWSFGQTFTGRQF

CDS (coding sequence)

>RcEXPA-10

ATGGGTTTTGTTGGAATTTATCTACTTGT TTTTCTAGCCATTTCCAAAAGAATTCA
AGGTTATGGAAGTGGATGGTCTAGAGCTCATGCTACCTTCTACGGAGGAGGTGAT
GCTTCTGGTACAATGGGGGGAGCTTGTGGCTATGGAAACCTTTACAGCCAAGGAT
ATGGAACAAGCACAGCTGCTTTGAGTACTGCTCTATTCAACAATGGACTAACCTG
TGGAGCATGTTTCGAAATCAAGTGTGTAATGATGCCAGGTGGTGCTTACCAGGT
TCCATCATTGTCACTGCAACAACTTTTGCCCTCCAAATAATGTTCTTCCAAGTAA
TGCAGGAGGCTGGTGCAATCCTCCTTTAAAACACTTTGATCTTCTCGACCTGTTT
TTCAACACATAGCTAATTTCAAGGCAGGAATAGTCCCTGTTCAAGTACAGAAGGGT
GGCTTGTAGGAAAAGTGGGGGGATAAGGTTCACTATAAATGGTCATTACTTCTC
AATCTTGTCTTGTAAACAATGTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT
CAAAGGATCTAGAAGTGGTTGGCAGCCAATGTCTCGCAACTGGGGCCAAAATTG
GCAAAGCAACTCTTATCTAAATGGTCAAGCACTCTCTTTTAAGGTCACAACAAGT
GATGGACACACTGTCATCTCCAACAATGTTGCTCCCCCTAACTGGTCGTTTGGCCA
AACCTTCACTGGCAGACAGTTTTAG

Nucleotide

>RcEXPA-10

ATGGGTTTTGTTGGAATTTATCTACTTGT TTTTCTAGCCATTTCCAAAAGAATTCA
AGGTTATGGAAGTGGATGGTCTAGAGCTCATGCTACCTTCTACGGAGGAGGTGAT
GCTTCTGGTACAATGGGTAAGAATCAAATCTAATCAGAACCTGTCATTAAGCATT
TCCTAATATAGTAGTTCCTGGCTTAAGTAATTATTGGTTTGCTGTAGGGGGAGCTT
GTGGCTATGGAAACCTTTACAGCCAAGGATATGGAACAAGCACAGCTGCTTTGAG
TACTGCTCTATTCAACAATGGACTAACCTGTGGAGCATGTTTCGAAATCAAGTGT
GTAATGATGCCAGGTGGTGCTTACCAGGTTCCATCATTGTCACTGCAACAACT
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TTAAAACACTTTGATCTTTCTCGACCTGTTTTTCAACACATAGCTAATTTCAAGGC
AGGAATAGTCCCTGTTTCAGTACAGAAGGTAAGATACTACAATCTTCATGAGAAAT
ATAATAATAATTATTTTAATACGGTCTCAGAGCCTCTCTGATCAAGCAATTGAC
GAGATTGTTAGGTTTGAAGTCTGCCAGTAATGACAGGCACTCAACCACTGGGCTT
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GTGGCTTGTTAGGAAAAGTGGGGGGATAAGGTTCACTATAAATGGTCATTCATACT
TCAATCTTGTCTTGTAACAAATGTTGGTGGTGCTGGTGATGTTGTATCTATCTCC
ATCAAAGGATCTAGAAGTGGTTGGCAGCCAATGTCTCGCAACTGGGGCCAAAATT
GGCAAAGCAACTCTTATCTAAATGGTCAAGCACTCTCTTTTAAGGTCACAACAAG
TGATGGACACACTGTCATCTCCAACAATGTTGCTCCCCCTAACTGGTCGTTTGGCC
AAACCTTCACTGGCAGACAGTTTTAG