

## IDENTIFICATION

**Species:** *Elaeis guineensis*

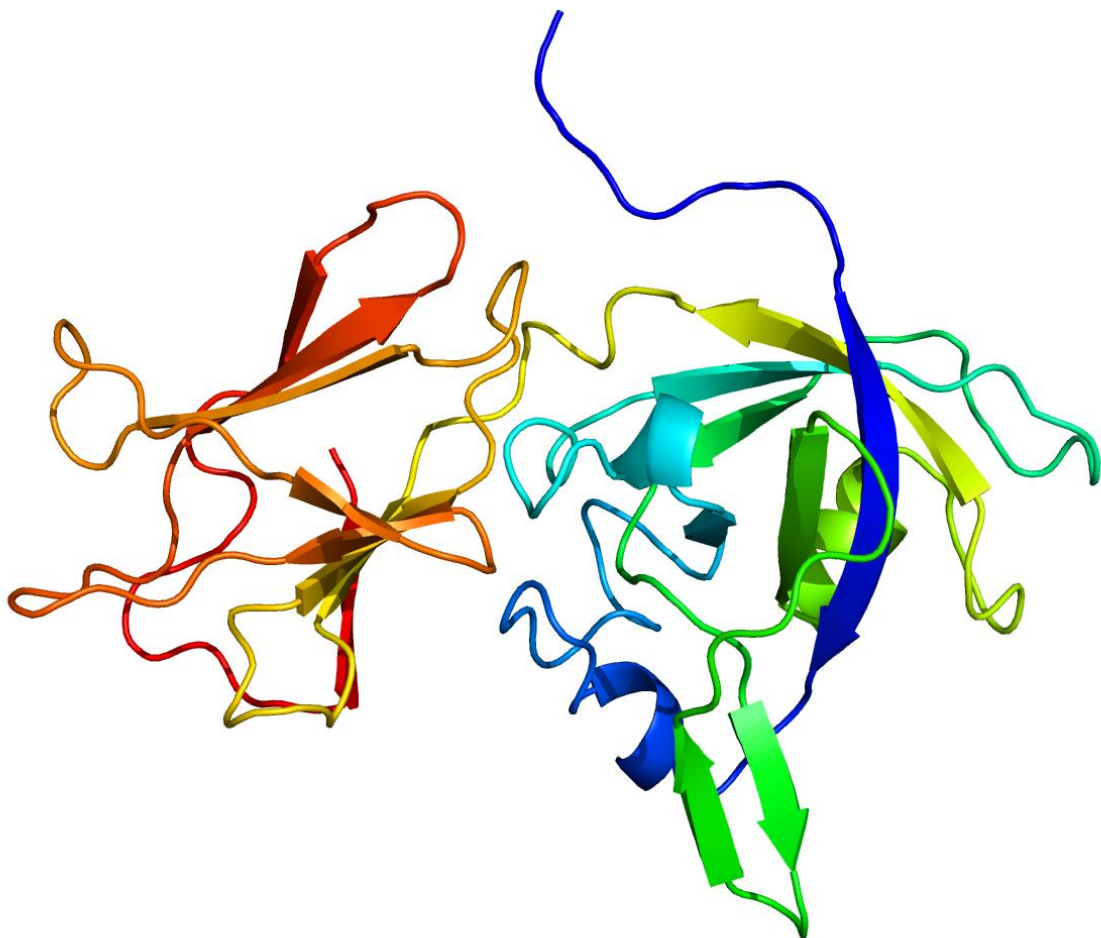
**Locus:** XP\_010921302

**Gene Model:** XP\_010921302.1

**Description:** EgEXPA-11

**Family:** Alpha Expansin

**3D structure:**



## GENOME DATABASES

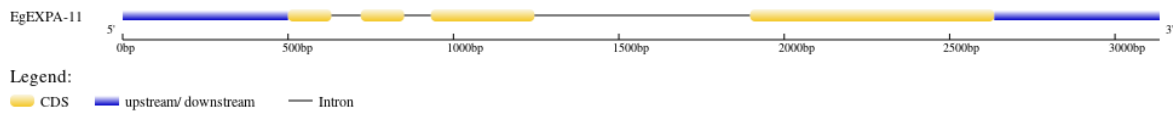
NCBI: [https://www.ncbi.nlm.nih.gov/genome/?term=txid51953\[orgn\]](https://www.ncbi.nlm.nih.gov/genome/?term=txid51953[orgn])

KEGG: <https://www.genome.jp/entry/T03921>

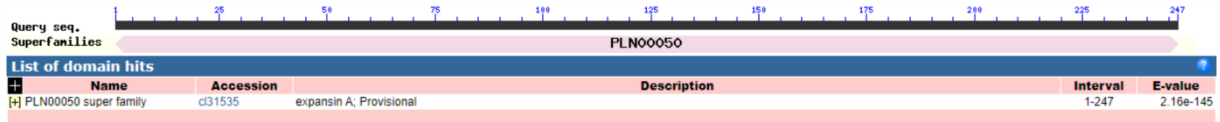
## EXTERNAL RESOURCES

-

## GENE STRUCTURE



## DOMAIN ARCHITECTURE



## SEQUENCES

### Peptide

>EgEXPA-11

MEFIALSLVSLLTIFGAVHGYGGGWSDAHATFYGGGDASGTMGGACGYGNLYSQG  
YGTNTAALSTALFNSSLSCGACFEIKCSNDGSWCLPGSIIVTATNFCPPNNALPNDNG  
GWCNPLQHFDSLQPVFQRIAQYKAGIVPVQYRRVPCVKNGGIRFTINGHSYFNLVLI  
SNVGGAGDVTAVSIKGSQTGWQPMSRNWQNWQSNLYLNGQSLSFQVTTSDGRTV  
TSMDVAPNNWSFGQTYSGGQL

### CDS (coding sequence)

>EgEXPA-11

CTGCTTTATCTGTTCCCTTTCCTTTCAGCTCCCTCCATCCATGTCTATAAATACACCT  
CTCCTTCCCTCACACCTTCCCTCATCCTCTCTCATTCCTTTTCTTTTGGGAAGTTAGGCT  
CTCATTTC AACCCCTCTGGAAATGGAGTTTATTGCCCTCTCCCTAGTTTCCCTTCTC  
ACCATCTTCGGAGCCGTTTCATGGATATGGTGGTGGGGTGGTCTGATGCACATGCTA  
CCTTTTATGGAGGTGGTGTGCTTCTGGGACAATGGGAGGGGCTTGTGGGTATGG  
AAATCTCTACAGTCAAGGATATGGGACAAACACAGCAGCATTGAGCACTGCTCTG  
TTCAACAGTGGACTGAGCTGTGGAGCTTGCTTCGAGATCAAATGTTCGAATGATG  
GGAGCTGGTGTCTCCCGGGATCTATAATTGTCACTGCAACAACTTCTGCCACC  
AAACAATGCTCTTCCAAACGATAATGGAGGGTGGTGCAACCCTCCCCTGCAGCAC  
TTTGATCTCTCTCAGCCAGTTTTCCAGCGTATTGCTCAGTACAAAGCAGGCATTGT  
CCCTGTTCAATACAGAAGGGTACCCTGTGTGAAGAACGGGGGAATCAGGTTACCC  
ATTAATGGTCACTCTTACTTCAACCTGGTGTGCTGATCTCCAATGTAGGTGGGGCTGG  
GGACGTGACGGCAGTGTCTATAAAGGGATCCCAGACTGGGTGGCAGCCAATGAG  
CCGCAACTGGGGCCAGAAGTGGCAGAGCAACAGCTACCTCAATGGCCAGTCCCT  
CTCCTTCCAAGTCACCACCAGCGATGGCCGCACTGTTACCTCCATGGACGTCGCC  
CCTAACAACTGGAGCTTCGGCCAGACCTACTCTGGTGGGCAGCTTTGAGCCTCTA  
ATTAAGCCAACAACGAATTCCCTCTGACCTTAGTATCAGTCTGGTGGAGTGACTG  
AAGTCTACGTATACTATTGTCTCACGGTGGGGTTCTCTTTTGATATGGCCCTACTT  
TGTCTGCTGAGTCTTTTCCCTTTTTTATTTCTTGTTTTCTTATGATTGACCTTCTCTT  
CCTGGCCTTGTATATGGTGGCAGAGGAGGACACTATCCAAGGGGTGGTGTGAGA  
GGTCTTTCTAGCTCTTAGGGAGTCCCATGGGGTTGTGTTAATGGGGAGGACAAAT  
GGCTGAGGTGAACCAAGGTTGGTCACCCGCCATGAATGCTTTTCTTTTCATGT

ACTTCTCTGTGACAGTGGGAAGCGAGATTGTAATCAGCTTTGCTGCTAAAATATT  
ATAAGATATCGAATAGATATATAATTATATTTTTGAAAGA

**Nucleotide**

>EgEXPA-11

AGTTATAGGAAAAGATCAGAAAAATTCACCTTTTTTTTTTTGACTTTTTATCATCTG  
ACAAACAGCAGCCCAAAAAGAGGAATTACTAAGATGACTGCCTCTAGTCGGCTTT  
ACACATTTTAAAGGTCTATGGTGTGCCAATGCTGTTCTCCAGAAGGTCCCCACAA  
GTGTTTGACAGCACCCAATTTTATCTGCAGAGGATAAGATTCATAGAATTTAGTT  
GGAAAAACGGAAAGGTTCAATTACTTTCTCTTATTTTATGTGTTACACTTTATCAA  
CTCAATTAATAACAATTTAGTAAGTGAAGGACCTATTATTGTTCACTTTATTT  
ACCCTCACACCAAATTTAGCTTAAAATGAACAGTAGATCATAGTCAGGATGGTGA  
TGAAAGGCTACCTAAACAAGGCAAAAGAAATTTGTGTTTTCTATTATTGGAGTCT  
GAGCAATCTAGTTTCAGTTAGTTGTTAGGATACTGTTCTTCCACTGGTCAATTTGC  
TCTGCTTTATCTGTTCCCTTTCCCTTCAGCTCCCTCCATCCATGTCTATAAATACACC  
TCTCCTTCCCTCACACCTTCCCTCATCCTCTCTCATTCTTTTCTTTTGGGAAGTTAGGC  
TCTCATTTCAACCCCTCTGTAAGCACAAAGCTTCCACCCTGCTTTGCTCTAAAAGCC  
TCTACTTCTTTTAAATCCCCACTCATTCTATGTTGCCTTTTTTTGCTGCAGGGAAAT  
GGAGTTTATTGCCCTCTCCCTAGTTTCCCTTCTCACCATCTTCGGAGCCGTTTCATG  
GATATGGTGGTGGGTGGTCTGATGCACATGCTACCTTTTATGGAGGTGGTGTATGC  
TTCTGGGACAATGGGTAAGCGCAGAGTCCACCCAGTAAATTCCCAAATGCTATGA  
CTACTTCTCTTCAACTCATTAACTCTTTCCCTTCCCTCCAGGAGGGGCTTGTGGGTA  
TGAAATCTCTACAGTCAAGGATATGGGACAAACACAGCAGCATTGAGCACTGC  
TCTGTTCAACAGTGGACTGAGCTGTGGAGCTTGCTTCGAGATCAAATGTTCGAAT  
GATGGGAGCTGGTGTCTCCCGGGATCTATAATTGTCACTGCAACAAACTTCTGCC  
CACCAAACAATGCTCTTCCAAACGATAATGGAGGGTGGTGAACCCCTCCCCTGCA  
GCACTTTGATCTCTCTCAGCCAGTTTTCCAGCGTATTGCTCAGTACAAAGCAGGCA  
TTGTCCCTGTTCAATACAGAAGGTAAACACTTCCATCAGCAACTCGATCATCTTAT  
AGCTCTGATTATACCGTTAAAAGTAACTCCTGGTGAACGAAACAGGGGATTTAT  
ACTGCACCTTGGGTCCGCAGACACATTATCCGTATTCCCTCGTAGCTCTAGCTTCTT  
GCCTCCAATCTTTAGAAACTCCCACATCCAACAGAACCGGTTTCCCTAAATATTTTT  
AAACTCAATACCACAAACTTTTCTAAGTTTGACTCCTTGCACCTAGAAGCCTTGTT  
CCCTTTGCTGCTCTTCTCTGTCTTTTTTCTTTTAAAATGTTTTGATATCAGCTTGA  
ATTACATAGCACAAATATCGTTTTTCAATGGTTTTCTGCATCACTGGGACCCCAAA  
AGCAACTCGTAGAGAACCCTTCTGATTCCAGTAGCAGTGGCATCCAACCTTAAGAG  
AACATTCAAAAGCAGAGGCTTGAAATGAAACATTATAATCTTCTTCTTTTAAA  
GAGATCCTTTATTAACAGAAATCCCCTCTCCCTTTTCTTCAAACAAAAAGTCTTT  
ATTTATTATAGGCGAACACACTCCATATAAGTCACAAGCAACCTTCCCTGTCGCT  
CTCTCTGGGATCTAAAATACTGAAGTTCTGAAACAAAAGGCAACCTTTTTTTCATCT  
TGCAGGGTACCCTGTGTGAAGAACGGGGGAATCAGGTTCACTTAATGGTCACT  
CTTACTTCAACCTGGTGTGCTGATCTCCAATGTAGGTGGGGCTGGGGACGTGACGGC  
AGTGTCTATAAAGGGATCCCAGACTGGGTGGCAGCCAATGAGCCGCAACTGGGG  
CCAGAACTGGCAGAGCAACAGCTACCTCAATGGCCAGTCCCTCTCCTTCCAAGTC  
ACCACCAGCGATGGCCGCACTGTTACCTCCATGGACGTCGCCCTAACAACCTGGA  
GCTTCGGCCAGACCTACTCTGGTGGGCAGCTTTGAGCCTCTAATTAAGCCAACAA  
CGAATTCCCTCTGACCTTAGTATCAGTCTGGTGGAGTGACTGAAGTCTACGTATA

