

## IDENTIFICATION

**Species:** *Elaeis guineensis*

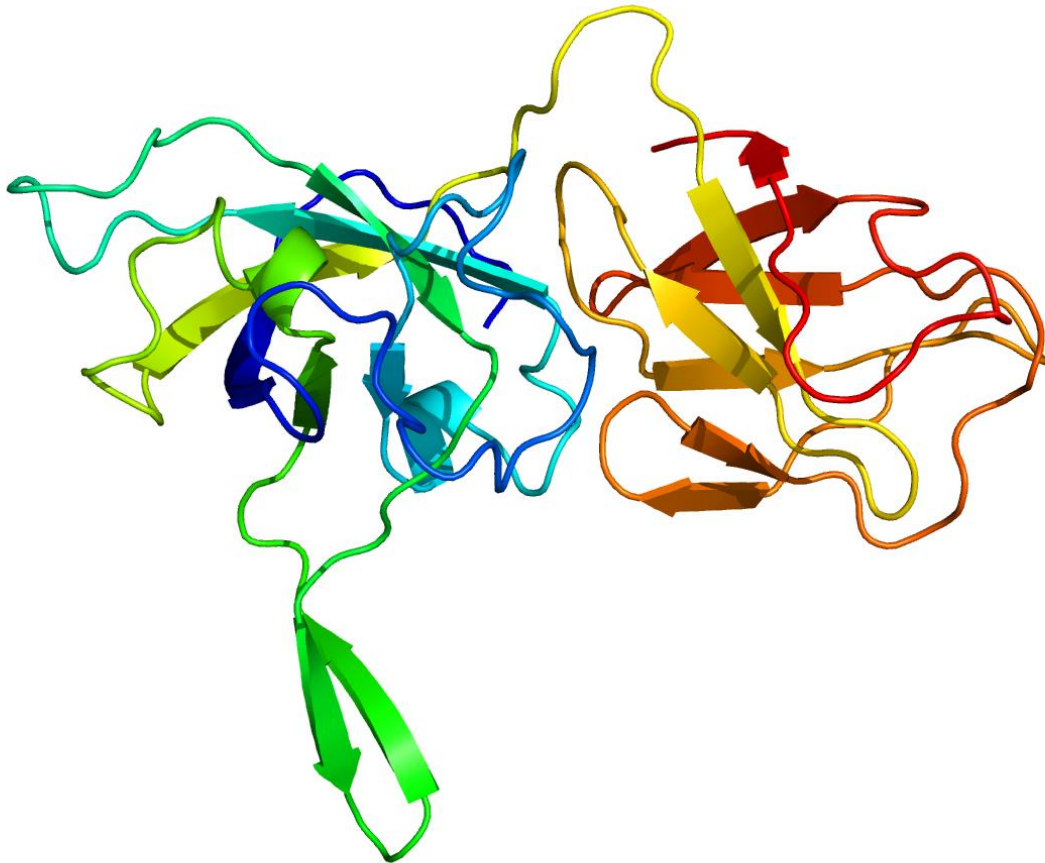
**Locus:** XP\_010922733

**Gene Model:** XP\_010922733.1

**Description:** EgEXPA-12

**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>

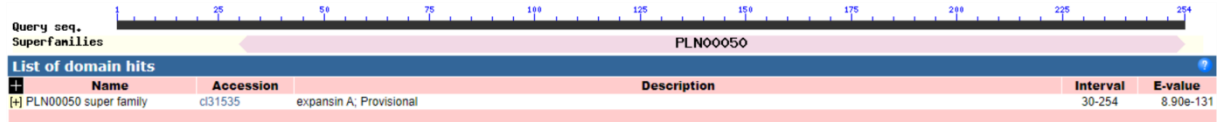
## EXTERNAL RESOURCES

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## GENE STRUCTURE



## DOMAIN ARCHITECTURE



## SEQUENCES

### Peptide

>EgEXPA-12

MGVPCSLSNALFLLLSSFSFLVHSIFGSDSWESAHATFYGGGDASGTMGGACGYGN  
LYSQGYGTSSAALSTALFNGLSCGSCYELRCDDDPKWCLPGTIVVTATNFCPPNYA  
LANDNGGWCNPPRQHFDLAEP AFLRIAQYRAGIVPVSFRRVPCVKKGGIRFTINGHSY  
FNLVLVTNVAGAGDVHAVSIKGSKTGWQAMSQNWGQNWQSNAYLDGQSLSFRVT  
TSDGRTVTSYDVVPAGWHFGQTFEGDQF

### CDS (coding sequence)

>EgEXPA-12

CAATTCGCCCTCAACCCAGACAGCTCATGTGCGTTTTGATTTGTTCTTTACTGCAA  
TTTGTTCACAGCCTTGCGGGCTCGGACTCGACTCGCGAGAACGGCCAACTTGTCT  
CCGTATACAAAGGGATTTAGGAAAATCCCCACCCACCCTCTTCTATAAATATG  
AAATACCACCTCCCTCCCACTTCCCCTTACAAGCAAACCAGACACACTCTTGAA  
CCCCACCTTTTCTGTCTCTCTTCTCTTAGCTCCATTTCTCTCAAAGCCTCTCCAATG  
GGGGTCCCAAGCTGCTCTCTCTCCAATGCTCTTCTCCTCCTCCTCTCTTTCTCC  
CTCTTTGTGCACAGTATTTTCGGGGACTCCGATTGGGAGAGTGCGCATGCCACGT  
TCTACGGTGGCGGCGATGCATCGGGAACAATGGGAGGTGCTTGTGGCTATGGCA  
ACCTCTATAGCCAAGGTTATGGCACGAGCTCCGCCGCCCTTAGCACGGCACTGTT  
CAACAATGGCCTCAGCTGTGGGTCGTGCTACGAGTTGAGGTGCGACGACGACCCC  
AAGTGGTGCCTGCCGGGGACCATTGTGGTCACTGCCACCAACTTCTGCCCTCCAA  
ATTATGCCCTTGCCAACGACAATGGAGGGTGGTGCAACCCCCCTCGCCAGCACTT  
TGACTTGGCCGAGCCTGCCTTCCTCCGGATCGCTCAATACCGTGCCGGGATCGTG  
CCCGTGTCTTCAGAAGGGTGCCATGTGTGAAGAAGGGTGGGATTAGATTCACCA  
TTAATGGTCACTCTTACTTCAATTTGGTCTTGGTCACCAATGTTGCGGGTGCCGGC  
GACGTGCATGCCGTGTCCATCAAGGGATCCAAGACTGGCTGGCAGGCGATGTCAC  
AAACTGGGGACAAAAGTGGCAAAGCAACGCATACCTCGATGGACAGAGCCTCT  
CCTTCCGAGTACCACCAGCGACGGGAGGACCGTCACCAGCTACGATGTCGTGCC  
CGCCGGCTGGCATTTCGGGCAGACCTTCGAAGGGGACCAATTCTAAAGCGTCCAG  
GACTTGCTAGGCTAATTATCGATATTTTTCTTTGTCGCACCATTTGCATTGGTTTT  
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GGTGGTCTAGTTTGGTTGGTAGCCCTCGGTCCTCATCGCATGGATCTAGATGTCTG  
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CTATTTGTGTAAACAAAGTGTTCTATAAGTATTACAGAGGTTTGTATTTTTTCATTC  
TACGTTATTATCCTCTCTTGCAGTATTTATTACGAGGACTCTATGTAAAATTTGGG  
TGAGCTCTTGAGATGTTTGTATGGGTAGCTTTTTTCCTTTTACGAGAATAACTTCATC  
GGATACGTCAACCGTTATTACCGAGCAGATATATAAATGCGACAAGAACTTAATC  
GAGGAAGAGGACAAGCTGCCGGACAAGCTGCCACGGCTTTCTCGCTAAATCTTTT  
CTTTGACATTTTTTTCTTTAGGAAGGCATTTAGATCACTACGACAGATCGGAGGCT  
GCGAAAGAGATCCAGTGGTTCGTGTTACCATTATCCTTGTTTGGTGTGCATGCGTGG  
GAGGAACCAATGTCCCTTTCTCCATTAATAAATTTTGGTGGTAAGTTTCATGTGACAG  
CCTAAACGTTTCATGTGACCTAATTTACTTTTCTTTATTCTAATTGTGTGGTAGAGTT  
TTGACGAACTCAATTGGAGAACGGATGATGGAGCCACGTAATACTAATTTGGA