

## IDENTIFICATION

**Species:** *Elaeis guineensis*

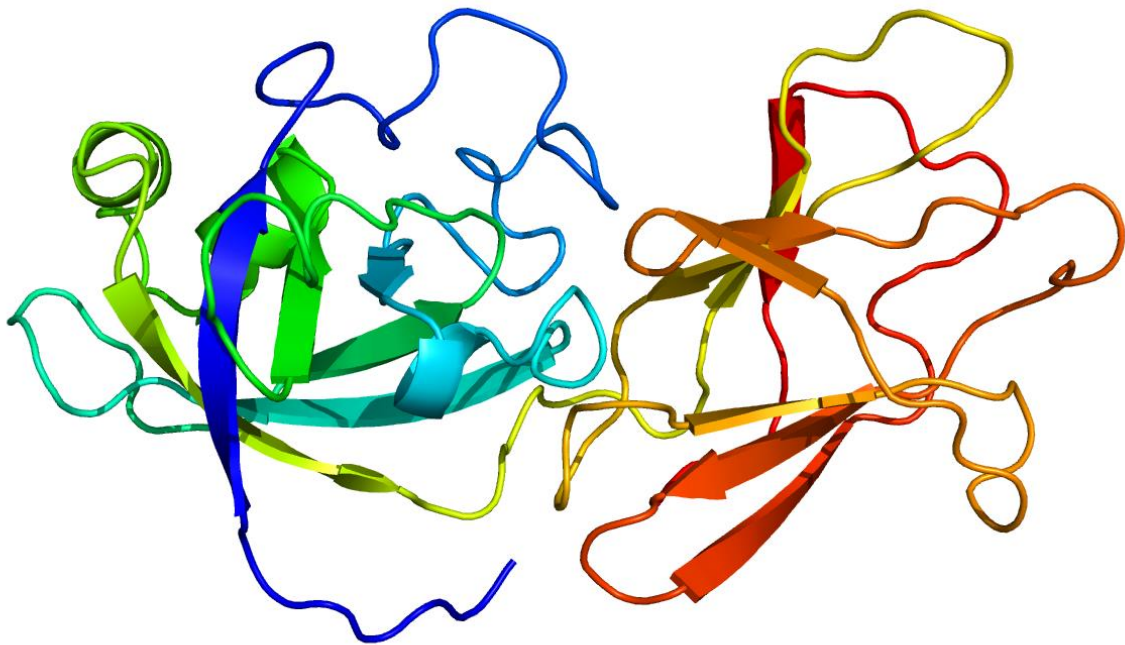
**Locus:** XP\_010919650

**Gene Model:** XP\_010919650.1

**Description:** EgEXPB-05

**Family:** Beta 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>

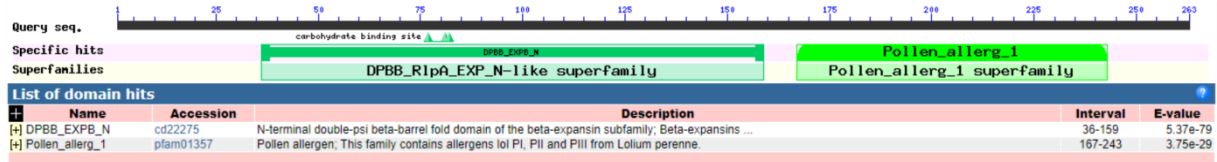
## EXTERNAL RESOURCES

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## GENE STRUCTURE



## DOMAIN ARCHITECTURE



## SEQUENCES

### Peptide

>EgEXPB-05

MATSLLATFLSLSCLFTLSFCFHTKHFALPMAGHDWSPAGATWYGSAHGAGSDGGA  
CGYRNAVDQAPFSAMIAAGSPSLFKSGKGCACGYVMCTTHEACSRKPVTVVITDE  
CPGGVCLKESAHFDSLGTAFGAMAKPGMADELNRNAGILPIQYSRVACEYPGKTITFH  
VDSGSNPYYMAVVVEFEDGDGDLSAVELKDGSAEWRAMAQSWGAVWRLDSGSTL  
HGPLSIQLTSQYSGKKLVANNVIPAGWKPGATYRSFVNYS

### CDS (coding sequence)

>EgEXPB-05

CCACCAGCAACGGCTAATATCCAAGTCCCCTAATACCTCTAGTCGCAGGAGAGTG  
AGCATAGAGAAATGGCTACTTCTCTCCTGGCTACTTTTCTTAGCTTGTCTTGCCTC  
TTTACTTTGAGCTTCTGCTTCCATAACCAAACTTTGCTTTGCCGATGGCCGGACA  
TGACTGGTCGCCGGCCGGAGCAACTTGGTATGGAAGTGCCCATGGAGCCGGAAG  
TGATGGGGGAGCTTGTGGATATCGCAATGCTGTGGATCAAGCCCCCTTTTCTGCC  
ATGATTGCCGCCGGAAGTCCTTCTCTTCAAGTCAGGCAAGGGCTGTGGTGCTT  
GCTATCAGGTGATGTGCACCACTCACGAGGCATGTTCAAGGAAGCCGGTGACGGT  
CGTGATCACCGACGAATGCCCCGGCGGTGTATGCTTAAAAGAATCCGCTCATTTC  
GATCTCAGCGGCACCGCATTTCGGGGCGATGGCCAAGCCGGGCATGGCTGATGAA  
CTAAGGAACGCTGGAATCCTCCAATCCAATACTCAAGAGTTGCATGCGAGTATC  
CAGGCAAGACGATCACCTTCCATGTGGACTCTGGTTCTAATCCCTACTACATGGC  
AGTGGTGGTGGAGTTCGAGGATGGTGACGGAGACCTGTCTGCTGTGGAGCTCAA  
GGATGGTTCTGCCGAGTGGCGTGCCATGGCACAATCATGGGGTGCGGTATGGAG  
GCTCGACTCTGGATCGACGCTCCATGGGCCGTTGTCGATTGAGTTGACGTCGCAA  
TACTCCGGCAAGAAGCTGGTGGCCAACAACGTGATTCCGGCGGGGTGGAAGCCA  
GGAGCCACCTATCGGTCTTTTGTAACTATAGCTAGTTATGAGAATTTGTGTCTCT  
CCACGTACCATACTATATATAGGGTGCATGTGGTAGCTAAGCATGCCCATGTATG  
GTTTTATTAGTGTGCTTCTAGCTTGTATGATCGCGTGTGATCTAATATTAATGAATG  
GTGATGGATTATGTTCCGTTTGCATGATATGAAAAGGTGTATCACCAAAGGATG  
CTGGTA

### Nucleotide



CGTCACAAACTGTGCACCCACATGGGTTGCCTACTTCTGCCGAGCATTGGAAATA  
TTTAAATGGATAGCAGTTTCTCTTATTTGGGTTTGCCTCTCCCTTGAAACTTGGAA  
AACCTACCATTTGTGATTCCCTTGTGACCGTGGTGTACCCCAGAAGAGTAAAACG  
TAAAGAACAACCTAGGAAAATAATTTTTGGCTCCCCCATATCCATTAGCTCGTG  
TAGCACACCTTCTACCCGTGTTATGACAACAGTATTTAACTTATAGTAACATAATT  
TTTGACCATATTGTAATAAGCTAAATATACAAAGGTAAGGAAAACAGTATCCAGA  
TCATAAAAAGGAAAACAGTATTTAACTTATAGAGTAACATAATTTGTGTCCTAA  
ATTAGTCATTTAAGCATT