

IDENTIFICATION

Species: *Elaeis guineensis*

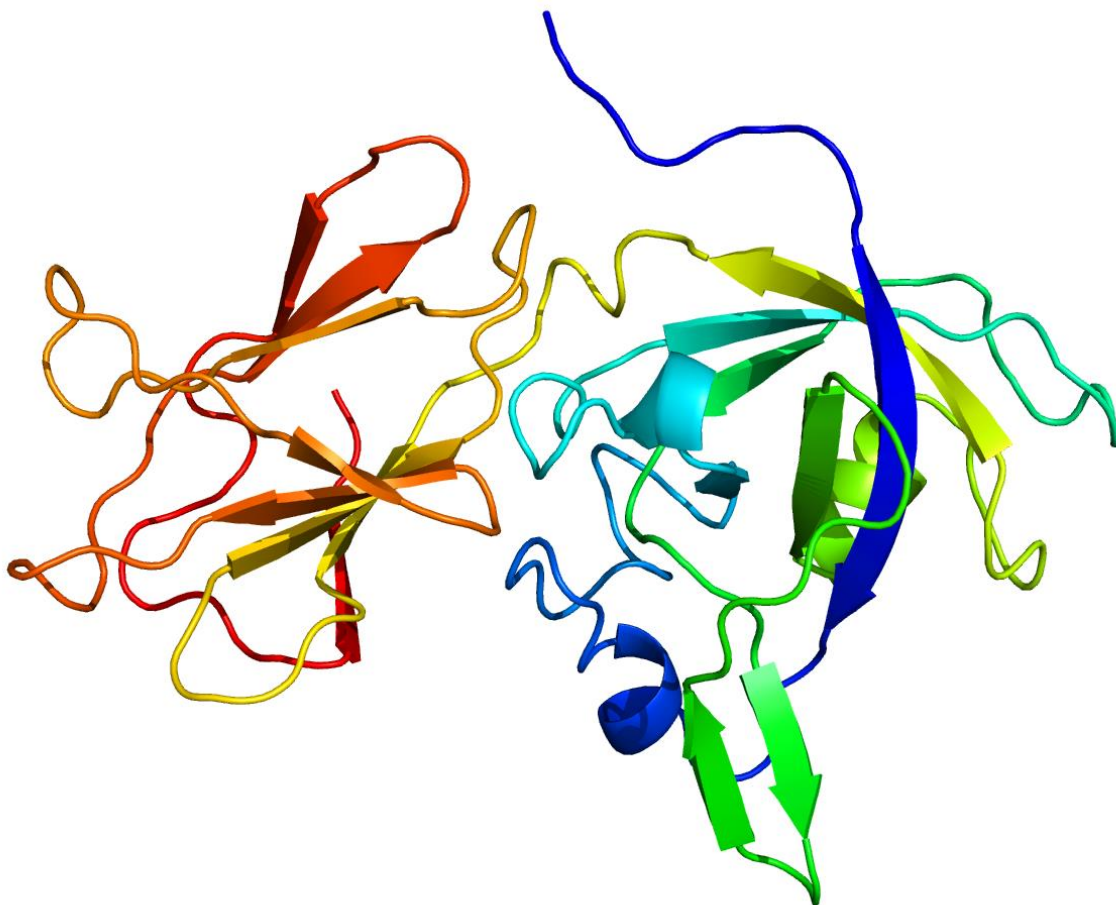
Locus: XP_010921134

Gene Model: XP_010921134.1

Description: EgEXPA-10

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>

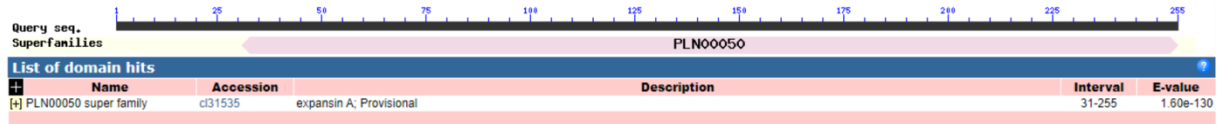
EXTERNAL RESOURCES

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GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>EgEXPA-10

MASPKCSLPNAVLSFFFSSLCFFASQALGDSGWQTGHATFYGGGDASGTMGGACGY
GNLYSQGYGTNTAALSTALFNGLSCGACYEMQCANDPQWCLPGSIIVTATNFCPPN
YALPNDNGGWCNPPLQHFDLAEPAFLQISQYRAGIVPISFRRVPCVKKGGIRFTVNGH
SYFNLVLISNVGGAGDVNAVSIKGSKTGWQAMSQNWGQNWQSNAYLDGQSLSFQV
TTSDGRTVTSYDVVPANWQFGQTFEGGQF

CDS (coding sequence)

>EgEXPA-10

CAAAAGCCACAACCTTTCCTCTCTCTCTCTCTCTCTCTACTCTAACCCTCCCCTCCT
CTCCAATGGCATCCCCAAAGTGCTCCCTCCCCAATGCTGTCCTCTCCTTCTTCTTTT
CTTCCTTGTGCTTCTTTGCATCACAAGCGTTGGGGGACTCCGGGTGGCAGACGGG
ACACGCCACATTCTACGGCGGTGGCGATGCCTCCGGCACAATGGGAGGGGCTTGT
GGGTACGGTAACCTCTACAGCCAGGGGTATGGGACCAACACTGCGGCCCTCAGC
ACCGCTCTCTTCAATAACGGGCTCAGCTGCGGCGCGTGCTACGAGATGCAGTGCG
CGAATGACCCCCAGTGGTGCCTCCCGGGCTCCATCATCGTCACCGCCACCAACTT
CTGCCCCCCTACTACGCCCTCCCCAACGACAACGGTGGGTGGTGCAACCCTCCC
CTGCAGCACTTCGACCTCGCCGAGCCTGCCTTCTCCAATCTCCCAATACCGGG
CTGGCATCGTCCCATCTCCTTCCGCCGGGTGCCCTGTGTGAAGAAGGGAGGGAT
AAGGTTACCGTCAATGGCCACTCCTACTTCAACTTGGTGCTGATCTCCAATGTCG
GCGGGGCCGGCGACGTGAATGCGGTGTCGATCAAGGGGTCAAGACCGGGTGGC
AGGCTATGTCGCAAACTGGGGGCAGAACTGGCAGAGCAATGCATACCTCGACG
GTCAGAGCCTCTCCTTCCAGGTCACCACCAGCGACGGAAGGACTGTCACCAGCTA
CGATGTCGTGCCGCAACTGGCAGTTCGGCCAGACCTTCGAGGGAGGCCAATTC
TAGGCCTCGATCGCCACTGTAAAGGGTTAAATTGTTTTTAAGGGTTTGGGAGGG
AAGCCTCTCTTGAAAGAGGTTGGGGCCTGGTTGAAAGCTGAGGTAGCTTTATGTA
CTAGCACCCGCTGAGAAAGGCCTATGGTAAATTTATTAGACATATAGGAGTTCGG
TTTGTTCTTGTGGCAATTTAGATTGAATGCCTTGTGGAAAATTCGGAAATCAAG
GCCTTGGGTGTATACCATAGGAATCCTCGAAACACAATATGTGATTGTGTGGAGG
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GTAATATCTGTAACAGCTGATTGGTCTCAAATAAGAATAAGCAATATGTTATTTG
CAGTA

AGGTTGTGGCTTTTGCTGCTTGGTTAGTGAAGGAGAGGGAGGGGGGCTATATGTA
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AATTCTCCACCGCTCTTTTAATTATGGGGTTGATTTGTGGGACAATCCTGTCTAAA
TATATGAATATGAATGCAGATTCCAAAAAGTTAATATACTTTAAGCTATCACTTT
ATAAAATGTACACTCAAATGGAATATGTAGTCACCAAACAGTTGGTAGACAAAC
AAATGTGACATATCAAGAGATGAAAAGGGAACGCAATTGTGTTAAAATTGCTGG
GAAAAACGCAAATTACTGTA