

IDENTIFICATION

Species: *Elaeis guineensis*

Locus: XP_010938009

Gene Model: XP_010938009.1

Description: EgEXPA-21

Family: Alpha Expansin

3D structure:



GENOME DATABASES

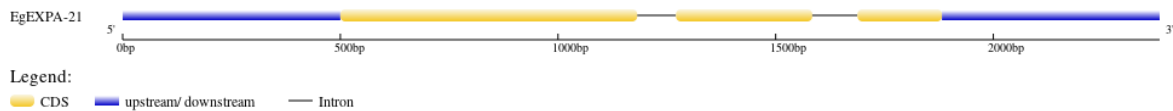
NCBI: [https://www.ncbi.nlm.nih.gov/genome/?term=txid51953\[orgn\]](https://www.ncbi.nlm.nih.gov/genome/?term=txid51953[orgn])

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

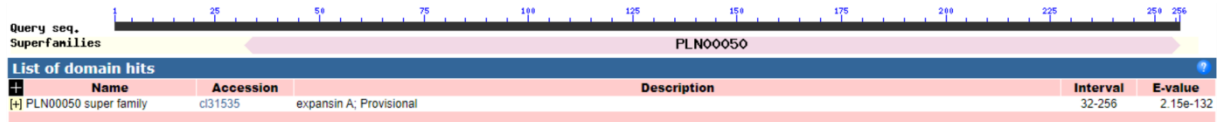
EXTERNAL RESOURCES

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GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>EgEXPA-21

MASPKFSLSNSALSFFFFASLCFFASQALGDSGWQNAHATFYGGGDASGTMGGACG
YGNLYSQGYGTNTAALSTALFNGLSCGSCYEMRCADDPQWCLPGSIIVTATNYCPP
NYALPNDNGGWCNPPREHFDLAEP AFLQIAQYRAGIVPISYRRVPCVKKGGVRFTIN
GHSYFNLVLITNVAGAGDVHAVSIKGSNTGWQAMSRNWGQNWQSNGYLNGQSLSF
QVTSSDGKTVTSYNVVPANWQFGQTFEGEQF

CDS (coding sequence)

>EgEXPA-21

CCAAGCAACAAACACCTCCATTCCTTCGTA CTCTCCAATGGCGTCCCCAAAG
TTCTCGCTCTCGAACTCCGCCCTCTCCTTCTTCTTTGCTTCCTTGTGCTTCTTTG
CATCGCAAGCCTTGGGGGACTCCGGATGGCAGAACGCACACGCCACGTTCTACG
GCGGTGGCGATGCCTCCGGCACGATGGGAGGGGCTTGTGGATATGGCAACCTCTA
CAGCCAGGGGTACGGGACCAACACCGCGGCCCTCAGCACCGCTCTCTTCAACAAC
GGGCTCAGCTGCGGCTCGTGCTACGAGATGCGGTGCGCTGACGACCCCCAGTGGT
GCCTCCCAGGCTCCATCATCGTCACCGCCACCAATTACTGTCCCCGAACTACGC
CCTCCCCAACGACAACGGCGGGTGGTGAACCCTCCCCGCGAGCACTTCGACCTC
GCCGAGCCTGCCTTCCCTCCAAATTGCCAGTACCGTGCCGGCATCGTCCCCATCTC
CTACCGTAGGGTCCCCTGTGTGAAGAAGGGAGGGGTAAGGTTACCATCAATGG
CCACTCCTACTTCAACTTGGTTCTCATCACCAATGTCGCTGGGGCCGGAGACGTG
CATGCGGTGTCGATCAAGGGGTCCAACACCGGATGGCAGGCCATGTCGCGAAAC
TGGGGCCAGAATTGGCAGAGCAATGGCTACCTCAACGGCCAGAGCCTCTCCTTCC
AGGTCACCTCCAGCGACGGGAAGACCGTCACCAGCTACAACGTCGTGCCGGCCA
ACTGGCAGTTCGGCCAGACCTTTGAGGGAGAACAATTCTAGGCCTCCATTGTTAG
GGGGTCTTAAGGGTTTGGGGTTTGGGAGGATGGCCTCTTTGACTTTGAGAGA
GGTTTGGGCCTGGTTGAATGCTGAGGTGGCTTTATTAGCACCCGCTGAGATGGCC
TAAATAGTAGACATATTAGACATAGATGGTCGCTTTGTTTCTTGTGGCAATTA
GATTGAATGCCTTGTGGAGATTAAGAAATCAAGGCCTTGGGTGTATAGAATTGGA
ATCCTCAACATATTATAATATGATTGTGTGGGGGATGGTATGTCAATTAGAGGAA
AGTATGATGTTTGCTTTGTGTATTTCAAACATAATATTGTAATCGATTGTTCTCC
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Nucleotide

>EgEXPA-21

CAATTGTACCAAATAAAGAACTTATTTCTTCGTAGTTTAAAAACCCAATCACCA
AGCCGTTACGGCTGGTAGTCTTTGGACATAGAGGTAAATTAAGGTGACCTGCT
TTTCATCATCAAAAAAGAAGGCCAAAAAAGGGTGACCTGCTAGTCTTCC
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CCATGTTCCAAATAATAATATTATAAATACTTAAGCTATCAAGGGAACCTTTAT
ACAACCTGCACAATTAAGTGCACATGAAAGTACCAAATGGTTGGTAAAGATTACA
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