

IDENTIFICATION

Species: *Elaeis guineensis*

Locus: XP_010933564

Gene Model: XP_010933564.1

Description: EgEXLB-02

Family: Expansin Like Beta

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>

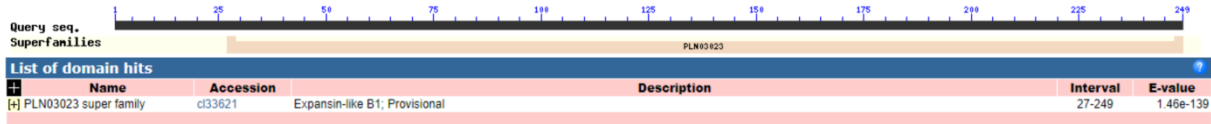
EXTERNAL RESOURCES

-

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>EgEXLB-02

MASILTFSCLLSLFFFFPIFSSSQSTFTCSRATYYGSPDCSGTTPRGACGYGELGRSLNNG
DVGAVSRLYRNGTGCGACYQVRCTHPQFCNEDGAKIVVTDYGGQDNTDFILSARGF
VKLARSNMANELMAFGVIDVEYRRIPCQYPGYNMMVKVTEHSKFPDYALALIIYQAG
QKDILAVELWQEECQEWKGMRKAYGGVWDMANPPRGPMNARILTGDDSGQNWV
QLNGVIPSGWKAGVAYDTAIQLD

CDS (coding sequence)

>EgEXLB-02

TCTCCTCCATAGCATCTCACCTCACTCCTTTCTTCTCCTGTTTGGCCTGTTAACCTT
TCACAAAGCTTGTCAATTATTCTCAGGGGGCAACCATGGCCTCAATTCTCACCTTCT
CTTGCCTACTATCTCTCTTCTTCTTCTTCCCTATATTCTCAAGCTCACAGAGTACCT
TCACTTGCTCGCGAGCAACCTACTATGGTAGCCCGGATTGCTCGGGCACTCCAAG
AGGAGCATGCGGGTATGGTGAGCTTGGTAGAAGCCTTAATGGCGGCGATGTCCG
GGCTGTTTCTAGGCTGTATCGAAATGGCACGGGCTGCGGTGCATGCTACCAAGTG
AGGTGCACCCATCCACAATTCTGCAACGAGGATGGTGCAAAGATTGTGGTCACTG
ACTATGGTCAGGGGGATAACACTGACTTCATCCTCAGTGCCAGGGGGTTTGTAA
GCTTGCAAGATCAAACATGGCTAATGAACTGATGGCTTTTGGTGTGATAGACGTC
GAGTACAGGAGGATCCCATGTCAATACCCAGGATAACAATATGATGGTTAAGGTC
ACAGAACACAGCAAGTTCCTGACTACTTGGCCCTCATCATCATCTATCAAGCAG
GCCAGAAGGACATATTGGCCGTCGAATTGTGGCAGGAGGAATGCCAGGAATGGA
AGGGGATGCGCAAAGCCTATGGTGGAGTTTGGGACATGGCGAATCCTCCAAGGG
GCCCAATGAATGCGAGAATTTTAAACAGGTGATGACAGTGGGCAAATTTGGGTCC
AGTTGAACGGTGTATCCCTTCAGGTTGGAAGGCAGGGGTGGCGTATGACACGGC
CATTAGCTAGACTAGGACTCTCCAATGATTCTAGATATCATGGGAAAGACCAG
ACCCACTTATAAATTGATCATTAGCAATTAATAAAGTTGGTACTTGGGGTGTGTG
ACTGCTTTTGGCTTGTATGCCTTTATGTATGTGCAATAAGAATGGTGATTCCATGC
TTTGTGGTTTGGTTAGATGAATATATAATAAAGGAACCTTCTGTTTAGAT

Nucleotide

>EgEXLB-02

GTCCAGAGTTTGAATTATATATAATGGGGGAAGTGGTGATCAAATGATTATTTTT
TTTGATCCACGGCCCCCTCCATATGGTTTCCAACCATTACTCTGTTCTGAATTTTT
TTTGTGAGTTTCTTCTATAATTTTGCCAGTAATGCTCAATGCGCAACAGAGGGTTA
AAAGAAAAAAAAAATTTTTTTGCAAAGAACATGTGGAAACCTACATCAGTTCC
ATTTACAAATGATAATAGATATTGCACGAGGGCATTCTATTCACAACCTTTATATA
ATAGTATTTACCTCCGTTACATTCACCTAATGACGGGGATTATGATCCATGAACC
AATATGGATGTGGTTTTACCAAAAATTTATTTTAGTACCATTTTCTAGTCTTTAAA
CATGGTGTACACCATACTATCATGTCAATAAGTGCTCCCATGTCAATAACATCTC
TTAATACTGAAATCATCATGTTGAGGTCGTGCTTATGCCAACCAAAAACCAATAAT
AATCTAAACAGAAAGTTCCTTTTTATTATATATTCATCTAAACCAAAACAAAGCAT
GGAATCACCATTCTTATTGCACATACATAAAGGCATCAAGCCAAAAAGCAGTCAC
ACACCCCAAGTACCAACTTTTTTAATTGCTAATGATCAATTTATAAGTGGGTCTGG
TCTTTCCCATGATATCTAGGAATCATTGGAGAGTCCTAGTCTAGCTGAATGGCCGT
GTCATACGCCACCCCTGCCTTCCAACCTGAAGGGATAACACCGTTCAACTGGACC
CAATTTTGCCCACTGTCATCACCTGTTAAAATTCTCGCATTTCATTGGGCCCTTGG
AGGATTCGCCATGTCCCAAACCTCCACCATAGGCTTTGCGCATCCCCTTCCATTCT
GGCATTCTCTGCATCCAGGAAGAGATCAACATGAATTAGATTCATGGACATGA
TTCTAAGAGACATGGGTTATGGCCTATATGAATCTTTACCTGCCACAATTCGACG
GCCAATATGTCCTTCTGGCCTGCTTGATAGATGATGATGAGGGCCAAGTAGTCAG
GGAACCTGCTGTGTTCTGTGACCTTAACCATCATATTGTATCCTGGGTATTGACAT
GGGATCCTTTATCAAGAAAACAAAGGGAGAGAAAAAAAATAATGTTAGAAGTC
ATAAAGCAACAAATCTTTTTAGTTTTCACTCAAAAATATTTCTATATTTTATCAAT
TTTTGCAAATAATGAATAAAACCTAGTAAAGATACGTATAACAAGCTCTCATTCT
TCTGTAAGTAGAAGTAATTCTGCATTAAGATCATACTTAGTAGCATATTTTCATCA
TTTGATGGCCATGTTATCTTGGTATGCTTTGTGTTAATTTCACTATGATATTTATCT
TTCTTTTTTCTCTTTTAGTTCCAGCAGTTTTGGTGGAACTAAGATGTGTTCTCTTCT
TTCAATGCTGGTCCATTAATATATTATGCATGATGGGGTTTAATTAACCTACTA
GGGAGTTCCACCAGCTAAAATGTCCCCATCAGTCTGAAATCCAAATGGTCCATTA
ATATATTAGAGCTCAGAAATCTATCATAAACTACCCATGGTCCGTCCTCACCTCT
GTACTCGACGTCTATCACACCAAAAGCCATCAGTTCATTAGCCATGTTTGATCTTG
CAAGCTTAACAAACCCCTGGCACTGAGGATGAAGTCAGTGTTATCCCCCTGACC
ATAGTCAGTGACCACAATCTTTGCACCATCCTCGTTGCAGAATTGTGGATGGGTG
CACCTCACTTGGTAGCATGCACCGCAGCCCGTGCCATTTGATACAGCCTAGAAA
CAGCCCCGACATCGCCGCCATTAAGGCTTCTACCAAGCTCACCATAACCCGCATGC
TCCTCCTATTGCATCCAAAACCATTAGACAAAAACTAGGCATTAACCCGACTATA
ACACTAAACATGAAAGTATAGATAGCATAGCACCATAGTGCCATAAATAAATG
CATGTGTTAATGAGTTTGTAAGAGTTCTATTACTTGGAGTGCCCGAGCAATCCGG
GCTACCATAGTAGGTTGCTCGCGAGCAAGTGAAGGTAAGTCTGTGAGCTTGAGAAT
ATAGGGAAGAAGAAGAAGAGAGATAGTAGGCAAGAGAAGGTGAGAATTGAGGC
CATGGTTGCCCCCTGAGAATAATGACAAGCTTTGTGAAAGGTTAACAGGCCAAAC
AGGAGAAGAAGGAGTGAGGTGAGATGCTATGGAGGAGACATGCTCTATATTTA
TAGCAGCGCATGCAAGAGATGCTTGCCAGGCTTGATGTGGCTAAAAGGAAGAT
AACTTATTAACCTGCTATTATCATCTGGTCCATAGGAAAAGGTGGCGTTTGGTGC
CCATGGAACACCCTTACATACCCACAAGACCCTTCCATAGAGCAAGAAGCATT
TTCTTGCCCTAACCCATAATTGTGTTAAATTTAATAGTATTCGTACATTTGGTGC
GTGCCTTTTGGATTTAAGAAATACAGAGCGTGTGAGAACACCTTAACCTAGTGGTC
AATTGCCAATAGTCTTCCCAGATGGACTCGATCGTAGCCATCCGATCAATTGAT

GGGTCGGTTGTGATTGCATGCCGGCTTCTTAGTGATTGTCTTACGTCAGATACATG
CATCCCTTTTCTGAGTGTTGAGTCCAAGCATTGAGCACGGAGTCTTACCAACTTCT
CAATAAAGTGGAGAGTTTGGTGATAATCACTCATTCTACCA