

IDENTIFICATION

Species: *Arachis ipaensis*

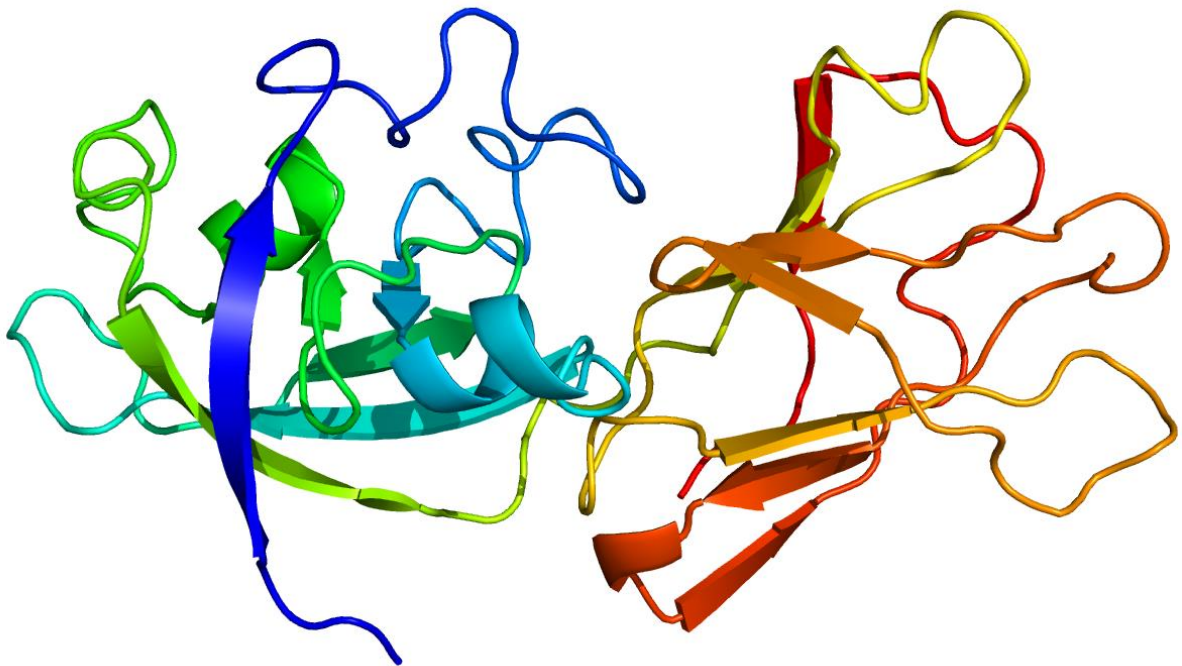
Locus: XP_020976206

Gene Model: XP_020976206.1

Description: AipEXLB-05

Family: Expansin Like Beta

3D structure:



GENOME DATABASES

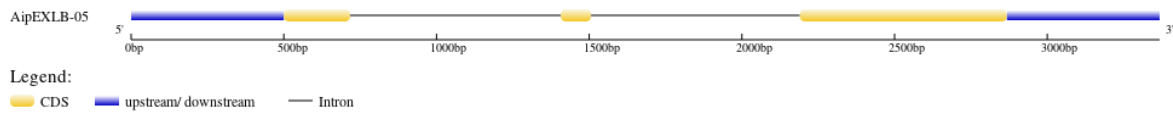
NCBI: https://www.ncbi.nlm.nih.gov/genome/35711?genome_assembly_id=315604

KEGG: <https://www.genome.jp/entry/T04301>

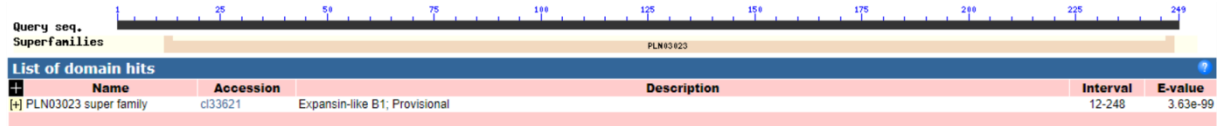
EXTERNAL RESOURCES

<https://peanutbase.org/organism/Arachis/ipaensis>

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>AipEXLB-05

MELNNLKRQIGIFCVLLILPALCSAAFTKSRAIFYSTSDGLGTPTGRCGYGDYGRTVH
GGSVAGVSNLWRDGVGCGLCYQVRCTNPSLCNSNGAYLVVTDYAGDRTDFIMSP
AAFSSLGVNSTANDELRLKLTVDIEYQRISCSYPGQNIKIKESSTNPGYLSIVLFNVG
GTCDVIAIQLSQSGSNTWLSLQRVDGAVFQISNPPSGTLRFRFQVNCGSLQWRLPKN
DIPANWRAGATYDTGIQF

CDS (coding sequence)

>AipEXLB-05

CTTTATGGTTGCTACCCATAGTCACAAACAAGCCTTCACTCATCATTATATTTAA
CTTGTTCAATTTCTGAGCTGTCTTGAGACATGGAGCTTAATAATTTGAAGCGCCAGA
TCGGAATTTTTGTGTTCTATTGATCTTACCAGCACTATGCAGTGCTGCGTTTACA
AAATCCAGAGCAACATTTTATAGTACCTCTGATGGTTTAGGGACTCCAAGTGGAC
GCTGTGGGTACGGCGACTATGGAAGGACGGTCCACGGAGGAAGTGTCGCCGGTG
TGTCAAACCTCTGGAGAGATGGAGTTGGCTGTGGTCTTTGTTATCAGGTGAGGTG
CACAAACCCATCGCTGTGCAACAGTAATGGAGCATACTTGGTGGTAACAGACTAC
GGTGCAGGAGATAGAACAGATTTTATAATGAGCCCAGCGGCCTTCTCAAGTTTGG
GAGTCAACTCAACAGCAAATGATGAACTCAGGAACTAGGCACCGTTGATATTG
AATACCAGAGGATTTTATGCAGTTACCCTGGCCAAAACATTGCGATCAAATTTAA
AGAGAGTAGCACCAACCCTGGTTACTTGTCTATTGTACTTTTCAATGTTGGTGGAA
CATGCGATGTCATTGCTATTGAGTTGTCGCAGTCGGGCAGCAACACATGGCTTTCT
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TCAGATTCAGATTTCAAAGTTAATTGCGGTTCTGGACTTCAATGGAGGCTCCCCAA
GAATGACATCCCTGCTAACTGGAGGGCTGGTGCCACTTATGACACTGGCATTGAG
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CCTCGTGTAATTTGTTTTGTTGTCTTTTGTGGTGTGAGACTAGAAAATAATGGGGC
TACTTGTCCGTCAAATATATGGATCTGAAGAAATAAATGTGGTGCATTTCTCCTT
TCTTAA

Nucleotide

>AipEXLB-05

ATTTTATTTTATCCGAATGGGTCAAATTTTGCTACAAGCTAAGATAATTATGCCAT
CGTCCACAGCATCCACATACCACATACGCTACGTCATTCTTCTAACTTCTAATCTT
TCCCGATTCTCATTAGCCGCCAACAAGGGTCAAGAAAATAATTTCAAACATA
AACTATTAATAAATATCCAAAATATCAATTTATTTTAAATGATATAAATTTTAA
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TATATCTAAAGGAATGGATTCTCTCCATTTTTTTTAAACTTAAGAGAATAAAATG
TGAATTTTTATCTTTAATTTTATAAGTGGGACCAAATTAATAAAAAGAGAAAA
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CTTTATGGTTGCTACCCATAGTCACAAACAAGCCTTCACTCATCATTATATTTAA
CTTGTTCAATTTCTGAGCTGTCTTGAGACATGGAGCTTAATAATTTGAAGCGCCAGA
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AAATCCAGAGCAACATTTTATAGTACCTCTGATGGTTTAGGGACTCCAAGTACGT
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