

IDENTIFICATION

Species: *Arachis ipaensis*

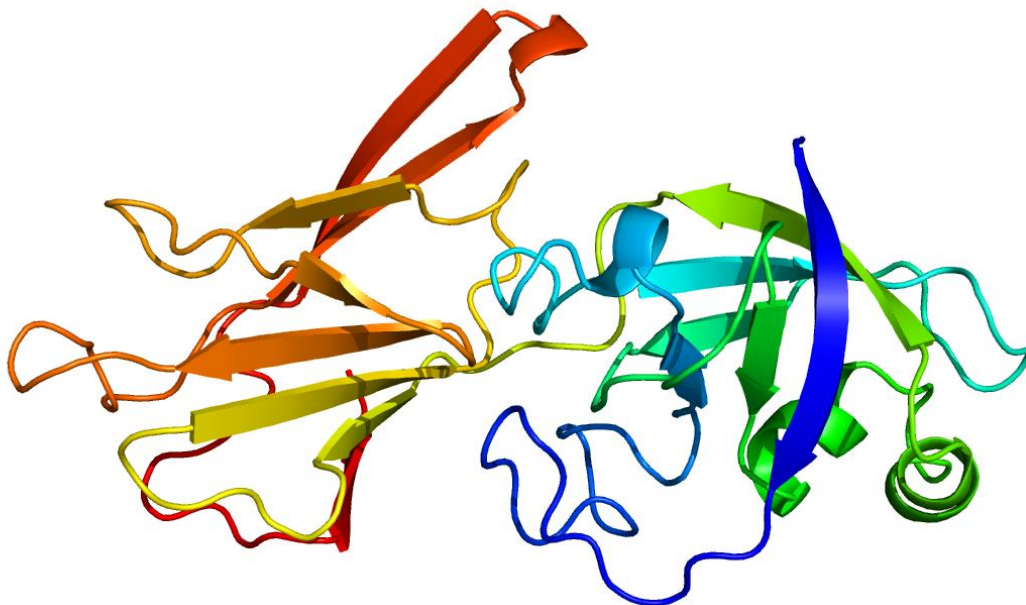
Locus: XP_016186083

Gene Model: XP_016186083.1

Description: AipEXPB-01

Family: Beta Expansin

3D structure:



GENOME DATABASES

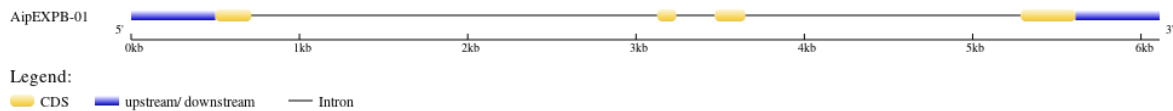
NCBI: https://www.ncbi.nlm.nih.gov/genome/35711?genome_assembly_id=315604

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

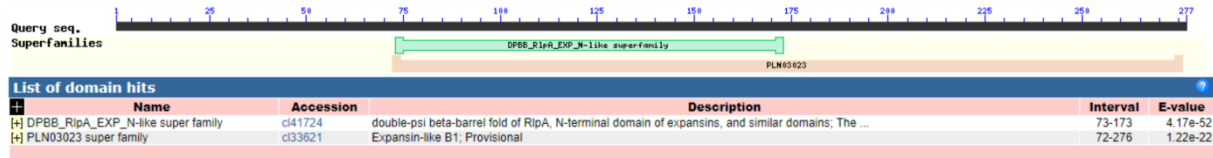
EXTERNAL RESOURCES

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

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>AipEXPB-01

MSKSGPKLATVARVKALTEVQTMVLFIFEGTEKLHLILVLLLCVGMTIVIEMAPSSSF
RSKENADAEAKEGCGACSYGKTVESPPISKLTAAVGHYIFRQGYGCGACYEVKCTD
NAACSGKPVTVVVSDECPSCSGYHFNLSGAASFASIANPGQQDILRKLQVNLQYRRV
SCSFGRSIAFRMGENSEPNKLEVSMEYVNGDADIHIENGPEQGLEISHVWGATWSVF
AGGYAIQPPFNFTLVQRYPDGTKGKTILVPNIFTQDWKIGQVYQSTINF

CDS (coding sequence)

>AipEXPB-01

ATGTCAAAGTCGGGACCAAATAGCGACGGTTGCCAGAGTAAAGGCTTTGACG
GAGGTGCAGACGGGAATGGTGTGATTTTGGAGGGACGGAGAAGTTGCATCTG
ATCCTAGTCCTCCTCCTCTGTGTTGGAATGACGATTGTGATAGAGATGGCTCCTCC
TTCGTCTTTCAGATCCAAAGAAAATGCAGATGCAGAAGCAAAGAAGGATGTGG
TGCATGTAGTTATGGTAAACTGTGGAGAGTCCTCCAATTTCTAAATTGACAGCG
GCTGTAGGCCATTATATTTTTCGTCAAGGTTATGGATGTGGTGCTTGTACGAGGT
GAAATGCACAGATAATGCAGCATGTTCAAGGAAGCCAGTGACAGTGGTGGTAAG
TGATGAATGCCCATCGTGTTCAGGATAACCATTTCAATCTCAGTGGCGCCGCTTTTG
CTTCCATTGCAAATCCAGGTCAACAAGATATTCTTCGTAAACTTGGACAAGTCAA
CCTTCAATACAGAAGGGTTTCATGCTCATTGGACGTTCTATAGCATTTAGAATGG
GTGAAAATTCTGAACCAAATAAATTAGAAGTATCAATGGAATACGTAAATGGAG
ATGCAGATATTCATATAGAAAATGGTCCTGAACAAGGTTTAGAGATTTCTCATGT
GTGGGGTGCAACTTGGAGTGTTTTTGCTGGTGGTTATGCTATAACAACCTCCATTCA
ATTTTACACTCGTTCAACGTTATCCCGATGGCACCAAAGGAAAGACCATTCTGGT
TCCTAATATATTCACACAGGATTGGAAGATCGGTCAAGTTTATCAATCAACGATA
AATTTCTAG

Nucleotide

>AipEXPB-01

ATGTATGTTTGGTATATTTGTAAGTTACTTGTATAAGAAGTCTCGTATATATATAT
ATGAAGATTGTCATTGAATTTGTTTATATATGCATTTTGTAAAAAGAAAAAGAAT
TTTTTATTTTTCAAAGAAACAGCAATACGGTTTCGAGTTAAAGGCTCATATTTTAT

CAAATAAATTAGAAGTATCAATGGAATACGTAAATGGAGATGCAGATATTCATAT
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AGTGTTTTTGCTGGTGGTTATGCTATAACAACCTCCATTCAATTTTACACTCGTTCA
ACGTTATCCCGATGGCACCAAAGGAAAGACCATTCTGGTTCCTAATATATTCACA
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TTATGCCGTCGGAAAGGATAAAGGAAAGAGCGTAGGGTGTGTATCGAATGTCAA
AGAGAATTCTTTTTGAGAGGCCAGGGTTTAGAAAAGCCATCTAAGATCTCTTTTA
GAGATAAGATCATTGGTGTAGAGAAATCCAAAGCCTTTCATTAGTAGGGTCTTT
ATTTAGGGATGGTATCTCAAAGTGATAGGTAATCAGAGTGATTTTCGTCCACCGA
ACATCAGTTTTACGAAAGAGGCGAAGAGCTATCTAACTGAACCATATCAGGAAG