

IDENTIFICATION

Species: *Oryza sativa* Kitaake

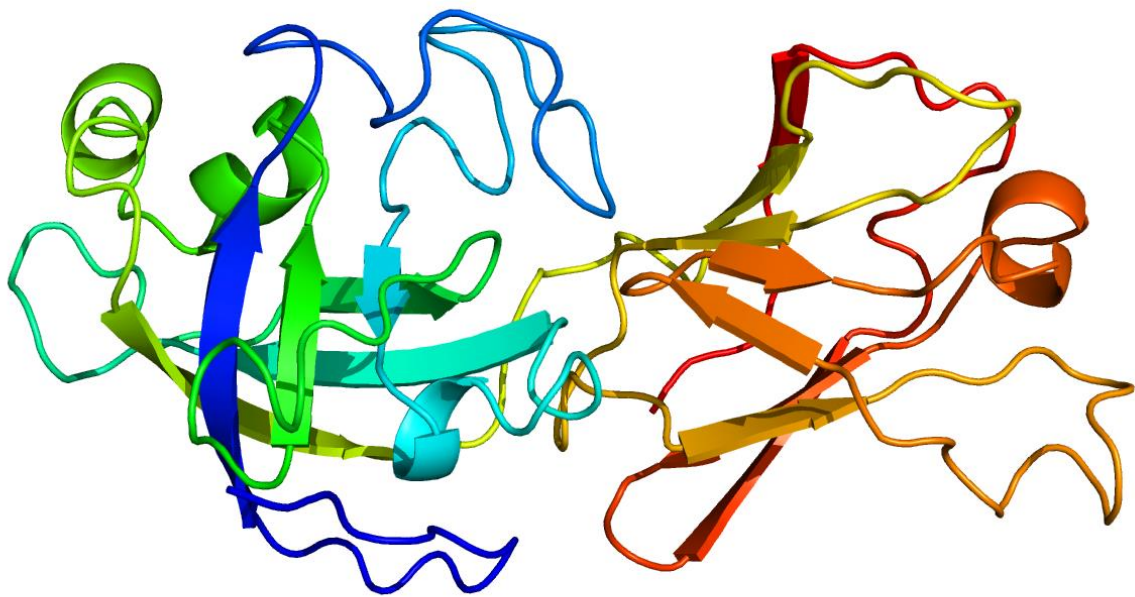
Locus: OsKitaake02g275100

Gene Model: OsKitaake02g275100.1.p

Description: OskEXPB-05

Family: Beta Expansin

3D structure:



GENOME DATABASES

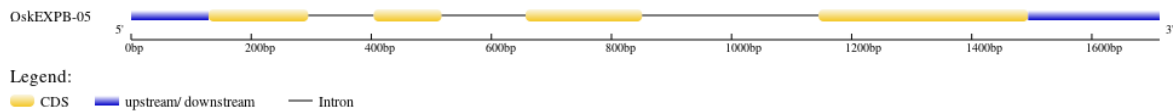
Phytozome: https://phytozome-next.jgi.doe.gov/info/OsativaKitaake_v3_1

KEGG:-

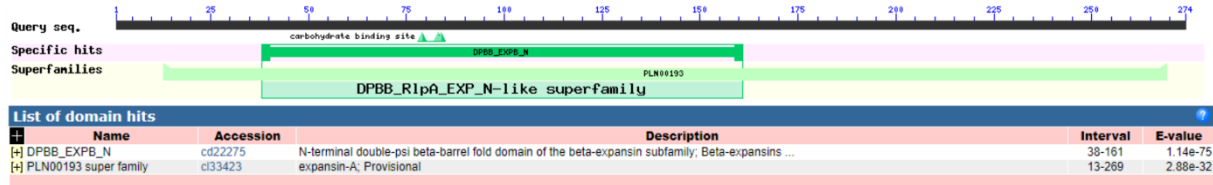
EXTERNAL RESOURCES

https://rice-genome-hub.southgreen.fr/bio_data/185326

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>OskEXPB-05

MALAAKLLPSIVAFVALACCVLRSSVASVDHHRKLSGWSIGGATWYGPANGSGTGDG
GACGYQGDVVGQPPFNSMIAAGSPSIYESGKGCSCYQVKCSGNPSCSGKPVTTVLTD
LCPGGACLEEPVHFDLSGTAFGAMAKPGQDDQLRNAGKLPVQYARVPCKWQGVDI
AFRVDAGSNQYYLAVLVEDEDGDGDLSAVDLMQSGSGGGGSWAAMQQSWGAV
WKYNSGPAPLQAPMSIRLTSGSGRTLVAASNVIPAGWQPGGTYRSIVNFRRED*

CDS (coding sequence)

>OskEXPB-05

ATGGCATTGGCAGCCAAGCTCCTCCCGTCCATCGTCGCGTTCGTGGCTCTCGCCTG
CTGCGTCTCCGCTCATCCGTCGCGTCCGTCGACCACCACCGGAAGCTCTCCGGCT
GGTCCATCGGCGGCGCGACGTGGTATGGCCCTGCCAACGGCTCTGGAACCGATGG
TGGCGCGTGTGGGTACCAGGGAGACGTCGGGCAGCCGCTTTCAACTCCATGATC
GCCGCCGGCAGCCCGTCCATCTATGAGTCCGGCAAGGGCTGCGGCTCTTGTTACC
AGGTGAAGTGCAGCGGCAACCCCTCTTGCTCCGGCAAGCCTGTGACCGTCGTCCT
CACCGACCTGTGCCCCGGCGGCGGTGCCTCGAAGAGCCCGTCCACTTCGACCTG
AGCGGGACGGCGTTCGGCGCCATGGCAAACCCGGCCAGGACGATCAGCTCCGC
AACGCCGGAAGCTCCAGTCCAATACGCTAGGGTGCCGTGCAAATGGCAGGGG
GTGGACATCGCGTTCGGGTGGACGCCGGCTCCAACCAGTACTACCTCGCCGTGC
TGGTCGAGGACGAGGACGGCGACGGCGACCTGTCGGCGGTGGACCTCATGCAGA
GCGGCGGCAGCGGCGGCGGATCTTGGGCGGCGATGCAGCAGTCGTGGGGCG
CGGTGTGGAAGTACAACCTCCGGGCCGGCGCCGCTGCAGGCGCCGATGTCCATCCG
CCTCACGTCCGGCTCCGGCCGGACGCTCGTCGCCAGCAACGTCATCCCCGCCGGG
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Nucleotide

>OskEXPB-05

CGACCTGCCAGCCACAGGTTGCAGCTGCCTATAAAATAGACAGACGGCAAGTTGT
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CGCGTTCGTGGCTCTCGCCTGCTGCGTCCTCCGCTCATCCGTCGCGTCCGTCGACC
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CAACGGCTCTGGAACCGATGGTACATCTACCTCACGGACTCGATCGATCATCACC
AGAGGATGGACCATATATGCGAGCGGCCTGCAGGCTTAATTAGTACTGACGAGG
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CCTGTGCCCCGGCGGCGCGTGCCTCGAAGAGCCCGTCCACTTCGACCTGAGCGGG
ACGGCGTTCGGCGCCATGGCAAACCCGGCCAGGACGATCAGCTCCGCAACGCC
GGCAAGCTCCCAGTCCAATACGCTAGGTAATCAAGATATCTATCTCTATCCATCT
GTATATCTCTATCTAGATCAATCAATCCCATATATATCCTACAGCTATAGCTAGCA
ACAGTCGATCAAGTGTGCGTAGTATATCTCGCATTGTCACATGCATTTAAACGCA
TCCGGGACAATTTCTTTGGGCTGCTTGTACGACGCACGCAAACCACGGGGCCCG
TGCATGCATGGCAGCCGTCGTGAACCGGTCGACCAACTGTGTGATCTCTTCCTCTC
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GATCCTTCAGC