

IDENTIFICATION

Species: *Oryza sativa* Kitaake

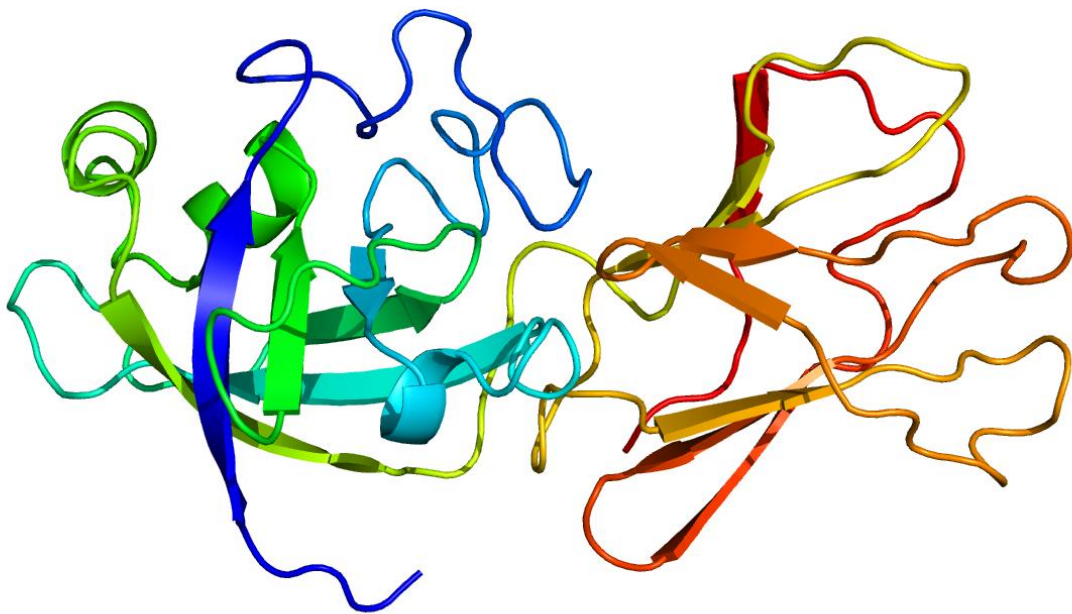
Locus: OsKitaake03g002800

Gene Model: OsKitaake03g002800.1.p

Description: OskEXPB-07

Family: Beta Expansin

3D structure:



GENOME DATABASES

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

KEGG:-

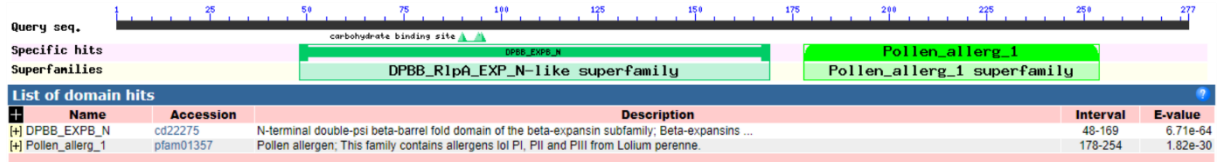
EXTERNAL RESOURCES

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

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>OskEXPB-07

MVSGDVGVVVYLLLVLVVVQGCKGSSAVQGEGRWYNESEAIGGAAAWGNAKAT
WYGQPNGAGAADNGGACGFKKVNQYPFMGMTSCGNQPLYKGGKGCSCYRVRNCN
RNPACSGNAQTVAITDMNYFPLSQYHFDLSGIAFGRLAKPGRADDLRRAGIIDVQFAR
VPCEFPLKVGHFVVEEGSSPVYLAVLVEYENGDDVAQVDLKEAGAGGGRWTPMR
ESWGSVWRLDSNHRLRAPFSIRIRSDSGKTLVAPDVIPLNWTPTFYRSFVQYSS*

CDS (coding sequence)

>OskEXPB-07

ATGGTTAGCGGTGATGTAGGAGTAGTAGTGTACTACCTGCTGCTAGTATTAGTGG
TGGTGCAGGGGTGCAAAGGCAGCAGCGCGGTGCAAGGTCGGTGGTACA
ACGAGAGCGAGGCCATCGGTGGTGCGGCGGGCGTGGGGGAACGCGAAGGCGACGT
GGTACGGGCAGCCGAACGGCGCCGGGGCGGCGGACAACGGCGGGGCGTGCGGG
TTCAAGAAGGTGAACCAGTACCCGTTTCATGGGGATGACGTCGTGCGGGAACCAG
CCGCTGTACAAGGGCGGCAAGGGCTGCGGCTCCTGCTACCGCGTCAGGTGCAATC
GAAACCCCGCCTGCTCCGGCAACGCCAGACCGTCCGATCACCGACATGAACTA
CTTCCCCTCTCCAGTACCACTTCGACCTCAGCGGCATCGCCTTCGGCCGCCTCG
CCAAGCCCGGCGCGCCGACGACCTCCGCGCGCGGGGATCATCGACGTGCAGTT
CGCGCGCGTGCCGTGCGAGTTCCCGGGCCTCAAGGTGGGATTCCACGTGGAGGA
AGGGTCCAGCCCCGTGTACCTGGCGGTGCTGGTGGAGTACGAGAACGGCGACGG
AGACGTGGCGCAGGTGGACCTCAAGGAGGCGGCGCCGGAGGAGGAAGGTGGA
CGCCGATGCGGGAGTCGTGGGGGTCGGTGTGGAGGCTGGACTCCAACCACCGCC
TGCGGGCGCCATTCTCCATCCGCATCCGGAGCGACTCCGGCAAGACGTTGGTGGC
ACCGACGTCATCCCCCTCAACTGGACGCCAACACCTTCTACCGTTCCTTCGTCC
AGTACTCCTCCTAG

Nucleotide

>OskEXPB-07

AGAGGAGGGGTACTTTCAATTCGTTGCTCTCCTCCCCGGCCGGTAGGCAGCAACA
AGCTGTAAGCACAAAGTATCGAAATGGTTAGCGGTGATGTAGGAGTAGTAGTGTA

CTACCTGCTGCTAGTATTAGTGGTGGTGCAGGGGTGCAAAGGCAGCAGCGCGGTG
CAGGGTGAAGGTCGGTGGTACAACGAGAGCGAGGCCATCGGTGGTGCGGCGGCG
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GCGCCGGAGGAGGAAGGTGGACGCCGATGCGGGAGTCGTGGGGGTTCGGTGTGGA
GGCTGGACTCCAACCACCGCCTGCGGGCGCCATTCTCCATCCGCATCCGGAGCGA
CTCCGGCAAGACGTTGGTGGCACCCGACGTCATCCCCCTCAACTGGACGCCAAC
ACCTTCTACCGTTCCTTCGTCCAGTACTCCTCCTAGCTAGCTACTCCTATACCCATT
AATTCTTCCCTAATTATTCCTTCTTGTTATTATATTCTACCCTTATATATATATA
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ATGCATGCATGGACTAGTAA