IDENTIFICATION

Species: *Oryza sativa Kitaake*

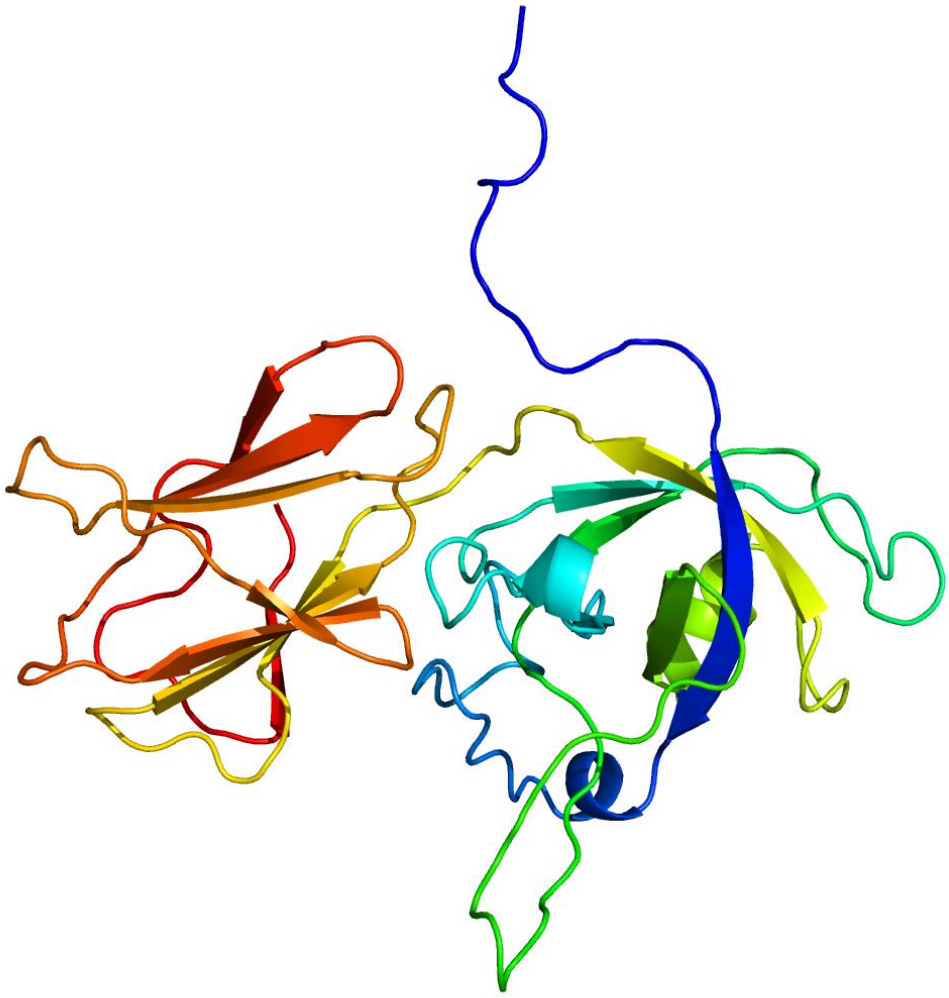
Locus: OsKitaake08g251200

Gene Model: OsKitaake08g251200.1.p

Description: OskEXPA-28

Family: Alpha Expansin

3D structure:



GENOME DATABASES

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

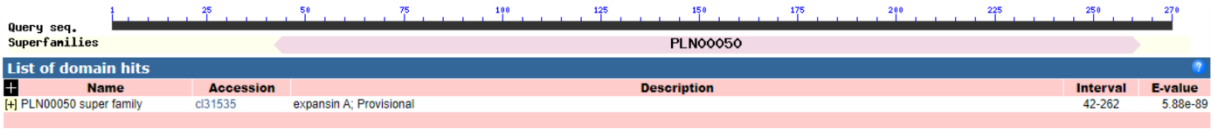
KEGG:-

EXTERNAL RESOURCES

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

GENE STRUCTURE

DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>OskEXPA-28

MWCTWALGRVVLAVVFLVALAAGDAAPPKVHRNHGKFTAGPWKQAHATFYGGR
DGSGTLDGACGYKDTSKEGYGVQTVAVSTPLFGAGAGCGACYEVKCVDSPDGCKV
GAAPLVVTATNLCPPNPGQSNDNGGWCNPPREHFDLSMPAFLQIAQEKAGIVPISYRR
VPCVKVGGIRYTITGNPYFNLVMVSNVGGAGDVAGLSVKGNKRVKWTPLKRNWGQ
EWQTSEVLTGESLTFRVMTGDHRKATSWHVLPPDWQFGVTYQATKNFN*

CDS (coding sequence)

>OskEXPA-28

ATGTGGTGTACGTGGGCGTTGGGGCGGGTGGTGTTGGCGGTGGTGTTCCTGGTTG
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CACGGCGGGGCCATGGAAGCAGGCGCACGCGACGTTCTACGGCGGGCGCGACGG
GTCCGGCACGCTGGACGGCGCGTGCGGGTACAAGGACACGTCCAAGGAAGGCTA
CGGCGTGCAGACGGTGGCGGTGAGCACGCCGCTGTTCGGCGCCGGCGCCGGCTG
CGGCGCCTGCTACGAGGTCAAGTGCGTGGACAGCCCCGACGGTTGCAAGGTCGG
CGCCGCCCCCTTGGTCGTCACCGCCACCAACCTCTGCCCCCCCAACCCCGGCCAG
TCCAACGACAACGGCGGCTGGTGCAACCCGCCGCGCGAGCACTTTGACCTCTCCA
TGCCGGCCTTTCTGCAGATCGCGCAGGAGAAGGCCGGCATCGTGCCCATATCGTA
CAGACGGGTGCCGTGTGTGAAGGTGGGTGGGATCAGGTACACGATAACCGGGAA
CCCGTACTTCAACCTGGTGATGGTGTCGAACGTGGGCGGGGCGGGTGACGTGGCA
GGGCTATCGGTGAAGGGGAACAAGAGGGTGAAGTGGACTCCGCTGAAGCGCAAC
TGGGGGCAGGAGTGGCAGACGTCGGAGGTCCTCACCGGAGAGTCGCTGACGTTC
AGGGTGATGACCGGCGACCACCGCAAGGCCACCTCCTGGCACGTCCTCCCCCCCG
ACTGGCAGTTCGGCGTCACCTACCAGGCTACCAAGAACTTCAACTAA

Nucleotide

>OskEXPA-28

GGAAATCTAATCCCCCGCAGCTACTAATTACTACTAACCGTTAAAAGTAGCCGCC
GGTTAATATTCGATCGATCGATCATGTGGTGTACGTGGGCGTTGGGGCGGGTGGT
GTTGGCGGTGGTGTTCCTGGTTGCGTTGGCTGCCGGCGATGCAGCGCCGCCCAAG
GTTCACCGGAACCACGGCAAGTTCACGGCGGGGCCATGGAAGCAGGCGCACGCG
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GCCCCGACGGTTGCAAGGTCGGCGCCGCCCCCTTGGTCGTCACCGCCACCAACCT
CTGCCCCCCCAACCCCGGCCAGTCCAACGACAACGGCGGCTGGTGCAACCCGCCG
CGCGAGCACTTTGACCTCTCCATGCCGGCCTTTCTGCAGATCGCGCAGGAGAAGG
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GTGTGAAGGTGGGTGGGATCAGGTACACGATAACCGGGAACCCGTACTTCAACC
TGGTGATGGTGTCGAACGTGGGCGGGGCGGGTGACGTGGCAGGGCTATCGGTGA
AGGGGAACAAGAGGGTGAAGTGGACTCCGCTGAAGCGCAACTGGGGGCAGGAG
TGGCAGACGTCGGAGGTCCTCACCGGAGAGTCGCTGACGTTCAGGGTGATGACC
GGCGACCACCGCAAGGCCACCTCCTGGCACGTCCTCCCCCCCGACTGGCAGTTCG
GCGTCACCTACCAGGCTACCAAGAACTTCAACTAATTCTTATCAATCATGCCAAC
CCAACCCAACCCAACAGCAAAATATGAAGGCTCTCTTACATGCATGAATGCTGAC
TACTGCAAATCTGGATCGAACCGATGATGATCATACTAGCTACAAATGTATATAT
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AAGGATCTGTTTCATACAAATCG