

IDENTIFICATION

Species: *Oryza sativa*

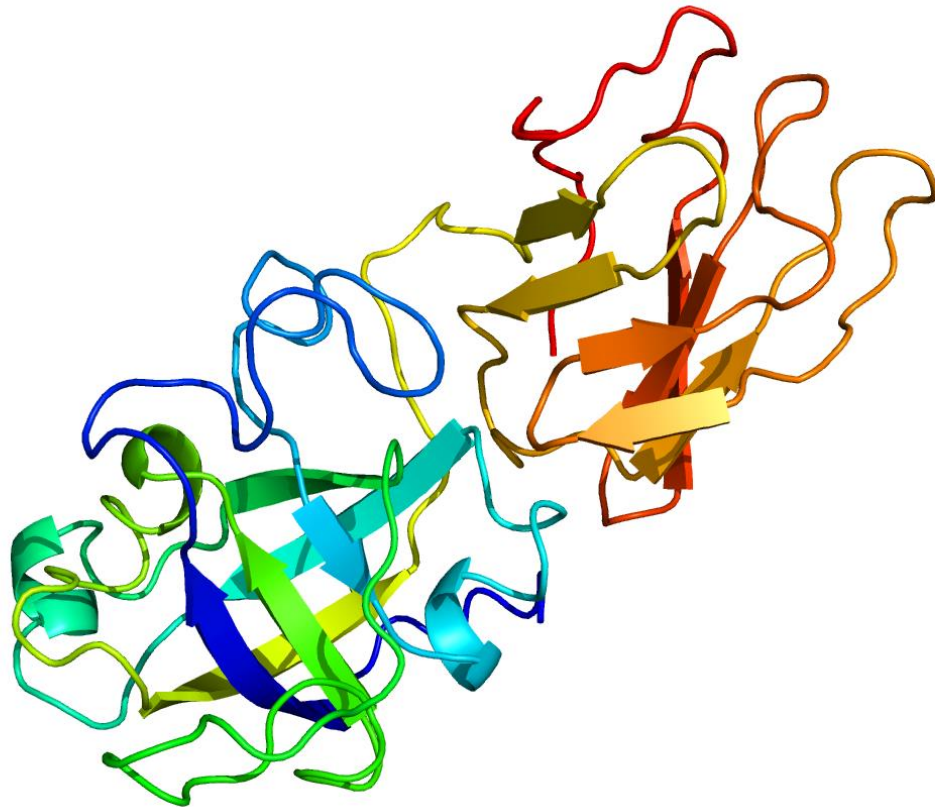
Locus: LOC_Os10g30330

Gene Model: LOC_Os10g30330.1

Description: OstEXPA-31

Family: Alpha Expansin

3D structure:



GENOME DATABASES

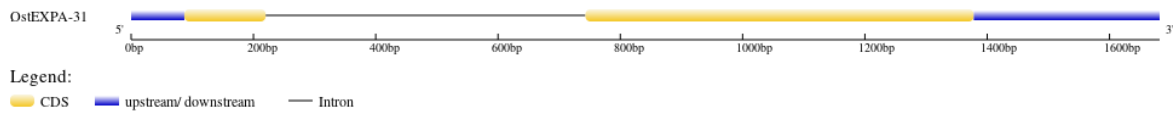
Phytozome: https://phytozome-next.jgi.doe.gov/info/Osativa_v7_0

KEGG: <https://www.genome.jp/entry/T01015>

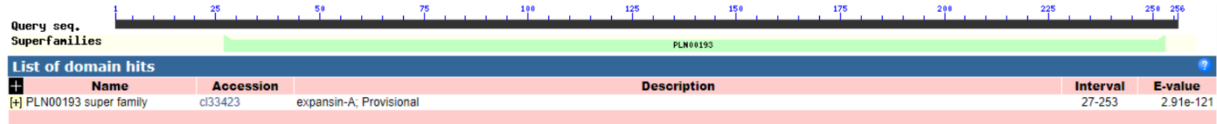
EXTERNAL RESOURCES

<http://rice.uga.edu/>

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>OstEXPA-31

MGAMAENLLVLCTILAARMALAAADDWIPATATFYGGNDGSGTMGGACGYGNLY
DQGYGLENAALSTALFNDGAACGQCYLIVCDTDKAGRWCCKPRGAVTVTATNLCPP
NVALPSDGGGWCNPPRRHFDMSQPAWERIGVYRAGIVPVLVYRRVRCWRRGGVRF
VGGFDHFELVLVANVAGSGSVAASVVRGAGTGWLQMSRNWGANWQSLAGLAGQP
LSFGVTTTGGQYILFQDVAPAGWKFGQTFSTSKQFDY*

CDS (coding sequence)

>OstEXPA-31

ATGGGCGCCATGGCTGAGAACCTCCTGGTTCTGTGCACCATCCTCGCGGGCGCGCA
TGGCGCTCGCCGCCGCGGATGATTGGATTCGCGCCACCGCCACGTTCTACGGCGG
AAACGACGGCTCCGGCACCATGGGCGGTGCGTGTGGGTATGGGAACCTGTACGA
CCAAGGGTACGGCCTCGAGAACCGCGGCGCTGAGCACGGCGCTGTTCAACGACGG
CGCGGCGTGCGGGCAGTGCTACCTCATCGTGTGCGACACCGACAAGGCCGGGCG
GTGGTGCAAGCCGCGGGGCGCGGTGACCGTGACGGCCACCAACCTGTGCCC GCC
CAACTGGGCCCTCCCAGCGACGGCGGCGGGTGGTGCAACCCGCCGCGGCGGCA
CTTCGACATGTTCGACCCGGCGTGGGAGCGGATCGGCGTCTACCGCGCCGGGATC
GTGCCGGTGCTCTACCGCCGCGTCCGGTGCTGGCGCCGCGGGCGGCGTCCGCTTCA
CCGTCGGCGGCTTCGACCACTTCGAGCTCGTGCTCGTCGCCAACGTCGCCCGG CAG
CGGCTCCGTCGCCGCCGTGTTCGGTCAGGGGCGCCGGCACCGGGTGGCTCCAGATG
TCGCGCAACTGGGGGGCCAATTGGCAGTCGCTCGCCGGGCTCGCCGGCCAGCCGC
TCAGCTTCGGCGTCACCACCACCGGCGGCCAGTACATACTGTTCCAGGACGTCGC
GCCGGCGGGGTGGAAGTTCGGCCAGACGTTCTCCACCTCCAAGCAGTTCGACTAC
TGA

Nucleotide

>OstEXPA-31

GCACTCAGTAACAACATCAAAATATTCAAGAACTTGTAGTTATTCAGGTCGATCT
CTTCCAGCCTGATCTGTTGTTTGAACGTCGCCATGGGCGCCATGGCTGAGAACCT
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AGTACGTCTAGTTTCGTTTTTCTCACTTTTTTTTCGTAGGAGTTGTACTCGTTTAGCA
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ACACGATGGGTATGCATGAGCAGGCGGTGCGTGTGGGTATGGGAACCTGTACGA
CCAAGGGTACGGCCTCGAGAACGCGGCGCTGAGCACGGCGCTGTTCAACGACGG
CGCGGCGTGCGGGCAGTGCTACCTCATCGTGTGCGACACCGACAAGGCCGGGCG
GTGGTGCAAGCCGCGGGGCGCGGTGACCGTGACGGCCACCAACCTGTGCCCCGCC
CAACTGGGCCCTCCCCAGCGACGGCGGCGGGTGGTGCAACCCGCCGCGGGCGGCA
CTTCGACATGTCGCAGCCGGCGTGGGAGCGGATCGGCGTCTACCGCGCCGGGATC
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TCAGCTTCGGCGTCACCACCACCGGCGGCCAGTACATACTGTTCCAGGACGTCGC
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TCCTTAATTTTGTAAATTATTATTAATTCATTGCCTATGCATGTAATTTTTTATTA
GATGAGTTAATGAAATGTTATTAACGAGGC