

## IDENTIFICATION

**Species:** *Oryza brachyantha*

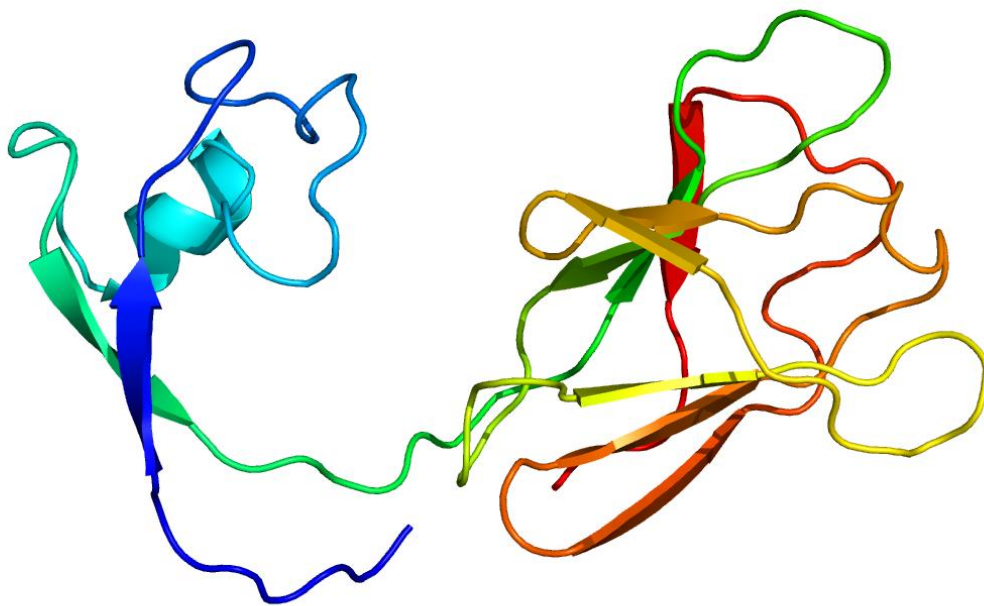
**Locus:** XP\_006651052

**Gene Model:** XP\_006651052.1

**Description:** ObEXPA-13

**Family:** Alpha Expansin

**3D structure:**



## GENOME DATABASES

NCBI: [https://www.ncbi.nlm.nih.gov/genome/10862?genome\\_assembly\\_id=1593936](https://www.ncbi.nlm.nih.gov/genome/10862?genome_assembly_id=1593936)

KEGG: <https://www.genome.jp/entry/T02995>

## EXTERNAL RESOURCES

<https://rice-genome-hub.southgreen.fr/organism/1941498>

## GENE STRUCTURE



## DOMAIN ARCHITECTURE

Query seq. MGSIFLQLVAVLALCFAPARSDWLPGTATFYGGADGSGTMARPHFDMAEPAWLQIGIYEAGIIPVLYQQVKCWRSAVRFINGFNMFELVLTNVAGSGSVASMSVKGSSPGWIQMSRNWGANWQCLAGLAGQALSFTVNSTGGQTIVFDGVVPAGWSFGQTYSTYKQFDY

Superfamilies

List of domain hits

Name	Accession	Description	Interval	E-value
PLN00193 super family	c133423	expansin-A, Provisional	42-170	4.26e-60

## SEQUENCES

### Peptide

>ObEXPA-13

MGSIFLQLVAVLALCFAPARSDWLPGTATFYGGADGSGTMARPHFDMAEPAWLQIGIYEAGIIPVLYQQVKCWRSAVRFINGFNMFELVLTNVAGSGSVASMSVKGSSPGWIQMSRNWGANWQCLAGLAGQALSFTVNSTGGQTIVFDGVVPAGWSFGQTYSTYKQFDY

### CDS (coding sequence)

>ObEXPA-13

ATGGGGAGCATTTCCTGCAGCTGGTGGCCGTTCTCGCGCTCTGCTTTGCACCGGC  
GAGGTCGACTGGCTCCCGGGCACCGCCACGTTCTACGGCGGCGCCGACGGCTCC  
GGCACGATGGCCCCGCCCTCACTTCGACATGGCCGAGCCCGCCTGGCTCCAGATCG  
GCATCTACGAGGCCGGCATCATCCCCGTCCTCTACCAGCAGGTGAAGTGCTGGAG  
GAGTGCAGGCGTGAGGTTCAACATCAACGGGTTCAACTACTTCGAGCTGGTGCTG  
GTGACCAACGTGGCCGGGAGCGGGTTCGGTAGCGAGCATGTCGGTGAAGGGGTCC  
AGCCCGGGGTGGATCCAGATGTCGAGGAATTGGGGCGCCAATTGGCAGTGCCTC  
GCCGATTGGCCGGCCAGGCTCTCAGCTTACGGTCAACTCCACCGGCGGCCAGA  
CCATCGTCTTCGACGGCGTTGTGCCGGCGGGGTGGTTCGTTCCGGCCAAACCTACAG  
CACCTACAAACAGTTTGACTACTAAGCTAGCTTCATACGTCAAGAGCAATTAATA  
GAGCATCGTCTGATCATCGAGCATTCTCTTTTTTCATTTCTTATTGATTAGCT  
CGAGAGCTAGCTCCGCGATCG

### Nucleotide

>ObEXPA-13

GCAAGAATGATTGTATGGCTAACATTCAGTTCAGCTACAGCCTGCGTAGCGTACA  
TGCTGGCTAGCAGAAACATTCGCGTGCATGCATGATCAGAGCATTCTGTTCTTG  
CTGCGCACAACGACCTGTTCACTTTGAACTTTGTAGCTGCACCCCAAGCAGTAGA  
GCTTAGACCAGCAAAACCAATCATAATTACGCGTAATTCAATCTCTGGACGTTGC  
AGAGCCATGTGCATGCGATCGTTGGAACAGTGATCGCATGTTTCAATAATGCATG  
CGACAATCATTCCTAGCTAAAGCTTGGTATGCAATCCATGCCCGTTCTGTTTACA  
GGCCTCCTGGATCACCATGCTATATAAGCACCAGCATTGCCGCAGACATCCTCAC  
CTCCAAAATCATTATCGCAAAACAATATCTATCTAGCTAGTAGCTACATAGTTT  
GCAACGAGGTTAATCTTCTCTCCATCGACTGCACAGAATCGAGCTAGCTAGGGGG

