

## IDENTIFICATION

**Species:** *Panicum hallii*

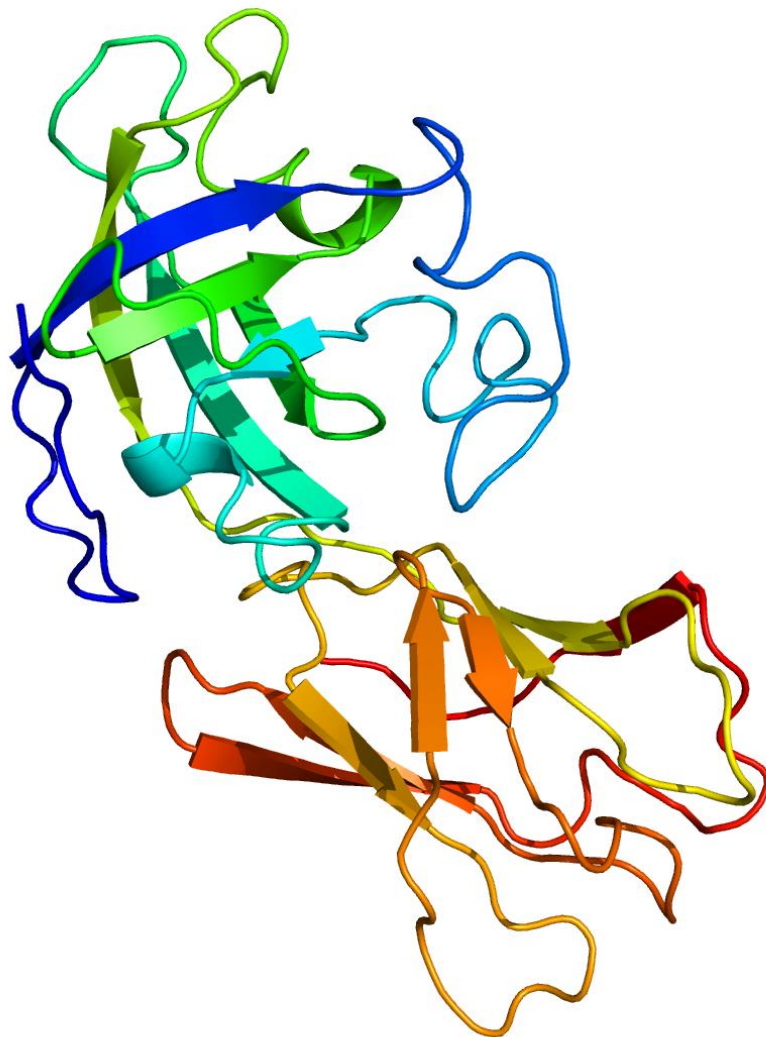
**Locus:** Pahal.9G403100

**Gene Model:** Pahal.9G403100.1.p

**Description:** PhEXPA-30

**Family:** Alpha Expansin

**3D structure:**



## GENOME DATABASES

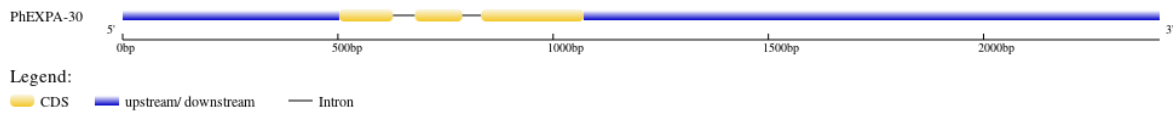
Phytozome: [https://phytozome-next.jgi.doe.gov/info/Phallii\\_v3\\_1](https://phytozome-next.jgi.doe.gov/info/Phallii_v3_1)

KEGG: <https://www.genome.jp/entry/T07366>

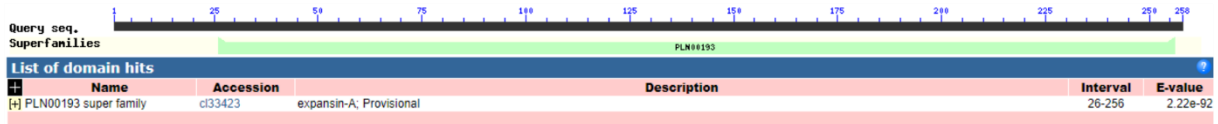
## EXTERNAL RESOURCES

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## GENE STRUCTURE



## DOMAIN ARCHITECTURE



## SEQUENCES

### Peptide

>PhEXPA-30

MASPSTAILALAVLVCAATAANARFTAMQWTPAHATFYGDETA AETMGGACGYG  
NLYATGYGTDTAALSTTLFKDGYGCGTCYQIRCASSPWCYRGSPVITVTATNLCPPN  
WAQDSNNGGWCNPPRTHFDLSKPAFMRMAQWRAGIVPVMYRRVPCVRRGGLRFA  
LQGNPYWLLAYVMNVAGAGDVAEMSVRSGRGAWVRMSHNWGFQAFQALGGR  
ALSFKVTSYTTRQTVVATNVAPANWCLGLTYQARVNFS\*

### CDS (coding sequence)

>PhEXPA-30

ATGGCTTCTCCATCCACAGCCATCTTGGCCCTCGCCGTCGCGTTGGTCTGCGCAGC  
CACCGCGGCGAACGCGAGGTTACGGCGATGCAGTGGACTCCGGCGCACGCCAC  
GTTCTACGGCGACGAGACCGCGGCCGAGACCATGGGTGGGGCGTGCGGGTACGG  
CAACCTGTACGCAACGGGGTACGGCACGGACACGGCGGGCGCTGAGCACGACACT  
GTTCAAGGACGGGTACGGGTGCGGGACGTGCTACCAGATCCGGTGCGCGAGCTC  
CCCCTGGTGCTACCGGGGCTCGCCGGTGATCACGGTGACGGCGACCAACCTGTGC  
CCGCCAACTGGGCGCAGGACTCCAACAACGGCGGCTGGTGCAACCCGCCGCGG  
ACCCACTTCGACCTCTCCAAGCCGGCGTTCATGCGGATGGCCCAGTGGCGCGCCG  
GCATCGTGCCGGTCAATGTACCGGCGGGTGCCCTGCGTGAGGCGCGGCGGCTCCG  
GTTGCGCTCCAGGGGAACCCCTACTGGCTGCTGGCGTACGTGATGAACGTGGCC  
GGCGCCGAGACGTCGCGGAGATGTGCGTGAGGAGCGGGCGCGGCGCGTGGGTG  
CGCATGAGCCACAACCTGGGGCGCGTCTTTTCAGGCGTTCGCGCAGCTCGGCGGCC  
GGGCGCTCAGCTTCAAGGTCACCTCCTACACCACCCGGCAGACCGTCTGTCGCCAC  
CAACGTCGCGCCGGCAAACCTGGTGCCCTCGGGCTCACGTACCAGGCCCGCGTCAAC  
TTCTCCTGA

### Nucleotide

>PhEXPA-30

CATCCGACGCCTCGCTGACGCGCCCCCGCGCCGCGGCACGCGTGTCCGGGGGTCCG  
GTGGCCGCCCCCGGCCTCGCCGTCTCTCCTCCTCCCTTCCCCATGTCCCCTCCC  
CACACCAGGCCACCACCTCTATATCCGTCCACGGCGCCGCGCTTCGCCCCAAC  
CGCGTCCGCGTGTCCAAAACATTCTGCGGCCTGCTGGAGGGCAGCACCAGGTATCA  
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GCGGCGCCTGCTTCCAGGTAGGCTCCTTCTTCCCCCAATTCTCAGTTTTTTCAGT  
CAAAGAATTTGGATTGAGCGAGGATCGCCCATTGCAGGTGAGGTGCGGGGACAG  
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CTCGTTCGAGCGGGCACTGGCGGGTGCCGTCGTCACGACGGGGGAGGTGAGGT  
CACGCGGACGTAGCTGAGCCGAGAGACATGCTCGGCAGATGCGGCCAGCGTGC  
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