

## IDENTIFICATION

**Species:** *Panicum hallii* HAL

**Locus:** PhHAL.5G111300

**Gene Model:** PhHAL.5G111300.1.p

**Description:** PhhEXPA-13

**Family:** Alpha Expansin

**3D structure:**



## GENOME DATABASES

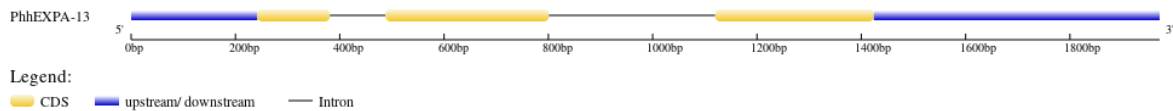
Phytozome: [https://phytozome-next.jgi.doe.gov/info/PhalliiHAL\\_v2\\_1](https://phytozome-next.jgi.doe.gov/info/PhalliiHAL_v2_1)

KEGG:-

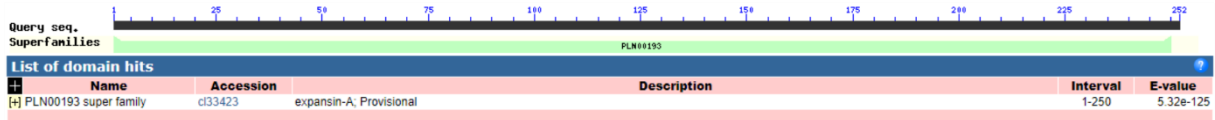
## EXTERNAL RESOURCES

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## GENE STRUCTURE



## DOMAIN ARCHITECTURE



## SEQUENCES

### Peptide

>PhhEXPA-13

MATANVFLLLCSTFCFLARRAAGDYGGWQSAHATFYGGGDASGTMGGACGYGNL  
YSTGYGTNTAALSTALFNDGASCGQCFELRCDNAGQSCLPGTITVTATNFCPPNYGLP  
SDDGGWCNPPRPHFDMAEPAFLQIAQYRAGIVPVA YRRVPCVKKGGIRFTINGHSYF  
NLVLVTNVAGAGDVQSVSIKGSSTGWQAMSRNWGQNWQSNLLDGQALSFKVTAS  
DGRCVTSNNAAPAGWQFGQTFEGGQF\*

### CDS (coding sequence)

>PhhEXPA-13

ATGGCGACCGCCAATGTCCTTCTCCTCCTGCTCTGCTCGACCTTCTGCTTCCTCGC  
CCGCCGGGCTGCCGGCGACTACGGCGGGTGGCAGAGCGCCACGCCACGTTCTA  
CGGCGGCGGCGACGCGTCCGGCACAATGGGCGGGGCGTGCGGGTACGGGAACCT  
GTACAGCACCGGGTACGGCACCAACACGGCGGGCGCTGAGCACAGCGCTGTTCAA  
CGACGGCGCCTCGTGCGGGCAGTGCTTCGAGCTCCGGTGCGACAACGCGGGGCA  
GTCGTGCCTGCCGGGCACCATCACCGTGACGGCCACCAACTTCTGCCCGCCCAAC  
TACGGCCTCCCCAGCGACGACGGCGGCTGGTGCAACCCGCCGCGCCCGCACTTCG  
ACATGGCCGAGCCGGCCTTCTCCAGATCGCGCAGTACCGCGCCGGCATCGTGCC  
CGTCGCGTACAGGAGGGTGCCGTGCGTGAAGAAGGGCGGGATCCGGTTCACCAT  
CAACGGCCACTCCTACTTCAACCTGGTGCTGGTGACCAACGTGGCCGGCGCCGGC  
GACGTGCAGTCCGTGTCCATCAAGGGCTCCTCCACCGGGTGGCAGGCCATGTCCC  
GCAACTGGGGCCAGA ACTGGCAGAGCAACTCGCTGCTCGACGGCCAGGCCCTCT  
CCTTCAAGGTCACCGCCAGCGACGGCCGCTGCGTACACAGCAACAACGCCGCGCC  
GGCCGGCTGGCAGTTCGGCCAGACCTTCGAGGGCGGCCAGTTCTAG

### Nucleotide

>PhhEXPA-13

GCCGCTCCGCCAGTCGTCCCCCACCACCTCCCTGGCCTCTATCTCTTTTGTCTC  
GGTTTCCCCTGGCCCTCCACGAAAGTTGCTAACGATTCCA ACTGCCGGGAGCACT  
GGCCGTTGGTTGGGTTGGGCCTATAAGTAGCTGGCCTCGGCGCGCCGCTCCCTTC  
ACAGCCAAGCAACTCTCGATCCCTAATCAGCAGCTCGAGCTCGCTTTAGCTCGAG  
AAGCAGTGTGTGTGTGCTGCAATGGCGACCGCCAATGTCTTCTTCTCCTGCTCTG  
CTCGACCTTCTGCTTCTCGCCCGCCGGGCTGCCGGCGACTACGGCGGGTGGCAG

AGCGCCACGCCACGTTCTACGGCGGGCGGCGACGCGTCCGGCACAATGGGTGAG  
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CCGCGCCGGCATCGTGCCCGTTCGCGTACAGGAGGTACGTGGGTCCAGACTTACTA  
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ATCAACGGCCACTCCTACTTCAACCTGGTGCTGGTGACCAACGTGGCCGGCGCCG  
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CGATGGCGACGTGTGCGGTGTGGTGAGTAGTCGATTGAAGAAG