

IDENTIFICATION

Species: *Panicum hallii*

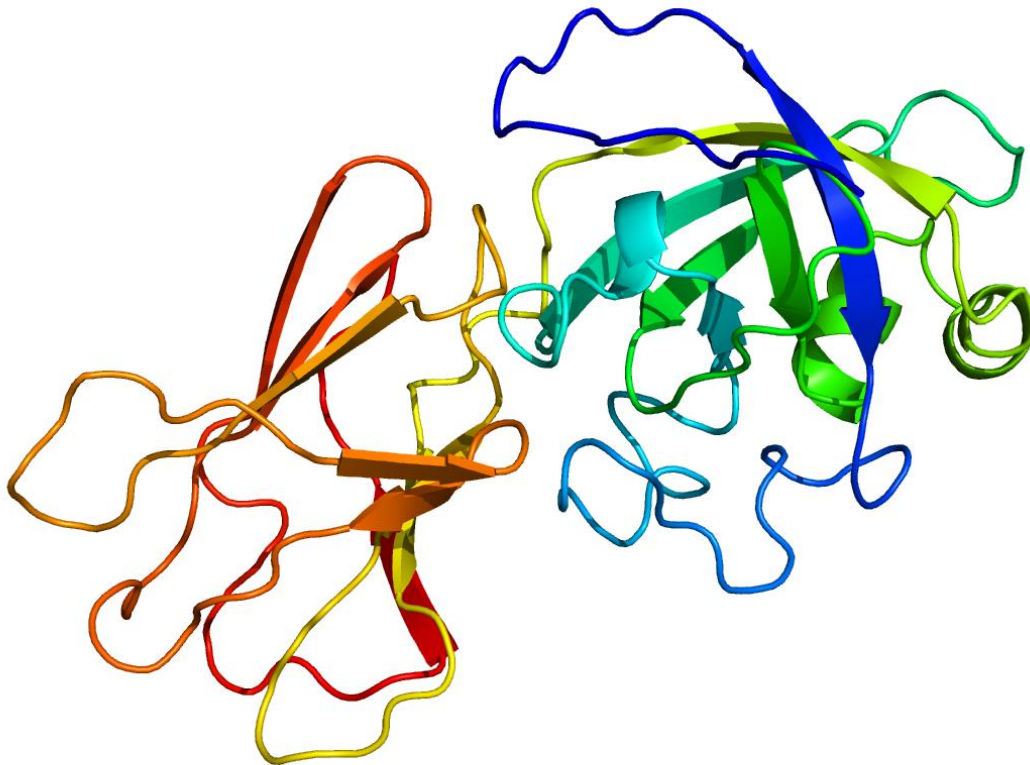
Locus: Pahal.9G388500

Gene Model: Pahal.9G388500.1.p

Description: PhEXPB-23

Family: Beta Expansin

3D structure:



GENOME DATABASES

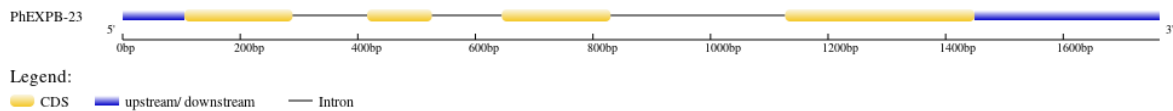
Phytozome: https://phytozome-next.jgi.doe.gov/info/Phallii_v3_1

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

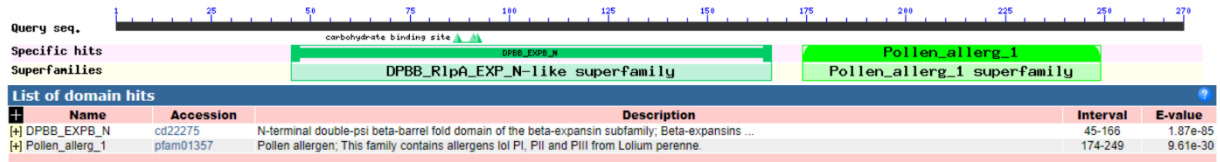
EXTERNAL RESOURCES

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GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>PhEXPB-23

MASMIAGSSKVVVALIFSLLVSYGSCARPPPVNLNASAFTADSNWEAARATWYGAPT
GAGPDDDDGGACGFKNVNLPPFSSMTSCGNEPLFKDGKGCSCYQIRCTNHAACSGN
PETVIITDMNYYPVSKYHFDLSGTAFGAMAKPGRNDELRHAGIIDIQFKRVPCDYPGQ
KVTFHVEEGSNPVYFAVLVEFEDGDGDAVQVDLMEASSGSWTPMRESWGSIWRLDS
NHRLQAPFSLRITNESGKQLVASNVIPANWVNPNTYYRSIVQY*

CDS (coding sequence)

>PhEXPB-23

ATGGCGTCCATGATCGCCGGCTCGTCCAAGGTGGTGGTTGCACTGATCTTCTCCCT
CCTTGTCTCGTATGGCTCGTGCCTAGGCCGCCCGGTGAACCTAACGCCTCTG
CCTTACCCGCCGACTCCAAGTGGGAGGCTGCCAGGGCCACCTGGTACGGCGCGCC
CACCGGCGCCGGCCCCGACGACGATGGTGGCGCCTGCGGGTTCAAGAACGTCAA
CCTGCCGCCGTTCTCGTCCATGACGTCGTGCGGCAACGAGCCCCTGTTCAAGGAC
GGCAAGGGCTGCGGCTCCTGCTACCAGATTCGATGCACTAACCACGCTGCGTGCT
CCGGCAACCCGGAGACGGTGATCATCACCGACATGAACTACTACCCGGTGTCCAA
GTACCACTTCGACCTCAGCGGCACGGCGTTCGGCGCCATGGCCAAGCCCGGCCGC
AACGACGAGCTCCGCCACGCCGGC ATCATCGACATCCAGTTCAAGAGGGTGCCCT
GCGACTACCCCGGGCAGAAGGTGACCTTCCACGTGGAGGAGGGCTCGAACCCTG
TCTACTTCGCGGTGCTCGTTCGAGTTCGAGGACGGCGACGGCGACGCTGTGCAGGT
GGACCTCATGGAGGCCAGCTCCGGGTCGTGGACGCCGATGCGCGAGTCCTGGGG
ATCCATCTGGAGGCTGGACTCGAACCACCGGCTGCAGGCGCCCTTCTCGCTGCGC
ATCACCAACGAGTCCGGCAAGCAGCTGGTGGCCAGCAACGTCATCCCGGCCAAC
TGGGTGCCCAACACCTACTACCGCTCCATCGTCCAGTACTAG

Nucleotide

>PhEXPB-23

AAACACTGATATCTTGTGTCTGCTCGGCACAAGCAGTAGCTACCTGCTTTCCTTCT
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GTATGGCTCGTGCGCTCGGCCGGTGAGCTTCAACGCCTCCGCCTTCACCGCCGAC
CCCAACTGGGAGGCCGCCAGGGCCACCTGGTACGGCGCGCCCACCGGCGCTGGT
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CACGCTGCGTGCTCCGGCAACCCGGAGACGGTGATCATCACCGACATGAACTACT
ACCCGGTCGCCAAGTACCACTTCGACCTCAGCGGCACGGCCTTCGGCGCCATGGC
CAAGCCCGGCCG CAGCGACGAGCTCCTCCATGCCGGCATCATCGACATCCAGTTC
AAGAGGTGGGTACCATGCATTGCAATGCTCGTTTTGCACAGAGCCGCGGAGCATA
ATCATTAGCTCGACCGTCGAGCTTGCCGTGTTTCTGTGGAGCCTTGTACTTTATTTG
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ATTCGCAGACATACTGTATTATTCTAGTACTTCCAATCCACTCCTAATTTGGCGTC
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GTTCGAGGACGGCGATGGCGACGTGGTGCAGGTGGACCTGATGGAGGCCAACTC
CGGGTCGTGGGCGCCGATGCGCGAGTCCTGGGGATCCATCTGGAGGATGGACTCC
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