IDENTIFICATION

Species: *Sorghum bicolor*

Locus: Sobic.001G306500

Gene Model: Sobic.001G306500.1.p

Description: SbEXPB-16

Family: Beta Expansin

3D structure:

GENOME DATABASES

Phytozome: https://phytozome-next.jgi.doe.gov/info/Sbicolor_v3_1_1
KEGG: https://www.genome.jp/entry/T01086

EXTERNAL RESOURCES

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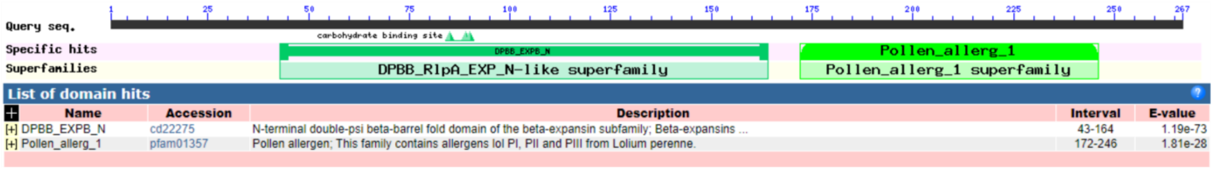
GENE STRUCTURE

DOMAIN ARCHITECTURE



List of domain hits

Name	Accession	Description	Interval	E-value
[+] DPBB_EXPB_N	cd22275	N-terminal double-psi beta-barrel fold domain of the beta-expansin subfamily; Beta-expansins ...	43-164	1.19e-73
[+] Pollen_allerg_1	pfam01357	Pollen allergen; This family contains allergens lol PI, PII and PIII from Lolium perenne.	172-246	1.81e-28

SEQUENCES

Peptide

>SbEXPB-16

MGSLANKIVAMAAVLAALVTGGSCAPKKFPPGPNITTNYNGQWLVARATWYGQPN
GAGPDDNGGACGIKNVNLPPYNGFTACGNVPIFKDGKGCGSCYEVRCKEMPECSGN
PITVFITDMNYEPIAPYHFDFSGKAFGSLAKPGLNDKLRHCGIMNVEFRRVRCKLGGK
IMFHVEKGSNPNYLAVLVKNVADDGNIVLMELEDKASPGFKPMKQSWGAVWRFDT
PKPIKGPFSIRLTSESGKKLVAPNVIPASWKPDTLYNSNIQF*

CDS (coding sequence)

>SbEXPB-16

ATGGGATCCCTCGCCAACAAAATCGTGGCCATGGCGGCTGTCCTTGCGGCGCTCG
TCACCGGCGGCTCGTGCGCGCCCAAGAAGTTCCCGCCTGGCCCCAACATCACAAC
CAACTACAACGGCCAATGGCTCGTTGCCAGGGCCACCTGGTACGGCCAGCCCAAC
GGTGCCGGCCCTGACGACAATGGCGGTGCGTGCGGGATCAAGAACGTGAACCTG
CCACCCTACAACGGCTTCACGGCCTGCGGTAACGTCCCCATCTTCAAGGACGGCA
AGGGCTGCGGCTCATGCTACGAGGTGAGATGCAAGGAAATGCCGGAGTGTTCGG
GCAACCCGATCACGGTGTTCATCACCGACATGAACTACGAGCCCATTGCACCCTA
CCACTTTGACTTCAGCGGCAAGGCCTTCGGCTCCCTGGCAAAGCCCGGGCTCAAC
GACAAGCTCCGCCACTGCGGCATCATGAACGTGGAGTTCAGGAGGGTGCGGTGC
AAGCTTGGGGGCAAGATCATGTTCCACGTTGAGAAGGGGTCCAACCCCAACTACC
TGGCCGTGCTGGTCAAGAACGTGGCGGACGACGGCAACATCGTGCTCATGGAAC
TCGAGGACAAGGCGTCGCCGGGGTTCAAGCCGATGAAGCAATCCTGGGGCGCCG
TGTGGAGGTTTGACACACCCAAGCCGATCAAGGGCCCCTTCTCCATCCGCCTCAC
CAGCGAGTCCGGCAAGAAGCTCGTCGCCCCAAACGTCATCCCGGCATCCTGGAA
GCCCGACACCCTCTACAACTCCAACATCCAGTTCTAA

Nucleotide

>SbEXPB-16

GTCACAAACACACAGAGCGACATTCGTCGAATATCACAGTTGAGCGCAAAGAAG
ACACCCGCGATGGGATCCCTCGCCAACAAAATCGTGGCCATGGCGGCTGTCCTTG
CGGCGCTCGTCACCGGCGGCTCGTGCGCGCCCAAGAAGTTCCCGCCTGGCCCCAA

CATCACAACCAACTACAACGGCCAATGGCTCGTTGCCAGGGCCACCTGGTACGGC
CAGCCCAACGGTGCCGGCCCTGACGACAATGGTATGTAAGGTTGCCTTGAGATTC
GGAATTCAATTCGGCCAGCAGTCGGTCAACCGATCGATCGATCATGCATGCATGT
GTTAATATGATGCAGGCGGTGCGTGCGGGATCAAGAACGTGAACCTGCCACCCTA
CAACGGCTTCACGGCCTGCGGTAACGTCCCCATCTTCAAGGACGGCAAGGGCTGC
GGCTCATGCTACGAGGTATGTACATTAGTATATAAATAGCAACCAAACCAAACAG
CACATGCATGAGAGAGAGAGAGATCATCTCACTAGGTGATCTTATATATACGCAG
GTGAGATGCAAGGAAATGCCGGAGTGTTCGGGCAACCCGATCACGGTGTTCATC
ACCGACATGAACTACGAGCCCATTGCACCCTACCACTTTGACTTCAGCGGCAAGG
CCTTCGGCTCCCTGGCAAAGCCCGGGCTCAACGACAAGCTCCGCCACTGCGGCAT
CATGAACGTGGAGTTCAGGAGGTAAATGCATATATTTTCATGCATGCTATATTGC
TGGCCAAGACGACGACGATCTCAGAAACACAATATATAGCTTCTCCATGATCGAT
CGATCTGTGTGTATATTTCAATATGCCATGCATGCACATGATGAAACAGGCAGCA
AAACTTATTACACGCTGTCCCGTCGTCCTACATGCAGGGTGCGGTGCAAGCTTGG
GGGCAAGATCATGTTCCACGTTGAGAAGGGGTCCAACCCCAACTACCTGGCCGTG
CTGGTCAAGAACGTGGCGGACGACGGCAACATCGTGCTCATGGAACTCGAGGAC
AAGGCGTCGCCGGGGTTCAAGCCGATGAAGCAATCCTGGGGCGCCGTGTGGAGG
TTTGACACACCCAAGCCGATCAAGGGCCCCTTCTCCATCCGCCTCACCAGCGAGT
CCGGCAAGAAGCTCGTCGCCCCAAACGTCATCCCGGCATCCTGGAAGCCCGACAC
CCTCTACAACTCCAACATCCAGTTCTAATAGACTTTGCATGCCCTTCATCCGGCAG
CAAGCCAAGTTGGCCGCTCATGTTTATTTGCACCAGAGAATGCACCGCTAATAAA
TAGTAGTACTGAGTCTTCTGCATTCTAGCTAGTATGTGATCCCTGTTGTTGTTCGG
GTTCATGATCAAATTCCAAACAGTGGAAAATAAAAAGATTGAATATATGTGTCAC
CATTGATGG