

IDENTIFICATION

Species: *Setaria italica*

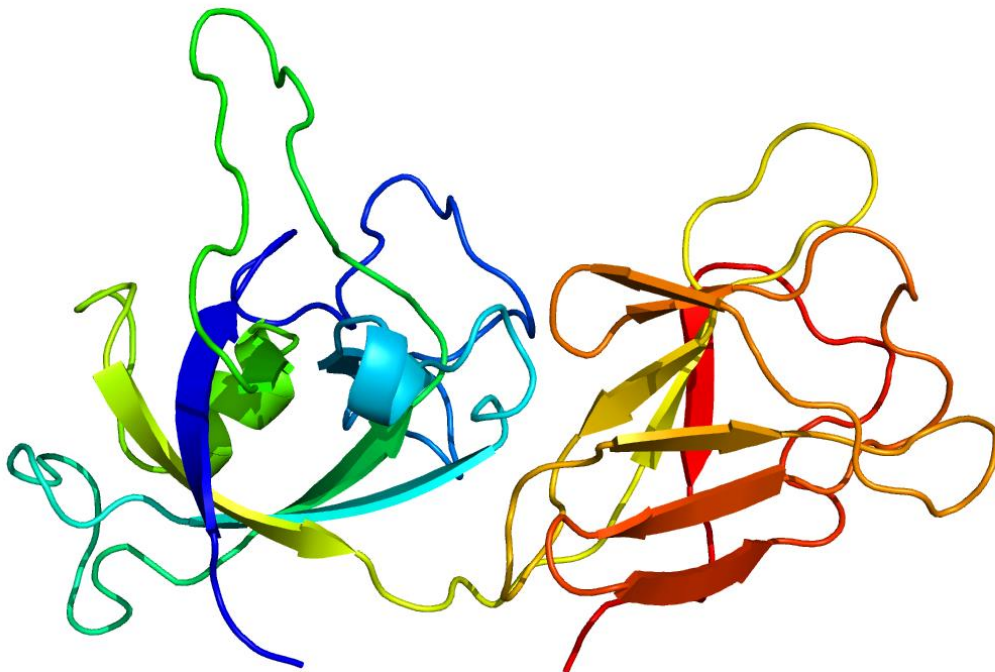
Locus: Seita.9G242100

Gene Model: Seita.9G242100.1.p

Description: SitEXPA-30

Family: Alpha Expansin

3D structure:



GENOME DATABASES

Phytozome: https://phytozome-next.jgi.doe.gov/info/Sitalica_v2_2

KEGG: <https://www.genome.jp/entry/gn:T02818>

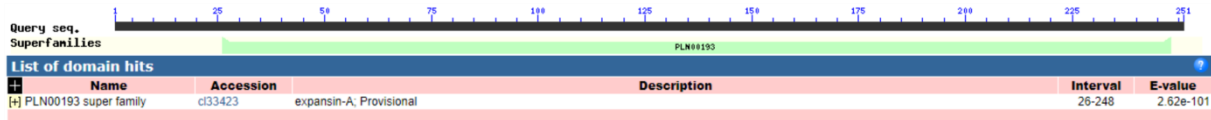
EXTERNAL RESOURCES

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GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>SitEXPA-30

MAKSLILCTVLLAACLALAAQGSPGTATFYGGADGWGTMGGACGYGNLYDAGY
GVLNAALSQTLFNDGASCGQCYTITCDGSRPGGQYCKPGNSITVTATNLCPANYALP
NGGWCGPGRPHFDMSQPAWENIGIYQAGVIPVLYQQVKCSRNGGVRFSIAGCNYFLL
VNIQNLGGSGSVGA AWIKGDNTGWIQMSRNWGANWQALAGLVGQGLSFAVTTTG
GQYIQFLNVAPAWWQFGQTYTTYQNFYY*

CDS (coding sequence)

>SitEXPA-30

ATGGCCAAGTCCCTGATCTTATGCACGGTCCTCCTTGCTGCGTGCCTCGCGCTCGC
CGCAGCCCAGGGCTCTCCGGGCACCGCCACGTTCTACGGTGGAGCCGACGGCTGG
GGCACCATGGGTGGCGCCTGCGGGTACGGCAACCTGTACGACGCCGGGTACGGC
GTGCTCAACGCGGCGCTGAGCCAGACGCTGTTCAACGACGGCGCGTCGTGCGGG
CAGTGCTACACCATCACGTGCGACGGATCACGCCCCGGCGGACAGTACTGCAAG
CCCGGCAACAGCATCACCGTCACGGCCACCAACCTGTGCCCGGCCAACTACGCC
TGCCCAACGGCGGCTGGTGC GGCCCGGGGCGCCCTCACTTCGACATGTCGCAGCC
GGCGTGGGAGAACATCGGAATCTACCAGGCCGGCGTCATCCAGTCCTGTACCAG
CAGGTCAAGTGCTCACGCAACGGCGGGCGTGCGCTTCAGCATCGCCGGATGCAACT
ACTTCTGCTCGTCAACATCCAGAACCTCGGCGGAAGCGGCTCCGTGGGCGCCGC
CTGGATCAAGGGAGACAACACCGGGTGGATCCAGATGTCCAGGAACTGGGGCGC
CAACTGGCAGGCGCTGGCCGGGCTCGTCGGCCAGGGGCTCAGCTTCGCCGTGACC
ACCACCGGCGGGCAGTACATCCAGTTTCTCAACGTGGCGCCGGCGTGGTGCCAGT
TCGGCCAGACCTACACCACCTACCAGAACTTCTACTACTAA

Nucleotide

>SitEXPA-30

GCCATACCTCGTCCTCACGAACGCACCTTCACTTCCATCTCGTTCTCTGCAGCTAC
CCTCTGCATTGGTGTCCGTGGATATGGCCAAGTCCCTGATCTTATGCACGGTCCTC
CTTGCTGCGTGCTCGCGCTCGCCGACGCCAGGGCTCTCCGGGCACCGCCACGT
TCTACGGTGGAGCCGACGGCTGGGGCACCATGGGTAAGCTTGCAAGCCTTGACA
GTTACACTTCGGTAGAAGAGCTACAATGCCTCACGAATTTTGCTAGCTGCGCGCG
TACTAATAGATTGGTATATACGCAGGTGGCGCCTGCGGGTACGGCAACCTGTACG

ACGCCGGGTACGGCGTGCTCAACGCGGCGCTGAGCCAGACGCTGTTCAACGACG
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GACAGTACTGCAAGCCCGGCAACAGCATCACCGTCACGGCCACCAACCTGTGCC
GGCCAACACTACGCCCTGCCAACGGCGGCTGGTGCGGCCCGGGGCGCCCTCACTT
GACATGTCGCAGCCGGCGTGGGAGAACATCGGAATCTACCAGGCCGGCGTCATC
CCAGTCCTGTACCAGCAGGTCAAGTGCTCACGCAACGGCGGGCGTGCGCTTCAGCA
TCGCCGGATGCAACTACTTCTGCTCGTCAACATCCAGAACCTCGGCGGAAGCGG
CTCCGTGGGCGCCGCCTGGATCAAGGGAGACAACACCGGGTGGATCCAGATGTC
CAGGAAGTGGGGCGCCAACCTGGCAGGCGCTGGCCGGGCTCGTCGGCCAGGGGCT
CAGCTTCGCCGTGACCACCACCGGCGGGCAGTACATCCAGTTTCTCAACGTGGCG
CCGGCGTGGTGGCAGTTCGGCCAGACCTACACCACCTACCAGAACTTCTACTACT
AAAAGTGGCGATTTCTTGCGGTTGGGTAAGATGGCAAGTGCGTCCTCGTAATTTG
GCCGGAGTGTGGGTGCACTTGGCGGCCGTCTGACCGTGGCATCTCTCCTATGTGA
TGCTCAGACAAAGCAAGAAGGGAGGCCCGAGGCCACATGTACCTATGGCCTGCA
TTTGTTTTCAACCTGTAGATACAAAAGCACATTATGTTTTCCCGATTACATGTACTG
CACATATTTTATTAAAGAGAAAACAGAGTTTT