

IDENTIFICATION

Species: *Setaria italica*

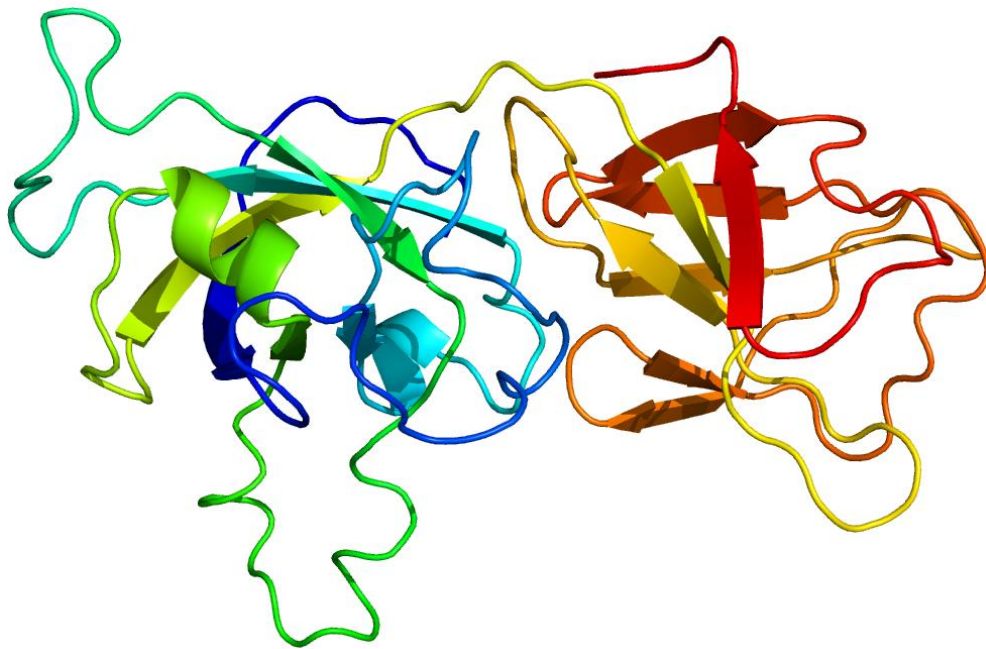
Locus: Seita.9G241800

Gene Model: Seita.9G241800.1.p

Description: SitEXPA-27

Family: Alpha Expansin

3D structure:



GENOME DATABASES

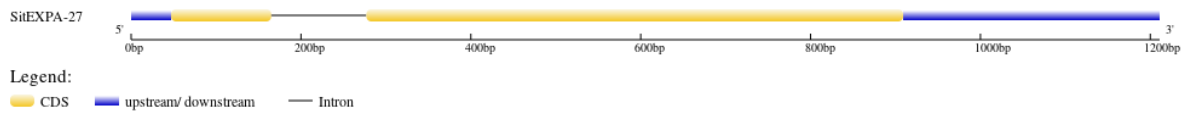
Phytozome: https://phytozome-next.jgi.doe.gov/info/Sitalica_v2_2

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

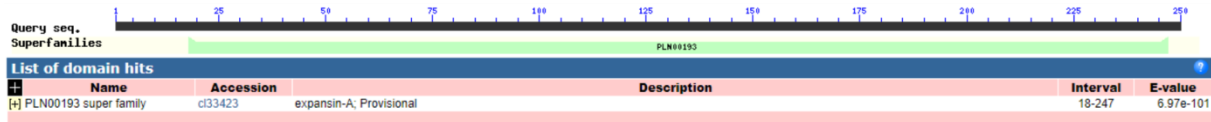
EXTERNAL RESOURCES

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GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>SitEXPA-27

MAKSLILCTALAACTIAAADWSQGTATFYGGPDGSDTMGGACGYENLYNAGYGIN
NAALSETLFDKDGASCGQCYLIICDGSRPGGQYCKHGTAITITATNLCPANYALPNGG
WCGPGRPHFDMSQPAWENIGVYQAGIPIVYQQVKCWRNGGVRFISIAGFNYFLLVNI
QNLAGSGSVGAAWIKGDNTGWIQMSRNWGTNWHALSGLVGQGLSFAVTSTGGQYI
QFLNVVPGWWQFGQTYNTYQNFYD*

CDS (coding sequence)

>SitEXPA-27

ATGGCCAAGTCCCTGATCTTGTGCACAGCGCTCGCGGCGTGCCTGACGATTGCCG
CCGCCGACTGGTCTCAAGGCACCGCCACGTTCTACGGCGGACCCGACGGTTCCGA
CACCATGGGCGGCGCTTGCGGTTACGAGAACCTGTACAACGCCGGGTACGGC
ACAACGCGGGCGCTGAGCGAGACGCTGTTCAAGGATGGCGCGTCTGCGGGCAG
TGCTACCTCATCATCTGCGACGGGTCACGCCCGGGCGGCCAGTACTGCAAGCACG
GCACGGCGATCACCATCACGGCCACCAACCTGTGCCCGGCAACTACGCGCTGCC
CAACGGCGGTTGGTGC GGCCCGGGGCGCCCCACTTCGACATGTCGCAGCCGGCG
TGGGAGAACATCGGCGTCTACCAGGCCGGC ATCATCCCCATCGTCTACCAGCAGG
TCAAGTGCTGGCGCAACGGTGGCGTGC GCTTACGATCGCCGGGTTCAACTACTT
CCTCCTCGTCAACATCCAGAACCTGGCCGGCAGCGGCTCCGTAGGCGCAGCCTGG
ATCAAGGGCGACAACACTGGGTGGATCCAGATGTCCAGGA ACTGGGGCACCAAC
TGGCATGCGCTCTCCG GACTAGTCGGCCAGGGGCTTAGCTTCGCCGTGACCAGCA
CCGGTGGG CAGTACATTCAGTTCCTTAACGTCGTGCCAGGATGGTGGCAGTTCGG
CCAGACCTACAACACATAACCAGAACTTCGACTACTGA

Nucleotide

>SitEXPA-27

AAAGTTAACCAAACAAAACCCTCACTGCCATCTCGTGCTCCACAGGAATGGCCAA
GTCCCTGATCTTGTGCACAGCGCTCGCGGCGTGCCTGACGATTGCCGCCCGCCGAC
TGGTCTCAAGGCACCGCCACGTTCTACGGCGGACCCGACGGTTCGGACACCATGG
GTAAGCTTACTGATGTGTTGCATTTTGGTGC AAGAGCATTCTTGCAA ACTGCACA
CTTACGTGCTGATGGCGTCCGGCCGTCGCTAATGCATGCGTATGTTTGATGTATA
GCGCGGCGCTTGC GGTACGAGAACCTGTACAACGCCGGGTACGGCATCAACAAC

GCGGCGCTGAGCGAGACGCTGTTCAAGGATGGCGCGTCGTGCGGGCAGTGCTAC
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GCGATCACCATCACGGCCACCAACCTGTGCCCGGCCAACTACGCGCTGCCAACG
GCGGTTGGTGCGGCCCGGGGCGCCCCACTTCGACATGTTCGCAGCCGGCGTGGGA
GAACATCGGCGTCTACCAGGCCGGCATCATCCCCATCGTCTACCAGCAGGTCAAG
TGCTGGCGCAACGGTGGCGTGCGCTTCAGCATCGCCGGGTTCAACTACTTCCTCC
TCGTCAACATCCAGAACCTGGCCGGCAGCGGCTCCGTAGGCGCAGCCTGGATCAA
GGGCGACAACACTGGGTGGATCCAGATGTCCAGGAACTGGGGCACCAACTGGCA
TGCGCTCTCCGGACTAGTCGGCCAGGGGCTTAGCTTCGCCGTGACCAGCACCGGT
GGGCAGTACATTCAGTTCCTTAACGTCGTGCCAGGATGGTGGCAGTTCGGCCAGA
CCTACAACACATAACCAGAACTTCGACTACTGAAACTTACAGGTAGCAGAGTGA
GATCGATCCTCGTTATATAGCCATCTATTGTGGTTCAAATTCGGTCGTATGTAGGG
TGTGTTGTATCTCTCCTACGTGGCCTCAGAACTGCATGTGTAAATGGCAGGGAGG
ATGAAGAAGGGATCCCACCCAGACCTTTAAGGCCCTCCTCAAAATTTTAATTCCT
CCTGTAGTTACAACACTTTTTTTTTGAGAATTATGCTTTTCAACACTGTACATCGA
ACTATAAGTTCTGTAGTGTGTTATGTGGCGACTTCCAAATTTTTGTGGTCAATACA
TA