

IDENTIFICATION

Species: *Setaria italica*

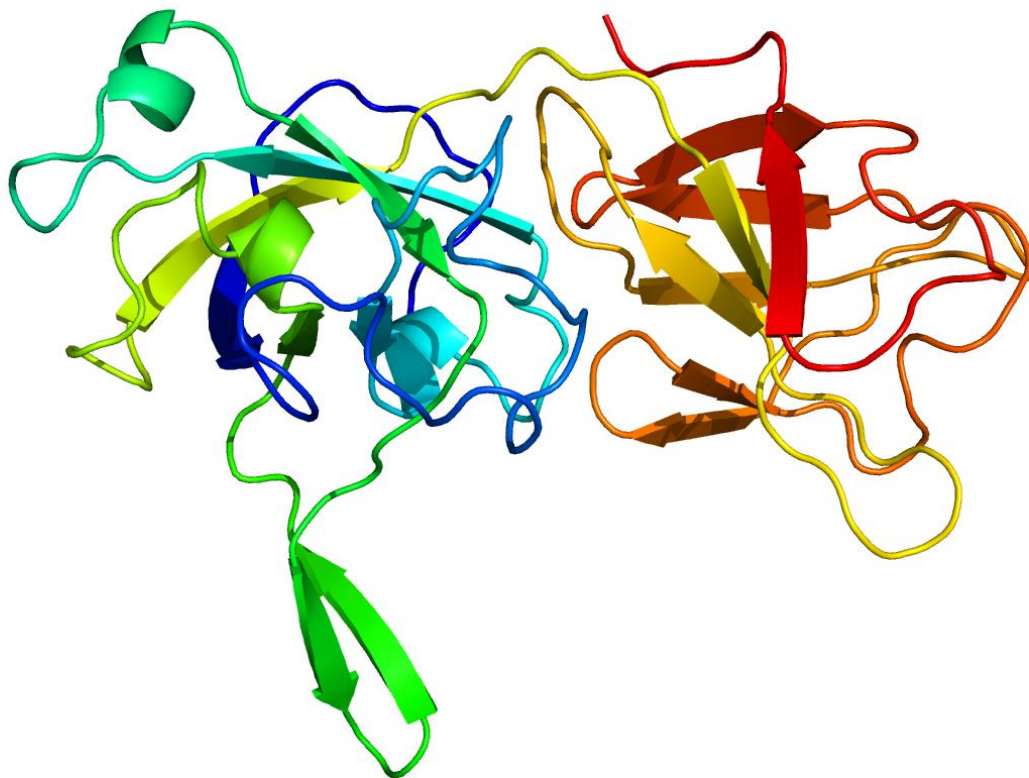
Locus: Seita.9G535900

Gene Model: Seita.9G535900.1.p

Description: SitEXPA-37

Family: Alpha Expansin

3D structure:



GENOME DATABASES

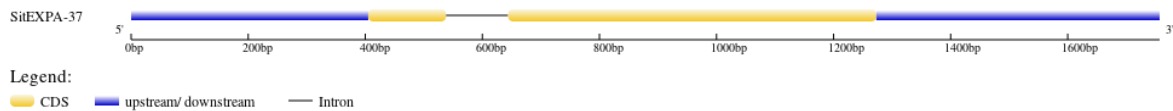
Phytozome: https://phytozome-next.jgi.doe.gov/info/Sitalica_v2_2

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

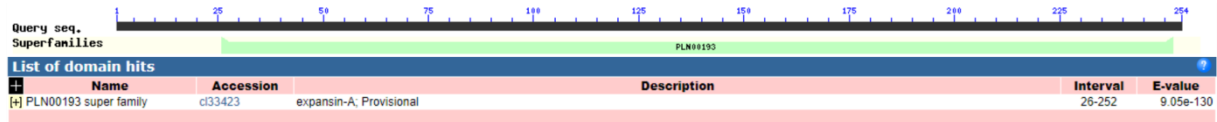
EXTERNAL RESOURCES

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GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>SitEXPA-37

MARKV SCHLLVIAVVAASLAATARAGWIRGSATFYGGADASGTMGGACGYGNLYS
TGYGTNTAALSSSLFNDGAACGECYQVMCDQNSQWCRPGVTVTVTATNLCPPDW
SKASNNGGWCNPPRQHFDMAQPAWEKIGVYRGGYVPVMYQRVSCSRNNGGVRFTIN
GNNYFELVLITNVAGPGLSVQIRGTRTGWITMSRNWGANWQANNYLNGQISIFR
VTATNGQTIEFWEVAGSGWRFGQFTNGQNFY*

CDS (coding sequence)

>SitEXPA-37

ATGGCGCGCAAGGTCTCGTGTCACTTGGTGGTGATCGCCGTCGTCGCCGCGAGCC
TCGCCGCGACGGCCCGGGCGGGATGGATCAGGGGCTCGGCGACGTTCTACGGCG
GCGCCGACGCCTCCGGCACAATGGGTGGCGCTTGGGGTACGGCAACCTTTACTC
GACGGGGTACGGGACGAACACGGCGGCGCTGAGCTCGTCGCTGTTCAACGACGG
GGCGGCGTGCGGGGAGTGCTACCAGGTGATGTGCGACCAGCAGAACAGCCAGTG
GTGCCCGCCGGGCGTGACGGTGACCGTGACGGCGACCAACCTGTGCCCGCCGGA
CTGGTCCAAGGCCAGCAACAACGGCGGCTGGTGCAACCCGCCGCGGCAGCACTT
CGACATGGCGCAGCCGGCCTGGGAGAAGATCGGGCTTACCGCGGGCGGGTACGT
CCCGGTCATGTACCAGAGGGTGTCTATGCTCCCGGAACGGCGGGGTGCGGTTACCC
ATCAACGGCAACAACACTTTCGAGCTGGTCTCATCACCAACGTCGCCGGCCCGG
GGTCGCTCAAGTCGGTGCAGATCAGGGGCACCCGGACCGGGTGGATCACCATGT
CCAGGAACTGGGGCGCCAACACTGGCAGGCCAACAACTACCTCAACGGCCAGAGCA
TCTCCTTCCGTGTCACCGCCACCAACGGCCAGACCATCGAGTTCTGGGAGGTTCG
GGGGTCCGGATGGCGGTTCCGGCCAGACCTTACCAACGGCCAGAATTTCTACTAG

Nucleotide

>SitEXPA-37

TGGCAGGGACGCCATGGCCGGCATAGAAAAATGGCGGAGTCGGCCGGCTGTGCA
GAGGCTGCAGAGAAGAAGAATCTTTCTTCGAATTGCCAATGGAACAGAGAGACT
TTTTGGACGGGAGGAGGAGGAGATGAGGAATCGTGGCATTAAAGGCGCACG
GCGCAGCGTCTGGGTGCGGCATGCATCGGCATGTGAGTCCGCGCCGGGGTCCGCG
CGCGTGAGCTCCGCTCCCCCGTCGCCGATTCTTAAAGCACCGCCGCGATC
ACCGCCATCTTCTCACTCATCCACCTCCCCGGCCGGTCTACTACTTCTCGGTTT

CTCCCACACATTGCCTCGAGCTTGCCACCTGTGAGTCTGTGACTGCCCAAGGG
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CTAAGCTGCCTCGTCTTGGTTGCAATGCAGTGCACCTTCCAGTGTCTGTCAATCGCT
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CCAGCAGAACAGCCAGTGGTGCCGGCCGGGCGTGACGGTGACCGTGACGGCGAC
CAACCTGTGCCCGCCGGACTGGTCCAAGGCCAGCAACAACGGCGGGCTGGTGCAA
CCCGCCGCGGCAGCACTTCGACATGGCGCAGCCGGCCTGGGAGAAGATCGGCGT
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CCAACGTCGCCGGCCCGGGTTCGCTCAAGTCGGTGCAGATCAGGGGCACCCGGA
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ACCTCAACGGCCAGAGCATCTCCTTCCGTGTCACCGCCACCAACGGCCAGACCAT
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GCGTACTGTTGCAGATTATATTGGTGCATTTTTCTAATGATGAAACGGCCATGCAT
GCTTGG