

IDENTIFICATION

Species: *Setaria italica*

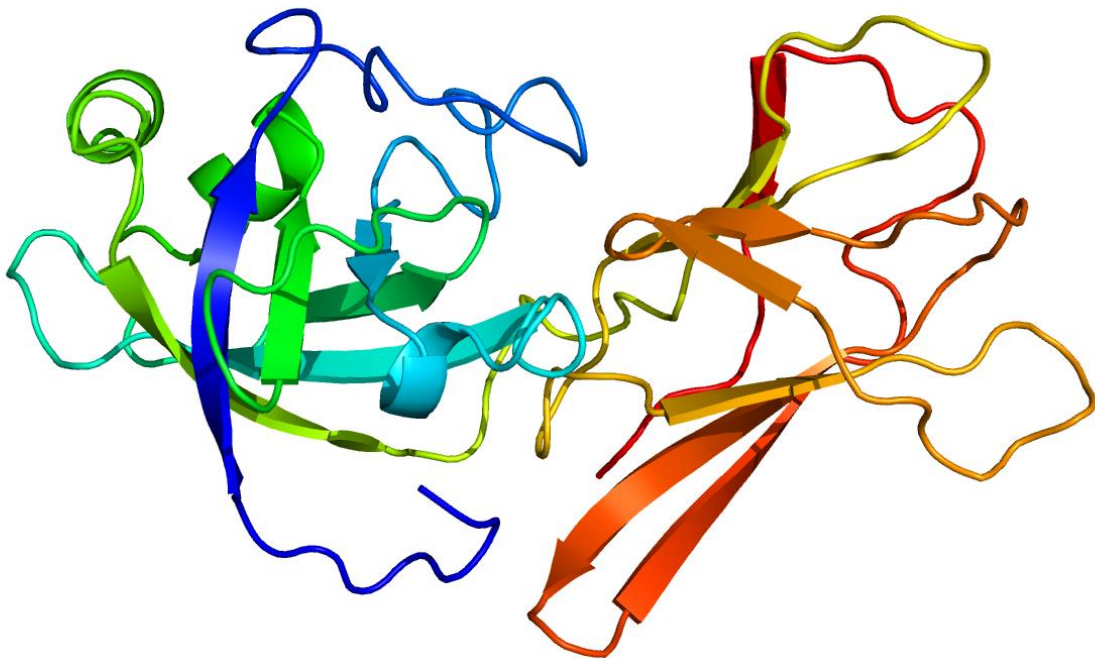
Locus: Seita.9G339600

Gene Model: Seita.9G339600.1.p

Description: SitEXLA-04

Family: Expansin Like Alpha

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

Query seq. Superfamilies

List of domain hits

Name	Accession	Description	Interval	E-value
PLN03023 super family	cl33621	Expansin-like B1; Provisional	32-252	8.51e-57

SEQUENCES

Peptide

>SitEXLA-04

MRSAASLSLVLLLVFVAVPSPARGCDRCVRRSKATYQASSLALNAGSCGYGSLAASL
NGGFLAAASPELYRGGVGGCAGCFQVRCRDELCSAAGTKVVVTDQARTSSNRTGLV
LSAAAYAAMARAGEAARLRAHRVVDVEYKRIPCEYANRNLSIRVEEKSRPPSQLSIR
FLYQGGQTDIVAVDVATVGSNNWRFMTREHGPAWSTAQAPAGPLQFRLVVTGGYD
GKWVWAESEVLPRRWEAGRVDYDGTGVQVADVAQEGCYPCDTHEWQ*

CDS (coding sequence)

>SitEXLA-04

ATGAGGAGCGCCGCGTCCCTGTCCCTCGTCTTGCTCCTCGTCTTCGTCGCGGTCCC
GTCTCCGGCTCGCGGCTGCGACCGCTGCGTGCGCCGGTCCAAGGCCACCTACCAA
GCCTCCTCGCTCGCCCTCAACGCCGTTCTTGCGGGTACGGCTCCCTGGCCGCGTC
CTTAAACGGCGGCTTCCTCGCCGCGGCCAGCCCCGAGCTCTACAGGGGCGGGCGTC
GGCTGCGGCGCCTGCTTCCAGGTGCGGTGCAGGGACAGCGAGCTGTGCAGCGCC
GCCGGCACCAAGGTGGTGGTGACGGACCAGGCGCGGACCTCCTCGAACCGCACG
GGCCTGGTGCTGAGCGCCGCGGCGTACGCGGCCATGGCCCGCGCCGGCGAGGCC
GCGCGGCTCCGGGCGCATCGCGTCGTGGACGTCGAGTACAAGAGGATCCCATGC
GAGTACGGAACCGCAACCTGTCCATCCGCGTGGAGGAGAAGAGCCGCGCCGCCG
AGCCAACCTGTCCATCAGGTTCTGTACCAGGGCGGCCAGACCGACATCGTCGCCG
TCGACGTCGCCACGGTCGGGTCTGTCGAACTGGCGGTTTCATGACGCGGGAGCACG
GGCCGGCGTGGAGCACGGCGCAGGCGCCGGCGGGGCCCTGCAGTTCGCGCTGG
TGGTGACCGGCGGGTACGACGGCAAGTGGGTGTGGGCGGAGTCCGAGGTGCTGC
CGCGGCGGTGGGAGGCCGGCCGCGTCTACGACACCGGGGTGCAGGTCCGCCGACG
TCGCGCAGGAAGGGTGCTACCCCTGCGACACGCACGAGTGGCAGTGA

Nucleotide

>SitEXLA-04

GTGGCCGCCCCCGGGCCTCAGCCTCACCGTCCTCTCTTCTTCTGTCCCCACC
ACTATATCCGTCCCACGGCGCCGCGCTCCGCTCCAACCGCGTCGCGTGTCCAAA
ACATTCTGCGGCCTGTTGGAGGGCAGCACCAAGTATCACAGTCTAGGGCCTACT
CTGGTTACTAGAAGGAGTACTCGCAGGCACCAGCTAGCTTCCGCACTGCGGCCAG
AACCAGAAACCAGAGCGGCAGCCTTGCGGCGCCCGCGTGGAGGCGTGGAGCATA

AAGCCGGCGCTCGCGCTGCTGGCAGCAATCCAATCCCCTGTTCTGCTCTGTTCTCC
CGAGTAATCACAATTCAAGCCTTCTTCGACCTCGAGCTCGTCGTCATGAGGAGCG
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GCGGCTGCGACCGCTGCGTGCGCCGGTCCAAGGCCACCTACCAAGCCTCCTCGCT
CGCCCTCAACGGTAATCAGGCATCCACAGGCTTCTGCGTTTCGGTTCATTTAATTT
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ATTCTCCGCGTGTGCGGTGGGCGAAACGGATTAATAAGCGGGGATCGCCATT
GCAGGTGCGGTGCAGGGACAGCGAGCTGTGCAGCGCCGCCGGCACCAAGGTGGT
GGTGACGGACCAGGCGCGGACCTCCTCGAACCGCACGGGCCTGGTGCTGAGCGC
CGCGGCGTACGCGGCCATGGCCC GCGCCGGCGAGGCCGCGCGGCTCCGGGCGCA
TCGCGTGTGGACGTCGAGTACAAGAGGTTGGTGGTTGCCCTGTTGCTCCTCCTTT
GTCGCCGCCCGCGGTGCCGTGCGCGAGTACGGCGTCGGTAGTGTGCGTCATTTTCG
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CGAGTACGCGAACCGCAACCTGTCCATCCGCGTGGAGGAGAAGAGCCGGCCGCC
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GGAACGTTTCGTCAGATTCAATGAGAGCGCTTCGAC