

IDENTIFICATION

Species: *Spirodela polyrhiza*

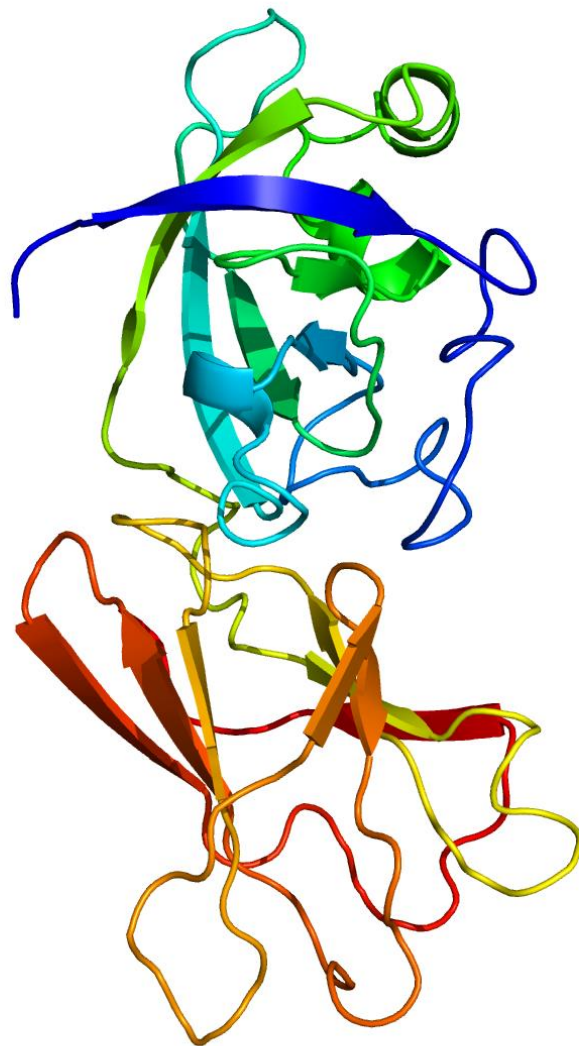
Locus: Spipo1G0075200

Gene Model: Spipo1G0075200

Description: SpEXLA-01

Family: Expansin Like Alpha

3D structure:



GENOME DATABASES

Phytozome: https://phytozome-next.jgi.doe.gov/info/Spolyrhiza_v2

KEGG:-

EXTERNAL RESOURCES

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GENE STRUCTURE



DOMAIN ARCHITECTURE

Query seq. Superfamilies

PLN03023

Name	Accession	Description	Interval	E-value
[H] PLN03023 super family	cl33621	Expansin-like B1; Provisional	28-249	4.27e-68

SEQUENCES

Peptide

>SpEXLA-01

MASYVFLLLLSYLLVSSASACDRCVHKSASYFSSPSLAGGACGYGAMATELYGGR
YPVAAAGSSLYREGVGC GGCFQIRCKNGKFCTGAGVKVVVTDLNKSNQTFVLSQP
AFLAMAKDGMGRTLKRLGNVDVEYKRVPC EYPTRHNL SFRVEESSRRPAHLVVKLL
YQGGQTDIVAVDVAQVGS SDWRYMTRDFGAVWSTGRAPAGALQFRLVVTGGYDG
KWWWA EKVLPLDWRTGAVYDAGVQISDIAQEGCSPCDSEVWK*

CDS (coding sequence)

>SpEXLA-01

ATGGCCAGCTATGTCTTCCTTCTCCTGTTGTCCTACCTTCTCGTCTCCTCTGCGTCT
GCATGTGACCGGTGCGTGCACAAGTCCAAGGCATCCTACTTCTCGTCACCGTCTT
CCCTCGCAGGCGGGGCCTGTGGGTATGGCGCTATGGCCACAGAGCTCTACGGAG
GAAGGTACCCTGTGGCGGCGGGCTCTTCCTTATACAGAGAAGGGGTGGGCT
GTGGAGGCTGTTTTTCAGATTCGGTGCAAGAACGGGAAGTTCTGCACCGGCGCGGG
GGTGAAGGTTGTCGTGACGGACCTGAACAAGAGCAACCAGACAGACTTCGTGCT
CTCCCAGCCGCGTTCCTGGCCATGGCCAAGGATGGAATGGGGAGGACCCTCAA
GAGACTCGGAAACGTCGACGTCGAGTACAAAAGGGTTCCTGCGAATACCCGAC
CCGCCACAACCTGTCATTCAGGGTGGAGGAGAGCAGCCGAAGGCCCGCTCACCT
GGTCGTCAAATTATTGTACCAGGGAGGCCAGACGGACATCGTCGCCGTCGACGTC
GCTCAGGTGGGCTCGTCGGATTGGCGGTACATGACCCGCGACTTCGGCGCCGTTT
GGAGCACCGGCCGCGCCCCCGCGGCCCTCCAGTTCCGGCTGGTGGTGACGGG
CGGCTACGACGGGAAGTGGGTCTGGGCGGAGAAGGTCCTGCCGCTGGACTGGAG
GACTGGGGCCGTCTACGACGCCGCGTCCAGATCAGCGACATCGCGCAGGAGGG
TTGCTCCCCCTGCGACTCCGAAGTCTGGAAGTGA

Nucleotide

>SpEXLA-01

ATGGCCAGCTATGTCTTCCTTCTCCTGTTGTCCTACCTTCTCGTCTCCTCTGCGTCT
GCATGTGACCGGTGCGTGCACAAGTCCAAGGCATCCTACTTCTCGTCACCGTCTT
CCCTCGCAGGTGCGCGCCG CAGTCGAATGACCCTTCCCCCTGCTGTTTCCGATA
GCTCCGGCGATCCTTATTTCTCTTTCTGCATACAGGCCGGGGCCTGTGGGTATGGC
GCTATGGCCACAGAGCTCTACGGAGGAAGGTACCCTGTGGCGGCGGGGCTCTT

CCTTATACAGAGAAGGGGTGGGCTGTGGAGGCTGTTTTTCAGGTAGGTAGAAGAC
AGACGAACCTAAATGCCCTTCTGGGGAGGCTGTTTTCAAGTGCTTCTGTTCCCTTG
GTCAGATTCGGTGCAAGAACGGGAAGTTCTGCACCGGC GCGGGGGTGAAGGTTG
TCGTGACGGACCTGAACAAGAGCAACCAGACAGACTTCGTGCTCTCCCAGCCGGC
GTTCCCTGGCCATGGCCAAGGATGGAATGGGGAGGACCCTCAAGAGACTCGGAAA
CGTCGACGTCGAGTACAAAAGGTGGGAGATGATCCGCCCAATCCTCTGCTGAGCT
CATCGATATCGTTTGCTAACTCGAGGCCCTCCGATCATGGGGGACTATCGATCA
GGGTTCCCTGCGAATACCCGACCCGCCACAACCTGTCATTCAGGGTGGAGGAGAG
CAGCCGAAGGCCCGCTCACCTGGTTCGTCAAATTATTGTACCAGGGAGGCCAGACG
GACATCGTCGCCGTCGACGTCGCTCAGGTGAGTAAGAATGCAGAAAGCTCTCTCT
GGGAACCTTACCTTCATCTCGCTCGCCGCCGGGGTTCCGGAATCTCCGCTGACGG
CGCCAGCGCTCGACGCAGGTGGGCTCGTCGGATTGGCGGTACATGACCCGCGACT
TCGGCGCCGTTTGGAGCACCGGCCGCGCCCCCGCCGGCGCCCTCCAGTTCCGGCT
GGTGGTGACGGGCGGCTACGACGGGAAGTGGGTCTGGGCGGAGAAGGTCCTGCC
GCTGGACTGGAGGACTGGGGCCGTCTACGACGCCGGCGTCCAGATCAGCGACAT
CGCGCAGGAGGGTTGCTCCCCCTGCGACTCCGAAGTCTGGAAGTGA