

## IDENTIFICATION

**Species:** *Selaginella moellendorffii*

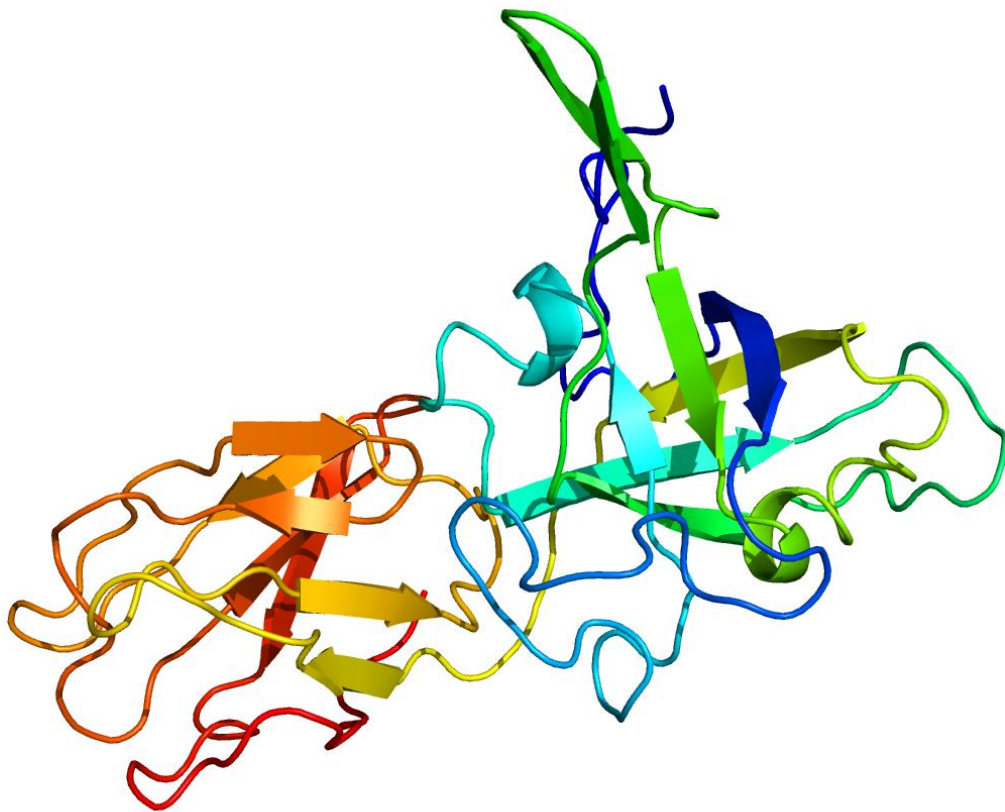
**Locus:** 75237

**Gene Model:** 75237

**Description:** SmEXPA-01

**Family:** Alpha Expansin

**3D structure:**



## GENOME DATABASES

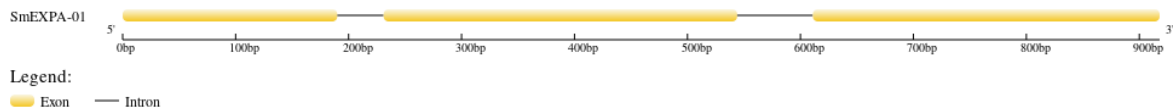
Phytozome: [https://phytozome-next.jgi.doe.gov/info/Smoellendorffii\\_v1\\_0](https://phytozome-next.jgi.doe.gov/info/Smoellendorffii_v1_0)

KEGG: <https://www.genome.jp/entry/T01496>

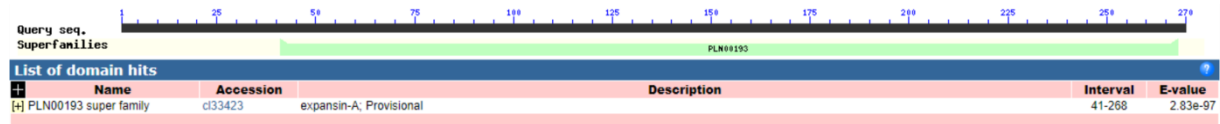
## EXTERNAL RESOURCES

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## GENE STRUCTURE



## DOMAIN ARCHITECTURE



## SEQUENCES

### Peptide

>SmEXPA-01

MRSVIACLLLCATLLVSVDHGRAASPKSLKKRATNAAKEIYNAGGWKQAFATFYGD  
ETARETMGGACGYGNLYQSGYGLMTAALSSTLFNSGYGCGQCYEITCTLSKHCYFG  
KSVVVTATNLCPPNWSKPSNNGGWCNPPRVHFDMSKPAFMKIAFWRAGIIPVSYRR  
VPCVRSGGMNFKLGGNRWWLMVFITNVGGSGDIKAVSVKGSRTGWIAMTRNWGV  
GFQVFKQLQGQSLFSMVTCTYSTGKTTVHNNVAPANWQLGSTYSKQL\*

### CDS (coding sequence)

>SmEXPA-01

ATGAGGAGTGTGATCGCGTGTCTTCTTCTCTGCGCCACTCTTCTCGTGTCTGTGGA  
TCATGGGAGAGCGGCATCGCCCAAAGCTTGAAGAAGCGGGCCACGAACGCCCGC  
GAAGGAGATCTACAACGCCGGCGGGTGAAGCAGGCATTCGCGACGTTCTATGG  
CGATGAAACAGCGAGGGAGACAATGGGTGGAGCTTGC GGCTATGGCAATTTGTA  
CCAATCCGGCTATGGATTGATGACGGCGGGCGCTGAGCAGTACGCTCTTCAACAGC  
GGCTATGGCTGCGGGCAGTGCTACGAGATCACTTGCACGCTATCGAAGCACTGCT  
ACTTCGAAAATCCGTGGTGGTGACCGCCACAAATCTTTGCCCGCCCAATTGGAG  
CAAGCCCTCGAACAATGGCGGCTGGTGAATCCGCCGCGCGTCCATTTGACATG  
TCCAAGCCGGCATTTCATGAAAATCGCGTTTTGGCGGGCGGGAATCATCCCAGTCT  
CCTATCGAAGGGTGCCATGCGTGCGATCCGGCGGCATGAATTTCAAGCTGGGCGG  
CAATCGCTGGTGGCTCATGGTGTTCATCACAAATGTGGGCGGCTCCGGTGATATC  
AAGGCGGTGTCGGTGAAGGGATCGAGGACGGGATGGATCGCCATGACGCGGAAT  
TGGGGCGTAGGGTTCCAAGTTTTCAAGCAGCTCCAGGGCCAAAGTCTCTCGTTCA  
TGGTCACTTGCTACAGTACCGGAAAGACTACTGTGCACAACAATGTGGCGCCCGC  
GAATTGGCAGCTCGGCAGCACCTATTCGCCAAGCAATTGTGA

### Nucleotide

>SmEXPA-01

ATGAGGAGTGTGATCGCGTGTCTTCTTCTCTGCGCCACTCTTCTCGTGTCTGTGGA  
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GAAGGAGATCTACAACGCCGGCGGGTGAAGCAGGCATTCGCGACGTTCTATGG  
CGATGAAACAGCGAGGGAGACAATGGGTAAAGAAGAACTTTGAGATCATATT  
TAAATTTGCGCAGGTGGAGCTTGC GGCTATGGCAATTTGTACCAATCCGGCTATG  
GATTGATGACGGCGGGCGCTGAGCAGTACGCTCTTCAACAGCGGCTATGGCTGCGG

GCAGTGCTACGAGATCACTTGCACGCTATCGAAGCACTGCTACTTCGGAAAATCC  
GTGGTGGTGACCGCCACAAATCTTTGCCCGCCCAATTGGAGCAAGCCCTCGAACA  
ATGGCGGCTGGTGCAATCCGCCGCGCGTCCATTTTCGACATGTCCAAGCCGGCATT  
CATGAAAATCGCGTTTTGGCGGGCGGGAATCATCCAGTCTCCTATCGAAGGTGA  
GAGAAGAAAAACGCGCGAGATTTTAGGGTTCTTCAGCTAAAAGTTTGAAAATTT  
CCTGTCAGGGTGCCATGCGTGCGATCCGGCGGCATGAATTTCAAGCTGGGCGGCA  
ATCGCTGGTGGCTCATGGTGTTTCATCACAAATGTGGGCGGCTCCGGTGATATCAA  
GGCGGTGTCGGTGAAGGGATCGAGGACGGGATGGATCGCCATGACGCGGAATTG  
GGGCGTAGGGTTCCAAGTTTTCAAGCAGCTCCAGGGCCAAAGTCTCTCGTTCATG  
GTCACTTGCTACAGTACCGGAAAGACTACTGTGCACAACAATGTGGCGCCCGCGA  
ATTGGCAGCTCGGCAGCACCTATTCCGCCAAGCAATTGTGA