

## IDENTIFICATION

**Species:** *Sphagnum fallax*

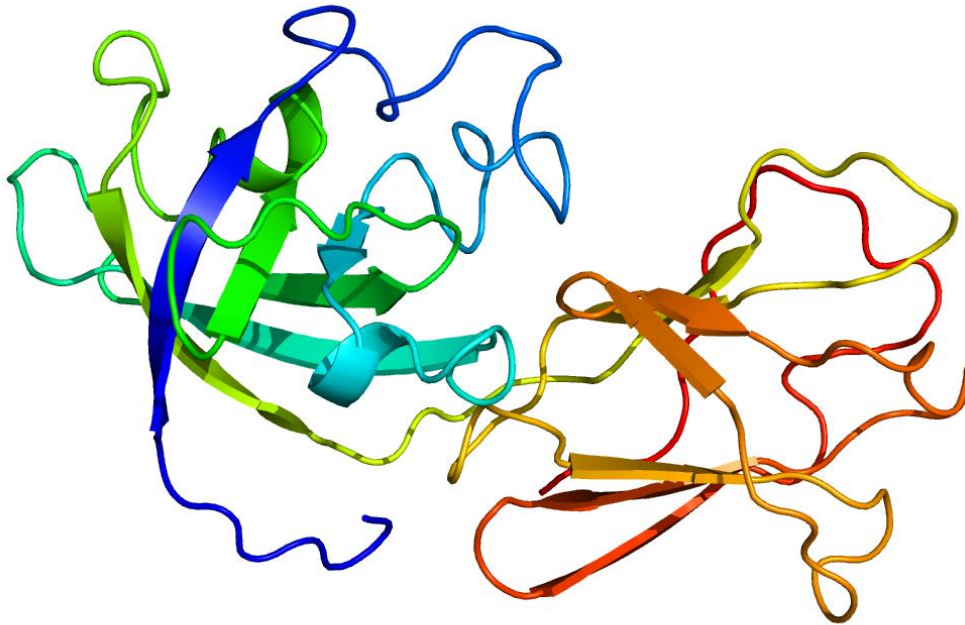
**Locus:** Sphfalx0005s0194

**Gene Model:** Sphfalx0005s0194.1.p

**Description:** SfEXPA-05

**Family:** Alpha Expansin

**3D structure:**



## GENOME DATABASES

Phytozome: [https://phytozome-next.jgi.doe.gov/info/Sfallax\\_v0\\_5](https://phytozome-next.jgi.doe.gov/info/Sfallax_v0_5)

KEGG:-

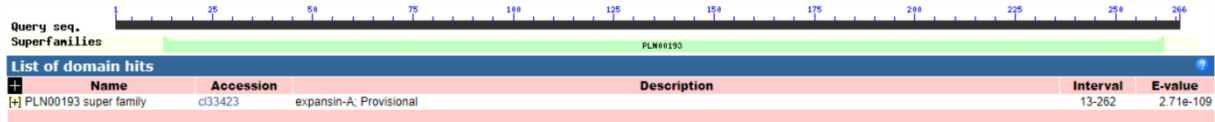
## EXTERNAL RESOURCES

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## GENE STRUCTURE



## DOMAIN ARCHITECTURE



## SEQUENCES

### Peptide

>SfEXPA-05

MARTFIAFLRTLCSAYSMIILVVFVFLPAVASGAVLDTGPWEQAHATFYGGSDASGTM  
GGACGYGNLYTEGYGTNTAALSTVLFNNGVSCGACFELQCYGSKWCLSSYKTVTIT  
ATNFCPPNLAEPDNGGWCNVPRPHFDMAMPAFLQMGQYVGGIIPVNYRRVPCIKSG  
GIRFTINGNPWFDLVLVTNVAGAGDVTAVSIRGGTGAWIQMTRNWGQNWQSGANL  
VGKTLSEFIVTTS DGRHVVSTNAAPSNWKFGQTFEGSQFSV\*

### CDS (coding sequence)

>SfEXPA-05

ATGGCGCGGACGTTTCATCGCATTCTAAGAACAACACTTTGCAGTGCGTACTCGATGA  
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GGGGCCCTGGGAGCAAGCGCATGCTACATTCTATGGCGGTAGCGACGCCTCTGGA  
ACAATGGGTGGTGC GTGGATATGGCAATCTGTACACTGAAGGATACGGCACC  
AACACAGCAGCCTTGAGCACCGTCTGTCAACAACGGAGTCAGTTGTGGAGCTT  
GCTTCGAGCTCCAATGCTACGGGAGCAAGTGGTGCTTGTCTTCTATAAAACCGT  
CACCATCACTGCCACCAACTTCTGTCCACCCAACCTCGCGGAACCCAGCGATAAC  
GGAGGATGGTGAATGTCCCTAGACCTCACTTCGACATGGCCATGCCTGCTTTCC  
TGCAGATGGGCCAGTATGTCGGCGGCATTATCCCTGTCAACTACAGAAGGGTTC  
ATGCATCAAGAGTGGAGGGATCCGGTTCACCATCAATGGGAATCCCTGGTTCGAC  
TTGGTACTGGTGACCAACGTGGCCGGCGCCGGAGACGTGACGGCAGTTTCCATCC  
GGGGGGGAACAGGGGCGTGGATTCAGATGACACGCAATTGGGGTCAGAACTGGC  
AATCCGGCGCTAACTTGGTGGGCAAGACCTTGTCGTTTCATCGTCACCACCAGCGA  
CGGCCGACATGTGGTCTCCACAAATGCCGCTCCATCCA ACTGGAAATTTGGACAA  
ACGTTCGAAGGCTCTCAATTCTCCGTCTAA

### Nucleotide

>SfEXPA-05

ATGGCGCGGACGTTTCATCGCATTCTAAGAACAACACTTTGCAGTGCGTACTCGATGA  
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GGGGCCCTGGGAGCAAGCGCATGCTACATTCTATGGCGGTAGCGACGCCTCTGGA  
ACAATGGGTATGTAGCTGATCTTGTACTAGTATCTGACGTGATCTGCAGCTCTCG  
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GTACATCTGGGTTTCTGGAATCCTGCAGGTGGTGCCTGTGGATATGGCAATCTGT  
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ACGGAGTCAGTTGTGGAGCTTGCTTCGAGCTCCAATGCTACGGGAGCAAGTGGTG  
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GGCTGCTGTGATCACAACAAATCTCTCCATTATTCAATTTGTTCCACTTACCTGTG  
CTCAGAGTCATCAGCTCTAAAGGTCAAATATGGACCAGATTATGCCTGAGAGCTA  
TCAAATGATTTCATCACAAGTGATATCTTTCTTTTAAACTTTTATCTATTTTAA  
TGAGAGTGTGTTCTCAGAGTTCCTAACATTGATTAATTGCATATTTGTAACACATG  
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GTCAATGACTTTCCATTAGACTGCTAGCTGTGATCAGAGCACACTGTGTGTAAC  
AAACCCCTATGTCAGTGGCTTTTCATTGGGTTGCTTGCTGTGATAGGAGCACATG  
GTTTCGTGTGTACGTGTGATCACAGCAGCCTAATGAAAAGAGACCCTTTTAGTCTG  
ACGAACATTCACGAATTCTGTGGCAGCTGATAGACGATTGTAGTACATAAATTTG  
ACGATCGTTGTACATGTATGCTTCTTTGCAGGGTTCCATGCATCAAGAGTGGAGG  
GATCCGGTTCACCATCAATGGGAATCCCTGGTTCGACTTGGTACTGGTGACCAAC  
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TTCTCCGTCTAA