

## IDENTIFICATION

**Species:** *Sphagnum fallax*

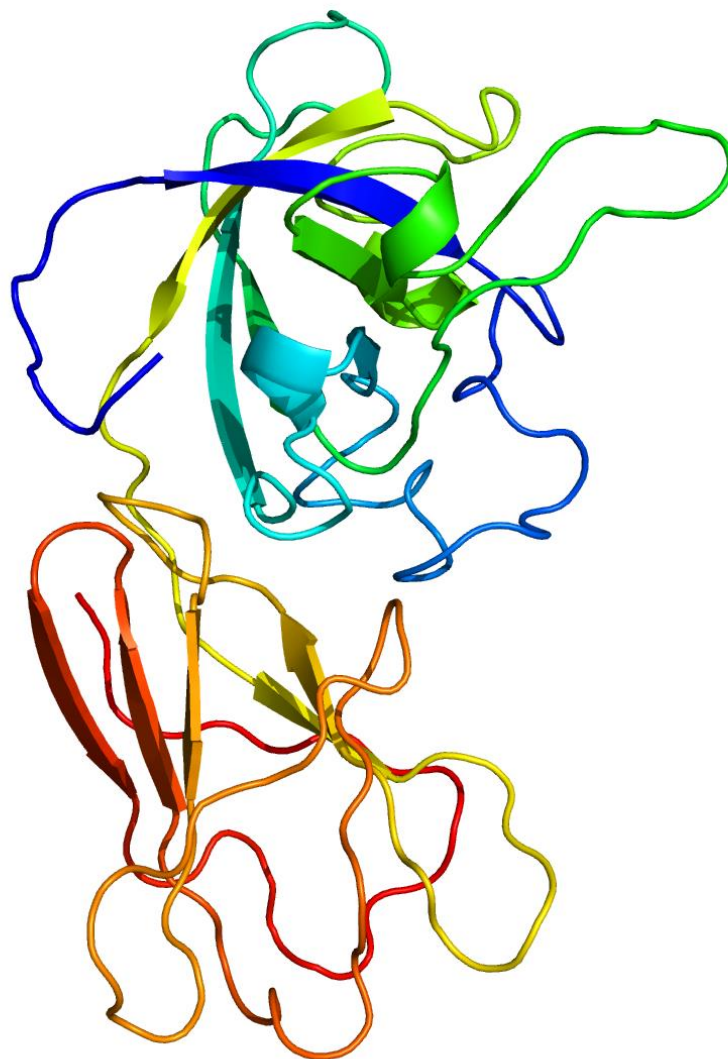
**Locus:** Sphfalx0288s0007

**Gene Model:** Sphfalx0288s0007.1.p

**Description:** SfEXPA-27

**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:-

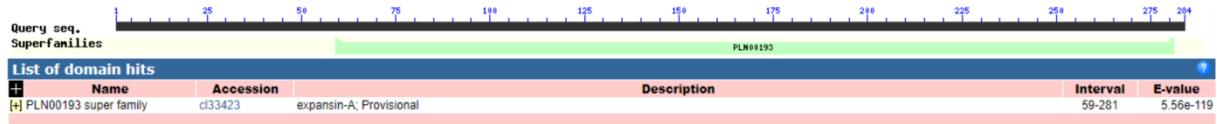
## EXTERNAL RESOURCES

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## GENE STRUCTURE



## DOMAIN ARCHITECTURE



## SEQUENCES

### Peptide

>SfEXPA-27

MLTPALFQHFQNAFDLVA VARTKSFHQLYFIMSQTMVGYAMGTLVMQVAMLLTVQ  
QVHGWDTAHATFYGGGDASGTQGGACGYGNLYTSGYGTNTVALSSALFNQGLSCG  
ACYEVACAGSEWCLPGKSITVTATNFCPPNPSPNDNGGWCNLPLQHFDMMAMPAYQ  
QIAAFQAGIVPVTYQRVSCIKSGGIHFTINGHSYFNLVLITNVGGAGDVQAVSIKGSNT  
GWQAMTRNWGQNWQNNANLDAQSLFSMVTTGDGQTLTSMNVAPAYWSFGQTYE  
GSQFS\*

### CDS (coding sequence)

>SfEXPA-27

ATGTTAACACCAGCTCTGTTTCAACATTTTGGCAATGCTTTCGACTTGGTAGCTGT  
AGCTCGGACAAAGTCGTTTCATCAACTTTATTTTATCATGTTCGCAGACAATGGTCG  
GATACGCGATGGGCACTCTGGTCATGCAGGTGGCTATGCTACTGACAGTGCAGCA  
GGTGCATGGATGGGACACCGCACATGCAACTTTCTACGGAGGCGGCGACGCCTC  
AGGCACGCAGGGAGGTGCTTGTGGGTACGGGAACCTGTACACTTCTGGGTACGG  
GACCAACACGGTGGCCCTGAGCTCGGCCCTTCAATCAAGGGCTGTCGTGCGGC  
GCCTGCTACGAGGTAGCGTGTGCGGGTAGTGAGTGGTGCTTGCCGGGCAAGTCCA  
TTACGGTGACAGCAACCAATTTCTGTCCCCGAATCCCAGTCTCCCAAACGACAA  
TGGCGGGTGGTGCAACTTGCCGCTCCAGCACTTCGACATGGCCATGCCCGCATA  
CAACAAATTGCGGCGTTCCAGGCTGGGATCGTGCCTGTGACTTACCAAAGGGTTT  
CATGCATCAAGTCTGGGGGCATTCACCTTACCATCAATGGACATTCCTACTTCAA  
CTTAGTGCTCATCACAATGTAGGAGGAGCTGGAGATGTGCAAGCTGTGTCCATC  
AAGGGCTCCAACACAGGATGGCAAGCCATGACAAGGAACTGGGGTCCAGAAGTGG  
CAGAACAAATGCCAACTTGGATGCTCAGAGCTTGTCTTCATGGTCACTACTGGTG  
ATGGCCAACTCTCACATCCATGAATGTGGCACCTGCCTACTGGTCCTTTGGACA  
AACATATGAGGGCTCTCAGTTTTTCATGA

### Nucleotide

>SfEXPA-27

TTGGTCTTGATCTTCTCAGGCTCTTGGGATCGAGCCGTAGCTGATCAGCATTGTTG  
CAGCTTATCGTCGATGTTAACACCAGCTCTGTTTCAACATTTTGGCAATGCTTTCG  
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CGTCGAGTTTTCCACTTCTTTTTGTCAGTCCCTTGTCCCTTCCGATAAGCTGAGAAT  
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GAATGATCACCTGGGTTTGCAACAGGAGGTGCTTGTGGGTACGGGAACCTGTACA  
CTTCTGGGTACGGGACCAACACGGTGGCCCTGAGCTCGGCCCTCTCAATCAAGG  
GCTGTCGTGCGGGCCTGCTACGAGGTAGCGTGTGCGGGTAGTGAGTGGTGCTTG  
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TCCCAAACGACAATGGCGGGTGGTGCAACTTGCCGCTCCAGCACTTCGACATGGC  
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TACCAAAGGCATTGATCTCTCTCCCTTCATCTTCATATTCTTTTGTGTATAAGCTG  
GATGCAAGGATGCCACCCTATTAGGGTCTCTTCCATTAGGATGCTGTGATCATA  
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GGTAAGAGATTTACCTGCTGATTTGAACAATTTATCATAACAGATTTGGACAGC  
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