

IDENTIFICATION

Species: *Sphagnum fallax*

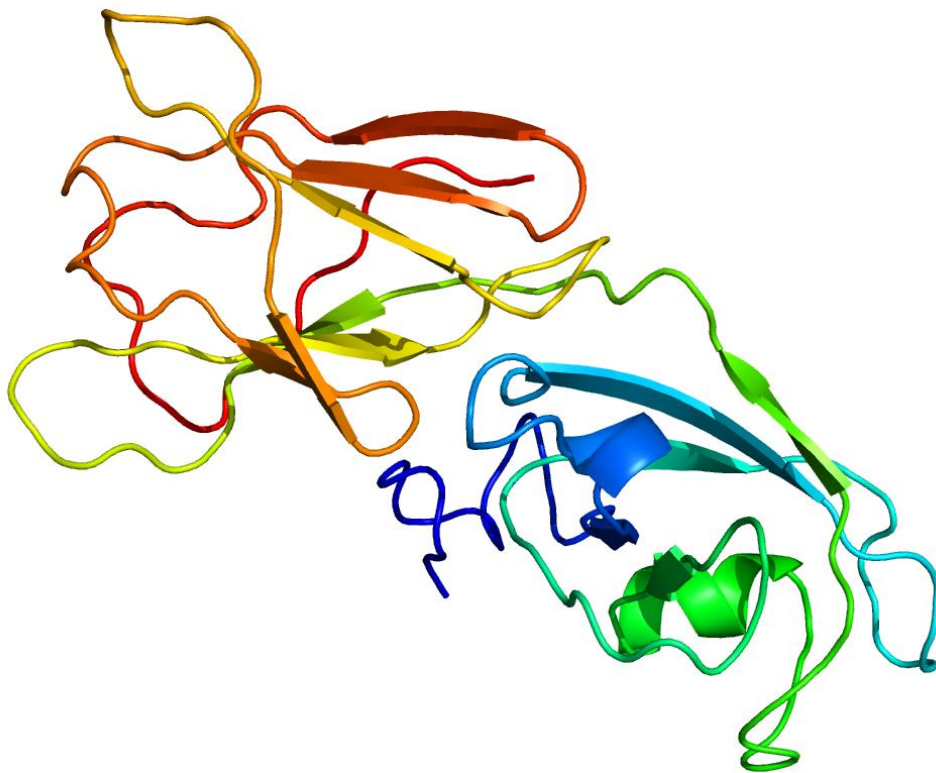
Locus: Sphfalx0028s0010

Gene Model: Sphfalx0028s0010.1.p

Description: SfEXPA-16

Family: Alpha Expansin

3D structure:



GENOME DATABASES

Phytozome: https://phytozome-next.jgi.doe.gov/info/Sfallax_v0_5

KEGG:-

EXTERNAL RESOURCES

-

GENE STRUCTURE



DOMAIN ARCHITECTURE

Query seq. `MHGRCDYIMYSEDGKIVLSTVIFPDLSDGKCYEDMKNVQMLSNPSILVTRTFQFPNPSEPNDNGGDFPLNHFTHQRFPLQIEYQAGVPLVYMDCTRSQGRFTTNGRPVNLVLSMGGSSGQCHVSMKGSNHNMIETPRMGGMGNNDPVGDSISPLVTTSDSSVTSVNHAFATISFQUTYEKRF*`

Super-families **PLN00050**

List of domain hits		Interval	E-value
Name	Accession	Description	
(+) PLN00050 super family	cI31535	expansin A; Provisional	1-208 1.41e-97

SEQUENCES

Peptide

>SfEXPA-16

MAGACGYTNVYSEGYGKTKTVALSTAMFNDGLSCGACYEIKCNAVQWCLSGNPSILV
TATNFCPPNPSEPNDNGGWCNPPLNHFDMAQPAFLQIAEYQAGIVPVLYRKVDCTRS
GGIRFTINGNPYFNLVLVSNVGGSGDVCAVSMKGSNMANWIPMSRNWQNWQCNDQ
DFVGGQISFLVTTSDGSSVTSVNVAPATWSFGQTYEGAQF*

CDS (coding sequence)

>SfEXPA-16

ATGGCTGGAGCATGTGGATATACAAATGTCTATAGTGAGGGCTATGGCACCAAAA
ACAGTGGCACTGAGCACTGCAATGTTCAACGATGGGCTTAGCTGTGGAGCTTGCT
ATGAAATCAAGTGTAATGCTGTCCAGTGGTGCTTATCTGGAAACCCCTCCATCTT
AGTCACAGCAACCAACTTCTGTCCCTCCCAATCCCTCTGAACCAATGATAATGGT
GGCTGGTGCAACCCTCCTCTCAACCATTTTGACATGGCCCAACCTGCTTTCCTTCA
AATTGCTGAGTACCAAGCTGGCATTGTTCCAGTCCTCTACCGCAAGGTGGATTGC
ACAAGAAGTGGAGGGATTAGGTTCAACATCAATGGCAATCCTTACTTCAATTTGG
TGCTGGTGAGCAATGTGGGTGGCTCTGGAGATGTGTGTGCAGTCTCCATGAAAGG
ATCCAACATGGCAAACCTGGATCCCAATGTCCCGAAACTGGGGTCAGAACTGGCA
ATGCAACCAGGATTTTGTGGGTCAATCCATCTCCTTCCTTGTCACTACTAGTGATG
GCAGCTCTGTAACCTCCGTGAATGTGGCACCTGCTACCTGGAGTTTTGGACAGAC
TTATGAAGGAGCTCAGTTCTGA

Nucleotide

>SfEXPA-16

GCTACTATGGAGTTTATAGTGGATATAACAGCCAAGAAGCATATTCCCACAACAG
CTTGAAGAAACCAGAGAGCTTAGCTTTAGCTTCTGCAGCTGCAGCATGGTCTGCT
GCACATGCAACTTTCTATGGAGGAGCAAATGCTGAAGGCACGATGGGTAATAAAA
TGACTTTCTTTCTTTTGAACTTTTTTTTCCCTCTTTTTTGTGTATTCCATTTTA
TGTGGTGAGATGTGGTGTGCAGTCAGATGGATTTCTTGGATAGCAGAACTTGGGG
AGTTGAGGAACTCACAATTTGTGGAGTTTGGAAATTTTTGTGGCAGCTGGAGCA
TGTGGATATACAAATGTCTATAGTGAGGGCTATGGCACAAAACAGTGGCACTGA
GCACTGCAATGTTCAACGATGGGCTTAGCTGTGGAGCTTGCTATGAAATCAAGTG

TAATGCTGTCCAGTGGTGCTTATCTGGAAACCCCTCCATCTTAGTCACAGCAACC
AACTTCTGTCTCCCAATCCCTCTGAACCCAATGATAATGGTGGCTGGTGCAACC
CTCCTCTCAACCATTTTGACATGGCCCAACCTGCTTTCCTTCAAATTGCTGAGTAC
CAAGCTGGCATTGTTCCAGTCCTCTACCGCAAGTAAGCAAAAAAAAAACTTTACAA
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GATTGTCCAAAATCTCTCTGCAGGTTCTTGAACTTTTGAAGGCTTCAATTTCTGAT
GGGTGCTTGGCATTCTTTTTGGGGTGTTTGGATGGATGGATGGATGGGTGGGTGG
TGATCTCTCATGGTAGGGTGGATTGCACAAGAAGTGGAGGGATTAGGTTACCCAT
CAATGGCAATCCTTACTTCAATTTGGTGCTGGTGAGCAATGTGGGTGGCTCTGGA
GATGTGTGTGCAGTCTCCATGAAAGGATCCAACATGGCAAACCTGGATCCCAATGT
CCCGAAACTGGGGTCAGAACTGGCAATGCAACCAGGATTTTGTGGGTCAATCCAT
CTCCTTCTTGTCACTACTAGTGATGGCAGCTCTGTAACCTCCGTGAATGTGGCAC
CTGCTACCTGGAGTTTTGGACAGACTTATGAAGGAGCTCAGTTCTGAAAATCAAA
CCCCACGCAACCAACCAACCAATCAACAACCAACCAACCAACTCCTGATATATAA
AATTCATATTCTTCAACAGTTATGAATCTATTTTCAACAGTTTTCTGATTTGTGCTT
CCTTTGTTTATTGATTTGGGATATGATTTGAATAATCACAATTGGGTAAATTTGTG
CTTAACGAATAATTAGGCTAAACCTCAATGCTAACTTTGAGTGCGACAAATTTCC
AATCAGTGCTTGCTTGTCTTTACCAGCAGCACATGCATCACAATCAAGATGTGAA
GAAGTACTACTAGTTCCAAGCTTTTTCTTGGTTTTTCACCGATTCAGGATTGAACT
TCTCTTGAGTGC