

IDENTIFICATION

Species: *Sphagnum fallax*

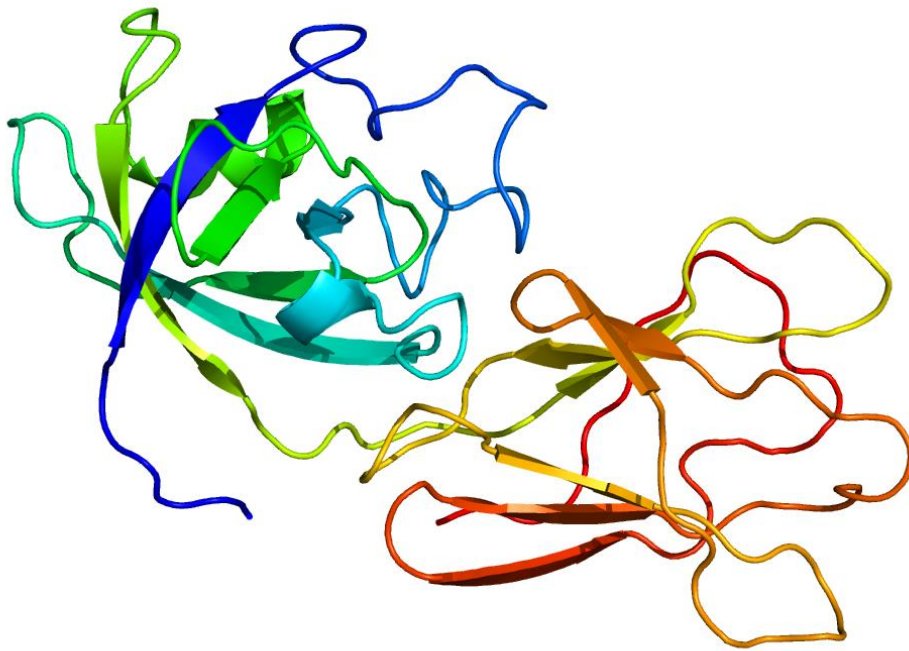
Locus: Sphfalx0005s0298

Gene Model: Sphfalx0005s0298.1.p

Description: SfEXPA-06

Family: Alpha Expansin

3D structure:



GENOME DATABASES

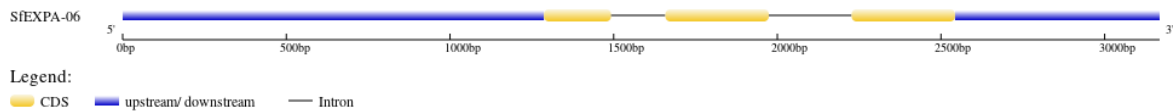
Phytozome: https://phytozome-next.jgi.doe.gov/info/Sfallax_v0_5

KEGG:-

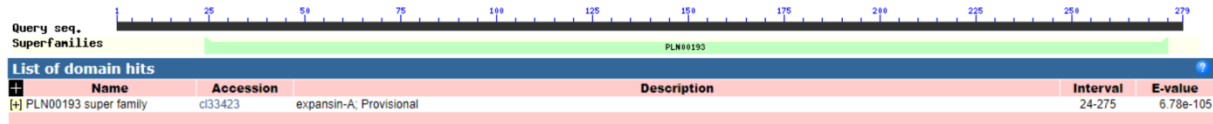
EXTERNAL RESOURCES

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GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>SfEXPA-06

MICGSIMEKRSTLLVLQLPMQQLVIMVIVLMIATSSRFFVSAGGYTGDTHWTPAHATF
YGGDDASGTQGGACGYGNLYSQGYGTNTAALSTALFDGGLRCGACYQLVCNQPRW
CVPGAPVLTVTATNLCPPNWALPNNDGGWCNPPLQHFDLAVPAFIQLAQPIAGIVPV
FYKRVACVRQGLRFTINGNPWFLLVLITNVGGAGDVQQVSVMSSELDWWMPMRQ
NWGQNWQFEGPILYGQSLSFMTTSDGQTVVSHNVADPYWEFGQTFEGSQFEW*

CDS (coding sequence)

>SfEXPA-06

ATGATCTGCGGCAGCATCATGGAGAAGAGGAGCACACTACTGGTGCTGCAGCTTC
CGATGCAGCAGCTAGTCATCATGGTTATAGTGTTGATGATCGCAACCAGCTCGCG
CTTTTTTGTGTCTGCTGGAGGTTACACTGGCGACACTCACTGGACTCCTGCCCATG
CTACCTTCTATGGCGGCGATGATGCCTCTGGCACTCAAGGTGGTGCATGTGGATA
TGGAACCTTTACAGCCAAGGCTATGGCACCAACACAGCAGCTCTGAGCACGGCT
CTTTTCGACGGTGGCCTGAGATGTGGAGCTTGCTACCAGCTGGTATGCAACCAAC
CTCGATGGTGCCTGGAGCACCAGTCTTGACGGTGACAGCCACGAATCTATG
TCCACCCAATTGGGCACTGCCAACACGACGGCGGGTGGTGCATCCTCCCCTC
CAGCACTTCGACCTCGCAGTGCCTGCCTTCATCCAGCTCGCCCAACCCATTGCTGG
AATTGTTCTGTCTTCTACAAAAGGGTAGCATGTGTGAGACAAGGAGGATTGCGC
TTCACCATCAACGGCAACCCATGGTTCCTGTTGGTGTGATCACAACGTGGGAG
GAGCCGGGGATGTGCAGCAAGTGTCCGGTGTGCTTTCGGAGCTGGACTGGTGGAT
GCCAATGCGGCAGAACTGGGGCCAGAATTGGCAGTTCGAAGGTCTTATTCTGTAT
GGCCAGTCTCTCCTTCATGACAACCACCAGTGACGGCCAGACCGTAGTCTCTC
ACAACGTTGCCGATCCCTACTGGGAATTCGGCCAAACATTTGAGGGTAGCCAATT
CGAGTGGTAA

Nucleotide

>SfEXPA-06

CTAGTAGTGTGTGCAGTGAGTAAAATTTGCACACTTGCTAAGAAGGTAGCAGCAG
CTCACTGCAAGAAGTCCTCCTTATAAGCTCAGCTCAGCTCAGCTCAGCTCAGCTT
AGCTAGTGTGTGCTCAGACTCAGCCTCATTCACTCTAGTATTGTGTCTCATGAGCT
CATGATCCCCCAGAAAAAATAAATACTCTCATCAATCCCTTCTTCCCACA

TCCTCACTAGATAGGGGATCAGTTGATCAGCAACATGATCAGCAGCTGATCTGCA
ACTAGTCTCATAATTTATAAGTGAACAACCCACCCACACACACAGTTCAAGAAAG
AAGAAAAGCTCTGGAGATGATATTTAGGTTAATGCCAGGTTTTTAAAGGGAGCTA
CTAGACATGAGAAGCTTGCTTGAGCTGCTGCTGCTTGTGGAGCTGCTACTTTTTG
ACGTGATGAGTTGCAGTACTTAGTACTTCTTCAGTTGCATAGAAAATTAAGATG
AGTATACTACTATTGGAACAAGCTCTATAGCTGCTTTCATGACTGTGTTAAGTCTG
CGCCA