

IDENTIFICATION

Species: *Sphagnum fallax*

Locus: Sphfalx0011s0210

Gene Model: Sphfalx0011s0210.2.p

Description: SfEXPA-11

Family: Alpha Expansin

3D structure:



GENOME DATABASES

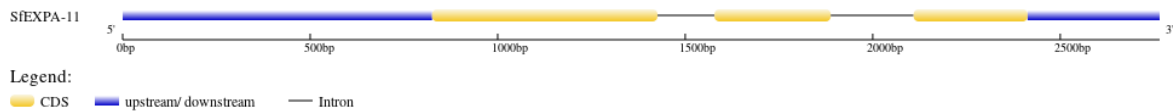
Phytozome: https://phytozome-next.jgi.doe.gov/info/Sfallax_v0_5

KEGG:-

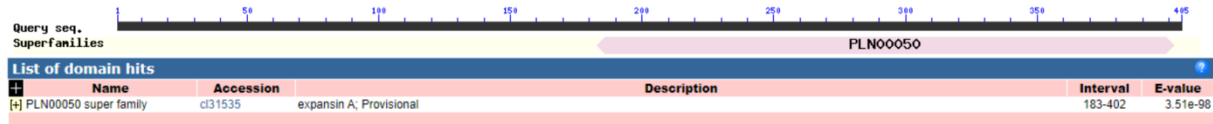
EXTERNAL RESOURCES

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GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>SfEXPA-11

MSTSSTTPQVLLLQPAALVGFVAALLWFVSGSVVIAAADLGSGGSSFDDSALEAIDN
FVVGGFATVSNVTTNSTIPSSPSDGASVPAASPANDQSSTASEKEQFSSTSSSSPTSS
PTSDENHDSSDDAPVDNGREFRLNAYNEYEKAAEEFVRSSSSTYNNPGTGETEGVSL
GASASVWWSRGATFYGGADASGTMGGACGYGNLYATGYGTATAALSTALFNNGA
MCGACYQLMCSGSPWCIPGAISVTATNFCPPNWAQASNNGGWCNPPRPHFDLAEPIF
LRIGHYKAGIIPVYRRINCVKAGGIRFTINGNPFNLVTITNVGGSGIVVAVRMRGDH
TAWYPMARNWGQNWQCSWKLVGQGIWFMVTTSDGRVTTSRVANANWRFQTFE
GAQVR*

CDS (coding sequence)

>SfEXPA-11

ATGTCGACGTCGAGTACTACTACCCCTCAGGTGCTTCTTCTTCAGCCCGCGGCGCT
AGTGGGATTTGTGGCTGCACTGTTGTGGTTTGTGAGCGGATCAGTAGTAATAGCA
GCAGCAGACTTGGGTTCCGGAGGATCAAGCTTCGATGATTCAGCGTTGGAGGCGA
TCGACAACTTCGTGGTTGGAGGTGGATTTGCGACTGTGAGCAATGTGACGACGAC
TAATAGCACGATCCCTTCATCACCATCGGATGGTGCTTCCGTGCCTGCAGCTAGC
CCGGCAAACGATCAATCATCGACAGCTAGTGAGAAGGAGCAATTCTCATCGACA
TCTTCTTCTTCTCCGACGTCGTCACCCACTAGTGATGAAAATCATGATAGCAGCGA
TGATGCGCCAGTAGATAACGGTCGAGAATTCAGATTGAATGCGTACAACGAGTA
CGAGAAAGCGGCTGAAGAGTTTGTGCGGTCTAGCTCCAGCACGTACAACAATCCT
GGGACCGGAGAACTGAAGGCGTCAGTCTTGGAGCGTCCGCATCTGTGGTATGGT
CTCGTGGAACCTGCAACTTTCTACGGTGGTGCTGATGCTTCCGGCACTATGGGTGG
AGCTTGCGGATATGGGAACCTGTACGCTACAGGCTACGGGACAGCTACCGCCGC
ATTGAGCACGGCATTGTTCAACAACGGAGCAATGTGCGGAGCCTGCTACCAACTC
ATGTGCTCCGGATCTCCCTGGTGTATTCCCGGAGCAATAAGTGTGACGGCGACCA
ACTTCTGCCCACCAACTGGGCTCAAGCTTCCAACAACGGCGGATGGTGCAACCC
ACCCAGGCCGCACTTCGACTTGGCAGAACCCATTTTCTTGAGAATTGGGCACTAT
AAAGCAGGCATCATTCCCGTTGTATATCGCAGGATCAATTGTGTCAAGGCAGGAG
GAATCCGGTTCACCATCAACGGGAACCCGTTTTTCAACCTGGTGACGATCACCAA
CGTGGGTGGATCTGGAATCGTGGTGGCGGTGAGGATGAGAGGGGATCACACAGC
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CGTGGGGCAAGGCATTTGGTTCATGGTCACCACAAGCGATGGCAGAGTCACAAC
ATCTCGTGTTGCAAATGCAAAGTGGAGATTCGGCCAGACCTTCGAAGGTGCACAG
GTCCGCTAA

Nucleotide

>SfEXPA-11

CGCGCGGGCTCAGCGACTCGCGAAGGGTTCGCGCGCGAGGGTTCGCGTCCCTGTAA
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CGAATCTCGCCATCTTGTGTCGTAATCCCCGAAGTCGAAAAGAAGACGGAAAAAT
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TCCAATCCGAAGTTTTTCATAGAACCTACATGCAAGAAGGATTCAATCTAGTGTGT
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