

IDENTIFICATION

Species: *Salix purpurea*

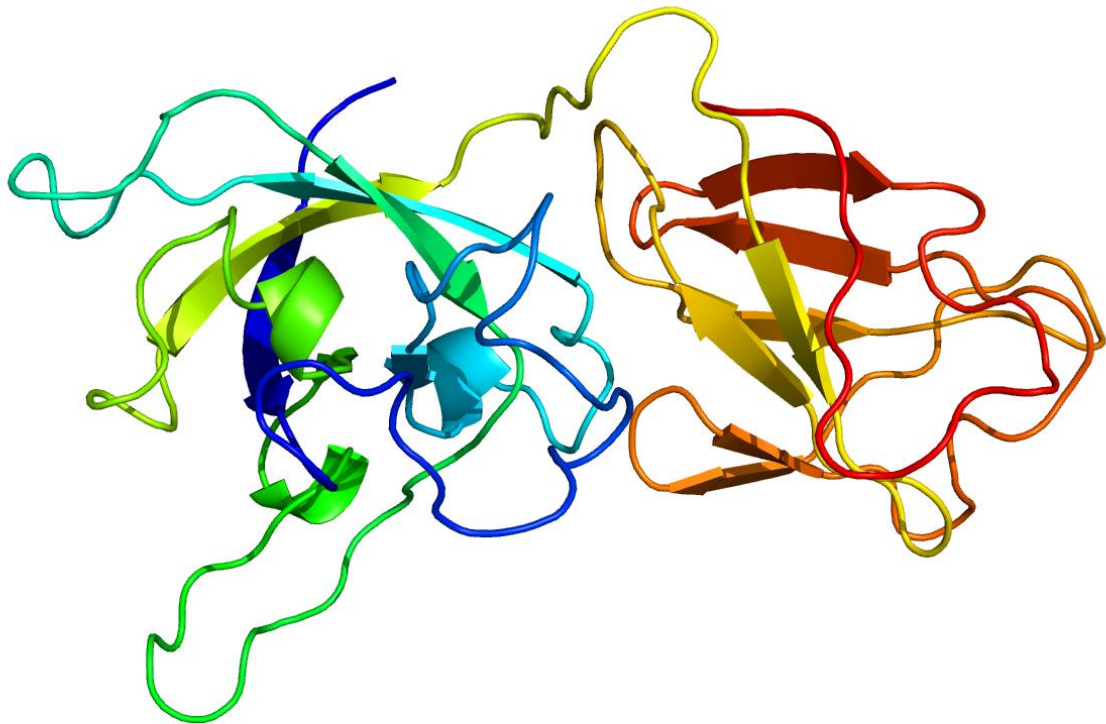
Locus: Sapur.013G138800

Gene Model: Sapur.013G138800.1.p

Description: SprEXPA-17

Family: Alpha Expansin

3D structure:



GENOME DATABASES

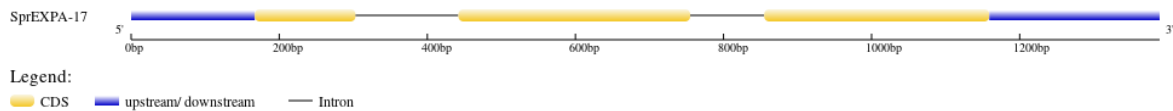
Phytozome: https://phytozome-next.jgi.doe.gov/info/Spurpurea_v5_1

KEGG:-

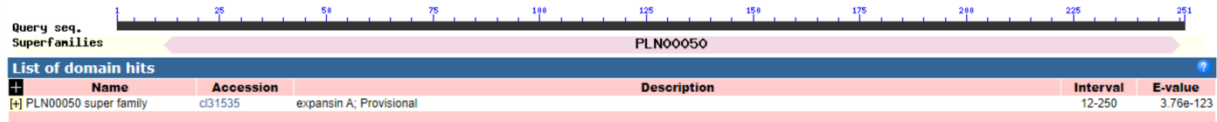
EXTERNAL RESOURCES

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GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>SprEXPA-17

MAAQAFASCLLLFICLHLQGVLADYGGWQGGHATFYGGGDATGTMGGACGYGNL
YSQGYGTNTAALSTALFNGLSCGACYEMRCDPRWCLPGSITVTATNFCPPNPSL
PNNNGGWCNAPLQHFDMAEPAFLQIAQYRAGIVPVAFRRVPCVKKGGIRFTINGHSY
FNLVLITNVGGAGDVHSVSIKGSKTGWQAMSRNWGQNWQSSSYLNGQSLSFQVTTS
DGRTVTSYNAVPAGWQFGQTFAGGQF*

CDS (coding sequence)

>SprEXPA-17

ATGGCAGCTCAAGCATTGCTTCATGTCTTCTCCTCTTCATCTGCTTGCACCTTCA
GGGCGTTTTGGCTGATTATGGAGGGTGGCAAGGTGGTCACGCCACTTCTATGGC
GGTGGTGACGCAACTGGCACAATGGGAGGAGCATGTGGATATGGAAATTTGTAC
AGTCAAGGTTATGGAACAACTGCAGCCCTAAGCACTGCCTTGTTCAACAATG
GCTTGAGCTGTGGGGCTTGTTATGAAATGAGATGCGACGACGCCAGATGGTG
TCTCCCTGGTAGCATCACTGTCACCGCTACAAATTTTTGCCCGCCGAACCCTTCTT
TGCCGAACAACAATGGCGGATGGTGCAACGCTCCGCTCCAACATTTTGACATGGC
TGAGCCTGCTTCTTGCAAATCGCTCAATACCGTGCCGGAATTGTGCCTGTAGCTT
TTAGAAGGGTGCCTTGTGTTAAGAAGGGGGGATTCGATTCACCATCAACGGCCA
CTCTTACTTCAACCTGGTTCTGATACCAATGTTGGCGGCGCCGGAGATGTCCATT
CAGTTTCAATCAAAGGCTCAAAAACAGGGTGGCAGGCCATGTCAAGAACTGGG
GCCAAAACCTGGCAGAGCAGCTCTTACCTCAATGGTCAGAGCCTATCTTTTCAGGT
CACCACCAGTGATGGCAGAACTGTCACAAGCTACAATGCGGTGCCTGCTGGCTGG
CAGTTTGGTCAGACTTTTGCAGGAGGCCAATTCTAA

Nucleotide

>SprEXPA-17

CACAACCTACTTATTAATGGGCTTTAGCTACTCTCTGGTTCGCTTATAAATAGCAC
TTCTTCTTTTCTTTACTTCAACAACACAAACACTTCATCCTCTTCTATAACATCCTC
TGTCTTGTAGTTTTGGTAGCACCATAACATCTGTCAGACAACCAGCGTTGGCAAT
GGCAGCTCAAGCATTGCTTCATGTCTTCTCCTCTTCATCTGCTTGCACCTTCAGG
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CCTAAGCACTGCCTTGTTCAACAATGGCTTGAGCTGTGGGGCTTGTTATGAAATG
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CGCTCCGCTCCAACATTTTGACATGGCTGAGCCTGCTTTCTTGCAAATCGCTCAAT
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GATTGATCTTTGATTTTGACAGGGTGCCTTGTTAAGAAGGGGGGGATTTCGATT
CACCATCAACGGCCACTCTTACTTCAACCTGGTTCTGATCACCAATGTTGGCGGC
GCCGGAGATGTCCATTCAGTTTCAATCAAAGGCTCAAAAACAGGGTGGCAGGCC
ATGTCAAGAACTGGGGCCAAAACCTGGCAGAGCAGCTCTTACCTCAATGGTCAG
AGCCTATCTTTTCAGGTCACCACCAGTGATGGCAGA ACTGTCACAAGCTACAATG
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TCTCACCACCCTTTTTTCACCGTTTTCTCTTCATCAAGCCTGGTTAATTAGTGGGA
ATTTGTATATTCATATTATGTGCTTCTTATAAGGACAAATTAAGAGGGAAAAAAG
CGTACTTTAGTGATGTTTGGAGGAGGAGGAGAAGTGGCCTTGTAAGCTGAGGTA
GCTAAATTTCACTATAGCACCCGCTTGCCCTTCCTCATATTATATATATATATA
TATATA