

IDENTIFICATION

Species: *Salix purpurea*

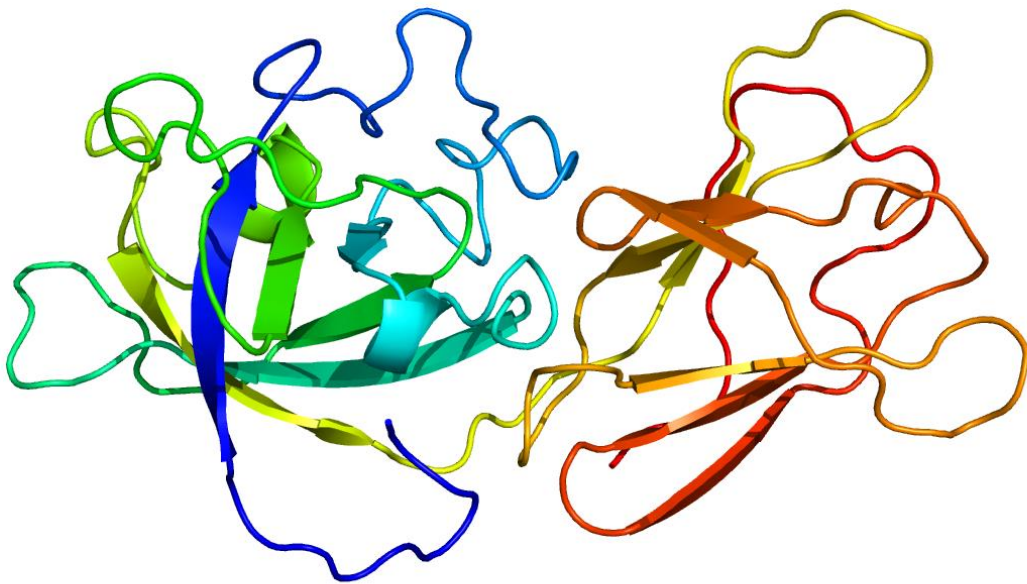
Locus: Sapur.013G056400

Gene Model: Sapur.013G056400.1.p

Description: SprEXPA-15

Family: Alpha Expansin

3D structure:



GENOME DATABASES

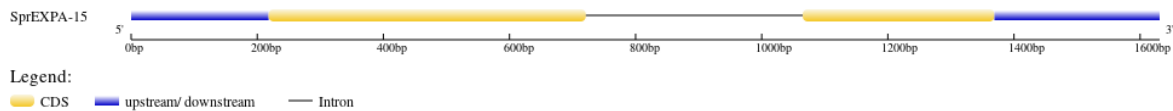
Phytozome: https://phytozome-next.jgi.doe.gov/info/Spurpurea_v5_1

KEGG:-

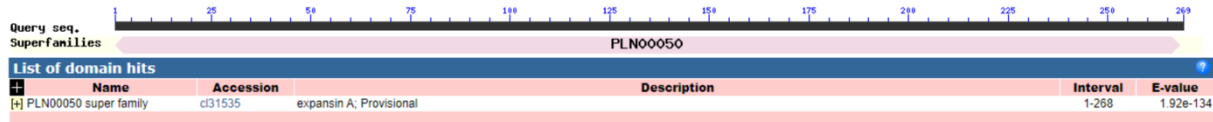
EXTERNAL RESOURCES

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GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>SprEXPA-15

MDFLGICLVVFLTMSKTIHGYGGGWSNAHATFYGGGDAAGTMGKYQNRNSNEIPASL
HLNQFMCTLQFTGGACGYGNLYSQGYGTNTAALSTALFKNGLACGACFELKCVND
DRWCLSGSIIITATNFCPPNSAGGWCNPPSQHFDSLQPAFQHLARFKAGIVPVVYRRV
ACRKAGGIRFTINGHSYFNLILVSNVGGAGDVVSVSVKGSRTGWQPMSRNWGQNW
QSSSYLNGQALSFKVTTSDGRSIISSNNVAPPSWAFGQTFHGGQF*

CDS (coding sequence)

>SprEXPA-15

ATGGATTTTCTTGGAAATTTGTCTCGTAGTCTTCCTGACCATGTCGAAAACACTATTCA
TGGCTATGGAGGTGGATGGTCTAACGCTCATGCCACCTTCTATGGAGGTGGCGAT
GCTGCCGGAACAATGGGTAAGTACCAAAATCGATCCAATGAGATACCTGCTAGTC
TACATCTCAATCAATTTATGTGTACGCTACAATTTACAGGAGGAGCTTGTGGCTAT
GGAAACCTCTACAGCCAAGGTTATGGGACAAACACGGCGGCGTTGAGCACAGCT
TTATTCAAGAATGGACTAGCTTGCGGAGCTTGTTTCGAGCTCAAATGTGTAAATG
ATGACAGGTGGTGTCTTTCAGGATCTATAATAATCACGGCAACAAATTTCTGCC
TCCAAACAGTGCCGGAGGGTGGTGAACCCGCCGTCCCAGCACTTCGATCTTCT
CAGCCTGCTTTTCAACATCTAGCTCGTTTCAAAGCAGGAATAGTCCCTGTCGTTTA
CAGAAGAGTTGCTTGTAGGAAAGCTGGAGGAATCAGATTCACAATAAATGGCCA
TTCATACTTCAACCTCATCCTCGTATCCAACGTTGGTGGCGCCGGCGATGTTGTCT
CCGTGTCCGTCAAAGGATCTAGAACTGGTTGGCAGCCGATGTCTCGCAACTGGGG
CCAAAATTGGCAGAGCAGCTCTTACCTGAATGGGCAAGCACTCTCCTTCAAGGTG
ACAACAAGTGATGGAAGATCTATCATCTCCAACAATGTCGCTCCTCCAAGCTGGG
CTTTTGGTCAGACCTTCCATGGAGGACAGTTCTAG

Nucleotide

>SprEXPA-15

GTTTTCTCCACAAACATCTATAAATACAGGTTCTTTCCCCAGCTTCTTCCTTGTCTT
TCCCTAGTCATTGACTTGAGCTTCCAAGCTGATTTCTTTGAGTTCAAATTTATTA
GGCCATTGTAAGCACAACTCATCAATAATTTCTTTTCCCACTTGCAAAAATAAT
CCATATCACAGATTAAGTGTGTGTTCTTTTGGCTGTCAGGAAATGGATT
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CTCTACAGCCAAGGTTATGGGACAAACACGGCGGCGTTGAGCACAGCTTTATTCA
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TGACCGAAATAAATCAAACAGAACGAAACTAAAACATTTTCAGTTATATTTGGCTG
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GTCTCCGTGTCCGTCAAAGGATCTAGAACTGGTGGCAGCCGATGTCTCGCAACT
GGGGCCAAAATTGGCAGAGCAGCTTTACCTGAATGGGCAAGCACTCTCCTTCAA
GGTGACAACAAGTGATGGAAGATCTATCATCTCCAACAATGTCGCTCCTCCAAGC
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CTAAATATATTAATAAACTGGAG