

IDENTIFICATION

Species: *Salix purpurea*

Locus: Sapur.004G169300

Gene Model: Sapur.004G169300.1.p

Description: SprEXPA-09

Family: Alpha Expansin

3D structure:



GENOME DATABASES

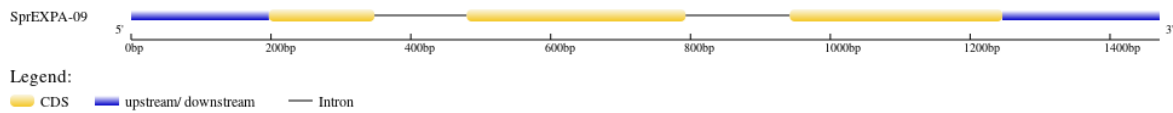
Phytozome: https://phytozome-next.jgi.doe.gov/info/Spurpurea_v5_1

KEGG:-

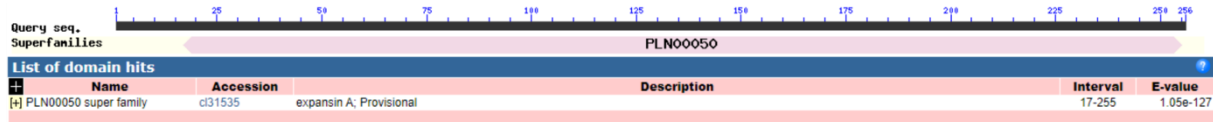
EXTERNAL RESOURCES

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GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>SprEXPA-09

MMAMKAMKDLVFVQLYLVLTFLLHGIYGDYGGWQSAHATFYGGSDASGTMGGAC
GYGNLYSQGYGTSTAALSTALFNGLSCGACFQIRCNNDPKWCHSSTITVTATNFCPP
NYALSNDNGGWCNPPLQHFDLAQPAFLQIAQFRAGIVPVLFRRVPCVKNGGIRFTING
HSYFNLVLITNVAGAGDVRAVSIKGSRTGWQTMSRNWQNWQSN SYLDGQSLSFR
VTSDGRTVTGYNVVPGNWRFQGTFEGGQL*

CDS (coding sequence)

>SprEXPA-09

ATGATGGCAATGAAAGCAATGAAAGATCTTGTGTTTCGTTTCAGCTATATCTTGTAC
TGACCTTTCTTCTTCATGGCATTATGGAGATTATGGTGGGTGGCAGAGTGCCCAT
GCCACATTCTACGGAGGTAGCGACGCGTCTGGCACCATGGGGGGTGCTTGTGGAT
ATGGAACCTGTACAGCCAGGGGTATGGAACAAGCACCCGACGCTCTAAGCACTG
CCCTTTTCAACAATGGCTTGAGCTGTGGTGCCTGCTTCCAGATACGCTGCAACAA
TGATCCCAAATGGTGCCATTCCAGTACCATTACTGTGACAGCCACCAACTTTTGCC
CTCCTAATTATGCTTTGTCTAATGACAATGGAGGCTGGTGCAACCCCCCTCTCAA
CATTTTGATTTGGCACAGCCTGCTTTCCTGCAAATTGCTCAGTTCGAGCTGGAAT
TGTTCTGTACTCTTCAGAAGGGTCCCATGTGTGAAGAATGGAGGCATTAGGTTTC
ACCATTAACGGTCATTCTACTTCAACCTGGTCCTGATAACCAATGTGGCAGGCG
CAGGTGATGTTTCGTGCTGTGTCTATCAAGGGATCTAGGACTGGCTGGCAAACCAT
GTCAAGAACTGGGGCCAAAATTGGCAGAGCAACTCATATCTCGATGGCCAGAG
CCTCTCCTTCAGAGTCACGACCAGCGATGGCAGGACAGTCACCGGCTACAATGTT
GTGCCAGGGAATTGGCGATTTGGACAACTTTTGAAGGAGGGGCAACTCTAG

Nucleotide

>SprEXPA-09

GGCTCTAATTATAGCTCTAACGTGACTACCTCTAACTTGCAGGTTGTAATAATCAA
CGAAGTCTACTCTGCTAATTGGGTCGCTACCTAAATCCCCAGAGTATAAATACCC
AACACGATTTCCCCAGAGTATAACACACTCGAGCCTAGCTACCCCGATATTTTCT
ACTACTTGTTTCTTAGTAACGACGCAAGAACATGATGGCAATGAAAGCAATGAAA
GATCTTGTGTTTCGTTTCAGCTATATCTTGTACTGACCTTCTTCTTCATGGCATTAT
GGAGATTATGGTGGGTGGCAGAGTGCCCATGCCACATTCTACGGAGGTAGCGAC

GCGTCTGGCACCATGGGTAAGCTAACCACGATAGACTGCTGATGCATTTATGATT
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TCCTGTACTCTTCAGAAGGTAATTTCAAAACGTCCTCAGTGACAAGATCATGGTA
TCAGCCACGACTGAACCTCAGTCTAGACCACCCAGAAGTTCTGCTACTGTAATAA
CTTTATGCTTGACTAGCTGGAACAGCATCATTTTAGTTTGTGGTTGTTTTTACAG
GGTCCCATGTGTGAAGAATGGAGGCATTAGGTTCCACCATTAACGGTCATTCCTAC
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ATTGGCAGAGCAACTCATATCTCGATGGCCAGAGCCTCTCCTTCAGAGTCACGAC
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