

IDENTIFICATION

Species: *Salix purpurea*

Locus: Sapur.001G092300

Gene Model: Sapur.001G092300.1.p

Description: SprEXPA-03

Family: Alpha Expansin

3D structure:



GENOME DATABASES

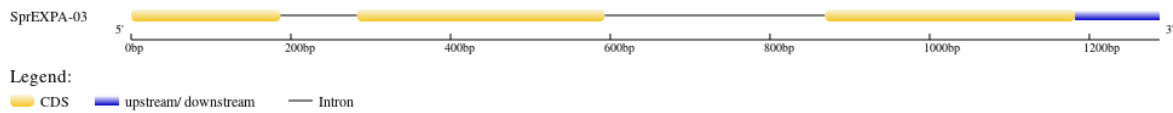
Phytozome: https://phytozome-next.jgi.doe.gov/info/Spurpurea_v5_1

KEGG:-

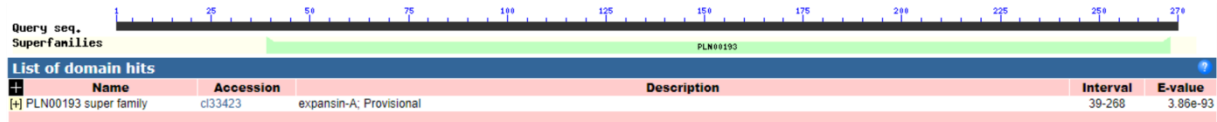
EXTERNAL RESOURCES

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GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>SprEXPA-03

MASSLHSWSSGFFFLIVLSTSAMFIGMAAGYSRAPSPATAFRPSLWSQAHATFYGDETA
RETMGGACGYGNLFQGTGYGTDVALSTTLFKSGYACGTCYQIKCTNAPACYGAIAT
VTATNICPPNWSKDSNKGWCNPPRVHFDMSKPAFMKIAQWKAGIVPVMYRRVPC
VRIGGLRFRFQNGYWLLVYVTNVGGGGDIASMWVKGSRTGWISMSHNWGASYQ
AFASLGGQALSFKITSYTTKQTVLALNVCPSNWA VGMTYKSSVNFR*

CDS (coding sequence)

>SprEXPA-03

ATGGCTTCCTCTCTTCATTCATGGAGCTCTGGCTTCTTCTTCCTGATAGTACTGTGC
ACATCGGCAATGTTTCATCGGAATGGCTGCAGGTTATAGCAGAGCACCCCTCTCCAA
CAGCGTTCAGGCCGAGCCTATGGTCGCAAGCCCATGCCACCTTTTATGGCGACGA
GACCGCTCGCGAGACCATGGGAGGGGCTTGCGGGTATGGGAATTTATTCCAAACC
GGATACGGAACCGATACAGTTGCACTGAGCACAACATTATTCAAAGCGGCTAT
GCCTGTGGGACTTGTTACCAGATAAAATGCACGAATGCTCCTGCATGCTATGGGG
CCATTGCAACAGTTACTGCTACGAACATCTGCCCTCCGAATTGGTCCAAGGATTC
TAACAAGGGCGGATGGTGCAACCCTCCTCGAGTTCACCTTCGACATGTCCAAGCCT
GCGTTCATGAAGATTGCTCAATGGAAGGCTGGGATAGTCCCAGTCATGTACCGAA
GAGTACCGTGTGTAAGAATTGGCGGGCTTCGATTCAGATTCCAAGGGAATGGGTA
CTGGTTGCTGGTGTATGTGACGAATGTAGGAGGAGGTGGTGACATTGCCAGCATG
TGGGTGAAGGGAAGCAGAACAGGATGGATTAGCATGAGCCATAACTGGGGAGCT
TCGTACCAGGCATTTGCAAGCCTTGGAGGCCAAGCTCTCTCTTTCAAGATCACTTC
TTACACAACCAAGCAGACTGTTCTTGCAATTGAATGTTTGTCTTCAAACCTGGGCTG
TAGGGATGACTTATAAATCATCTGTGAACTTCCGTTAG

Nucleotide

>SprEXPA-03

ATGGCTTCCTCTCTTCATTCATGGAGCTCTGGCTTCTTCTTCCTGATAGTACTGTGC
ACATCGGCAATGTTTCATCGGAATGGCTGCAGGTTATAGCAGAGCACCCCTCTCCAA
CAGCGTTCAGGCCGAGCCTATGGTCGCAAGCCCATGCCACCTTTTATGGCGACGA
GACCGCTCGCGAGACCATGGGTATGTTAATTATTCTCGTTTTGTTTTCCATAATTC
TACAACAAAATGCTCAATTAATATTCTGTCTGCTTCTTTTTTCTGGGGTTGATTTATT

CAGGAGGGGCTTGCGGGTATGGGAATTTATTCCAAACCGGATACGGAACCGATA
CAGTTGCACTGAGCACAAACATTATTCAAAGCGGCTATGCCTGTGGGACTTGTTA
CCAGATAAAATGCACGAATGCTCCTGCATGCTATGGGGCCATTGCAACAGTTACT
GCTACGAACATCTGCCCTCCGAATTGGTCCAAGGATTCTAACAAGGGCGGATGGT
GCAACCCTCCTCGAGTTCACCTTCGACATGTCCAAGCCTGCGTTCATGAAGATTGCT
CAATGGAAGGCTGGGATAGTCCCAGTCATGTACCGAAGGTATGCCAATATCTTTC
TGAATGCTTTTTACAAGTCAACTCTATGTGGGCCAAACGTTTTTGAGCAAGCTGCT
CATTGGTGCTAATTAACACTTAATTCCTATATATACGAGTAGTCTTGGATGCAGTT
TTCTCATGAATTCCTTCCATCGTGAACCTCTCTTAACTGGACTGGGAAAGTG
AATTTGGTTTATGCAAGCTAGCCTGATCGAGGGAATACAATTTGTCAACTCTGGT
TCGATCAGAGCTCTAATTATCCTTCATATCTTGCAGAGTACCGTGTGTAAGAATTG
GCGGGCTTCGATTCAGATTCOAAGGGAATGGGTACTGGTTGCTGGTGTATGTGAC
GAATGTAGGAGGAGGTGGTGTGACATTGCCAGCATGTGGGTGAAGGGAAGCAGAAC
AGGATGGATTAGCATGAGCCATAACTGGGGAGCTTCGTACCAGGCATTTGCAAGC
CTTGAGGCCAAGCTCTCTCTTTCAAGATCACTTCTTACACAACCAAGCAGACTG
TTCTTGCAATTGAATGTTTGTCTTCAAACCTGGGCTGTAGGGATGACTTATAAATCA
TCTGTGAACTCCGTTAGTGATGCCATGATCACTTCGTACACTATCCTTTTTTCTTT
TCTCCACCACATCTTCTCTATCAGGTCTTTTGAGGCCCTTGTTTTCCATCATGTTT
TTGCTTCCCC