

IDENTIFICATION

Species: *Salix purpurea*

Locus: Sapur.019G061000

Gene Model: Sapur.019G061000.1.p

Description: SprEXPA-28

Family: Alpha Expansin

3D structure:



GENOME DATABASES

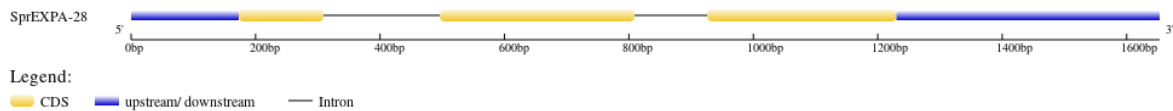
Phytozome: https://phytozome-next.jgi.doe.gov/info/Spurpurea_v5_1

KEGG:-

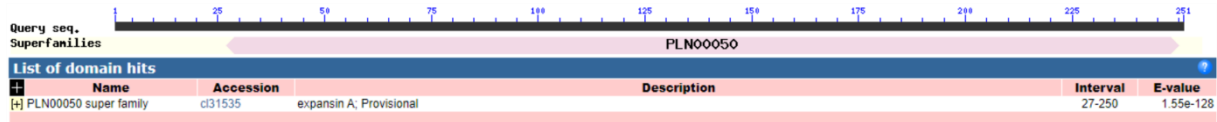
EXTERNAL RESOURCES

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GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>SprEXPA-28

MAMAATVSLLLFALSCLRGSYGDYGGWQSGHATFYGGGDASGTMGGACGYGNL
YSQGYGTDTAALSTALFNGLSCGSCYEMRCDNDPKWCLPGSITVTATNFCPPNSGL
ANDNGGW CNPPLQHFDMAEPAFLQIAQYRAGIVPISFRRVPCVKKGGIRFTINGHSYF
NLVLITNVGGAGDVHSVSIKGSKTGWQAMSRNWGQNWQSN SYLNGQSLSFQVTTS
DGRTVTSYNAAPAGWQFGQTFSGGQF*

CDS (coding sequence)

>SprEXPA-28

ATGGCAATGGCAGCTACTGTTTCTTCTTCTTGTGTTGCGCTCAGTTTGTGCCTGAG
AGGCTCTTATGGGGACTACGGAGGGTGGCAGAGTGGTCACGCCACCTTCTATGGC
GGCGGTGATGCTTCCGGGACAATGGGAGGTGCTTGCGGGTATGGCAATCTGTACA
GTCAAGGGTATGGTACGGACACTGCAGCGCTTAGCACTGCCCTGTTCAACAATGG
CTTGAGCTGCGGTTCTTGTATGAGATGAGATGTGACAATGACCCCAAATGGTGC
CTCCCTGGCTCAATCACCGTCACCGCCACTA ACTTCTGCCCCCTAACTCTGGCTT
GGCTAATGACAACGGTGGCTGGTGTAAACCCTCCCCTCCAACACTTCGACATGGCT
GAGCCAGCGTTCCTGCAAATTGCTCAGTACAGAGCCGGGATTGTGCCAATTTCTT
TCAGAAGGGTCCCCTGTGTGAAGAAAGGAGGAATAAGGTTCACCATCAATGGGC
ACTCTTACTTCAATCTGGTGCTGATCACGAATGTTGGTGGAGCAGGAGATGTTCA
CTCAGTGTCAATCAAGGGTTCTAAGACAGGGTGGCAGGCTATGTGCGAGGAACTG
GGCCAGA ACTGGCAAAGCAATTCCTACCTCAATGGCCAGAGTCTTTCCTTCCAG
GTGACCACAAGTGATGGTAGGACAGTGACCAGCTACAACGCAGCGCCGGCAGGC
TGGAATTTGGCCAGACATTTTCCGGCGGACAATTCTAG

Nucleotide

>SprEXPA-28

AATTTATTAGCTTGTCTCACCTTCATGCATGCGTCCACATCAAAACAGCCCTCGTC
GCCTATATAAAGTATACATACGCTCATTTCTTTTGTACAATCAACAAGCATCTGGG
CTTCGAATCTTTCTCACACAACTTTCCCCCTCACCTGATAGAAACCCAGCACCAG
AAACAATGGCAATGGCAGCTACTGTTTCTTCTTCTTGTGTTGCGCTCAGTTTGTGC
CTGAGAGGCTCTTATGGGGACTACGGAGGGTGGCAGAGTGGTCACGCCACCTTCT
ATGGCGGCGGTGATGCTTCCGGGACAATGGGTATGTTTCAGCAACTTTTCTTCTT

TATAGCTAGGGTGCATGCTACTAATTCTACTGAAAGGTTTTTCCAAATTCCTCCC
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TAGCACTGCCCTGTTCAACAATGGCTTGAGCTGCGGTTCTTGTTATGAGATGAGA
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TATAACCTCGGTCAATTATATAGTATCCATCATTACCAGATAGATTTACCTCGTCT
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AGGAGGAATAAGGTTACCATCAATGGGCACTCTTACTTCAATCTGGTGCTGATC
ACGAATGTTGGTGGAGCAGGAGATGTTCACTCAGTGTCAATCAAGGGTTCTAAGA
CAGGGTGGCAGGCTATGTTCGAGGAACTGGGGCCAGAACTGGCAAAGCAATTCCT
ACCTCAATGGCCAGAGTCTTTCCTTCCAGGTGACCACAAGTGATGGTAGGACAGT
GACCAGCTACAACGCAGCGCCGGCAGGCTGGCAATTTGGCCAGACATTTTCCGGC
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TCTATAAATGGTATACGAGAGAGGAGAGGGAGGGGGTAGGGTAGGGAAGCCATG
GCCAATGTGTCTGGCTGTAGCTGAGGTGGTTTATTAGCACCCGCTGGGCCTTTTTT
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CATCCTGTCCTGGTAGACTCAGTCCGCAATTTGGTCTGAAACCCAGTTGGAACCTC
TAAATTTGCTTACTTTATTGTACTGATTAATTTCTCTGGTTTTGTGCTTGATTTA
CGAGTATAATCCCGTCGTGCATCTATGTATATCATCAAATTTCTAGCCATTCTTTG
CACAGTAAATATCATTGCGCAGAATATTATAAATTATACTCTGGAG