

## IDENTIFICATION

**Species:** *Salix purpurea*

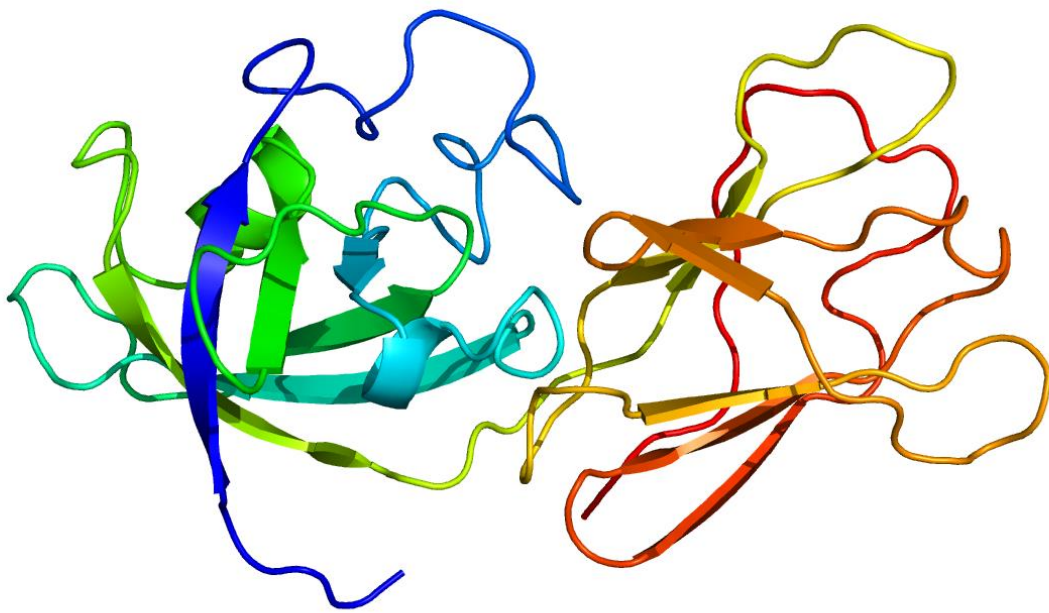
**Locus:** Sapur.004G056400

**Gene Model:** Sapur.004G056400.1.p

**Description:** SprEXPA-07

**Family:** Alpha Expansin

**3D structure:**



## GENOME DATABASES

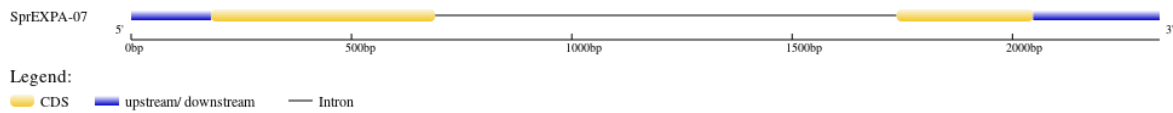
Phytozome: [https://phytozome-next.jgi.doe.gov/info/Spurpurea\\_v5\\_1](https://phytozome-next.jgi.doe.gov/info/Spurpurea_v5_1)

KEGG:-

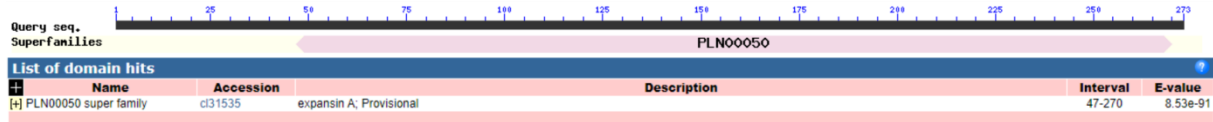
## EXTERNAL RESOURCES

-

## GENE STRUCTURE



## DOMAIN ARCHITECTURE



## SEQUENCES

### Peptide

>SprEXPA-07

MPPPSLQNPIHTLLKPLLFLFIFAATTSHTSSTTSSPTLSTTLSQWQSARATYYAASDP  
RDTVGGACGYGDLVKAGYGMATAGLSESMFERGEICGACFQIKCVDDLRCWIPGTSI  
IVSVTNFCAPNYGFASDGGGKCNPPNKHVFLPIEAFEKIAIWKATNMPVHYMRIKCR  
KEGGIRFTISGSGIFLSVLISNVAGAGDVTA VKIKGSRTGWLDMGRNWGQNWVNA  
NLQNQALSFEVTSSDSMTVISYNVAPKDWRFQTFEGKQFET\*

### CDS (coding sequence)

>SprEXPA-07

ATGCCACCGCCATCACTCCAAAACCCCATTCACACTCTCCTAAAACCCCTCCTTTT  
CCTCTTCATCTTCGCCGCCACCACCACCTCCCACACCTCTTCCACCACCTCCTCAC  
CAACTCTCTCCACCACCCTATCCCAATGGCAATCCGCACGCGCCACTTACTACGC  
AGCATCGGATCCCCGGGACACAGTAGGAGGGGCGTGTGGATATGGGGACTTAGT  
TAAAGCCGATATGGAATGGCAACTGCGGGGTTGAGTGAATCAATGTTTGAACGT  
GGAGAGATCTGTGGCGCGTGTTTTCAAATTAAGTGTGTTGATGATTTGAGGTGGT  
GTATTCCGGGGACTTCTATTATTGTTTCTGTCACAAATTTTGTGCTCCAAATTAT  
GGGTTCCGTTCTGATGGTGGTGGAAAATGTAATCCTCCTAATAAGCATTTTGTGCT  
GCCTATTGAAGCTTTTGAAGATTGCCATTTGGAAGGCCACTAATATGCCTGTT  
CATTATATGAGGATTAATGCAGAAAGGAAGGGGGGATTCGGTTTACCATCTCCG  
GCTCTGGTATTTTCTTTCGGTGCTGATCAGCAATGTCGCAGGTGCCGGAGATGTC  
ACTGCAGTGAAGATCAAAGGTTCAAGAACAGGCTGGCTTGATATGGGCAGGAAT  
TGGGGCCAGAAGTGGCATGTTAATGCTAATCTACAGAATCAAGCTCTCTCATTCG  
AGGTCACCAGTAGTGATAGTATGACTGTAATTTCTTACAATGTTGCTCCCAAAGA  
TTGGAGATTCGGACAGACCTTTGAAGGCAAGCAATTTGAGACTTGA

### Nucleotide

>SprEXPA-07

GGCAGCATGAGAGGATGTTCTTCAAACCTCACAACTGCTCATCAGCACAAAGAG  
AAGGAACTATAGCAGTAAAGCAATCTCAGTTTCCACCCTTCTGTTATAAAAT  
AACTAAGACAACCTCAACTTCGAAACAAATCCTTTCCTTTAACCCCCCAAACC  
TGTCTAAGACAGCGAAATGCCACCGCCATCACTCCAAAACCCCATTCACACTCTC  
CTAAAACCCCTCCTTTTCTTCTTTCATCTTCGCCGCCACCACCACCTCCCACACCTC

TTCCACCACCTCCTCACCAACTCTCTCCACCACCCTATCCCAATGGCAATCCGCAC  
GCGCCACTTACTACGCAGCATCGGATCCCCGGGACACAGTAGGAGGGGCGTGTG  
GATATGGGGACTTAGTTAAAGCCGGATATGGAATGGCAACTGCGGGGTTGAGTG  
AATCAATGTTTGAACGTGGAGAGATCTGTGGCGCGTGTTTTCAAATTAAGTGTGT  
TGATGATTTGAGGTGGTGTATTCCGGGGACTTCTATTATTGTTTCTGTCACAAATT  
TTTGTGCTCCAAATTATGGGTTTCGCTTCTGATGGTGGTGGAAAATGTAATCCTCCT  
AATAAGCATTTTGTGCTGCCTATTGAAGCTTTTGAAAAGATTGCCATTTGGAAGG  
CCACTAATATGCCTGTTTATTATATGAGGTAAGAATCTGAAAGCCCTCATGGATT  
TTGTTGTTTTTGAAGTTAAGTCTGTAAGTTAGGCACATATTTAGTCCTTTGAATTC  
GAGTTATGCTAGAGAAGATGAGCTGTCTAATTCTGTCAAGATTTCGAAATTTGAGT  
GTTTAGTTTGTAAATTTCAATGAATTTGTCTTCAGTTGCTTGAATCATTCTTGCTA  
ACATGCACTGATACTAAAATTTAGCCACTGAGAAGAAGAGAGTCCACTGCTAAAT  
TTGTTTCTTTGTGAATCTATTTCTTCTTTCATTATTATTTTTTTCTTTCAGCCCTCAGT  
TCCTTGTAGGACCCTTTAGACTGGCCATTCTGAATTATTTTACCAAGCTCCTTTTTT  
TCTAAATTATGGACACCCTGCTTTATGCTTTTTGCAGCTGCCATTGAAAGCTTAAA  
CTTTAGGAGTTGTTGATGGTTAGAAACATGAAGGTTTGTGTTGTGATAAAAAAATAA  
GTGCTTGGTGTAAATTTAGCAGCTAAGCAAGTAAGAGACCAGGGAGGGGGCAAT  
TTAAATTTAGTGCTTGGTGTGTCTTTGTTCAGTGTTAATGAGCGCCCCGTTTCTTGC  
TAACTTATATCATGGCATTATTTGTGGGGCTGCTGTCGAGAGATCACTGTTTTGGC  
TTTGAAAATTCAAAGGGGTTTTTATTAGCCTACACTTTTGGTTCATTGGTTGATGG  
AAAATACAAATAATGCATGATGGGAGACAGCCACTATCTCGTCTCAATCCTGCA  
TCAAAGAAGTAAAATATTCCTAATCACTAGTATATGATAGCGACAGTTCCTTT  
GCTAAATGTCTCTACGTATCTTTAACTGGAATTTGCTGAAAGTATTTCTGTTATTT  
TGACTGCTAGAGCAAAAAAATTGAATCACTCCAGAAAGAAGTAGACTTTCTCTT  
CTTTTTATGATGGCAATGGATGTATCACATTTTCATCTGAAACTTAAATGCAGGTTT  
TTGAAGCTTGCTACTGTTTTCAATTATTATTAATTTTTCTGCTTATCCTTGACTGTG  
ATTATGTTTGAACAGGATTAATGCAGAAAGGAAGGGGGGATTCGGTTTACCATC  
TCCGGCTCTGGTATTTTCCTTTCGGTGCTGATCAGCAATGTCGCAGGTGCCGGAGA  
TGTCACTGCAGTGAAGATCAAAGGTTCAAGAACAGGCTGGCTTGATATGGGCAG  
GAATTGGGGCCAGAACTGGCATGTTAATGCTAATCTACAGAATCAAGCTCTCTCA  
TTCGAGGTCACCAGTAGTGATAGTATGACTGTAATTTCTTACAATGTTGCTCCCAA  
AGATTGGAGATTCGGACAGACCTTTGAAGGCAAGCAATTTGAGACTTGACGTACA  
AGCAAGAGGATAAGATGATAGATAGATGAGGCCATTTCTTTCTTTTCTTTCTTGT  
TTTGTCTCCTGATAGGTGAAGATGTATGTATCTATGGTCCAAACGATTTGGTTTG  
AGAGAGTAAATTGTTAAAGTCTGTTGCTTTCTGAGTACCAATCCTGCCTTGTTTTG  
TCATTTAATGTCACGAAGAAGAAGCTCGAACTCCATGCTTTTGGAACCTAGCCTA  
GCTCACCGGGTTAACTCGGATTCTGTTCGATCGAAAAACCGAGTAGAAATTGACCT  
GGT