

## IDENTIFICATION

**Species:** *Salix purpurea*

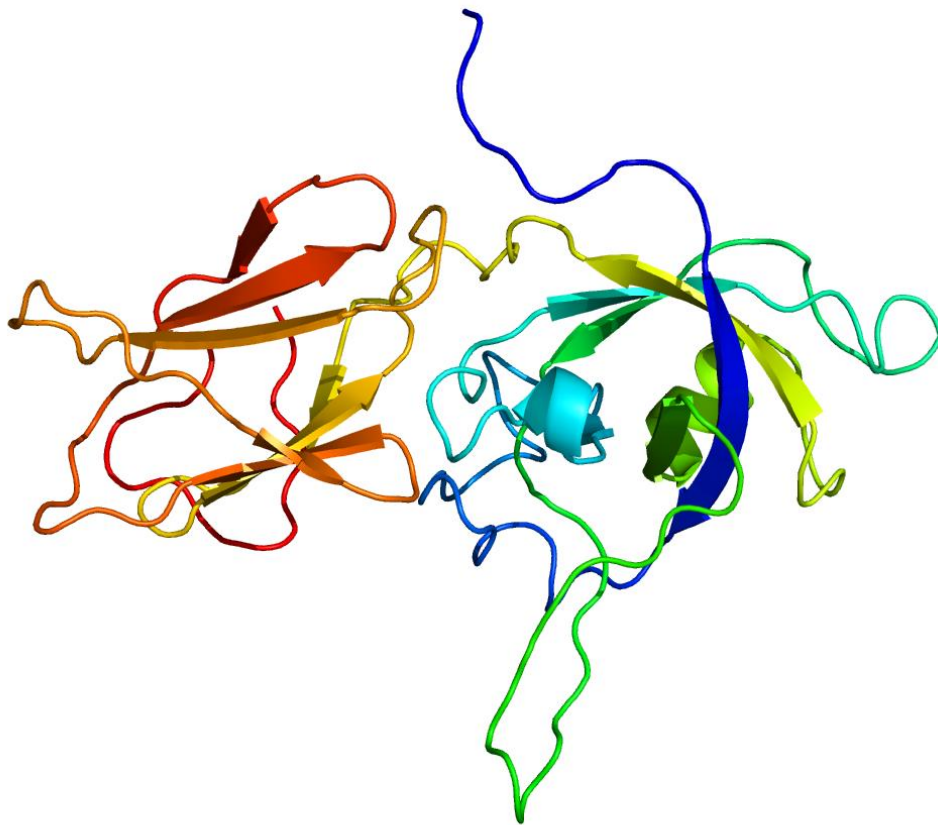
**Locus:** Sapur.016G088600

**Gene Model:** Sapur.016G088600.1.p

**Description:** SprEXPA-20

**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:-

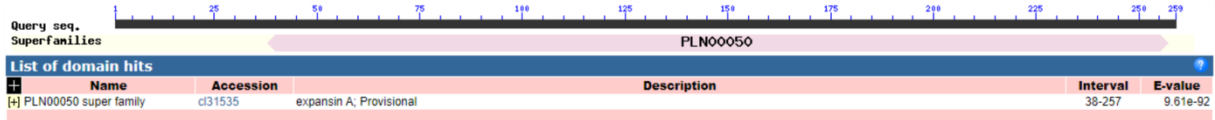
## EXTERNAL RESOURCES

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## GENE STRUCTURE



## DOMAIN ARCHITECTURE



## SEQUENCES

### Peptide

>SprEXPA-20

MASPLKPVLAALLLLTIAVPDCQAKSKPSLSGKQAIHHATFYEGGSGTFFGGACNYKD  
VAGQGYGMNTAALSSVLFKNGQACGACFEIKCADNPQWCKPGQPPLIVTATDHCPP  
NPSPNDNGGWCNVPREHFDVAKPVFSQLAEYKAGIPIHYRRVPCKKQGGIRFTILG  
NPWFYQVIVWNVKGAGDIVSVQVKGDDKLKWTQMERDWGATWKTSAILLGESLTF  
RVRASDKRYSTSWHVTPKNWQFGQTYEGKNFN\*

### CDS (coding sequence)

>SprEXPA-20

ATGGCATCTCCTTTGAAACCTGTGTTAGCAGCACTGCTGCTTTTAACCATTGCAGT  
GCCTGATTGCCAGGCAAATCAAACCTTCCCTCTCAGGGAAACAAGCCATTCAC  
CATGCAACTTTCTATGAAGGCGGCTCAGGGACATTTGGGGGAGCATGCAATTACA  
AAGATGTTGCAGGCCAAGGATATGGCATGAATACAGCTGCACTGAGCAGTGTTTT  
GTTCAAAAATGGACAGGCCTGTGGTGCTTGTTCGAAATCAAGTGCGCTGATAAC  
CCTCAATGGTGCAAGCCAGGGCAGCCACCTCTCATTGTCCTGCAACTGACCATT  
GCCACCAAATCCATCTCTCCAAATGACAATGGAGGCTGGTGCAATGTTCCACG  
TGAGCATTTCGATGTAGCCAAGCCTGTATTTAGTCAGCTTGCTGAGTACAAGGCC  
GGCATTATTCCAATCCACTATCGCAGGGTTCGTGCAAAAAGCAAGGAGGTATTA  
GATTCATAATTTGGGAATCCTTGGTTCTATCAGGTCATTGTGTGGAATGTGAA  
GGGAGCTGGAGATATTGTTAGTGTTCAAGTGAAGGGTGATGACAAGCTCAAGTG  
GACGCAAATGGAACGAGATTGGGGGGCAACTTGGAAAACCAGTGCTATTTTGCTT  
GGAGAGTCGCTAACCTTTCGTGTTAGAGCAAGCGATAAAAGATACTCCACTTCAT  
GGCATGTTACCCCTAAGAAGCTGGCAATTTGGCCAGACATACGAGGGCAAGAAGCTT  
CAACTAG

### Nucleotide

>SprEXPA-20

ATGGCATCTCCTTTGAAACCTGTGTTAGCAGCACTGCTGCTTTTAACCATTGCAGT  
GCCTGATTGCCAGGCAAATCAAACCTTCCCTCTCAGGGAAACAAGCCATTCAC  
CATGCAACTTTCTATGAAGGCGGCTCAGGGACATTTGGTATCGATTGATGGCTTC  
TTTTCCTTTTGCCCTTCTTTTCCGTCCAAATCCAACTTGCAATATGGTCTTTCCGT  
TAACTAAAAGCTTCAATATTGCGAGACTGCCTGCCAAGAGCAGTGGCAGTCT

GATGAGAACATTAATTTAATATTGTCAATAAGACTATATTGTAAAAAGAAGAAGA  
AAAACATGGAGTCCTCGCGCATCTGACGATTTTAACTGTAACCAACCCGTATATTA  
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CAATTACAAAGATGTTGCAGGCCAAGGATATGGCATGAATACAGCTGCACTGAG  
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CTGACCATTGCCACCAAATCCATCTCTCCCAAATGACAATGGAGGCTGGTGCAA  
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ACAAGGCCGGCATTATTCCAATCCACTATCGCAGGTCATATGACTTTTCAATTTCT  
TACCATTTAGCGATATTATAACCAGTTAGGAGGCCAGTTAGGAAGCTTAGGTCGAG  
TTTCTTAATTAAGGGTTCAATTTCCCTGCAGGGTTCCGTGCAAAAAGCAAGGA  
GGTATTAGATTCACTATATTGGGGAATCCTTGGTTCTATCAGGTCATTGTGTGGAA  
TGTGAAGGGAGCTGGAGATATTGTTAGTGTTCAAGTGAAGGGTGATGACAAGCTC  
AAGTGGACGCAAATGGAACGAGATTGGGGGGCAACTTGGAAAACCAGTGCTATT  
TTGCTTGGAGAGTCGCTAACCTTTCGTGTTAGAGCAAGCGATAAAAGATACTCCA  
CTTCATGGCATGTTACCCCTAAGAACTGGCAATTTGGCCAGACATACGAGGGCAA  
GAACTTCAACTAG