

IDENTIFICATION

Species: *Salix purpurea*

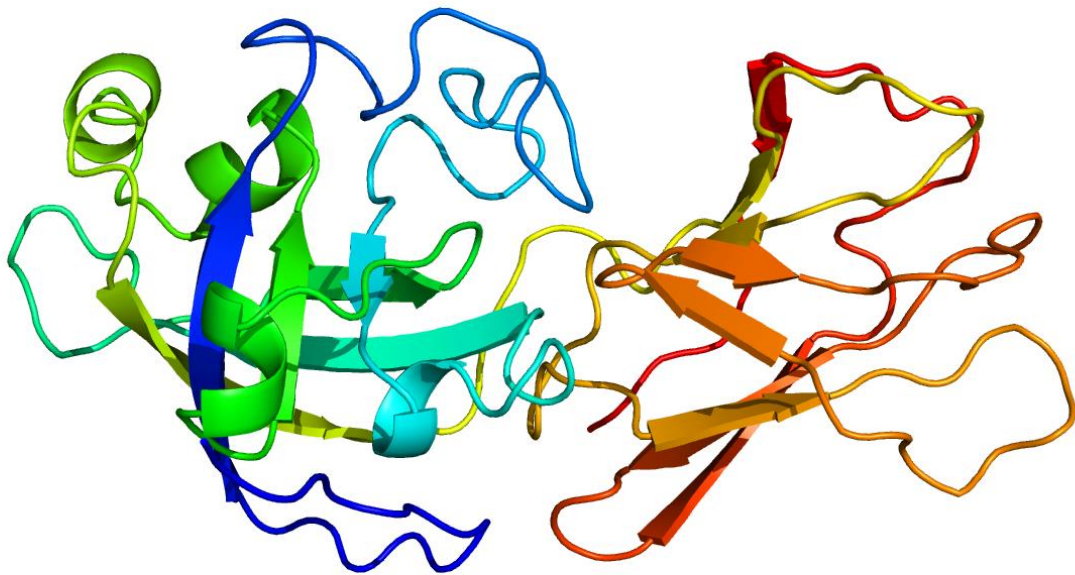
Locus: Sapur.019G097700

Gene Model: Sapur.019G097700.1.p

Description: SprEXPB-03

Family: Beta Expansin

3D structure:



GENOME DATABASES

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

KEGG:-

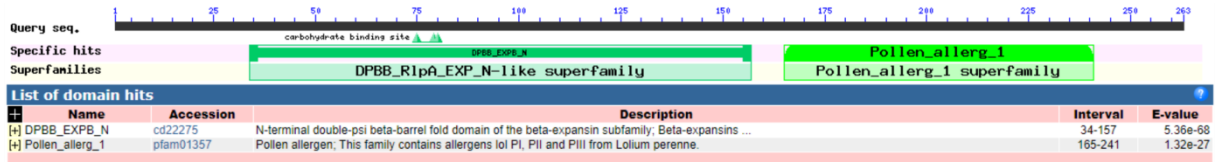
EXTERNAL RESOURCES

-

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>SprEXPB-03

MQLSGLYVMVFLKCF LAVSGQQIHSQHKVPDLHWKPATATWYGSPEGDGS DGGAC
GYGSLVDVKPLRARVGA VSPVLFKNGEGCGACYKVRCLDKSICSRRAV TIIVMDECP
GGYCSNGNTHFDLSGAA FGRMAISGENGLLRNKGILPVIYRRTPC KYPGKNIAFHVNE
GSTDYWLSLLVEFEDGD GDVGS MHIREAGGTEWLEMTHVWGANWCIVR GPLKGPF
SVKLTTLATGRTL SAREVIPRNWAPKATYTSRLNFLH*

CDS (coding sequence)

>SprEXPB-03

ATGCAGCTCTCGGGGTTATATGTTATGGTGTTCCTGAAGTGCTTTTTGGCTGTCTC
TGGCCAGCAAATTCATTCTCAACATAAAGTGCCTGACTTACACTGGAAACCGGCC
ACTGCAACCTGGTATGGCAGTCCTGAAGGTGATGGTAGTGACGGAGGGGCCTGT
GGGTACGGGTCATTGGTGGACGTGAAGCCATTGAGGGCCAGAGTTGGTGCAGTG
AGCCCAGTGCTCTTCAAGAATGGCGAAGGATGTGGGGCATGCTACAAAGTTAGG
TGCCTAGACAAGAGCATATGCTCAAGAAGAGCAGTGACCATAATTGTTATGGATG
AGTGTCCAGGTGGGTATTGCTCCAATGGTAACACCCACTTCGATCTTAGTGGTGC
AGCCTTTGGTCGGATGGCTATTTCCGGTGAGAATGGTCTGCTCAGGAACAAGGGT
ATACTCCCGGTCATTTATCGGGCGGACCCCATGTAAGTACCCAGGGAAGAACATTG
CCTTCCATGTCAATGAAGGCTCGACAGATTATTGGCTATCCCTTCTAGTAGAGTTT
GAAGATGGAGATGGCGATGTTGGATCGATGCATATACGAGAAGCAGGTGGCACT
GAGTGGCTAGAGATGACTCACGTATGGGGTGCAAATTGGTGTATTGTCAGGGGAC
CCTTGAAAGGACCGTTCTCCGTGAAATTAACGACACTAGCAACGGGAAGAACAC
TGTCAGCAAGAGAAGTGATTCCAAGAACTGGGCTCCGAAAGCTACTTACACCTC
CAGGCTCAATTCCTCCATTGA

Nucleotide

>SprEXPB-03

GAAATCACTTAAACAACAACACCCTTTAGTAAATAGTAAGTGAGTGAAGTGTTT
TTGTTTCAAAGAAACAACAAAACACTGTCCGCAGAGGTTGTAAAAACTGTTTCTTT
AACTGTTTTTCTTGGGTTCTCCGCCTGGGAAGCGATATTGTAAAGTAGAGATAGT

GGTGGCGGTGATTGGTGGCGCCGCCGTTTCGTAGAGAGACCATTTGGTGCAAAG
ACCCTTTCGGCTCACAAATGCAGCTCTCGGGGTTATATGTTATGGTGTCTTGAAGT
GCTTTTTGGCTGTCTCTGGCCAGCAAATTCATTCTCAACATAAAGTGCCTGACTTA
CACTGGAAACCGGCCACTGCAACCTGGTATGGCAGTCCTGAAGGTGATGGTAGTG
ACGGTGAGTGCTCACTTTATGTGCCCGGTATTGTTTTTCCAATTTTGTGATTTTTGG
TGCAGCATTTTTTTTTTCATCTTGGATCTCTTTTTCTTTGTTTTTCATGGTGGTCAAAC
TCGGTGACTTGACTCACTTTTCGCCTCGACCACTAGCTTGGTACAAGTTGATGGGG
AAAGTCATTTTTTACTTTCTCTTGTATTTTTTTTATCTATTTAATTACTGTTGATAA
AGAAACCATGTTCTCTCTCTTTTTGTAAAGAGACGGCGTGTACTCAGCGTAGCAAT
TTTGGCACCATGTTTCTTAATTAAGCTCTCACATTCCCAAACCTAAACTTGCATC
CCTAAATTATGTGACAACATGTAATGTCTGCAGGAGGGGCCTGTGGGTACGGGTC
ATTGGTGGACGTGAAGCCATTGAGGGCCAGAGTTGGTGCAGTGAGCCCAGTGCTC
TTCAAGAATGGCGAAGGATGTGGGGCATGCTACAAAGTTAGGTGCCTAGACAAG
AGCATATGCTCAAGAAGAGCAGTGACCATAATTGTTATGGATGAGTGTCCAGGTG
GGTATTGCTCCAATGGTAACACCCACTTCGATCTTAGTGGTGCAGCCTTTGGTCGG
ATGGCTATTTCCGGTGAGAATGGTCTGCTCAGGAACAAGGGTATACTCCCGGTCA
TTATCGGCGGTATGGATGGCAATAATCTTCTCCCTTTCTAGTTTACCCGCCTGTC
TCACTTCTCTTGATAATTTTGGTTTTTTTTCTTAATAGTTCTTTTTAAAAATGAAAT
AAAACCCCTTTTTGTAGGACCCCATGTAAGTACCCAGGGAAGAACATTGCCTTCC
ATGTCAATGAAGGCTCGACAGATTATTGGCTATCCCTTCTAGTAGAGTTTGAAGA
TGGAGATGGCGATGTTGGATCGATGCATATACGAGAAGTAAGCAATCTTCTTCCCT
TAATTTCTGTTGTTATTCATTACATCTCGGACTTTAGGCTCCGGAATCTTGGCCAT
GTCTAACTTTGTGGAGTGCAAAGTGAGATGCCATTTACTTCATGGGTGTCATGACTC
GACAAAGGTGCAAATAATATTGTCATCTTTTAGGGGTGCTGTTCTGCTAAAGTG
CTTCTTCGAAAGTGTTCACTTTCACTTTAAAAATAAAAAAGAACTGCCTAAACGTG
CTAAATCCAAGTAGTGCCCTCGCATGAAAAGCAAGTGTAATGCTAATTTTAGAAC
TTTTAGTTTGATTGGCAAGACATTATTTATACTAATATTTTGAAACGACAACACCT
TGTAGTCAGTCAAATGGCATGGCCCAGCATCACCCATTTCCCCCATCTTTGTTGG
GTAAACCCCAAAGCACTTTGTTTCCTGCTTGGGTTTTCTCTCCTGTATTTTAGTAT
TTTCTTGACTCGTTGCATAAATGGGCCACTCTCTGCAATTCAAGAACATGAAAAG
GGAAATCTAAGGACTTGGTGGATTCTAGTTTCTGAAAAGAGATCTGGATAATGAA
TGAAAACAGGGTATAAATCTCAATATTCAAATAGAAATTATATATGCAGATCTC
ACATGATTTTTCGTTTTCTAATTGACAGGCAGGTGGCACTGAGTGGCTAGAGATGA
CTCACGTATGGGGTGCAAATTGGTGTATTGTCAGGGGACCCTTGAAAGGACCGTT
CTCCGTGAAATTAACGACACTAGCAACGGGAAGAACAACACTGTCAGCAAGAGAAGT
GATTCCAAGAAACTGGGCTCCGAAAGCTACTTACACCTCCAGGCTCAATTTCTC
CATTGATACAGCTTCAAGCTTTTCTTGGTGTGAAATCACATGAGAGAAACAAACA
AGCCCATTTCTATGACAGGAAAACGTGCCTTGTGTTCCCTTGAAACAAAAGTAG
CCGTTCACTGGTGTGGTGTTTTTTTTTTTTTTATATATATATAGAAAAGTAGCCGTT
GGATTGCATAATGGCATCCAAAGCTCTTTTTTCTTTTTCTTTTTTCTTTTTTCTTTTTT
TTGATCTTTGCCCCCTACTTTTGTAGTGTGAAAGTGTTTAAATTTAGATCGTCAA
TGTAGCCCTCTCCAAAGGAGAGAGAGCGTATGATATTATGTATTTTCATGTTTGTGT
AAGTTTCTTAGGCCATTTGGGTCATCAATGAATCTGGACCGTTGAATGTTATTAGA
GATAGTACATGGTGGGACCTTGTTCATCATTTTTTCACTTCCATCTCATTGTTTTTC
AGTACCTTTTATCGAACAGAAATTAATGGTTGCATAGTTGAATGCCTG