

IDENTIFICATION

Species: *Trifolium pratense*

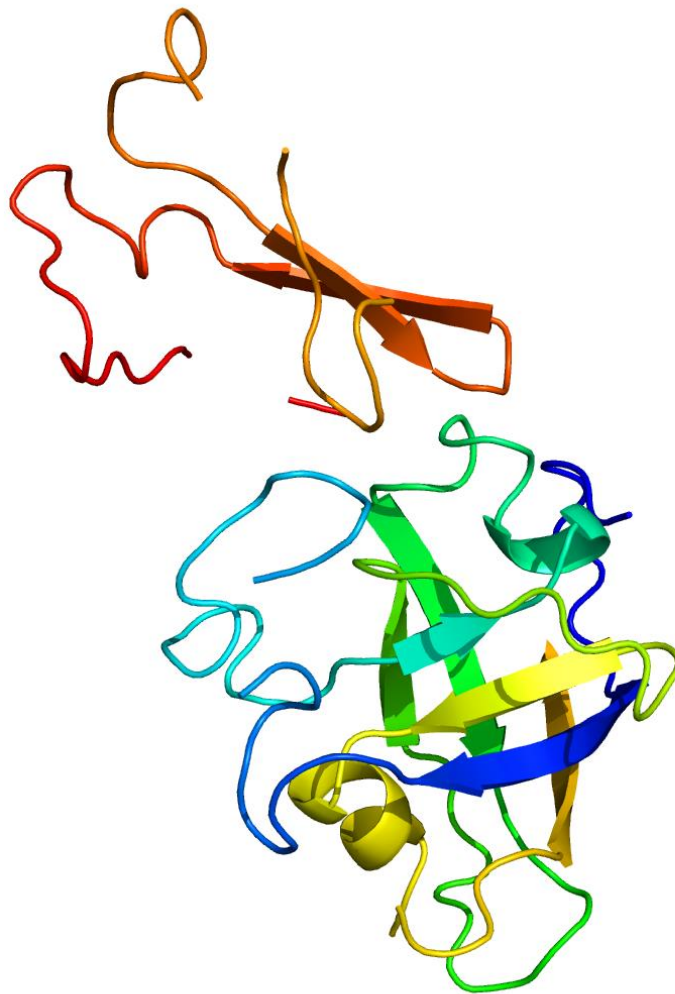
Locus: Tp57577_TGAC_v2_mRNA6621

Gene Model: Tp57577_TGAC_v2_mRNA6621

Description: TprEXPA-23

Family: Alpha Expansin

3D structure:



GENOME DATABASES

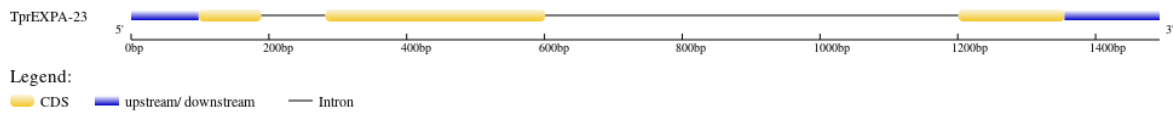
Phytozome: https://phytozome-next.jgi.doe.gov/info/Tpratense_v2

KEGG:-

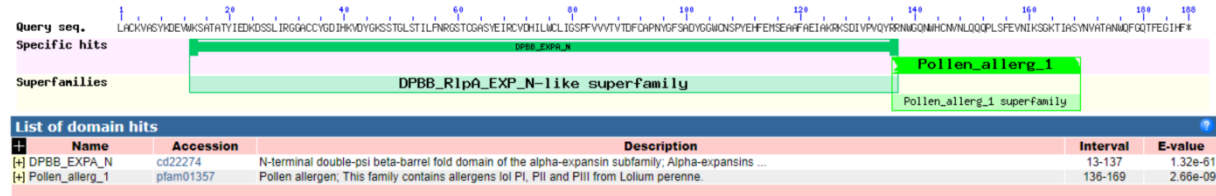
EXTERNAL RESOURCES

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GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>TprEXPA-23

LACKVASVKDEVWKSATATYIEDKDSSLIRGGACCYGDIHKVDYGKSSTGLSTILFN
RGSTCGASYEIRCVDHILWCLIGSPFVVVTVDFCAPNYGFSADYGGWCNSPYEHFE
MSEAAFAEIAKRKSDIVPVQYRRNWGQNWHCNVNLQQQPLSFEVNIKSGKTIASYN
VATANWQFGQTFEGIHIF*

CDS (coding sequence)

>TprEXPA-23

CTGGCATGCAAGGTTGCTTCTTACAAAGATGAAGTATGGAAATCTGCAACTGCAA
CATAATCGAAGATAAAGATAGTTCTCTCATAAGAGGAGGAGCTTGTGTTATGG
AGACATTCACAAGGTTGATTATGGAAAATCTAGTACAGGATTAAGCACCATTTG
TTCAATAGAGGTAGTACTTGTGGGGCTAGCTATGAGATTAGATGTGTTGATCATA
TCTTATGGTGTGTTGATTGGAAGTCCTTTTGTAGTTGTTACTGTTACTGATTTTTGTG
CACCGAATTATGGATTTTCAGCTGATTATGGTGGATGGTGTAAATTCTCCATATGAA
CATTTTGAGATGTCAGAAGCTGCATTTGCTGAAATTGCCAAGAGAAAATCTGATA
TAGTGCCAGTTCAATATAGAAGGAATTGGGGACAAAATTGGCATTGCAATGTGA
ATCTTCAACAACAGCCTCTATCCTTTGAGGTGAATATCAAAGTGGAAAAACAAT
CGCATCTTACAACGTTGCAACTGCAAATTGGCAGTTTGGACAGACATTTGAAGGA
ATACATTTCTAG

Nucleotide

>TprEXPA-23

CCATTGTTTAGTGTTATTGTTTCCATTCAAAGAAAAACTCTTCTTTTTGTCTAAC
ATGGGTGTTTTACAATCTTCATTTCTTTAACTGATTTTACTACTGGCATGCAAGGT
TGCTTCTTACAAAGATGAAGTATGGAAATCTGCAACTGCAACATACATCGAAGAT
AAAGATAGTTCTCTCATAAGAGGTATTAATTTCTCTTTATCTAATCTTAGCATAAG
TTCGTCTATATAATCACTTTTGTAGTTTGTAAAATGTGGTTAGTTGAGTATTGATTA
TAGGAGGAGCTTGTGTTATGGAGACATTCACAAGGTTGATTATGGAAAATCTAG
TACAGGATTAAGCACCATTTTGTTCATAGAGGTAGTACTTGTGGGGCTAGCTAT
GAGATTAGATGTGTTGATCATATCTTATGGTGTGTTGATTGGAAGTCCTTTTGTAGT

TGTTACTGTTACTGATTTTTGTGCACCGAATTATGGATTTTCAGCTGATTATGGTG
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AATTGCCAAGAGAAAATCTGATATAGTGCCAGTTCAATATAGAAGGTACAAAA
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TATCTTTTTCCATAAAAATAGCTTATTAATAAGTACTTGTAAGCTAATACATTGTA
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CTTAGGCTAGGCATATGGGTTTTACAAGTGAAATTTTTTGCTGGTGTGAATATTAT
GCAGAAATTCACAATGAGTGGAATTCACAATGAGTGGAAGTTATAATTTTTTGC
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CATTGCAATGTGAATCTTCAACAACAGCCTCTATCCTTTGAGGTGAATATCAAAA
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AGATAAATTTTTATGACTTGAATTTTGA ACTACTAACTGTGATTTATGACCCTTCC
AAGGCTTTTATTTTGACATGATGTTCAACTAATTAATGCTGTAACGATGT