

IDENTIFICATION

Species: *Trifolium pratense*

Locus: Tp57577_TGAC_v2_mRNA26650

Gene Model: Tp57577_TGAC_v2_mRNA26650

Description: TprEXLB-02

Family: Expansin Like Beta

3D structure:



GENOME DATABASES

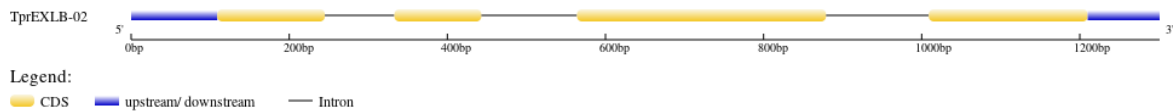
Phytozome: https://phytozome-next.jgi.doe.gov/info/Tpratense_v2

KEGG:-

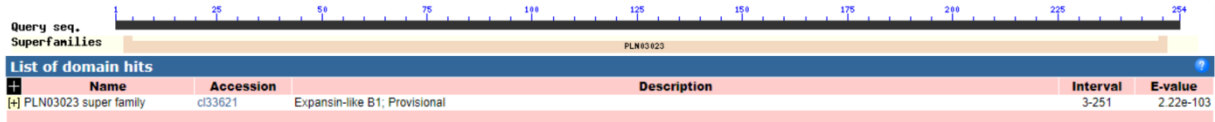
EXTERNAL RESOURCES

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GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>TprEXLB-02

MDLSFKYQFSLVCVILLFPALCSCKEYYAKSRASYGTS DGYGNSRGACGFGYYGKI
VNDGSVTA VSAKLWKN GEGCGACYQVKCKIPQLCDYNGTYVVVTDY GEGDRTDFI
TSPHAFSKLGRNAVASEK LKKYGVLDVEYKRVPCTFKGNNIVYQINENS RNPGYFAI
NVLYVGGTYDVT TVEIWQREQHQWVAMRRSYGAVFDFANPPEGEIRLRFQVSSNIE
AHYYVVS RFPVPAVWKAGATYSTKILPY*

CDS (coding sequence)

>TprEXLB-02

ATGGATCTTAGT TTTAAGTATCAATTTAGCCTTGTTTGTGTTATTCTGTTGTTTCCA
GCACTATGTAGCTGCAAAGAATATTATGCCAAATCTAGAGCTTCCTATTATGGCA
CCTCTGATGGCTATGGAAATTCAAGGGGAGCTTGTGGTTTTGGATACTATGGAAA
AATAGTGAATGATGGCAGTGT CACAGCTGTGTCTGCAAAGCTGTGGAAAAATGG
AGAAGGCTGTGGTGCATGCTATCAAGTAAAGTGCAA AATACCACAATTATGTGAT
TACAATGGAACATATGTTGTGGTAACTGACTATGGTGAGGGAGATAGA ACTGATT
TCATAACGAGTCCACACGCCTTCTCAA AATTAGGACGCAACGCAGTTGCATCTGA
AAAATTGAAGAAATATGGAGTATTGGATGTTGAATACAAAAGAGTTCCTTGTACA
TTTAAAGGCAACAATATTGTGTACCAAATCAATGAAAATAGTAGAAATCCTGGCT
ACTTTGCTATCAATGTTCTTTATGTTGGAGGAACTTATGATGTCACTACTGTTGAA
ATATGGCAGAGAGAACAACACCAATGGGTGGCGATGCGTAGATCTTATGGGGCA
GATTTGACTTTGCTAACCACCAGAAGGTGAAATCAGATTAAGATTTCAAGTGA
GTAGCAATATTGAAGCTCATTATTATGTGGTGTCAAGGTTCCAGTTCCTGCAGTT
TGGAAGGCTGGTGCTACTTATCCACTAAGATTCTGCCTTATTA

Nucleotide

>TprEXLB-02

CATCTCATACAAATATTTCACTTGTATAATTTCTTACCTTTCAAAGTAAAATAAA
TATTTCACTTGTATATTGTATTGCATTTCATAACTTGTGTTGCTTCATTAGACATGG
ATCTTAGTTTTAAGTATCAATTTAGCCTTGTTTGTGTTATTCTGTTGTTTCCAGCAC
TATGTAGCTGCAAAGAATATTATGCCAAATCTAGAGCTTCCTATTATGGCACCTCT
GATGGCTATGGAAATTCAAGTATGTCATATGATTGTGATCCTCCCTTTGTAGCTAG
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GCTTGTGGTTTTGGATACTATGGAAAAATAGTGAATGATGGCAGTGTCACAGCTG
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TAACTTTTCTTTCCTTTCATTTTTAATTTCAATATTTCCAATAAACCTTAGTAAAAG
AATGCTTTATCATCATTTAAACTTTACAAAATATAAATGATGGCGTACACTTAATT
TAGGTAAAGTGCAAATAACCACAATTATGTGATTACAATGGAACATATGTTGTGG
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CTCAAATTAGGACGCAACGCAGTTGCATCTGAAAAATTGAAGAAATATGGAGT
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TACCAAATCAATGAAAATAGTAGAAATCCTGGCTACTTTGCTATCAATGTTCTTTA
TGTTGGAGGAACTTATGATGTCACTACTGTTGAAATATGGCAGGTATATTACTTA
CACAATACTACTTTATTAGTATTTGACTAAATTTTGCTTATATTTAAAACCAGAAG
GACCGTATAATACAGATGGTCTATTTTTTTTATACAATCATCTAATTAGATTTTGTT
ATTCAGAGAGAACAAACACCAATGGGTGGCGATGCGTAGATCTTATGGGGCAGTA
TTTGACTTTGCTAACCCACCAGAAGGTGAAATCAGATTAAGATTTCAAGTGAGTA
GCAATATTGAAGCTCATTATTATGTGGTGTCAAGGTTCCCAGTTCCTGCAGTTTGG
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AGACTTCAGTTTAAAATCCCATAAACTGTTGTTTTATCAAAAAAAATGTGTGACT
AGAATAATGGGATTCGTGTATT