

IDENTIFICATION

Species: *Phaseolus vulgaris*

Locus: Phvul.008G232200

Gene Model: Phvul.008G232200.1.p

Description: PvEXPA-17

Family: Alpha Expansin

3D structure:



GENOME DATABASES

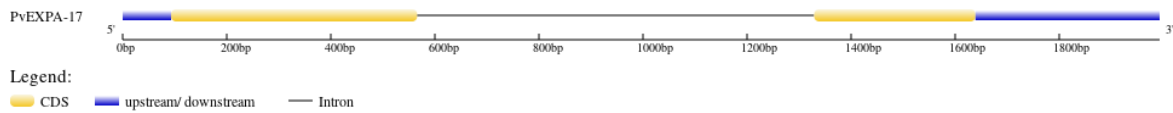
Phytozome: https://phytozome-next.jgi.doe.gov/info/Pvulgaris_v2_1

KEGG: <https://www.genome.jp/entry/gn:T03093>

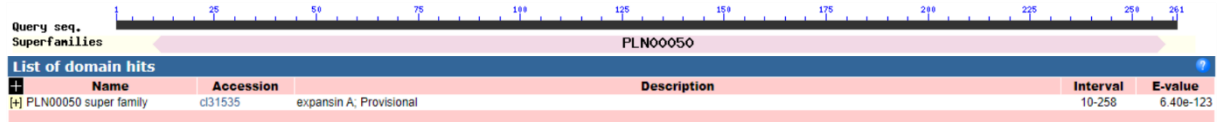
EXTERNAL RESOURCES

<https://www.pulsedb.org/organism/636>

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>PvEXPA-17

MASFQKLLAIVSLVTVLLASAEARIPGVYGGAWETAHATFYGGSDASGTMGGACG
YGNLYSQGYGVNTAALSTALFNSGLSCGACFEIKCADDPSWCHAGSPSILVTATNFCP
PNYALPSDNGGWCNPPRPHFDLAMPFLKIAEYRAGIVPVSYRRVPCRKQGGMRFTI
NGFRYFNLVLITNVAGAGDVVRTSVKGAKTGWMSMSRNWQNWQSNVAVLVGQSL
SFRVTASDRRTSTSWNIVPANWQFGQTFTGKNFRV*

CDS (coding sequence)

>PvEXPA-17

ATGGCTTCTTTTCAAAAACCTCCTTGCCATTGTTCCCTCGTTACCGTTCTTCTCGCT
TCCGCCGAGGCCCGAATCCCGGGCGTGTACGGCGGCGGCGCGTGGGAGACCGCG
CACGCCACGTTCTACGGCGGTAGCGACGCGTCGGGTACAATGGGAGGCGCGTGC
GGCTACGGGAACCTGTACAGCCAGGGGTACGGCGTGAACACGGCGGCCCTGAGC
ACTGCACTGTTCAACAGCGGGCTGAGCTGCGGAGCGTGCTTCGAGATAAAGTGCG
CGGACGACCCGAGCTGGTGCCACGCTGGCAGCCCCCTCGATCTTGGTGACGGCCAC
GAACTTCTGCCCTCCGAACTACGCTCTCCCCAGCGACAATGGAGGATGGTGCAAC
CCTCCAGACCACACTTCGACCTCGCCATGCCCATGTTCCCTCAAAATCGCTGAGT
ACCGCGCCGGAATCGTCCCCGTCTCTTACCGCAGGGTGCCTTGTCGAAAGCAGGG
AGGGATGAGGTTACGATCAACGGCTTCCGTTACTTTAACCTGGTTTTGATCACC
AACGTGGCCGGTGCAGGGGATGTCGTGAGGACGAGCGTGAAAGGGGCTAAGACT
GGGTGGATGAGTATGAGCCGCAACTGGGGTCAGAATTGGCAGTCAAACGCTGTT
CTGGTTGGTCAGTCACTCTCCTTCAGGGTGACAGCCAGTGACCGACGCACCTCCA
CCTCTTGGAACATTGTACCCGCCAATTGGCAATTTGGCCAAACCTTCACAGGCAA
AAATTCAGGGTCTGA

Nucleotide

>PvEXPA-17

TCCACAGAACTCAAACGCAGAGCGAGTTAGTTTCTAAAACCGTTCTTCTTTTCATA
ACTCCTAACAAAACCCTGCTCGGTCTTCCCCTCATAATGGCTTCTTTTCAAAAAC
TCCTTGCCATTGTTTCCCTCGTTACCGTTCTTCTCGCTTCCGCCGAGGCCCGAATCC
CGGGCGTGTACGGCGGCGGCGCGTGGGAGACCGCGCACGCCACGTTCTACGGCG
GTAGCGACGCGTCGGGTACAATGGGAGGCGCGTGC GGCTACGGGAACCTGTACA

GCCAGGGGTACGGCGTGAACACGGCGGCCCTGAGCACTGCACTGTTCAACAGCG
GGCTGAGCTGCGGAGCGTGCTTCGAGATAAAGTGCGCGGACGACCCGAGCTGGT
GCCACGCTGGCAGCCCCTCGATCTTGGTGACGGCCACGAACTTCTGCCCTCCGAA
CTACGCTCTCCCCAGCGACAATGGAGGATGGTGAACCCTCCCAGACCACACTTC
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CCGTCTCTTACCGCAGGTAACGTTACTTTACCCATTTTCGCTCCACACTTCGCCT
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TAAATATCAGTTATTAATAATTTGTGTTTCATAATTTAAAACATTAGAGTTGAAAA
AAACGGAATTTTCCGCATTTGGGATAGGTGTAGTTTTTGACACAATTGTCTAGAC
ACTAGCAATAAAAAAGTTAATAATTTTTTATAGTAAAGAAAGGGAGAAATTAATT
AACTTTAATATTGTAGGAGTATAAAAAAAGGGAGATTTTGATGTTTTATTATTTTA
TAATAAAATGAGAATAAAGGAAATAGAGTAAACGCGCTTGTTTGGCTTTTGGCCT
TCTGAGAGTACAAAGCGCAGAGACAGAAATGCGACGTCGTTTAAACCGACAAAG
TGACTGATATTCTTACACTGTGGCGGGGACTAGACAGTAGACAATAGGTAATTC
GTAATTCAGAAAAGTGAAAACAGATGAGAACCGTAGATGCTTATTTGGTGGCCCT
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TATCTT