

IDENTIFICATION

Species: *Helianthus annuus*

Locus: HanXRQChr12g0366791

Gene Model: HanXRQChr12g0366791

Description: HanEXPA-19

Family: Alpha Expansin

3D structure:



GENOME DATABASES

Phytozome: https://phytozome-next.jgi.doe.gov/info/Hannuus_r1_2

KEGG: <https://www.genome.jp/entry/T05101>

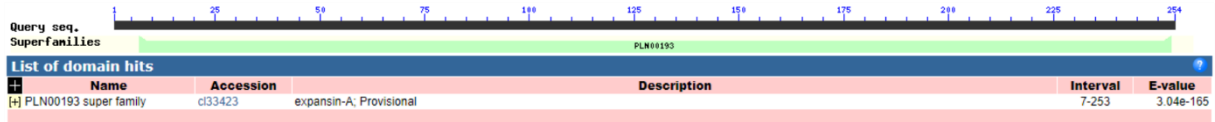
EXTERNAL RESOURCES

<https://www.heliagene.org/>

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>HanEXPA-19

MAKSCIILLSAICYLHVHSDAFTASGWTRAHATFYGGSDASGTMGGACGYGNLYTTG
YKTRTAALSTALFNEGGACGQCYKIICDYKADPRWCRKGASVTITATNFCPPNFAQP
NDAGGWCNPLQHFDMAQPAWEKIGIYAGGIIPVIYQRPCKKKHGVRFITINGRDYF
ELVLITNVGGAGSIQSVKIKGSKTDWQPMSRNWGANWQNSYLDGQSMSFMVTTSD
GVTKTFMDVVPANWGFQTFSSPLQF*

CDS (coding sequence)

>HanEXPA-19

ATGGCGAAAAGTTGCATTATTTTGTATCTGCAATCTGTTATCTGTTTGTTCATTC
GGATGCATTTACAGCATCGGGATGGACACGGGCTCATGCAACCTTTTATGGAGGC
AGTGATGCTTCAGGAACAATGGGGGGTGCTTGTGGATATGGTAACTTGTATACAA
CCGTTACAAAACAAGAACAGCTGCATTGAGTACTGCTCTTTTAAACGAAGGTGG
CGCATGCGGCCAATGCTACAAGATCATATGCGATTACAAGGCAGACCCAAGGTG
GTGCCGAAAGGAGCATCGGTAACCATCACCGCCACCAACTTCTGCCACCAAAT
TTTGCTCAGCCTAACGATGCCGGGGGCTGGTGCAACCCACCCCTCCAACATTCG
ATATGGCTCAGCCCGCTTGGGAAAAAATCGGCATTTATGCTGGTGGCATCATCCC
TGTTATCTATCAAAGAGTACCATGCAAGAAGAAACATGGAGTTAGATTCACAATA
AACGGTCGAGATTATTTGAGCTTGTTTAATAACTAATGTTGGAGGGGCTGGAT
CAATCCAATCGGTGAAGATTAAGGGTTCGAAAACCGACTGGCAGCCGATGTCAA
GGAATTGGGGAGCTAACTGGCAATCAAATTCCTTATCTCGACGGACAATCTATGTC
CTTCATGGTCACAACCTAGTGATGGTGTCACTAAAACCTTCATGGATGTCGTCCTG
CAAACCTGGGGTTTTGGTCAAACCTTCTCGAGTCCTTTGCAATTCTAA

Nucleotide

>HanEXPA-19

ATCTTCTAAAGCCATCTTATTCATTCTCATTTCGATCCAACCTCTTTGCAGACCGAG
AATGGCGAAAAGTTGCATTATTTTGTATCTGCAATCTGTTATCTGTTTGTTCATT
CGGATGCATTTACAGCATCGGGATGGACACGGGCTCATGCAACCTTTTATGGAGG
CAGTGATGCTTCAGGAACAATGGGTATATTTCTTTTCTAGCTAAACTTACTTGTT
AACTATCAATTTATGTAGGCGTAAAAGATTTTATTATAAATATTTTTACCATTTT
GACATTAATTTTTGTATGACGATTAACAAGGTTTCGTTTTTATTAGTGAACCAA

ACAATAAACATTTAATCGATATTAGCACATTTTATTTTACTGTTAACAAAGGGATT
TGGTAACTTGTATGCAACCGGGTACAAATCAAGAACAATAAGAAACAAACGGGT
TAAACCTATAACTAATTTTAAGGTTATATATATCTTGTGCAGGGGGTGCTTGTGGA
TATGGTAACTTGTATAACAACCGGTTACAAAACAAGAACAGCTGCATTGAGTACTG
CTCTTTTAAACGAAGGTGGCGCATGCGGCCAATGCTACAAGATCATATGCGATTA
CAAGGCAGACCCAAGGTGGTGCCGGAAAGGAGCATCGGTAACCATCACCGCCAC
CAACTTCTGCCACCAAATTTTGCTCAGCCTAACGATGCCGGGGGCTGGTGCAAC
CCACCCCTCCAACATTTTCGATATGGCTCAGCCCGCTTGGGAAAAAATCGGCATTT
ATGCTGGTGGCATCATCCCTGTTATCTATCAAAGGTCATCTATCTCTCTTTTAATTT
TTTGCCGAACCTTTTTTTTTTTTTTTTTTTGTGGCCAAAAGACTGATGTTTTTGGTT
TGACTGGTTTTTCAGAGTACCATGCAAGAAGAAACATGGAGTTAGATTCACAATAA
ACGGTCGAGATTATTTTGAGCTTGTTTTAATAACTAATGTTGGAGGGGCTGGATC
AATCCAATCGGTGAAGATTAAAGGGTCGAAAACCGACTGGCAGCCGATGTCAAG
GAATTGGGGAGCTAACTGGCAATCAAATTCTTATCTCGACGGACAATCTATGTCC
TTCATGGTCACAACCTAGTGATGGTGTCCTAAAACCTTCATGGATGTCGTCCCTGC
AACTGGGGTTTTGGTCAAACCTTCTCGAGTCCTTTGCAATTCTAAATGTTGAACA
ACAAATGTGGTTTTAAATGGTTTTAAGGTTTAGAGATTCGGGGTTTTCAAAGTGCCA
GCGGCGTGTACTCTTTTTATAGAAGCAGCCCGCGGGGTTTTCTTTCTTTCTTTTT
TTAATCTTAGTTGTGTTTTTATAATAACTATATGGATTGTGCTCGTTATACTTGTG
TATTCTTTGACAATTATGTAATGAAAACCACTGCTTTGAGCATCATTTTTAGCTTA
TCATTCAATAGACTAAGCAGTTTAGCAATCTGTTCATTAGTCAAAGTACTCATAG
AAGAAG