

IDENTIFICATION

Species: *Helianthus annuus*

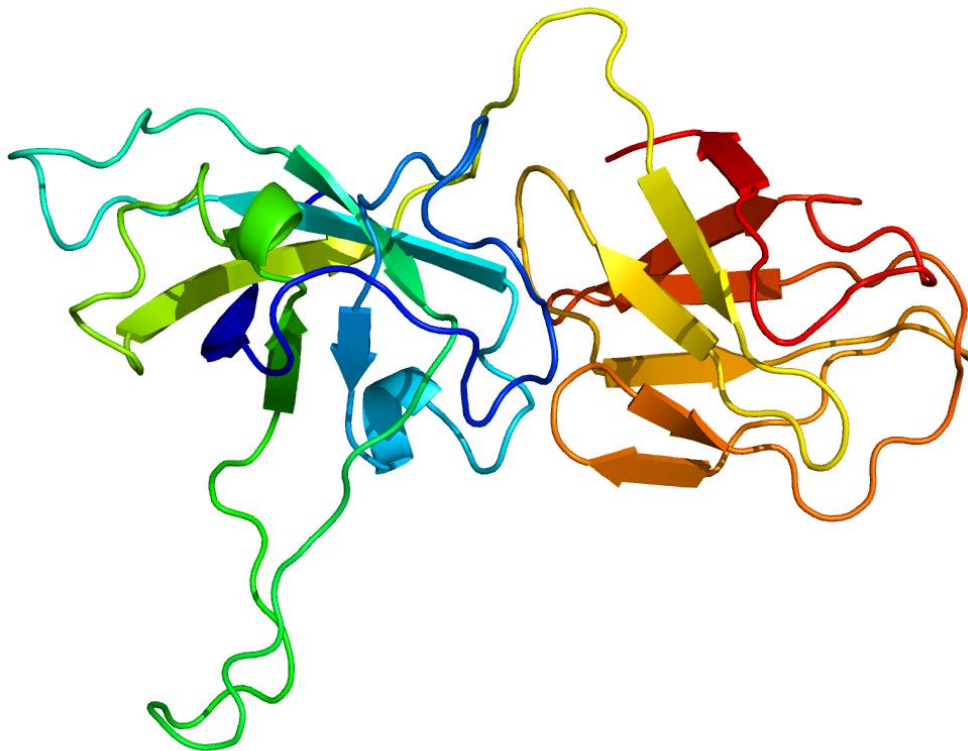
Locus: HanXRQChr08g0227911

Gene Model: HanXRQChr08g0227911

Description: HanEXPA-12

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>

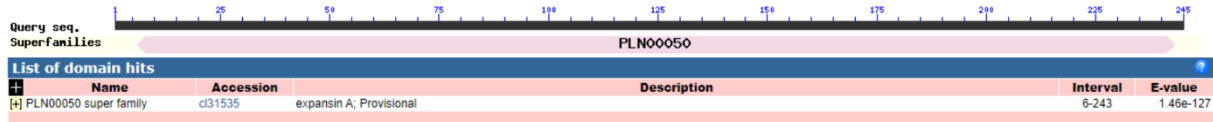
EXTERNAL RESOURCES

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

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>HanEXPA-12

MKSIVIFIFSSLLLVSFPSIVNGGWLNHAHATFYDDGTMGGACGYGNVYRQGYGTNNV
ALSSALFNDGLSCGACFQIMCVNDRQWCLPGSIVVTATNFCPPNPALPSEKGGWCNP
PLRHFDLSQPAFLRIAQYKAGIVPVA YRRVPCVRRGGIRFQMNGHSYFNLVLITNVGG
AGDVHAVA IKGSRGTGWQQMKQNWGQNWQSDTYFNGQSLFRVTTSDGRTVVSNN
VVPANWSFGQTFSGSQFR*

CDS (coding sequence)

>HanEXPA-12

ATGAAATCCATTGTTATTTTCATTTTCTCTAGCTTATTGCTTGTTAGTTTTCCGTCA
ATCGTTAACGGCGGTTGGCTCAATGCGCATGCCACATTCTACGACGACGGCACAA
TGGGTGGTGCTTGTGGGTATGGGAATGTGTATCGTCAAGGGTATGGTACAAACAA
TGTAGCATTAAAGTAGCGCTTTGTTCAACGATGGTTTGAGTTGTGGGGCATGTTTTT
AAATCATGTGTGTTAATGATCGTCAATGGTGTTTACCGGGTCCATTGTTGTCACC
GCCACCAACTTCTGCCCACCGAACCCCGCCTTACCTAGCGAGAAAGGCGGCTGGT
GCAACCCTCCTCTACGTCATTTTGTCTATCTCAACCTGCCTTCTTACGCATTGCTC
AGTACAAAGCTGGAATTGTTCCCTGTTGCTTATAGAAGGGTACCCTGCGTGAGAAG
GGGTGGAATTAGGTTCCAAATGAACGGACACTCCTACTTCAATTTGGTGTTAATT
ACAAATGTGGGTGGTGCTGGTGACGTGCACGCGGTGGCAATTAAGGGTCAAGA
ACAGGATGGCAACAAATGAAACAAAACCTGGGGGCAAACTGGCAATCCGACACT
TATTTTAAACGGGCAGTCTCTATCTTTAGGGTCACCACAAGTGATGGTTCGGACTGT
GGTGTCCAACAATGTTGTCCCCGCTAATTGGTCTTTTCGGGCAGACCTTCAGCGGTT
CCCAATTCGTTGA

Nucleotide

>HanEXPA-12

ATGAAATCCATTGTTATTTTCATTTTCTCTAGCTTATTGCTTGTTAGTTTTCCGTCA
ATCGTTAACGGCGGTTGGCTCAATGCGCATGCCACATTCTACGACGACGGCACAA
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TTTTTTTTTTAAAACGGTAATTCACACACTCTGTATGTATAACAGGTGGTGCTTGT
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GCGCTTTGTTCAACGATGGTTTGAGTTGTGGGGCATGTTTTCAAATCATGTGTGTT

AATGATCGTCAATGGTGTTCACCGGGTCCATTGTTGTCACCGCCACCAACTTCTG
CCCACCGAACCCCGCCTTACCTAGCGAGAAAGGCGGCTGGTGCAACCCTCCTCTA
CGTCATTTTGATCTATCTCAACCTGCCTTCTTACGCATTGCTCAGTACAAAGCTGG
AATTGTTCCCTGTTGCTTATAGAAGGTATATAAATTATTAATTTTCATGAGATGCCT
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TACGTAGTGAACCGTCTCTAAACGAATCACGTGCTTAGTGATCAGTCGTGAACCG
TGACAAAAGTTTTTTTATATCTACTTATTTAATAAAGAAACGAATATGAACAAGA
TATTTGTCTACTTAATTAATTAATAAAGAAACGAATATGAACAAGAAGCTTTTT
TATATCTACTTAGAAACTTTTGTATGCATTACTTGTCTTAATCATGCGATGAT
ATTGGTATTTAGATTTTCATTTATATATTGTAGTTTACTTTTCATTTACATG
TGTTATAACAAATATGATTGAATACAACTAGAACAAACAAAGTTTGATTCTTTA
AAGCTTGTGTTTAGTATGTAATAATCGTTTAATTCATCTCAATAAAGTACCAAAAT
GACAAATTACAAACAAATGACAGGTAAACAGGAAACAAGTTGCACCGCAAAAAT
ATGCTCTCTTTTTGCATGCTCTCTTTTTCTCCAATTTGTTTACATGCCTAAACATTG
CAATCTAATACCAAACTATTTTAGTAAAATTTTTGTTCTTGTCTTCTAGGGTACC
CTGCGTGAGAAGGGGTGGAATTAGGTTCCAAATGAACGGGACACTCCTACTTCAAT
TTGGTGTTAATTACAAATGTGGGTGGTGCTGGTGACGTGCACGCGGTGGCAATTA
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TGGTCGGACTGTGGTGTCCAACAATGTTGTCCCCGCTAATTGGTCTTTCGGGCAG
ACCTTCAGCGGTTCCCAATTCGTTGA