

IDENTIFICATION

Species: *Helianthus annuus*

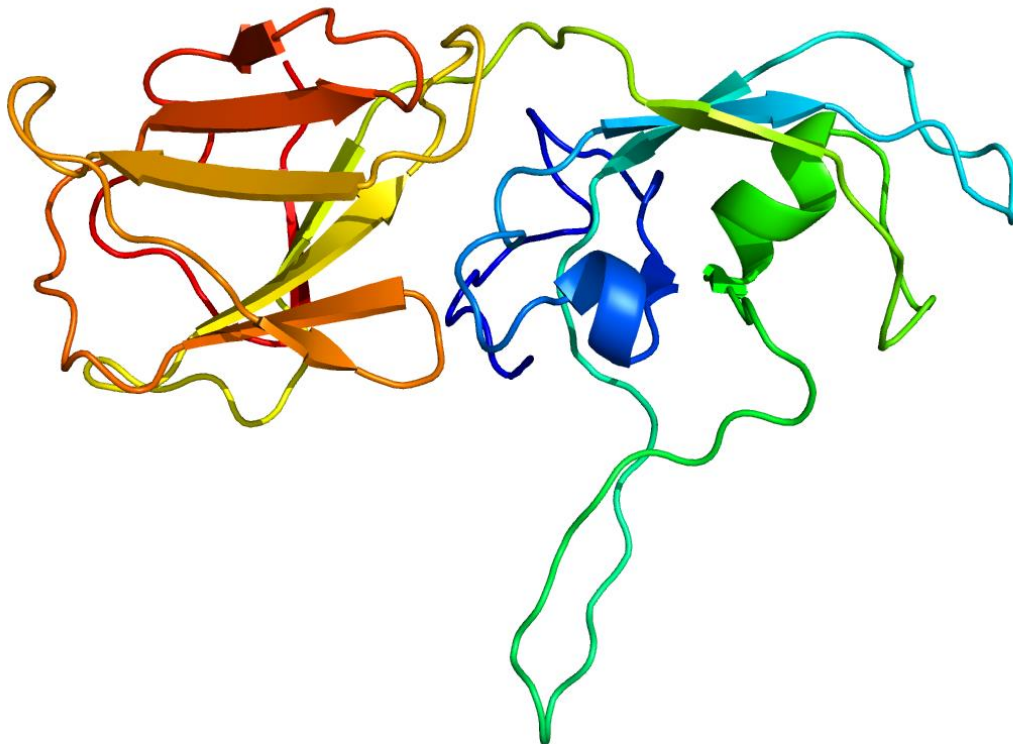
Locus: HanXRQChr12g0378681

Gene Model: HanXRQChr12g0378681

Description: HanEXPA-26

Family: Alpha Expansin

3D structure:



GENOME DATABASES

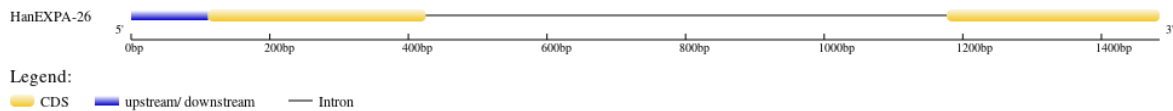
Phytozome: https://phytozome-next.jgi.doe.gov/info/Hannuus_r1_2

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

EXTERNAL RESOURCES

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

GENE STRUCTURE



DOMAIN ARCHITECTURE

Query seq. MGGACGYGNVYRQGYGTNNVALSSALFNDGLSCGACFQIMCVNDRQWCLPGSIVV
TATNFCPPNPALPSEKGGWCNPPLRHFDLSEPAFLRIAQYKAGIVPVAYRRVPCVRRG
GIRFQMNGHPYFNLVLITNVGGAGDVHAVAIAKGSRTGWQQMKQNWGQNWQSDTY
FNGQSLFSMVTTSDGRTVVSNNVVPANWSFGQTFSGSQFR*

Superfamilies PLN00050

Name	Accession	Description	Interval	E-value
PLN00050 super family	cl31535	expansin A, Provisional	1-206	6.73e-118

SEQUENCES

Peptide

>HanEXPA-26

MGGACGYGNVYRQGYGTNNVALSSALFNDGLSCGACFQIMCVNDRQWCLPGSIVV
TATNFCPPNPALPSEKGGWCNPPLRHFDLSEPAFLRIAQYKAGIVPVAYRRVPCVRRG
GIRFQMNGHPYFNLVLITNVGGAGDVHAVAIAKGSRTGWQQMKQNWGQNWQSDTY
FNGQSLFSMVTTSDGRTVVSNNVVPANWSFGQTFSGSQFR*

CDS (coding sequence)

>HanEXPA-26

ATGGGTGGTGCTTGTGGGTATGGGAATGTGTATCGTCAAGGGTATGGTACAAACA
ATGTAGCATTAAAGTAGTGCTTTGTTCAACGATGGTTTGAGTTGTGGGGCATGTTTT
CAAATCATGTGTGTTAATGATCGTCAATGGTGTTTACCGGGTTCCATTGTTGTCAC
CGCCACCAACTTCTGCCACCGAACCCCGCCTTACCTAGCGAGAAAGGCGGCTGG
TGCAACCCTCCTCTACGTCATTTGATCTATCTGAACCTGCCTTCCTACGCATTGC
TCAGTACAAAGCTGGAATTGTTCCCTGTTGCTTATAGAAGGGTACCCTGCGTGAGA
AGGGGTGGAATTAGGTTCCAAATGAACGGACACCCCTACTTCAATTTGGTGTAA
TTACAAATGTGGGTGGTGCTGGTGACGTGCACGCGGTGGCAATCAAAGGGTCAA
GAACAGGATGGCAACAAATGAAACAAAACCTGGGGGCAAACTGGCAATCCGAC
ACTTATTTTAAACGGGCAGTCTCTATCTTTTATGGTCACCACAAGTGATGGTCCGAC
TGTGGTGTCCAACAATGTGGTCCCCGCTAATTGGTCTTTCGGGCAGACCTTCAGC
GGTTCCAATTCGTTGA

Nucleotide

>HanEXPA-26

ATGGGTATGCAGTACTGATCATAATTATCTCAAATTTGTTGTGTTGTTTATTATT
ATTATTATTATTATTTTTAAAACGCTAACTCACACACTCTGTATGTATAACAG
GTGGTGCTTGTGGGTATGGGAATGTGTATCGTCAAGGGTATGGTACAAACAATGT
AGCATTAAAGTAGTGCTTTGTTCAACGATGGTTTGAGTTGTGGGGCATGTTTTCAA
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ACCAACTTCTGCCACCGAACCCCGCCTTACCTAGCGAGAAAGGCGGCTGGTGCA
ACCCTCCTCTACGTCATTTGATCTATCTGAACCTGCCTTCCTACGCATTGCTCAG
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CTAAATGTATTTTGGTAATCTACTTAAAATACCAACATATTTTACAAAAGATTAT
CAGACCGAATGCGTAGTGAAGTGTCTCTAAACGAATCACGTAAGTAGTGATCAGT
CGTGAACCGTGATAAAGTTTTTTTATATCTACTTATTTAATAAAGAAACGAATATG
AACAAGATATTTGTCTACTTAATTAATTAATAAAGAAACGTATATGAACAAGAA
GTTTTTTTGTATCTACTTAGAAACTTTTGTATTATGCATCACTTGTTTCTTAATCATG
CGATGATATTGGTATTTGGATTTTCATTTATATATTTTAATTTAATTTTCATTTTCAT
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GCAAAAATATGCTCTCTTTTTGTCATGCTCTCTTTTTCTCCAATTTGTTTACATGCCT
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CCACAAGTGATGGTCCGACTGTGGTGTCCAACAATGTGGTCCCCGCTAATTGGTC
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