

IDENTIFICATION

Species: *Helianthus annuus*

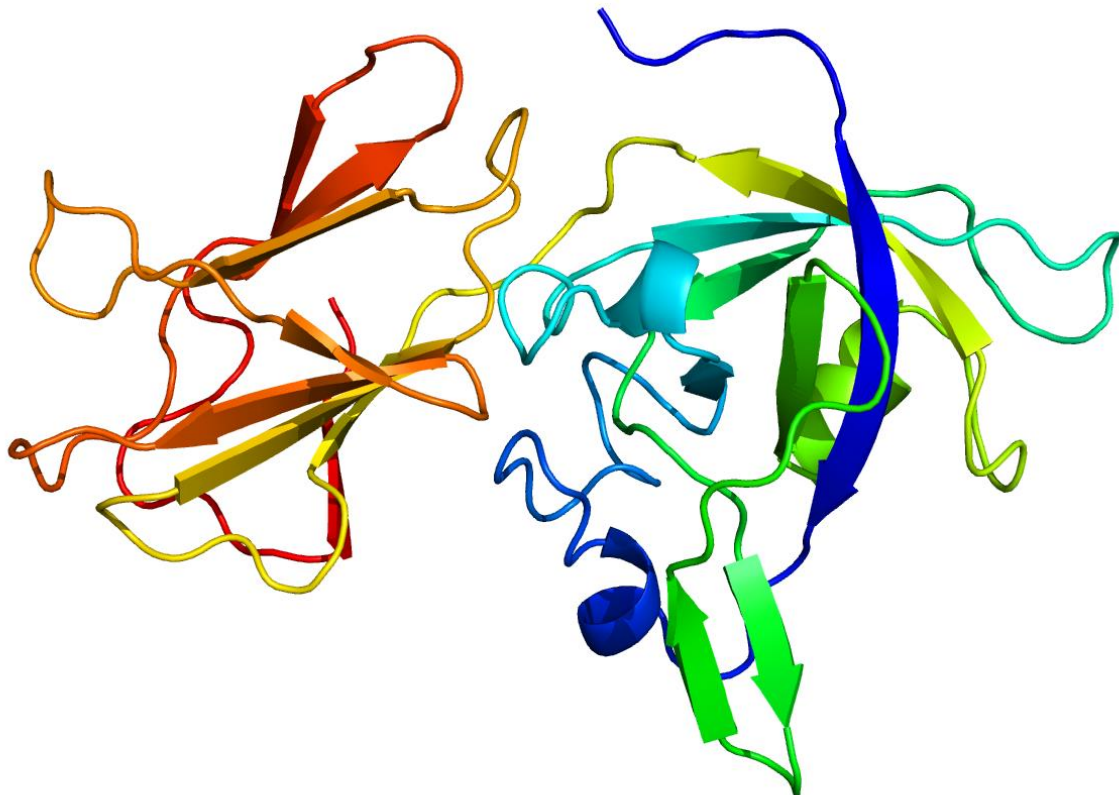
Locus: HanXRQChr09g0270611

Gene Model: HanXRQChr09g0270611

Description: HanEXPA-16

Family: Alpha Expansin

3D structure:



GENOME DATABASES

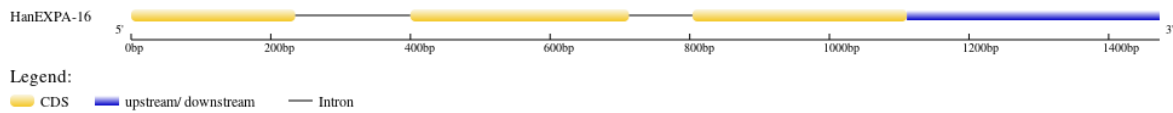
Phytozome: https://phytozome-next.jgi.doe.gov/info/Hannuus_r1_2

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

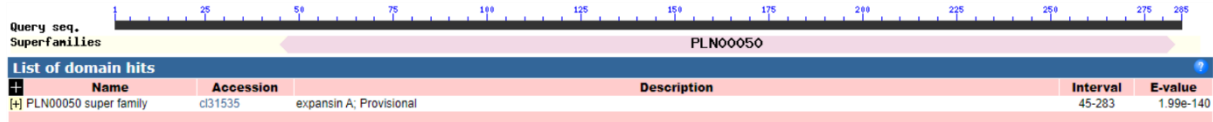
EXTERNAL RESOURCES

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

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>HanEXPA-16

MILLKCPSQPSIYSHLNSLYIPPPSSFSTICVAKMTPFGLLLAVAILSMASLVQANNGG
WVDAHATFYGGGDASGTMGGACGYGNLYSQGYGTNTAALSTALFNNGMSCGACF
EIKCAGEPKWCHPGSIVVTATNFCPPNNALPNNDGGWCNPPQHFDLSQPVFQOMA
QYRAGIVPVHYRRVPCMKKGGIRFTVNGHSYFNLVLITNVGGAGDVTRVAIKGSKTR
WVPMSRNWGQNWQSNANLDGQALSFKVTTSDGRTVVCNNAVPASWSFGQTFTGG
QFT*

CDS (coding sequence)

>HanEXPA-16

ATGATTTTACTGAAATGCCCTCTCAACCATCTATTTATTCCCACCTCAACTCCCT
CTACATTCCACCCCCTCTTCTTTTTCATCAACCATTTGTGTAGCAAAAATGACTC
CATTTGGGCTTCTTTTAGCTGTGGCTATTCTCTCAATGGCCTCTTTGGTTCAAGCC
ACAATGGTGGTTGGGTTGATGCTCATGCTACCTTCTATGGAGGTGGTGTATGCTT
CTGGCACTATGGGTGGGGCTTGTGGGTATGGGAAGTTATACAGTCAAGGGTATGG
TACAAACACAGCAGCACTAAGTACAGCACTATTCAACAATGGAATGAGCTGTGG
AGCTTGCTTTGAAATCAAGTGTGCAGGTGAACCAAAATGGTGTCCACCCTGGTCT
ATAGTAGTCACTGCAACCAACTTCTGCCACCAACAATGCATTACCCAACAATG
ATGGAGGCTGGTGCAACCCTCCCAACACCATTTTGACCTCTCTCAGCCTGTGTTT
CAGCAAATGGCTCAATACAGAGCTGGAATTGTTCTGTTTCATTACAGAAGGGTGC
CATGTATGAAGAAAGGTGGGATCAGGTTTACGGTGAATGGACACTCATATTTCAA
CTTGGTGTCTGATAACAAACGTAGGAGGAGCAGGGGATGTAACAAGGGTTGCAAT
CAAAGGTTCAAAGACCAGATGGGTACCCATGTTCGAGAAACTGGGGTCAGAACTG
GCAGAGCAACGCAAATCTTGACGGTCAGGCGTTGTCTTTCAAGGTGACCACGAGT
GATGGACGTACTGTCTGCAACAACGCGGTGCCCGCCAGTTGGTTCGTTTGGAC
AGACGTTTACCGGCGGACAGTTCAGTTACTTAG

Nucleotide

>HanEXPA-16

ATGATTTTACTGAAATGCCCTCTCAACCATCTATTTATTCCCACCTCAACTCCCT
CTACATTCCACCCCCTCTTCTTTTTCATCAACCATTTGTGTAGCAAAAATGACTC
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AACAATGGTGGTTGGGTTGATGCTCATGCTACCTTCTATGGAGGTGGTGATGCTT
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ACAAACACAGCAGCACTAAGTACAGCACTATTCAACAATGGAATGAGCTGTGGA
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AGCAAATGGCTCAATACAGAGCTGGAATTGTTCCCTGTTTATTACAGAAGGTATGT
TTTATGTTTTAAACTCATGCAAAAGGCACAAGATTGGTACTTTATGAATCTTTAAA
ATTAAGTCTTGACATATTCTTGTGATTAGGGTGCCATGTATGAAGAAAGGTGGGA
TCAGGTTTACGGTGAATGGACACTCATATTTCAACTTGGTGCTGATAACAAACGT
AGGAGGAGCAGGGGATGTAACAAGGGTTGCAATCAAAGGTTCAAAGACCAGATG
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CGGTCAGGCGTTGTCTTTCAAGGTGACCACGAGTGATGGACGTA CTGTCGTCTGC
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