

IDENTIFICATION

Species: *Helianthus annuus*

Locus: HanXRQChr15g0463181

Gene Model: HanXRQChr15g0463181

Description: HanEXPA-35

Family: Alpha Expansin

3D structure:



GENOME DATABASES

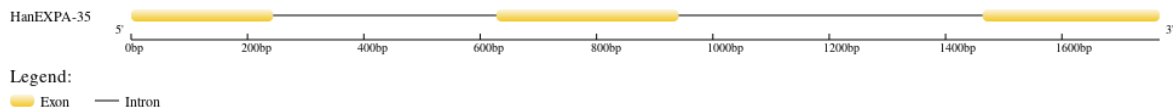
Phytozome: https://phytozome-next.jgi.doe.gov/info/Hannuus_r1_2

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

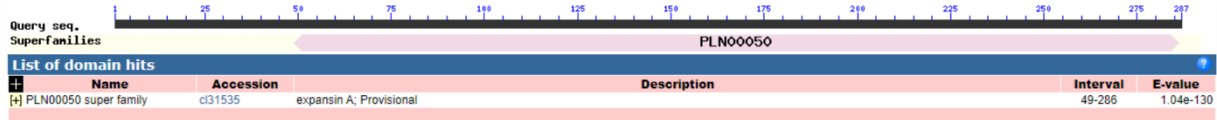
EXTERNAL RESOURCES

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

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>HanEXPA-35

MHTSSSTLFYTHIPYLYLPNLPPLSNHLSLSISLLIVNLMGFLLPFSIILLAFRTTHGLKG
GWQKAHATFYGGEDASGTMGGACGYGNLYSDGYGTNTAALSTALFNGLSCGSCF
QLRCIDDPKWCIQGVITITATNYCPPNYALANDNGGWCNPPLRHFDSLQPAFLKIAQY
RAGIVPVA YRRVPCIKKGGMRFTINGHSYFNLVLITNVGGAGDIHGVSIKGSKTGWQ
TMTRNWGQNWQSN SYLDGQSL SFRVTASNGRVVTSYHVVP SGWKFGQTFQGGQF*

CDS (coding sequence)

>HanEXPA-35

ATGCACACTTCTTCATCTACTCTTTTTTACACACATATCCCCTATTTATACCTTCCA
AATCTCCCTCCTCTTTCAAACCATCTCTCTCTCTATCTCTCTCCTCATTGTGAAT
TTGATCATGGGTTTTCTCTTGCCATTTAGTATCATCCTCTTGGCTTTCCGTACCACC
CATGGCTTAAAAGGGGGTTGGCAAAGGCTCATGCAACATTTTACGGCGGCGAA
GATGCATCTGGCACCATGGGTGGTGTGCTTGTGGCTACGGAAACCTCTACAGCGACG
GTTACGGCACAAACACCGCAGCGTTGAGCACCGCACTATTCAACAACGGGCTGA
GCTGCGGTTCTTGCTTCCAGTTGCGGTGTATTGATGATCCGAAATGGTGCATTCAA
GGCGTCATCACCATCACTGCCACCAACTATTGCCCGCCCAATTACGCACTCGCCA
ATGACAATGGCGGGTGGTGCAACCCCCACTCCGCCATTTTGATTTGTGCGAGCC
CGCTTTCTTGAAGATTGCACAATATCGCGCTGGAATCGTCCCCGTTGCCTATCGGA
GGGTGCCATGTATAAAGAAAGGAGGAATGAGGTTCAACAATTAATGGTCACTCTTA
CTTCAACTTGGTTTTGATCACCAACGTCGGCGGTGCGGGGGATATCCATGGGGTC
TCGATCAAAGGGTCGAAAACAGGGTGGCAAACGATGACAAGAACTGGGGTCAA
AACTGGCAAAGCAACTCTTATCTAGACGGTCAAAGCCTCTCTTTTAGAGTAACAG
CCAGTAACGGAAGAGTTGTAACCAGCTACCACGTCGTACCTTCTGGTTGGAAGTT
CGGTCAAACGTTTCAAGGTGGTCAGTTTTAA

Nucleotide

>HanEXPA-35

ATGCACACTTCTTCATCTACTCTTTTTTACACACATATCCCCTATTTATACCTTCCA
AATCTCCCTCCTCTTTCAAACCATCTCTCTCTCTATCTCTCTCCTCATTGTGAAT
TTGATCATGGGTTTTCTCTTGCCATTTAGTATCATCCTCTTGGCTTTCCGTACCACC
CATGGCTTAAAAGGGGGTTGGCAAAGGCTCATGCAACATTTTACGGCGGCGAA

GATGCATCTGGCACCATGGGTATGTGTTTATGTTTGTCTTTGCACGCGTGACTTGT
TATTAACATAAACGTCATATAACATGTCATGCAAGTGTGCGTATATATAAACCTA
AACTTTAAACCTTAAAAGTAGTTAGTTGACAGGGAGAAAACAGATCACCGTTAGT
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TTTCAACTGAGTTCGTAACATAATTATTCAAGGTCAAAACTATAAGAAAACGATAA
TAAATACCAATATTAATTGATTTTGTCCCAATTTTTTTTTTTTTATCATTTTGTATTGT
GACACAACATAGGGTGGCACCCACCTCTTTGGTGACTTAACATTTTTGTGAACA
ATTTAATGCTCAGGTGGTGCTTGTGGCTACGGAAACCTCTACAGCGACGGTTAC
GGCACAAACACCGCAGCGTTGAGCACCGCACTATTCAACAACGGGCTGAGCTGC
GGTTCTTGCTTCCAGTTGCGGTGTATTGATGATCCGAAATGGTGCATTCAAGGCGT
CATCACCATCACTGCCACCAACTATTGCCCGCCAATTACGCACTCGCCAATGAC
AATGGCGGGTGGTGCAACCCCCACTCCGCCATTTTGTATTGTCGCAGCCCGCTTT
CTTGAAGATTGCACAATATCGCGCTGGAATCGTCCCCGTTGCCTATCGGAGGTAT
GACATGTAACATTCATTTATCGAGCCTGTGCGTCTAAACAAACCTATTATTTATCT
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CACAATTAATGGTCACTCTTACTTCAACTTGGTTTTGATCACCAACGTCCGGCGGTG
CGGGGGATATCCATGGGGTCTCGATCAAAGGGTCGAAAACAGGGTGGCAAACGA
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GCCTCTCTTTTAGAGTAACAGCCAGTAACGGAAGAGTTGTAACCAGCTACCACGT
CGTACCTTCTGGTTGGAAGTTCGGTCAAACGTTTCAAGGTGGTCAGTTTTAA