

IDENTIFICATION

Species: *Helianthus annuus*

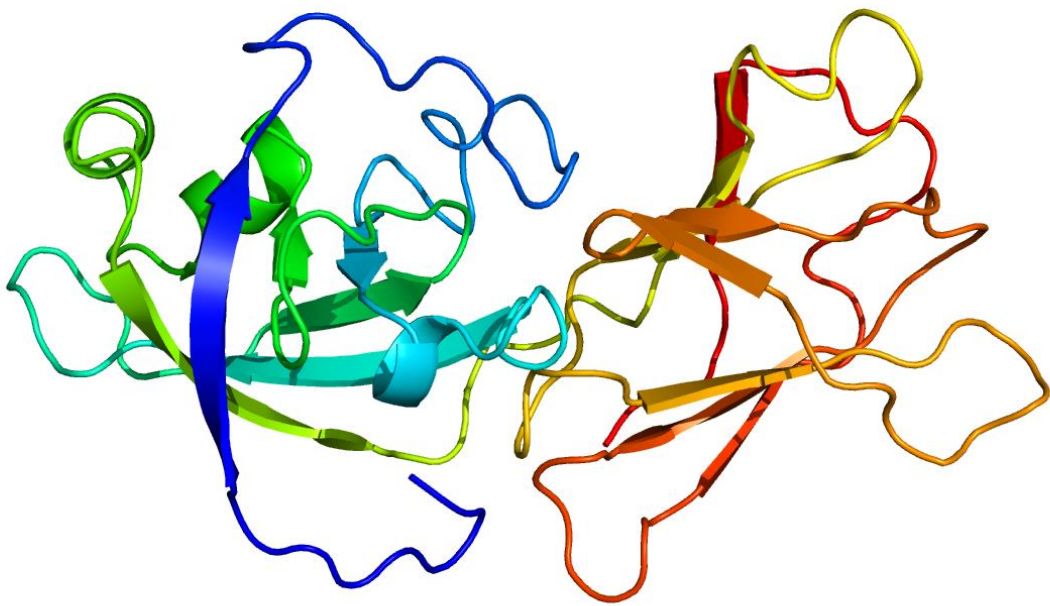
Locus: HanXRQChr17g0559441

Gene Model: HanXRQChr17g0559441

Description: HanEXLA-02

Family: Expansin Like Alpha

3D structure:



GENOME DATABASES

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

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

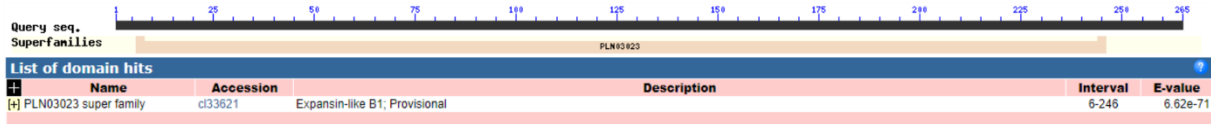
EXTERNAL RESOURCES

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

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>HanEXLA-02

MGLFNLCFLWLLISVSSTNACDRCLHQSKAAFFSTPSSLSSGACGYGSSASSLYGSH
LAAAVGSIYKSGSGCGACFQVRCKDSKVCCKAGTQVIVTDLNKNNDTDFVMTPRAF
MAMANKGMAHSLLKLG VADVEYKRVP CDYKGNLTVRVEESTKKPNYLALKFLY
QGGQTEIVGVDVAQV GSSSWTYMTRNYGAVWDTSRAPAGPLQLRLVVTSGYDGK
WIWAKSVMPVDWTIGGVYDCGVQINDIAQEGCGECDDQNWKS*

CDS (coding sequence)

>HanEXLA-02

ATGGGATTGTTCAATCTTTGTTTCCTCTGGTTGCTTCTGATCTCAGTTTCTTCAACA
AATGCTTGCGATAGATGTCTACATCAAAGCAAAGCGGCCTTCTTCTCCACACCTT
CTTCTCTTTCTTCTGGAGCATGCGGGTATGGTTCATCAGCTAGCAGCTTGTATGGC
AGCCACCTTGCTGCAGCTGTTGGTAGCATTACAAATCGGGTTCGGGTTGTGGGG
CATGCTTTCAGGTGAGATGCAAGGATTCTAAGGTGTGTAGCAAGGCCGGGACTCA
GGTCATAGTAACTGATCTCAATAAAAACAACGACACCGATTTTGTGATGACCCCT
AGAGCTTTCATGGCCATGGCTAACAAAGGGTATGGCCACAGCTTATTA AAACTTG
GTGTTGCCGACGTTGAATATAAAAAGAGTACCTTGTGATTACAAAGGCAACA ACTT
AACTGTAAGAGTTGAAGAATCTACCAAAAAGCCTAATTATCTTGC ACTCAAATTC
TTATACCAAGGAGGTCAAACAGAAATAGTGGGCGTTGACGTTGCTCAGGTTGGGT
CATCAAGTTGGACTTACATGACTAGAACTATGGGGCTGTCTGGGACACCAGCCG
AGCTCCTGCAGGACCACTGCAACTCCGCCTGGTGGTCACCTCCGGCTATGATGGA
AAGTGGATATGGGCCAAGAGTGTTATGCCGGTCGATTGGACCATTGGAGGTGTGT
ATGATTGTGGCGTACAAATCAATGACATTGCTCAAGAAGGGTGTGGTGAATGTGA
TGACCAAAAATTGGAAAAGTTAA

Nucleotide

>HanEXLA-02

AAAGTTAAAAAAAAAAAAAAAAAAGAAAGAACCTATAAATAGACATGTAATTCT
TCCCCTCTTGAATCACAGAGACACACTAAACAAAAAATGGGATTGTTCAATCTT
TGTTTCCTCTGGTTGCTTCTGATCTCAGTTTCTTCAACAAATGCTTGCATAGATG
TCTACATCAAAGCAAAGCGGCCTTCTTCTCCACACCTTCTTCTTTCTTGTAA
CAACGTTTTCTATCTATGTATCTATGTATCTATCTATCTATCTATCACTTGT

GTTGAATTGAGTTATAATAAAAATGAATAGCTGGAGCATGCGGGTATGGTTCATCA
GCTAGCAGCTTGTATGGCAGCCACCTTGCTGCAGCTGTTGGTAGCATTACAAAT
CGGGTTCGGGTTGTGGGGCATGCTTTCAGGTGAGATGCAAGGATTCTAAGGTGTG
TAGCAAGGCCGGGACTCAGGTCATAGTAACTGATCTCAATAAAAACAACGACAC
CGATTTTGTGATGACCCCTAGAGCTTTCATGGCCATGGCTAACAAGGGTATGGCC
CACAGCTTATTA AAACTTGGTGTGGCCGACGTTGAATATAAAAAGGTAAATATTAT
ATTATTTTTTTTTTTCTAAACATCTCCATCATAACATATGGTATTGTGATGTAAAAC
AGAGTACCTTGTGATTACAAAGGCAACA ACTTAACTGTAAGAGTTGAAGAATCTA
CCAAAAGCCTAATTATCTTGCACTCAAATTCTTATACCAAGGAGGTCAAACAGA
AATAGTGGGCGTTGACGTTGCTCAGGTTGGGTCATCAAGTTGGACTTACATGACT
AGAAACTATGGGGCTGTCTGGGACACCAGCCGAGCTCCTGCAGGACCACTGCAA
CTCCGCCTGGTGGTCACCTCCGGCTATGATGGAAAGTGGATATGGGCCAAGAGTG
TTATGCCGGTCGATTGGACCATTGGAGGTGTGTATGATTGTGGCGTACAAATCAA
TGACATTGCTCAAGAAGGGTGTGGTGAATGTGATGACCAAAAATTGGAAAAGTTA
ACACACACGACATTCTATTTTGGGTTGTCATAAGGATTCTGGTAACATAACAATAA
TAGTGTAGATGGAGTAACAAAATGTTATGGACTAGCTGATGTATTAGGTTGGAAT
CACGTATATGATAT