

IDENTIFICATION

Species: *Helianthus annuus*

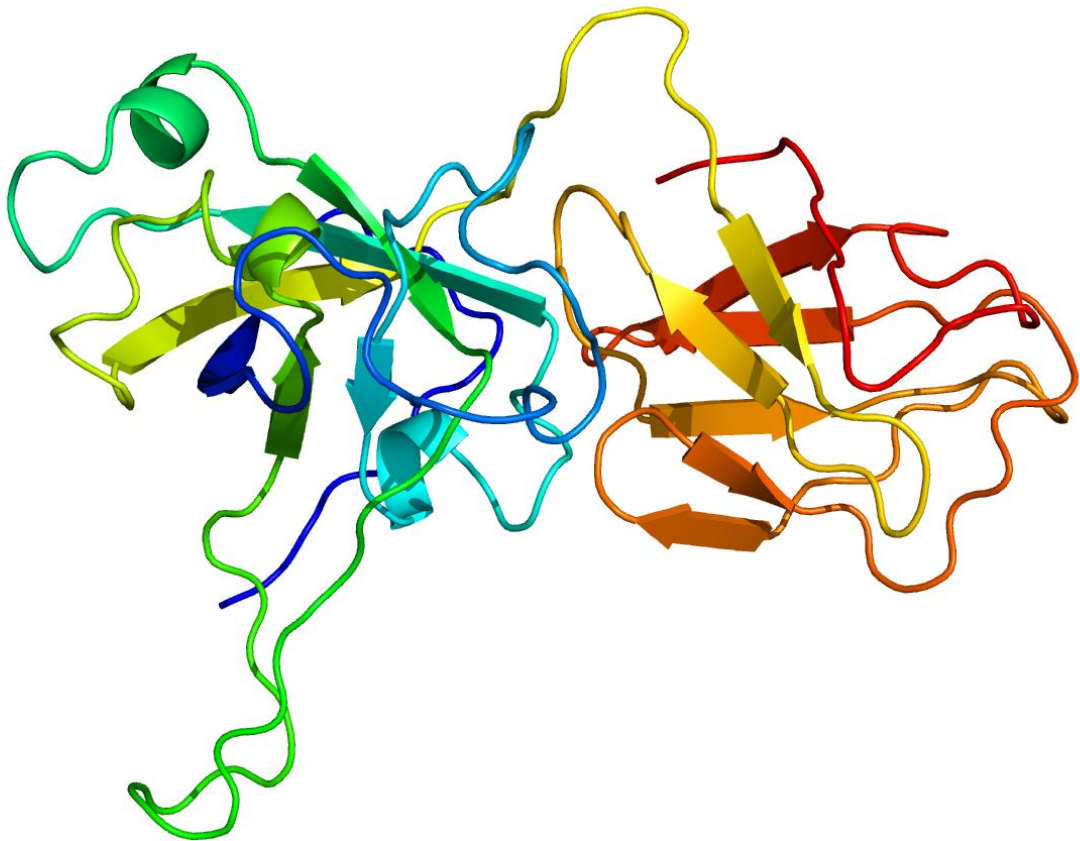
Locus: HanXRQChr12g0369581

Gene Model: HanXRQChr12g0369581

Description: HanEXPA-20

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>

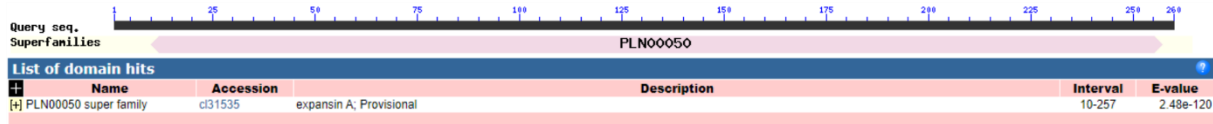
EXTERNAL RESOURCES

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

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>HanEXPA-20

MKVTTTTTLCYILLTAAITNARIPGVYTGPPWETAHATFYGGSDASGTMGGACGYG
NLYSQGYGVNTAALSTALFNGLSCGACFEMKCTDDPQWCLPGNPSIFITATNFCPP
NFAQPSDDGGWCNPPRPHFDLAMPMLKFAKYRAGIVPVS YRRVPCRKQGGIRFTIN
GFRYFNLILISNVAGAGDITQAWVKGSNTEWMSLSRNWGQNWQSNVVLIGQSLSFR
VRGSDGRTSTSKNIVPSDWHFGQTF TGKNFRV*

CDS (coding sequence)

>HanEXPA-20

ATGAAGGTTACTACTACTACTCTATGCTACATTTTACTGTTAACCGCGATAAC
GACCAACGCTCGTATCCCCGGAGTCTACACCGGTGGCCCGTGGGAAACCGCCAC
GCCACGTTTTACGGTGGCAGTGATGCTTCTGGCACCATGGGTGGAGCATGTGGTT
ATGGTAATCTGTACAGCCAAGGCTACGGAGTGAACACCGCAGCGCTAAGCACCG
CGCTGTTCAACAACGGGCTGAGCTGCGGTGCTTGTTCGAGATGAAATGTACGGA
TGATCCTCAATGGTGCCTTCCCGGCAATCCTTCTATTTTCATTACCGCTACCAATT
TCTGCCCCCGAATTTTCGCTCAACCTAGTGACGATGGCGGGTGGTGTAAACCGCC
TCGCCCCCATTTTGATCTCGCCATGCCGATGTTTCTTAAGTTCGCTAAGTACCGTG
CTGGGATTGTCCAGTCTCTTACCGCCGGGTCCGTGCCGAAAACAAGGAGGGAT
CCGGTTCACCATAAACGGTTTCCGCTACTTCAACTTGATTTTGATTAGTAATGTAG
CGGGTGCGGGCGATATCACCCAGGCGTGGGTAAAAGGTTCGAACACCGAGTGGA
TGAGTCTTAGCCGAAACTGGGGTCAAACTGGCAGTCGAATGCGGTGTTGATCGG
ACAATCGCTTTCGTTCCGGGTTAGAGGCAGTGATGGTAGAACTTCTACCTCCAAG
AACATTGTACCTTCCGATTGGCATTTTGGGCAGACTTTTACCGGAAAGAATTTTCG
GGTTTGA

Nucleotide

>HanEXPA-20

TTCACCACTTTCCTACTTCTCTACACCTCTGTTTCTGCTTCAACAATGAAGGTTACT
ACTACTACTACTCTATGCTACATTTTACTGTTAACCGCGATAACGACCAACGCTCG
TATCCCCGGAGTCTACACCGGTGGCCCGTGGGAAACCGCCACGCCACGTTTTAC
GGTGGCAGTGATGCTTCTGGCACCATGGGTGCGTCTTCAACAATCTTCCACCTTC
TTTATTTTTAGTTATAACAATTCAATTCAATTAAGAAAAAAGAAAATAACAGAA

ATTTTATTCAATTTTGTGTGTAACGTTTTTAGGTGGAGCATGTGGTTATGGTAAT
CTGTACAGCCAAGGCTACGGAGTGAACACCGCAGCGCTAAGCACCGCGCTGTTC
AACACGGGCTGAGCTGCGGTGCTTGTTCGAGATGAAATGTACGGATGATCCTC
AATGGTGCCTTCCC GGCAATCCTTCTATTTTCATTACCGCTACCAATTTCTGCCCC
CCGAATTTTCGCTCAACCTAGTGACGATGGCGGGTGGTGTAAACCGCCTCGCCCC
ATTTTGATCTCGCCATGCCGATGTTTCTTAAGTTCGCTAAGTACCGTGCTGGGATT
GTCCCAGTCTCTTACCGCCGGTTAGTAATATTTCTATTTTGGGTAAAACGAGCAGT
ACCCGGGTAAATATTTCTACTTTTGGGTAAAAGGAACAGTACCCGGGTAAAATTC
ATTTAAATAAAAAATATTAACGACTAAAAAAGGTTTAGCTAATTAGCCCACCCGG
GGCCTACCTACTAAACCTCGGTAAAATTTTATTATTAAAAAAACATAATTATA
AAATTTTAGCTAATTAGTTCATCCGGGGCCTACGAGTCCCCGAGAAGGGAAATTT
ACTACTGGAGTACTGGGTCTAACAATTAATAATATTTTATAGGGTTCGGTGCCG
AAAACAAGGAGGGATCCGGTTCACCATAAACGGTTTCCGCTACTTCAACTTGATT
TTGATTAGTAATGTAGCGGGTGCGGGCGATATCACCCAGGCGTGGGTAAAAGGTT
CGAACACCGAGTGGATGAGTCTTAGCCGAAACTGGGGTCAAACCTGGCAGTCGA
ATGCGGTGTTGATCGGACAATCGCTTTCGTTCCGGGTAGAGGCAGTGATGGTAG
AACTTCTACCTCCAAGAACATTGTACCTTCCGATTGGCATTTTGGGCAGACTTTTA
CCGGAAGAATTTTCGGGTTTGAAATTTGGAATCGGGTTAAGACCCGGGTGGTT
GACGGGTCGAAATATCTATTGGAAAAAGAATATAATTGTTGTTTTTAATTTAGGG
AAAAAGAGAAAACAATAGCGGAGTGCTTGTGTTGATTTTTTGACTATTGTAAAGT
GCTTATCCTTGTAAGGAAAGCTGAAGTGGCTATGGTTGTTATGTCTACGAGCCCG
CAGCTTTGAATATTCTTTTTTTAAATATACATTATATAAACTTCATGGCTTATTA
ATTAATATATGTTGTTTAGAAGTTGAC