

IDENTIFICATION

Species: *Helianthus annuus*

Locus: HanXRQChr06g0165191

Gene Model: HanXRQChr06g0165191

Description: HanEXPA-05

Family: Alpha Expansin

3D structure:



GENOME DATABASES

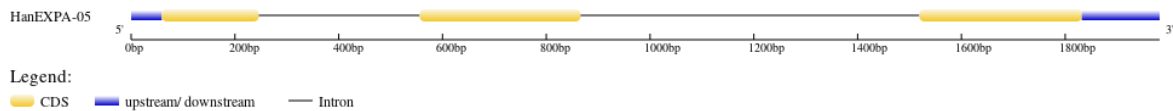
Phytozome: https://phytozome-next.jgi.doe.gov/info/Hannuus_r1_2

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

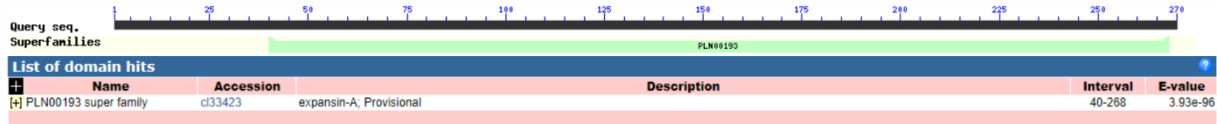
EXTERNAL RESOURCES

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

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>HanEXPA-05

MASFQRSTMFCLFFMITIFIPFGSVLAGAAYA VPRAPT VYRPSWTLAHATFYGDESA
SSTMGGACGYGNLMTNGYGTNTAALSSTMFNNGYACGQCYQMRCVQSPWC SKGIA
TVTATNLCPPNWSQDSNNGGWCNPPRTHFDMAKPAFMQIAQWKAGIVPVMYRRVP
CVRKGG LRFSFQNGYWLLVYVMNVGGAGDIKSMWVKGTKTAWISM SHN WGASY
QAFATLRGQALSFR L TSYTTKQTITAYNVAPANWNVGLTYQANVNFH*

CDS (coding sequence)

>HanEXPA-05

ATGGCTTCATTCCAACGTTCAACAATGTTTTGCCTCTTCTTTATGATCACAATATT
CATCCCGTTTGGATCGGTCTTAGCTGGAGCTGCGTATGCGGTCCCTCGTGCACCTA
CTGTGTACCGCCCGAGTCCATGGACTCTCGCCCATGCCACGTTTTATGGAGACGA
GTCCGCCTCTTCAACCATGGGAGGTGCATGTGGATATGGAAACTTGATGACTAAC
GGATATGGCACGAACACAGCCGCACTGAGCTCGACAATGTTTAAACAACGGTTATG
CATGCGGGCAATGTTATCAAATGCGGTGTGTGCAATCTCCATGGTGCTCGAAAGG
CATTGCCACGGTCACCGCCACCAACCTCTGCCCTCCAACTGGTCTCAGGATTCT
AACAAACGGTGGATGGTGCAACCCGCCTAGGACCCATTCGACATGGCCAAACCC
GCTTTTATGCAAATAGCCAATGGAAAGCCGGCATTGTCCCCGTCATGTATCGTA
GGGTGCCTTGTGTGAGGAAAGGTGGTCTTAGATTTTCTTTCCAAGGAAATGGCTA
CTGGTTGCTAGTCTATGTAATGAACGTTGGTGGCGGGGTGACATCAAGAGCATG
TGGGTAAAGGGAACCAAGACGGCTTGGATAAGCATGAGCCATAACTGGGGAGCA
TCGTATCAAGCTTTTGAACACTTCGTGGTCAAGCATTGTCGTTTAGGCTAACCTC
GTACACAACCAAGCAGACCATAACGGCTTACAATGTCGCCCCGGCTAATTGGAAC
GTCGGGTTGACTTACCAAGCCAATGTAACTTTCACTAA

Nucleotide

>HanEXPA-05

AAATATCTCTCAACCGTTTTTGAAGTATAACACGCAAAAAACAACATAAGCACAA
ACAATGGCTTCATTCCAACGTTCAACAATGTTTTGCCTCTTCTTTATGATCACAA
TATTCATCCCGTTTGGATCGGTCTTAGCTGGAGCTGCGTATGCGGTCCCTCGTGCA
CCTACTGTGTACCGCCCGAGTCCATGGACTCTCGCCCATGCCACGTTTTATGGAG
ACGAGTCCGCCTCTTCAACCATGGGTACTACTTTATCTTTATACACACACAAAGA

GTGTAATTTTTTTGTTTATAAAGGTTTTATCGTTAAAACCGATAAAAATAACGCTCG
TTATTTCTATTTTATTCTAGGTAAATATTATATCTAACATGACTAGGACATGTTAG
GGGCTAACCTATAAATCTATTTTTGTACATAGTACATAAACTCATGTTATCTTTCA
AAAATTCGAAAATTCTCATAACGAATTTTTGGGTAGTGGCACAGCTTGTTGCTCG
TTACCTTCTATCTCGATGTGATTTCTTATTTTCAAGATAATATTGAACATATCAG
GAGGTGCATGTGGATATGGAACTTGATGACTAACGGATATGGCACGAACACAG
CCGCACTGAGCTCGACAATGTTTAAACAACGGTTATGCATGCGGGCAATGTTATCA
AATGCGGTGTGTGCAATCTCCATGGTGCTCGAAAGGCATTGCCACGGTCACCGCC
ACCAACCTCTGCCCTCCAACTGGTCTCAGGATTCTAACAACGGTGGATGGTGCA
ACCCGCCTAGGACCCATTTTCGACATGGCCAAACCCGCTTTTATGCAAATAGCCCA
ATGGAAAGCCGGCATTGTCCCCGTCATGTATCGTAGGTATGTTTCTTCGTTGAGTA
CTAATTGAATAACTAGAGAAAATAAAACATAATGAATGTTATTTTTTTATATTG
ATAACTCTTAATAAGCTCTTTATCTATTTACATATAGATATAGAACAAGATAATT
ATTAAAGTAAACATATAGATATAATAACGAAATAATGCAATCATATCTAGGTTGC
AAACGAAACAAACGTTTCGGCGGATAAATTCGTGAAGCGTTCGGCGGGAAATTCGT
TTGTGTTTGTTCGTTTATTAATAAATGAACACGAACAAGAAATTCTGTTTCGGTTA
GTTACATGAACAGAGCCCGTTTCGTAATTCATTTATGTCCGTGAACGTTTGGTAAG
GTGTTTCGATAGTTCACTAGTGTTCAGTTTTTATATTTTATTTAAATACTTCAAAA
TTTCTACAAATAAAATATTTAATAAGTGTGTCAGTGTATTATATATTATGTTTCATGAA
CGTTTGTTCGTTTGTTCGTTTTTTTTTCCATTTGTGTTTCATGAACATTAGTTTGTTCAT
TTGTATTCATCAACATTCATTTTAGTTCGTCGCATAAACAGTTCGTGAACACATAT
ATTTCTTAACAAACCGCCCTAATCATATCCAAATATATTTCTAATAACTCAGTTAT
ATTCCTTTTTTTGTATAGGGTGCCTTGTGTGAGGAAAGGTGGTCTTAGATTTTCTT
TCCAAGGAAATGGCTACTGGTTGCTAGTCTATGTAATGAACGTTGGTGGCGCGGG
TGACATCAAGAGCATGTGGGTAAAGGGAACCAAGACGGCTTGGATAAGCATGAG
CCATAACTGGGGAGCATCGTATCAAGCTTTTGCAACACTTCGTGGTCAAGCATTG
TCGTTTAGGCTAACCTCGTACACAACCAAGCAGACCATAACGGCTTACAATGTGC
CCCCGGCTAATTGGAACGTCGGGTGACTTACCAAGCCAATGTTAACTTTCACTA
ATCAGTCGACATCAATGTGGTGTGATTTTTGCCAAAATAGAATTTGTGGCATGT
ATTTTTACATTTTAAGTTGTATAACTTTTGTGTTGATTGTGATACGTATGAACCT
GTTAAGAACGACTAATTATGAGAAAACCTTGACTTGCT