

IDENTIFICATION

Species: *Helianthus annuus*

Locus: HanXRQChr13g0415791

Gene Model: HanXRQChr13g0415791

Description: HanEXPA-29

Family: Alpha Expansin

3D structure:



GENOME DATABASES

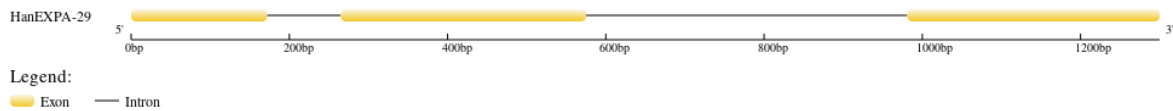
Phytozome: https://phytozome-next.jgi.doe.gov/info/Hannuus_r1_2

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

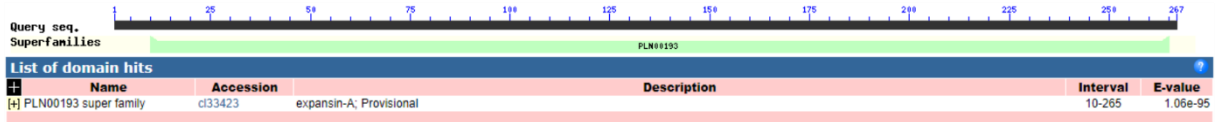
EXTERNAL RESOURCES

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

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>HanEXPA-29

MASFYYPWSFCCFFSIVTLIFSGFVKPSVA VYHGYVPSPWTLAHATFYGDESASATM
GGACGYGNLITNGYGTNTAALSSTLFSDDYACGQCYQIRCVQSKWCYKGYTTVTAT
NLCPPNWSKDSNNGGWCNPPRTHFDMAKPAFMKIAQWKAGIVPVMYRRVPCNAIR
KGGIRFSFQNGYWLLVYVMNVGGAGDIRNMWVKGTGTGWISMShNWGASYQAF
ATLKGQALSFRLLSYTTKQTITAYNVAPANWNLGLTYQAKVNFH*

CDS (coding sequence)

>HanEXPA-29

ATGGCTTCTTTTACTATCCATGGAGCTTTTGCTGCTTCTTTAGCATTGTCACACTC
ATTTTCTCCGGGTTTCGTAAAGCCTAGTGTAGCTGTCTATCATGGCTACGTTCCGAG
CCCATGGACCCTAGCCCACGCCACATTTTATGGCGATGAGTCTGCATCTGCAACT
ATGGGGGGGTGCTTGTGGATATGGGAACCTTGATTACTAACGGATACGGAACCAATA
CAGCTGCATTGAGCTCAACGCTCTTTAGCGATGGATACGCATGTGGTCAGTGTTA
CCAAATACGGTGTGTCCAGTCCAAATGGTGCTACAAAGGTTATAACAACGTTACT
GCCACCAACCTTTGCCACCTAACTGGTCTAAGGATTCAAACAACGGAGGATGGT
GCAACCCTCCCCGAACCCATTTTCGACATGGCTAAGCCC GCGTTCATGAAAATTGC
TCAATGGAAAGCCGGCATTGTCCCAGTCATGTACCGCAGGGTTCATGCAATGCC
ATCAGGAAAGGTGGGATCAGATTTTCTTTTCAAGGAAATGGGTATTGGTTGTTGG
TGTATGTGATGAATGTTGGTGGTGCGGGTGACATCCGTAATATGTGGGTCAAAGG
GACCAAGACCGGTTGGATCAGCATGAGCCATAACTGGGGTGCTTCTTACCAAGCT
TTCGCAACTCTTAAGGGTCAAGCCCTATCCTTCAGGCTAACTTCATACACCACAA
AACAGACTATTACGGCTTACAATGTCGCCCCCGGCTAACTGGAACCTAGGGTTGAC
CTACCAAGCCAAAGTCAACTTCCATTAA

Nucleotide

>HanEXPA-29

ATGGCTTCTTTTACTATCCATGGAGCTTTTGCTGCTTCTTTAGCATTGTCACACTC
ATTTTCTCCGGGTTTCGTAAAGCCTAGTGTAGCTGTCTATCATGGCTACGTTCCGAG
CCCATGGACCCTAGCCCACGCCACATTTTATGGCGATGAGTCTGCATCTGCAACT
ATGGGTGTGTAATACATGCATGTAACATAGTCTAATTATCATCTAATGGTTTATAA
TATGGTGTCTAAATAACAATATTTTAAATCAATGTTTATAGGGGGTGCTTGTGGAT

ATGGGAACTTGATTACTAACGGATACGGAACCAATACAGCTGCATTGAGCTCAAC
GCTCTTTAGCGATGGATACGCATGTGGTCAGTGTTACCAAATACGGTGTGTCCAG
TCCAAATGGTGCTACAAAGGTTATACAACCGTTACTGCCACCAACCTTTGCCAC
CTAACTGGTCTAAGGATTCAAACAACGGAGGATGGTGCAACCCTCCCCGAACCA
TTTCGACATGGCTAAGCCC GCGTTCATGAAAATTGCTCAATGGAAAGCCGGCATT
GTCCCAGTCATGTACCGCAGGTGCATTTCTATTACTTTAGTGAAATGGAAAATCA
CTAGCTTGGTCATTTTGACCGATGAGTCTGACAAAATAGCTTTGAATTTTTTTCT
TTTACACAAAATCGTTTGGCTTATCTTCTTTTTAGTTAAGAACTATTT CAGCCAA
CCAGAAGCTTCTACATAGCACACCGTGTGTGTTGATGTAGCAGGTTTCTATCTAG
CGCATGATAATGGATTTCTTGAGCCAACATTA AAAATTTGTTGCGCAAAGATTGAA
ATCTGCTACGCCAAGGGACAATTATTGGTTGATTGGAGATTTTAAATCAA ACTCA
TTTTTCAACAAGTTGGAACCTTTTCTTCAACATGT TAACTTAATACGAATTTGACT
AACCGCTAGCTTTCTAACCAAATTATGGGTATTTTAGGGTTCCATGCAATGCCATC
AGGAAAGGTGGGATCAGATTTTCTTTTCAAGGAAATGGGTATTGGTTGTTGGTGT
ATGTGATGAATGTTGGTGGTGCGGGTGACATCCGTAATATGTGGGTCAAAGGGAC
CAAGACCGGTTGGATCAGCATGAGCCATAACTGGGGTGCTTCTTACCAAGCTTTC
GCAACTCTTAAGGGTCAAGCCCTATCCTTCAGGCTAACTTCATACACCACAAAAC
AGACTATTACGGCTTACAATGTCGCCCCGGCTAACTGGAACCTAGGGTTGACCTA
CCAAGCCAAAGTCAACTTCCATTAA