

IDENTIFICATION

Species: *Capsella grandiflora*

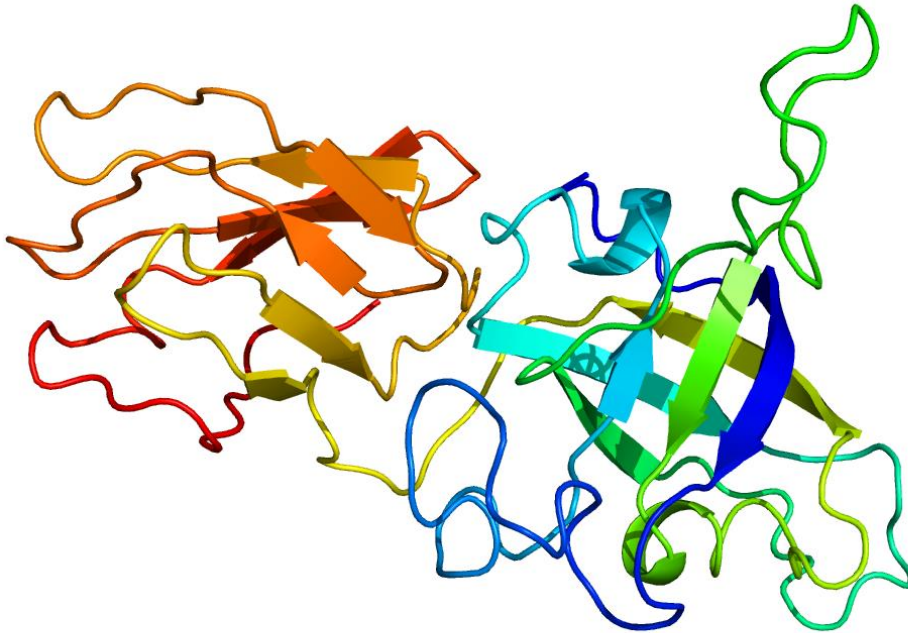
Locus: Cagra.18121S0005

Gene Model: Cagra.18121S0005.1.p

Description: CgrEXPA-22

Family: Alpha Expansin

3D structure:



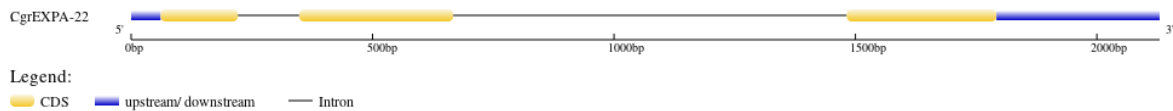
GENOME DATABASES

Phytozome: https://phytozome-next.jgi.doe.gov/info/Cgrandiflora_v1_1

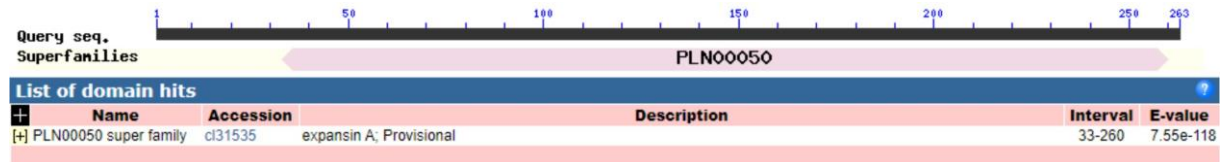
EXTERNAL RESOURCES

-

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>CgrEXPA-22

MTATAFGICLWLAVTASFLLTASDAKIAGVYSGGPWQNAHATFYGGSDASGTMGGA
CGYGNLYSQGYGVNTAALSTALFNNGYSCGACFEIKCTDDPRWCVPGNPSILVTATN
FCPPNFAQASDNGGWCNPPREHFDLAMPFLKIGLYRAGIVPVSYRRVPCRKVGIR
FTVNGFRYFNLVLVTNVAGAGDINGVSVKGSKTDWVRMSRNWGQNWQSNVLIQ
SLSFRVTASDRRSSTSWNVAPPSWQFGQTFSGKNFRV*

CDS (coding sequence)

>CgrEXPA-22

ATGACGGCGACTGCGTTTGGGATCTGCTTGTGGTTGGCCGTTACGGCTTCTTTTCT
CTTAACAGCTTCAGACGCCAAAATCGCCGGCGTTTACAGCGGCGGACCATGGCAG
AACGCACACGCCACTTTCTACGGTGGTAGTGACGCCTCTGGAACCATGGGCGGCG
CGTGTGGGTACGGGAAGTTGTACAGCCAAGGATACGGTGTGAACACGGCGGCCT
TGAGCACTGCTCTGTTCAACAACGGGTATAGCTGCGGTGCTTGCTTCGAGATCAA
GTGTACCGACGACCCGAGATGGTGTGTGCCGGAAACCCCTCGATTCTTGTTACG
GCGACGAACTTTGTCCGCGGAATTTGCTCAGGCGAGTGACAACGGAGGATGGT
GCAATCCTCCGCGTGAGCACTTTGATCTAGCTATGCCTATGTTCTCAAGATCGGT
CTCTACCGTGCAGGCATTGTCCCCGTCTCCTATCGCAGGGTACCTTGTCGGAAGGT
AGGAGGGATAAGATTCACAGTAAACGGGTTCAGATACTTCAATCTCGTTCTGGTA
ACTAACGTTGCCGGTGCCGGAGATATCAACGGAGTTAGCGTAAAGGGATCAAAG
ACAGATTGGGTGAGGATGAGTAGGAAGTGGGGACAGAACTGGCAGTCCAACGCC
GTCCTTATCGGCCAATCACTCTTTTCAGAGTCACCGCTTCTGACCGACGCTCCTC
TACCTCGTGGAACGTTGCTCCTCCCTCGTGGCAGTTTGGTCAGACTTTCTCCGGCA
AAACTTCCGAGTCTGA

Nucleotide

>CgrEXPA-22

TCCCGCTTTCTCTCAGTACTATCCAATACACTTCTCTCTCTCTCTCTCACCTCT
ATAATGACGGCGACTGCGTTTGGGATCTGCTTGTGGTTGGCCGTTACGGCTTCTT
TTCTCTTAACAGCTTCAGACGCCAAAATCGCCGGCGTTTACAGCGGCGGACCATG

GCAGAACGCACACGCCACTTTCTACGGTGGTAGTGACGCCTCTGGAACCATGGGT
ATTACCATATTCACCGTTTTTAATTTTCATTTTCATACGTAACCATAAATTATGATTC
CTAACTTGTTAATTTTTTTTATAAAGTTCCTGACTTTTTCTTGTGCTCTGTTTTGTG
GGTTTTGCTAGGCGGCGCGTGTGGGTACGGGAACCTTGTACAGCCAAGGATACGGT
GTGAACACGGCGGCCTTGAGCACTGCTCTGTTCAACAACGGGTATAGCTGCGGTG
CTTGCTTCGAGATCAAGTGTACCGACGACCCGAGATGGTGTGTGCCGGGAAACCC
CTCGATTCTTGTTACGGCGACGAACTTTTGTCCGCCGAATTTTGTCTCAGGCGAGTG
ACAACGGAGGATGGTGCAATCCTCCGCGTGAGCACTTTGATCTAGCTATGCCTAT
GTTCCCTCAAGATCGGTCTCTACCGTGCAGGCATTGTCCCCGTCTCCTATCGCAGGT
TACTCCTCTCTCTCTCTGATTTTTTTTTTATTTTTTACCGATTTGGTTTTCGCCG
GCGAATATAATTTGGTGAATCGATAAGAATTTAACAGTAAATAGGTACGGTGAA
GAATTCTAACTAGCCAGTATATATAGTCACAGCTGTTGTTTACATAAACACGCAT
ATGGATGTTGATAATACATTAGTAACTTTTGCTAATCTAGATTATGTAATAATGAG
ATTAATAATGTTTTAGAGGGAAGTCTTTTCGTTGTGTAACATAAATCAGAGG
ATTTAGTGTTTGATTTTACTTGCTACTATAATATGGTAGAGAAATAGTATAATT
TTTTACAACTTAATTAAGACACCTTTTTTCATGTGAAATAGAAAATTTTTAAGATT
TCTTATTGAGATAGATAGTAATAAATAATAATAGTCGAAAATAAAAATAAAAAC
GCTTGAAGTTGTATTTTGATTGTATGTTTTTTTTATTAATAAAGTGAAAAGATATTT
GTACCGACTACCGAACATGTTATTATGAACTATCTGTGTGTTTTGTTTTCTCTAG
GTTTTCTACTTTCTAGCACTTTTTAAGATAACGGCCTATTGAGTTTCAGAGTTCAGA
AACTGAAACCATCGCTCTCAATAGTATTATTATTATCTCAATATTTCTATTTG
TTTTTTTTTTAACTCTGAAACATTTTTATTTTTAAAATTATCTTTTTGGGAAAAGAA
GCAGGCAGGACACAGTAACCCAGAGATCCATCTCCCTCTTTCTTTACCTCTTTGTC
TTGTTGTTAATAATTGTTCTGTTTCCTCTGAAGGGTACCTTGTCGGAAGGTAGGAG
GGATAAGATTCACAGTAAACGGGTTTCAGATACTTCAATCTCGTTCTGGTAACTAA
CGTTGCCGGTGCCGGAGATATCAACGGAGTTAGCGTAAAGGGATCAAAGACAGA
TTGGGTGAGGATGAGTAGGAACTGGGGACAGAAGTGGCAGTCCAACGCCGTCCT
TATCGGCCAATCACTCTCTTTTCAGAGTCACCGCTTCTGACCGACGCTCCTCTACCT
CGTGGAACGTTGCTCCTCCCTCGTGGCAGTTTGGTCAGACTTTCTCCGGCAAAAA
CTTCCGAGTCTGACTGAAGTCTCTCTGAAACCACACCCACACACACACCCAAAA
GAATCAAAATCTTTTTTCTTTTTTTTTCTCCATTACTTAAAAGAGAGATGTTGTTA
TTTTTATATTTTAATATGGCTCAGACATTTTCCAGCCCTGGGGTTCTCCCTTTAAT
TTCTCGGGAAAATTTGCCGGTGGCTTCGGGAAATTATTTAGTTTTATTTGTTGGT
GGCATCTTCTTCTGCTTAGCTAATAAAAAGCCAGAGAGAGTGTAAACAAAACAGT
CTGTGATTTGAGTCTGATGGACCTTGTAATGGGCCCTTGGGCCAAGTTATTTATAA
AAATCTTAAATTCGG