

IDENTIFICATION

Species: *Capsella grandiflora*

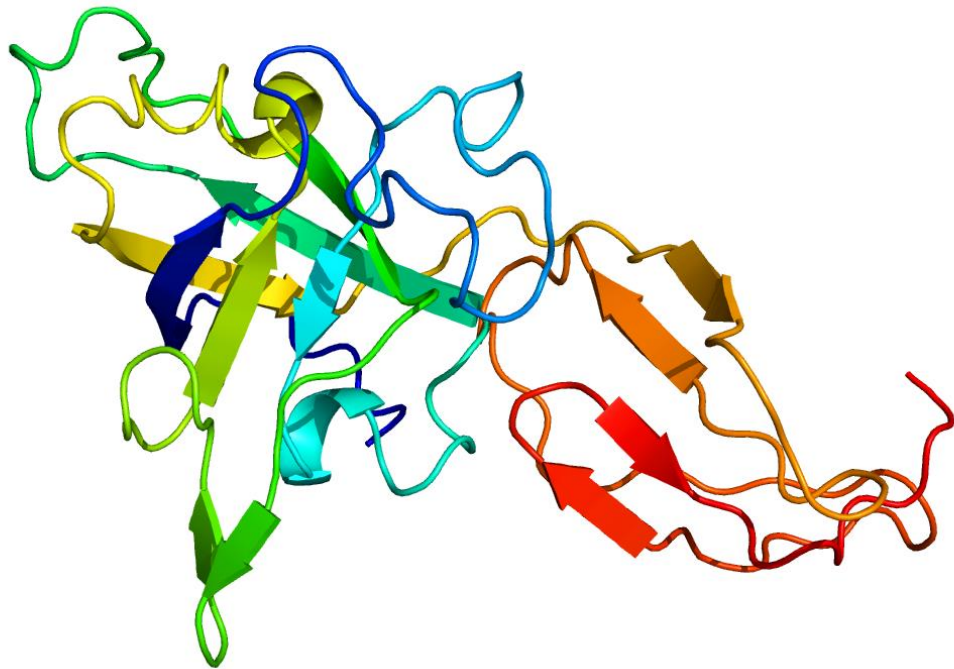
Locus: Cagra.6845S0001

Gene Model: Cagra.6845S0001.1.p

Description: CgrEXPA-20

Family: Alpha Expansin

3D structure:



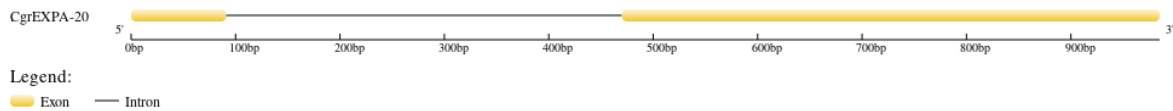
GENOME DATABASES

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

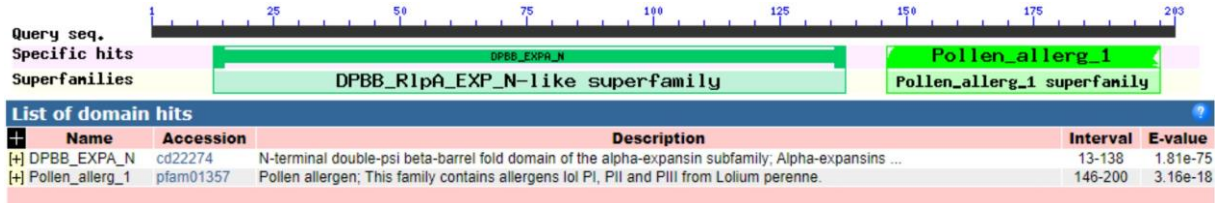
EXTERNAL RESOURCES

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GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>CgrEXPA-20

MSTGAATAVTD AWDNARATFYGDIEGGGTMKGDCGYGNLFEQGYGLETTALSAAL
FNNGATCGACFEIKCVDNPQACIEGAKPIRV TATNFCPANYTKTVGVWCNPPQKHFD
LSLPMFLKIAKYKAGVVPVKYRRVLC PHKQGGVKFQLSGNPYFLMVLVYNVGHVG
DVSEVRVKGSKSGWFMHRNWGQVWDTGLKLTGES*

CDS (coding sequence)

>CgrEXPA-20

ATGAGCACCGGTGCTGCTACTGCTGTCACAGACGCCTGGGACAATGCTCGTGCCA
CTTTTTACGGTGATATAGAGGGTGGAGGA ACTATGAAAGGAGATTGTGGGTACG
GTAATCTCTTCGAGCAAGGCTACGGTTTAGAGACGACGGCTCTAAGTGCAGCTTT
GTTCAACAATGGAGCTACGTGCGGTGCATGCTTCGAGATTAAGTGCGTAGACAAT
CCACAAGCGTGCATCGAAGGAGCCAAACCTATACGCGTCACAGCCACCAATTTCT
GCCAGCAA ACTACACCAAACAGTAGGTGTTTGGTGCAATCCGCCG CAGAAAC
ATTCGACCTCTCGTTACCAATGTTTCTCAAGATCGCTAAGTACAAAGCCGGAGTT
GTTCCGGTGAAATATAGGCGAGTTTTATGCCCGCATAAACAAGGTGGTGTCAAGT
TTCAGTTATCAGGAAATCCTTATTTCTTGATGGTCTTGTTTACAACGTTGGACAT
GTTGGTGATGTGTCTGAGGTTAGGGTGAAAGGTTCCAAGAGTGGTTGGTTTCAGA
TGCATCGGAATTGGGGACAGGTGTGGGATACAGGCTTGAAGTTAACCGGAGAGA
GT

Nucleotide

>CgrEXPA-20

ATGAGCACCGGTGCTGCTACTGCTGTCACAGACGCCTGGGACAATGCTCGTGCCA
CTTTTTACGGTGATATAGAGGGTGGAGGA ACTATGAGTACGTTTACTCATTAAAA
TAACACATACCTGTTATATGATCAATATTTTTTTTTTTTTTTTAAAATGTTAATAATA
AGTTATTTAGAATTAGTATTATCCTTAAGAGCAA AATAGTTGAAACTTTTTTTTTTG
GATGGTGTGTAGTGTAGGTCGTATAAAAACAATGAATTGTCGAATTTTGTGATACA
ATGAGTTTTTCAAATTTTGTGAACCAAAGAATAGTTTGA ACTAATTATGTCATGCA

ACGTTGTGTTTGATCGCATACATATTTATAACAAATGGAGAAGCTAGATACGTTAT
ATAATTAGTCCTACACACATAATATATATATATCAGTGTTAAATTGAATCAAAAC
CAACAATCTAATTGAGGTGTAAACAGAAGGAGATTGTGGGTACGGTAATCTCTTC
GAGCAAGGCTACGGTTTAGAGACGACGGCTCTAAGTGCAGCTTTGTTCAACAATG
GAGCTACGTGCGGTGCATGCTTCGAGATTAAGTGCGTAGACAATCCACAAGCGTG
CATCGAAGGAGCCAAACCTATACGCGTCACAGCCACCAATTTCTGCCAGCAAAC
TACACCAAACAGTAGGTGTTTGGTGCAATCCGCCGCAGAAACATTTCGACCTCT
CGTTACCAATGTTTCTCAAGATCGCTAAGTACAAAGCCGGAGTTGTTCCGGTGAA
ATATAGGCGAGTTTTATGCCCGCATAAACAAGGTGGTGTCAAGTTTCAGTTATCA
GGAAATCCTTATTTCTTGATGGTTCTTGTTTACAACGTTGGACATGTTGGTGATGT
GTCTGAGGTTAGGGTGAAAGGTTCCAAGAGTGGTTGGTTTCAGATGCATCGGAAT
TGGGGACAGGTGTGGGATACAGGCTTGAAGTTAACCGGAGAGAGT