

## IDENTIFICATION

**Species:** *Capsella grandiflora*

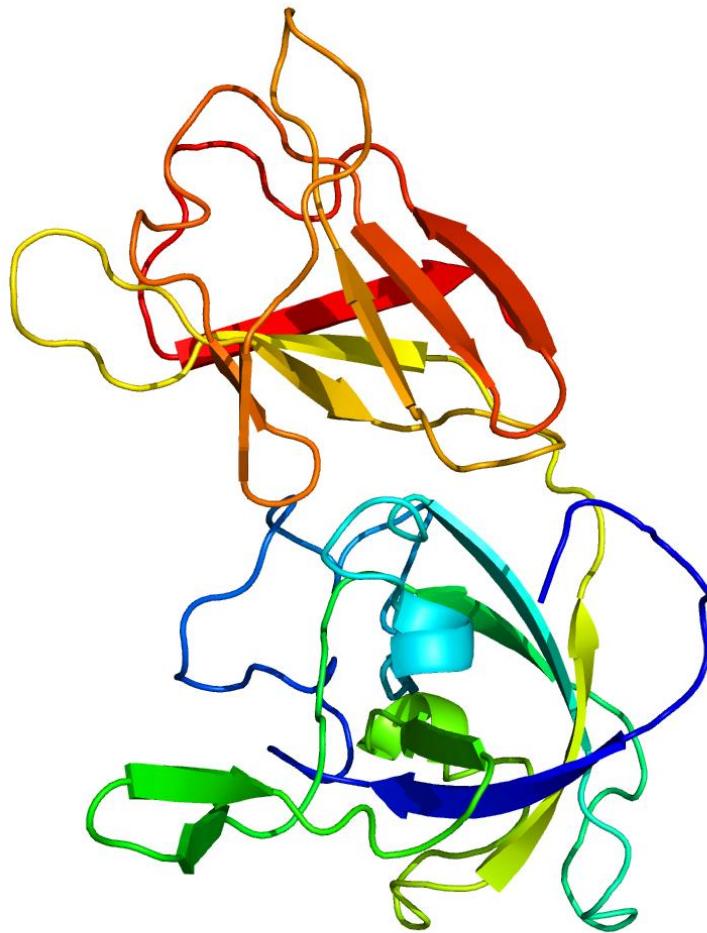
**Locus:** Cagra.1504S0034

**Gene Model:** Cagra.1504S0034.1.p

**Description:** CgrEXPA-12

**Family:** Alpha Expansin

**3D structure:**



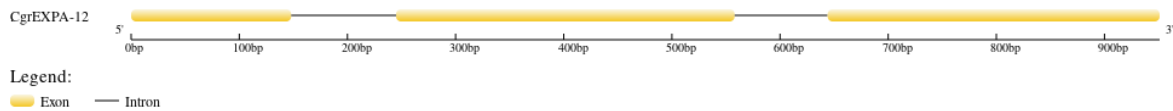
## GENOME DATABASES

Phytozome: [https://phytozome-next.jgi.doe.gov/info/Cgrandiflora\\_v1\\_1](https://phytozome-next.jgi.doe.gov/info/Cgrandiflora_v1_1)

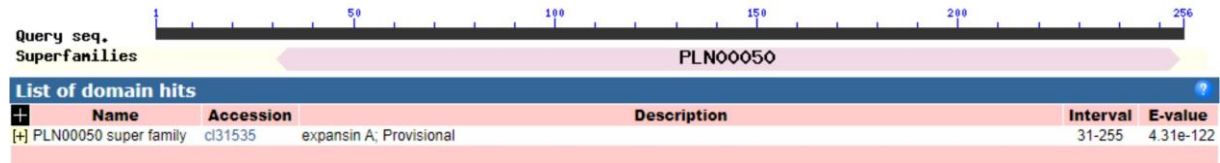
## EXTERNAL RESOURCES

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## GENE STRUCTURE



## DOMAIN ARCHITECTURE



## SEQUENCES

### Peptide

>CgrEXPA-12

MNLILYSQILFVSLCTLSCCFYLINSDDNGGWDRGHATFYGGADASGTMGGACGYG  
NLNSQGYGLQTAALSTALFNNGQRCGACFELQCEDDPEWCIPGSIIVSATNFCPPNFA  
LANDNGGWCNPLKHFDLAQP AFLQIAHYRAGIVPVAFRVPCEKGGGIRFTINGNP  
YFDLVLITNVGGAGDVRAVSLKGSKTNQWQMSRNWQNWQSN TYLRGQSLSFQV  
IASDGRAVVSYDVVPADWQFGQTFEGGQF\*

### CDS (coding sequence)

>CgrEXPA-12

ATGAATCTTATACTTTATTCTCAGATTTTATTTGTTTCACTATGTACCCTCAGTTGC  
TGCTTCTACCTTATTA ACTCCGACGACAACGGAGGCTGGGATAGAGGCCATGCCA  
CCTTTTACGGCGGAGCTGATGCATCCGGCACTATGGGTGGTGC GTGTGGGTACGG  
TAACTTAAACAGCCAAGGCTATGGGCTACAAACCGCGGCTCTGAGCACTGCTTTG  
TTCAACAACGGACAGAGATGTGGGGCTTGCTTTGAGCTACAGTGTGAGGATGATC  
CTGAGTGGTGCATCCCTGGTTCCATCATCGTCTCAGCTACAACTTCTGTCCACCA  
AACTTTGCCTTAGCCAATGATAATGGTGGTGGTGTAACTCCTCCCCTCAAGCACTT  
TGACTTAGCCCAGCCTGCCTTCTCCAAATTGCTCACTACCGAGCTGGGATCGTTC  
CTGTTCGATTTTGAAGGGTTCCATGTGAGAAAGGTGGAGGTATAAGGTTCACAAT  
AAATGGGAATCCGTATTTGACCTCGTGCTGATCACAACGTGGGTGGTGGTGGG  
GATGTAAGGGCCGCTCTTTGAAAGGATCAAAGACTAATCAGTGGCAATCCATGT  
CAAGAACTGGGGACAGAATTGGCAAAGCAACTTACCTTAGAGGTCAAAGCC  
TCTCTTTTCAAGTCATTGCTAGTGACGGTTCGAGCTGTTGTGAGCTACGATGTTGTG  
CCTGCTGATTGGCAGTTCGGTCAAACCTTTTGAAGGCGGACAATTTTAA

### Nucleotide

>CgrEXPA-12

ATGAATCTTATACTTTATTCTCAGATTTTATTTGTTTCACTATGTACCCTCAGTTGC  
TGCTTCTACCTTATTA ACTCCGACGACAACGGAGGCTGGGATAGAGGCCATGCCA  
CCTTTTACGGCGGAGCTGATGCATCCGGCACTATGGGTACTTTAACGACTACTTTT  
TCCATGAGCTCACTTATAATCCACA AATTGATATGTTAACATGTCTAACAGTTGAC

TTGTTGGGGTTTAAATTGTAGGTGGTGCCTGTGGGTACGGTAACTTAAACAGCCA  
AGGCTATGGGCTACAAACCGCGGCTCTGAGCACTGCTTTGTTCAACAACGGACAG  
AGATGTGGGGCTTGCTTTGAGCTACAGTGTGAGGATGATCCTGAGTGGTGCATCC  
CTGGTTCCATCATCGTCTCAGCTACAAACTTCTGTCCACCAAACCTTTGCCTTAGCC  
AATGATAATGGTGGTGGTGTAAATCCTCCCCTCAAGCACTTTGACTTAGCCCAGC  
CTGCCTTCCTCCAAATTGCTCACTACCGAGCTGGGATCGTTCCTGTGCGCATTTCGA  
AGGTATAGGTTTCACTAGCTAGAAACACCTTAATCTCAAGTTTGAAACTATATAT  
GTAACAAATTTATATGTCCACTTATAATGACAGGGTTCCATGTGAGAAAGGTGGA  
GGTATAAGGTTCAACAATAAATGGGAATCCGTATTTGACCTCGTGCTGATCACAA  
ACGTGGGTGGTGGTGGGGATGTAAGGGCCGTCTCTTTGAAAGGATCAAAGACTA  
ATCAGTGGCAATCCATGTCAAGAACTGGGGACAGAATTGGCAAAGCAACACTT  
ACCTTAGAGGTCAAAGCCTCTCTTTTCAAGTCATTGCTAGTGACGGTCGAGCTGTT  
GTGAGCTACGATGTTGTGCCTGCTGATTGGCAGTTCGGTCAAACCTTTTGAAGGCG  
GACAATTTTAA