

IDENTIFICATION

Species: *Capsella grandiflora*

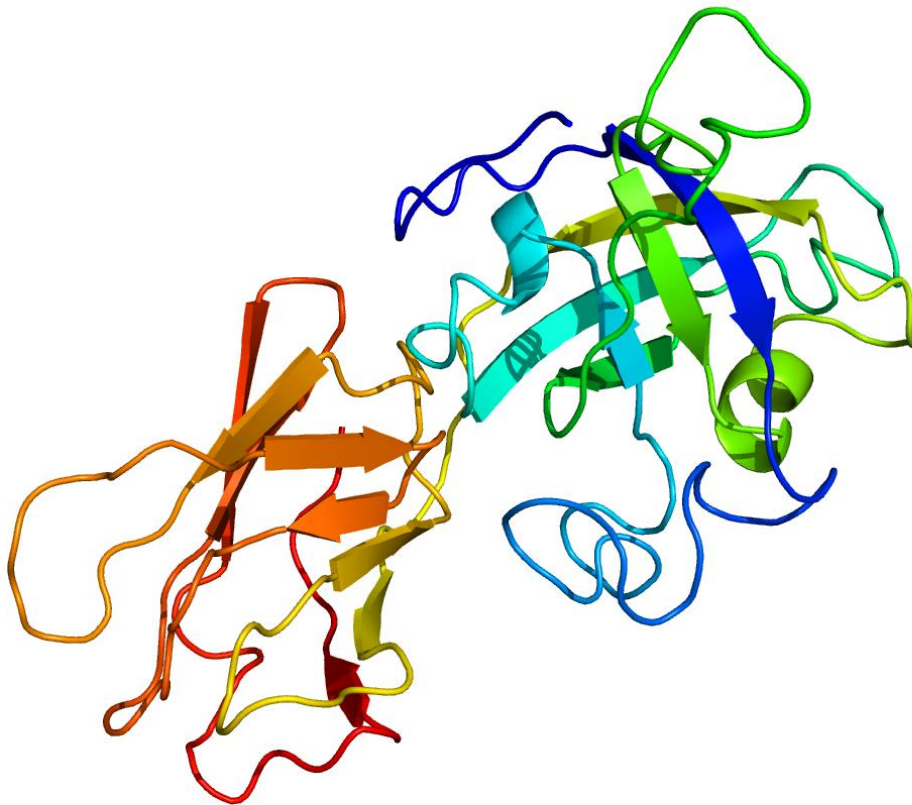
Locus: Cagra.0003S0041

Gene Model: Cagra.0003S0041.1.p

Description: CgrEXPA-01

Family: Alpha Expansin

3D structure:



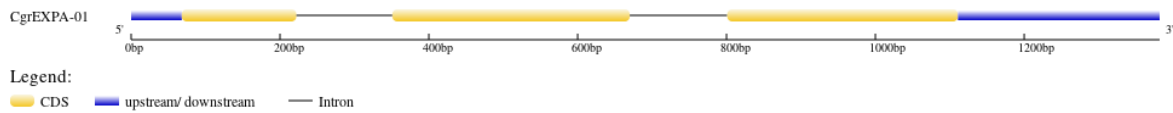
GENOME DATABASES

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

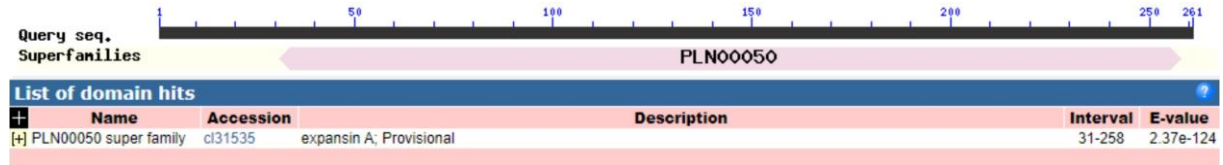
EXTERNAL RESOURCES

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GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>CgrEXPA-01

MAISSILLTIPLFLLLSLTHAGIPGVYSGSSWLTAHATFYGGNDASGTMGGACGYGD
LYSQGYGTNTAALSTALFNSGQSCGACFEVKCVNDPKWCHPGSPSVFVTATNFCPPN
LAQPSDNGGWCNPPRAHFDLAMPVFLKIAQYRAGIVPISYRRVACRKS GGIRFTINGH
RYFNLVLITNVAGAGDIVKASVKSSKSGWMGLTRNWGQNWQSNVVLVGQSL SFRV
TSSDRRTSTSWNIVPSNWQFGQTFVGKNFRV*

CDS (coding sequence)

>CgrEXPA-01

ATGGCAATCAGTTCATCGATTCTCTTAACCATAATCCCTCTCTTTCTCCTCTTAAG
CCTCACCCACGCCGGAATCCCTGGCGTTTACTCTGGCAGCTCTTGGCTAACCGCTC
ACGCCACTTTCTACGGCGGCAATGACGCTTCCGGAACCATGGGTGGCGCTTGCGG
ATACGGGGATTTATACAGCCAAGGGTACGGAACAAACACGGCAGCGCTAAGCAC
AGCGTTGTTCAACAGTGGCCAAAGCTGCGGGGCATGCTTTGAAGTTAAATGTGTC
AATGATCCCAAATGGTGTACCCGGGTAGTCCTTCCGTCTTCGTAACCGCAACCA
ACTTTTGCCCTCCAAACTTAGCCCAACCTAGCGACAATGGCGGCTGGTGCAACCC
GCCACGTGCTCACTTCGACCTTGCAATGCCCGTTTTTCTCAAGATCGCTCAGTATC
GCGCCGGCATTGTCCCATCTCTTACCGCAGGGTGGCATGTAGGAAGAGTGGAGG
GATAAGGTTACGATCAACGCCACCGTTACTTCAACTTAGTGCTGATCACGAAC
GTGGCAGGAGCAGGAGACATCGTGAAGGCGAGCGTGAAAAGTTCAAAGAGTGGT
TGGATGGGTTTGACTAGGAACTGGGGACAGA ACTGGCAGTCAAATGCCGTTCTTG
TTGGTCAGTCACTTTCTTTCCGTGTACATCCAGTGACCGCAGAACCTCTACTTCA
TGGAACATCGTTCCTTCGAACTGGCAGTTTGGACAAACCTTTGTCGGAAAGAATT
TCAGAGTCTAA

Nucleotide

>CgrEXPA-01

CCAAGTTCCTCCCTTAGCCTTCTTTCTAGTTTAAACAATCTTCTTATTCTCTCTCCAT
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GCTAACCGCTCACGCCACTTTCTACGGCGGCAATGACGCTTCCGGAACCATGGGT
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CGGGGCATGCTTTGAAGTTAAATGTGTCAATGATCCCAAATGGTGTACCCGGGT
AGTCCTTCCGTCTTCGTAACCGCAACCAACTTTTGCCCTCCAACTTAGCCCAACC
TAGCGACAATGGCGGCTGGTGCAACCCGCCACGTGCTCACTTCGACCTTGCAATG
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TAAGCTTGAGTTTTGTTGTATAGGGTGGCATGTAGGAAGAGTGGAGGGATAAGGT
TCACGATCAACGGCCACCGTTACTTCAACTTAGTGCTGATCACGAACGTGGCAGG
AGCAGGAGACATCGTGAAGGCGAGCGTGAAAAGTTCAAAGAGTGGTTGGATGGG
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TCACTTTCTTTCCGTGTCACATCCAGTGACCGCAGAACCTCTACTTCATGGAACAT
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TAAAGTGAATCGATGAAATCAAACATACGAAGTGGTAGAAACAAATTAAGAAA
CCTCACTTTCAAATTCGAACATATTTGTAATTTGTATTTTCTGTTAATGGTTTTTT
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GCCCGCAGCTCTTAATTTACATGGTTTGCTTGTAATGTGTGAATTTTCATCATA