

IDENTIFICATION

Species: *Citrus sinensis*

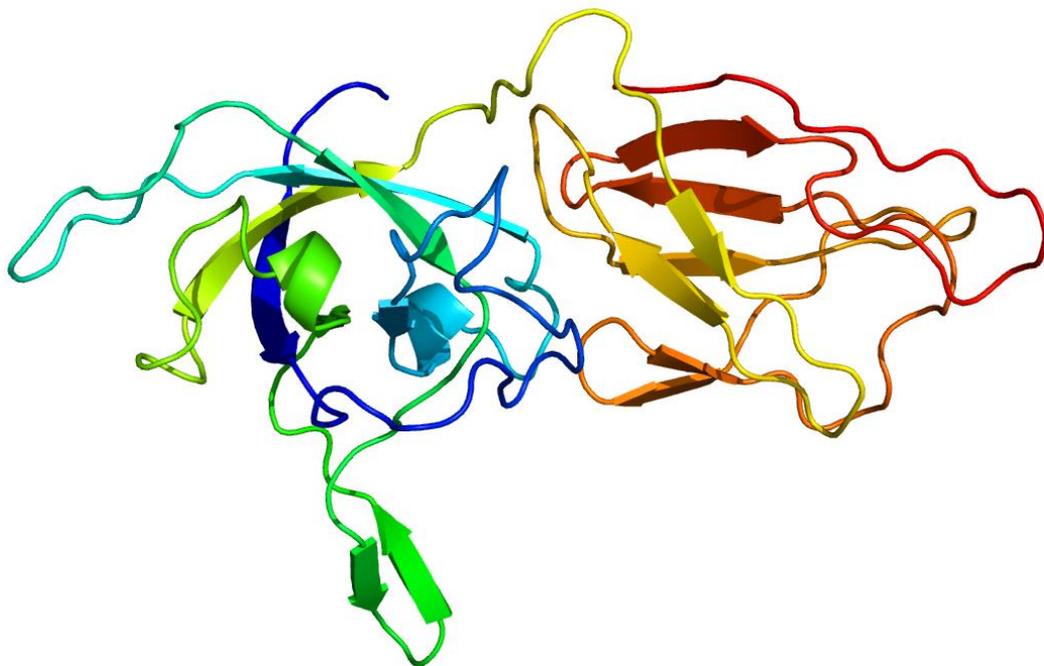
Locus: orange1.1g023962m

Gene Model: orange1.1g023962m

Description: CisEXPB-01

Family: Beta Expansin

3D structure:



GENOME DATABASES

Phytozome: https://phytozome-next.jgi.doe.gov/info/Csinensis_v1_1

Kegg: <https://www.genome.jp/entry/T02983>

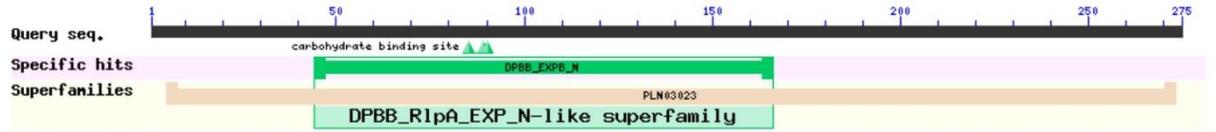
EXTERNAL RESOURCES

<https://www.citrusgenomedb.org/organism/Citrus/sinensis>

GENE STRUCTURE



DOMAIN ARCHITECTURE



List of domain hits					
	Name	Accession	Description	Interval	E-value
[+]	DPBB_EXP_N	cd22275	N-terminal double-psi beta-barrel fold domain of the beta-expansin subfamily; Beta-expansins ...	44-166	4.33e-77
[+]	PLN03023 super family	cl33621	Expansin-like B1; Provisional	5-273	7.76e-44

SEQUENCES

Peptide

>CisEXPB-01

MAHVFRYPISFFTLVFMFPLFLHSCWCFNPKLLNITMAESGSDWSPAGATWYGSPTG
AGSDGGACGYGAAVEQAPFSALISAGGPSLYKSGKGCACGYQVKCTHPECSGNPVT
VVITDECPGGPCVSESVHFDLSGTAFGAMAISGKADQLRNVGVLQIQHRRVECNYPG
MRIA FHVDSGSNPNYFATLIEYEDGDGLASVDLQQALDSSDSWLPQRSWGAVW
KLNYGSTLRAPFSLRLTAAESGKALVAKGVIPAGWQPGQTYRSLVNFTP*

CDS (coding sequence)

>CisEXPB-01

ATGGCACATGTTTTTCGATATCCCATATCATTTTTCACTCTTGTATTCATGTTTCCT
CTTTTCCTGCACTCATGTTGGTGCTTCAATCCCAAGCTACTTAATATCACCATGGC
AGAGTCGGGGTCTGATTGGTCCCCGGCTGGGGCAACGTGGTACGGTAGCCCTACT
GGTGCAGGAAGCGATGGTGGCGCTTGTGGGTACGGAGCGGCAGTGGAGCAAGCC
CCGTTCTCCGCACTGATTTCTGCTGGAGGCCCTCTTTGTACAAATCTGGCAAAGG
ATGTGGAGCCTGTTATCAGGTA AAAATGTACACATCCGGAATGCTCGGGAAATCCA
GTGACAGTGGTCATTACTGATGAATGCCCTGGGGGACCCTGTGTTTTCAGAATCAG
TTCATTTGACTTAAGTGGCACTGCTTTTGGAGCTATGGCAATTTCTGGCAAAGGCT
GATCAACTCCGTAACGTTGGGGTCTTACAGATTCAGCACAGAAGAGTTGAGTGCA
ACTATCCTGGCATGAGGATAGCATTTACGTTGATTCAGGCTCAAACCCTAACTA
TTTTGCGACACTGATTGAGTACGAAGATGGTGACGGTGACCTTGCTTCAGTTGAC
CTGCAACAAGCTCTGGACTCATCCGACTCGTGGCTTCCCATGCAACGGTCATGGG
GTGCTGTTTGGAACTTAACTATGGATCCACTTTACGTGCTCCGTTTTCGCTCCGT
TTAACGGCAGCCGAATCTGGGAAAGCTCTTGTAGCAAAGGAGTTATTCCGGCTG
GTTGGCAACCTGGACAACTTACCGATCACTTGTC AATTTTACACCCTAG

Nucleotide

>CisEXPB-01

GTTCATTGTGTACAATAATATGGCACATGTTTTTCGATATCCCATATCATTTTTCA
CTCTTGTATTCATGTTTCCTCTTTTCCTGCACTCATGTTGGTGCTTCAATCCCAAGC

TACTTAATATCACCATGGCAGAGTCGGGGTCTGATTGGTCCCCGGCTGGGGCAAC
GTGGTACGGTAGCCCTACTGGTGCAGGAAGCGATGGTACGTATTTCAATGGAGA
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TGCTGATTACAATTA AATTGCCTAATTAATTCTATACTAAAGTAATTAATCTACT
CCAGGTAAAATGTACACATCCGGAATGCTCGGGAAATCCAGTGACAGTGGTCATT
ACTGATGAATGCCCTGGGGGACCCTGTGTTTCAGAATCAGTTCATTTGACTTAA
GTGGCACTGCTTTTGGAGCTATGGCAATTTCTGGCAAGGCTGATCAACTCCGTAA
CGTTGGGGTCTTACAGATTCAGCACAGAAGGTACGTACGTAATTAATTAGTACAT
GTTGAAATTTCCAAATTTTTTAAAGTCACCATACGTCAAATGGCCACTTTAATTA
TTTGCAGAGTTGAGTGCAACTATCCTGGCATGAGGATAGCATTTACGTTGATTC
AGGCTCAAACCCTAACTATTTTGCGACACTGATTGAGTACGAAGATGGTGACGGT
GACCTTGCTTCAGTTGACCTGCAACAAGCTCTGGACTCATCCGACTCGTGGCTTCC
CATGCAACGGTCATGGGGTGCTGTTTGGAACTTAACTATGGATCCACTTTACGT
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