

IDENTIFICATION

Species: *Theobroma cacao*

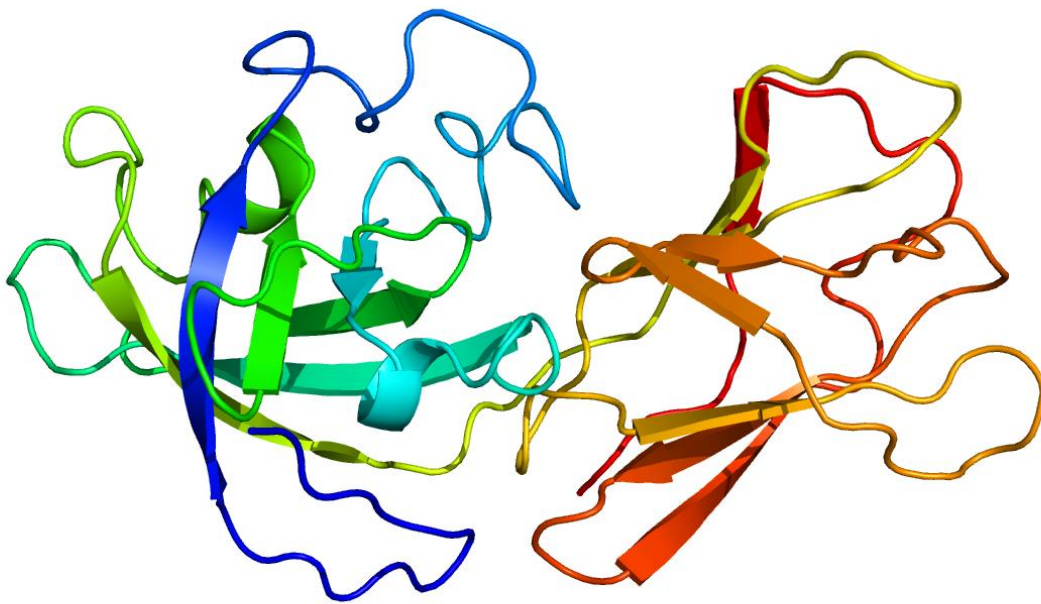
Locus: Thecc.03G268000

Gene Model: Thecc.03G268000.1.p

Description: TcEXPA-06

Family: Alpha Expansin

3D structure:



GENOME DATABASES

Phytozome: https://phytozome-next.jgi.doe.gov/info/Tcacao_v2_1

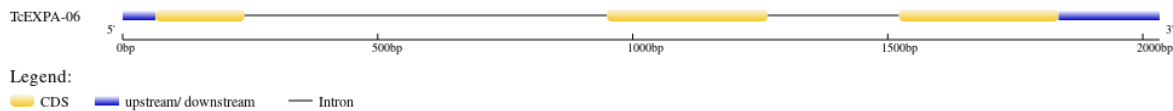
KEGG: <https://www.genome.jp/entry/gn:T02994>

EXTERNAL RESOURCES

<https://www.cacaogenomedb.org/>

<https://cocoa-genome-hub.southgreen.fr/node/4>

GENE STRUCTURE



DOMAIN ARCHITECTURE

Query seq. Superfamilies

List of domain hits

Name	Accession	Description	Interval	E-value
PLN00193 super family	cl33423	expansin-A, Provisional	12-266	6.09e-97

SEQUENCES

Peptide

>TcEXPA-06

MASSSSYSWSWCFRFFSLTLTTLAIISKPSVA APIFRPSPWALAHATFYGDETA SETMG
GACGYGNLFSNGYGTDTAALSTTLFNNGFACGTCYQIKCVQSSWCYSGVPFTT VTAT
NLCPPNWAQDSNNGGWCNPPRAHFDMSKPAFMKIAQWKAGIVPVMYRRVPCVRPG
GLRFSFQNGYWLLVYVMNVGGGGDIQNMWVKGSRTGWISM SHNWGASYQAFAT
LGGQSLSFKLTSYTTKETIIAWNVAPANWNVGLTYSTNLNFH*

CDS (coding sequence)

>TcEXPA-06

ATGGCTTCTTCTTCTTCTTATTTCATGGTCCTGGTGCTTTAGGTTCTTTTCGTTGACA
CTTACAACGTTGGCCATCATCAGCAAACCTTCTGTTGCTGCTCCAATTTCCGGCC
AAGCCCTTGGGCCCTTGCCCATGCCACCTTTTATGGCGATGAAACCGCCTCCGAG
ACAATGGGAGGAGCTTGTGGATATGGGAATTTGTTTTCCAATGGTTACGGTACGG
ACACAGCTGCTCTGAGCACAACATTGTTCAACAATGGGTTTGCTTGCGGGACTTG
CTACCAGATAAAATGTGTCCAGTCATCTTGGTGCTACAGTGGGGTTCCTTTCACCA
CAGTAACTGCTACTAACCTTTGCCCTCCAAATTGGGCCCAAGACTCCAACAATGG
TGGCTGGTGCAACCCTCCTCGAGCCCACTTTGACATGTCCAAGCCCGCTTTCATGA
AAATTGCTCAGTGGAAGGCTGGCATTGTCCCTGTTCATGTACCGAAGGGTACCGTG
CGTAAGGCCAGGCGGGCTTAGGTTCTTTTCCAAGGAAATGGGTAAGTTGTTGTTG
GTGTATGTGATGAATGTAGGAGGAGGTGGTGACATTCAAACATGTGGGTAAA
GGAAGCAGAACAGGGTGGATCAGCATGAGCCATAACTGGGGAGCATCATAACAG
GCATTTGCAACTCTCGGAGGCCAATCTCTTTCCTTCAAGCTCACTTCATACACAAC
CAAGGAGACCATCATAGCTTGAATGTTGCACCTGCAAATTGGAATGTAGGATTG
ACTTACAGCACAAATCTGAACTTCCATTAA

Nucleotide

>TcEXPA-06

AATGCACATTACACAATATTGTACAATTTTGTCTCTAAAAGGTCTCCCAAGGAA
GAATAAGCCATGGCTTCTTCTTCTTCTTATTTCATGGTCCTGGTGCTTTAGGTTCTTT
TCGTTGACACTTACAACGTTGGCCATCATCAGCAAACCTTCTGTTGCTGCTCCAAT
TTCCGGCCAAGCCCTTGGGCCCTTGCCCATGCCACCTTTTATGGCGATGAAACCG
CCTCCGAGACAATGGGTATGTCGTTTTTTTAACTTTTCATTGGTGTATTATAGGG

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TCATTGGTGTCAATAGCTAATCAAGATTGATCTTTGAAGCGCATGCTCATTGTTA
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AGCTGCTCTGAGCACAACATTGTTCAACAATGGGTTTGCTTGCGGGACTTGCTAC
CAGATAAAATGTGTCCAGTCATCTTGGTGCTACAGTGGGGTTCCTTTCACCACAG
TAACTGCTACTAACCTTTGCCCTCCAAATTGGGCCCAAGACTCCAACAATGGTGG
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GTGCTTAAGATTCAACCTTATACTCGTTGGATATACCCAAATCCCCTCTAAAACCA
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GCCAGGAGAATAATTATACCTGCTCTTCGTTTGGT