



# CAGL0K04037g [Help!](#)

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## CAGL0K04037g

tr|Q9P8N8 *Candida glabrata*  
1, 3-beta-glucan synthase,  
identified start

*Candida glabrata* Complete  
CDS.

ORF from

[Cagl0K:372546..378239](#) sense

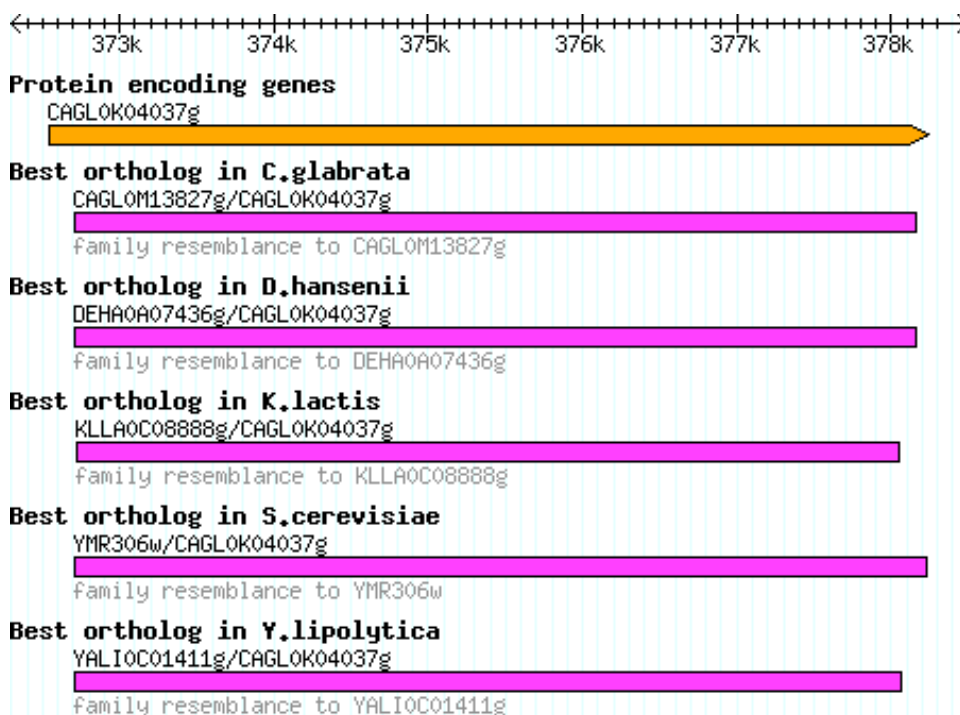
(p)

Predicted protein is 1897 aa

Synonyms:

CAGL0K04037g|CAGL-

IPF2142|CAGL-CDS0043.1



## Theoretical

Molecular weight: 217.6 kDa

Avg residue weight: 114.7 Da

Isoelectric point: 7.8

Charge: 23.5

(InterPro domains cartoon)

## Protein family

Family [GLR.23](#) sckdy: 13 proteins (3 3 3 2 2)

## Results

<a href="#">S.cerevisiae blastp</a>	<a href="#">Uniprot blastp</a>
<a href="#">C.albicans blastp</a>	<a href="#">N.crassa blastp</a>
<a href="#">C.glabrata blastp</a>	<a href="#">K.lactis blastp</a>
<a href="#">D.hansenii blastp</a>	<a href="#">Y.lipolytica blastp</a>

## CDS translation product

>gnl|GLV|CAGL0K04037g Translation product.

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QANYTPSQLSYSNNGMGSNGMNSGSSTPVYGNYPNAIAMTLPNDPYPAWTADPQSPVS  
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SLEASDFRWKTKMMLTPIERVROVALYMLIWGEANQVRFTSECLCFIYKCADSYLESPL  
CQORTEPIPEGDYLNRVITPIYQFIRNOVYEIVDGRYVKREKDHNKIIGYDDVNQLFWYP  
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KWAGAQLSRRFVFLCGILGVNLGPLIFVFAYEKDQVQSKAGHAAVAVTFPIAVATVLFV  
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LSIFIVFIAFVPIVVQELERGLWKTQRFRRHILSLSPMFEVFAQIYSAALLSDMTV  
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SALLFSPFIFNPHQFSWEDFFLDYRDYIRWLSRGNNKYHKNSWIGYVRMARSRITGFKRK  
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IRPPIYSLKQSRRLKRMVKRYLTLYIIIFLVFAGAIVGPAAVAASHVPQDIGHTLTGPFHN  
IVQPRNKSNNDTGLQISTYSNHYYTHTPSLKTWSTIK

## Predicted mRNA for coding sequence

>gnl|GLV|CAGL0K04037g tr|Q9P8N8 Candida glabrata 1, 3-beta-glucan synthase,  
identified start [Candida glabrata] Complete CDS.

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GAACAACAACAAGGUGGUGAAGGUUACUACGAUGAGUACGGACAACCCAAUAUAAUUAAC  
AUGAACGACCCACAGCAAGGUCAAAUGCCACAACAACAACCUGGUGGUUAUGAGAACGAC  
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## CDS chromosomal neighborhood

>gnl |GLV |CAGL0K04037g -500,+200 neighborhood

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 TCCTAGCCGCCATTCTCTTCTACCTTTATTTGGTCTCTTTTCTAACTTTGAGATCTGGG  
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 CACTTTGTACAAGAATTAAGGACATCATACAGCGGTAAACTTTTTACAACACTACAAGTC  
 TTTTGTCTTTCTTCTCATCGAAGAAAACAGGAATAGACACAAAAAAGAGAGTAAGTG  
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TGCAAATTCGACATATAGTAATCATTACTACACACATACGCCATCTCTAAAGACCTGGT  
CCACTATAAAA**TAA**AGAGGCAATAGATAATCCCCTAATTGAGTATGATTTTCAAGAATTT  
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CGATGGTAACAATAACAGTCTATATTTTTATCTT

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