	A R	265_Cna1	
	00.49/	07.0%	
	99.4%	97.0%	
WM276_Cna1 ← H99_Cna1			
В		96.7%	
R265_Cna1 1 WM276_Cna1 H99_Cna1	MASPATQTAN VIAAINNRSNLVI	PEIDFTQHQLENGEVVSTTERVIKDVQAPAMYV PEIDFTQHQLENGEVVSTTERVIKDVQAPAMYV PEIDFTQHQLENGEIVSTTERVIKDVQAPAMYV	PTDD
R265_Cnal 6 WM276_Cnal H99_Cnal	QFFSKVDKTKPDIAFLKNHFYRE	Catalytic GRLTEEQALYILEKGGELLRSEPNLLEVDAPIT GRLTEEQALYILEKGGELLRSEPNLLEVDAPIT GRLTEEQALYILEKGGELLRSEPNLLEVDAPIT	VCGD
R265_Cna1 12 WM276_Cna1 H99_Cna1	IHGQYYDLMKLFEVGGNPADTRY	LFLGDYVDRGYFSIECVLYLWSLKMWYPDTLFL LFLGDYVDRGYFSIECVLYLWSLKMWYPDTLFL LFLGDYVDRGYFSIECVLYLWSLKMWYPDTLFL	LRGN
R265_Cna1 18 WM276_Cna1 H99_Cna1	HECRHLTDYFTFKLECKHKYSET	VYNACMESFCNLPLAAVMNKQFLCIHGGLSPEL VYNACMESFCNLPLAAVMNKQFLCIHGGLSPEL VYNACMESFCNLPLAAVMNKQFLCIHGGLSPEL	HTLD
R265_Cnal 24 WM276_Cnal H99_Cnal	DLRSINRFREPPTQGLMCDILWF	DPLEDFGSEKTNDNFLHNHVRGCSYFFTYNAAC DPLEDFGSEKTNDNFLHNHVRGCSYFFTYNAAC DPLEDFGSEKTNENFLHNHVRGCSYFFTYNAAC	QFLE
R265_Cnal 30 WM276_Cnal H99_Cnal	RNNLLSIIRAHEAQDAGYRMYR	TKTTGFPSVMTIFSAPNYLDVYSNKAAVLKYES TKTTGFPSVMTIFSAPNYLDVYSNKAAVLKYES TKTTGFPSVMTIFSAPNYLDVYSNKAAVLKYES	NVMN
R265_Cnal <mark>36</mark> WM276_Cnal H99_Cnal	IRQFNCTPHPYWLPNFMDVFTWS	LPFVGEKITDMLIAILNCCTKEELEEEDEEFPI LPFVGEKITDMLIAILNCCTKEELEEEDEEFPI LPFVGEKITDMLIAILNCCTKEELEEEDEEFPI Cnb binding	GALE
R265_Cnal 421 WM276_Cnal H99_Cnal	TTDVESAAERRQIIKNKILAVGE	MSRVFSLLREESERVSELKS TAGSNALPAGMLA MSRVFSLLREESERVSELKS TAGSNALPAGMLA MSRVFSLLREESERVSELKS TSGSNALPAGMLA CaM binding	SGAE
R265_Cna1 48 WM276_Cna1 H99_Cna1	GIKET IQGFEDARKSDIENERLE	PDIIDPDEDKPASPSASPIMPATFKETTSEILH PDIIDPDEDKPASPSASPIMPATFKETTSEILH PDIIDPDEDKPASPSASPIMPATFEEIPSEIPY Autoinhibitory	DSPI
R265_Cna1 54 WM276_Cna1 H99_Cna1	IGTFVTPISSAIVSGSPGSPGT	TSPSVGGPPLTAWRPGHORRTSLGTTKTSPSTR ISPSVGGPPLTAWRPGHGRRTSLGTTKTSPSTR TSPSIGGPPLTAWRPGHGRRTSLGTTKTSPSTR	RRSL
R265_Cna1 60 WM276_Cna1 H99_Cna1	<sup>1</sup> ENTMHLIRDVVGGKDAQGDGQLE ENTMHLIRDVVGGKDAQGDGQLE ENTMHLIRDVVGGKDAQGDGQLE	RLAEVISSPTKGGQDERE	

Figure S1 Amino acid identity and pairwise alignments of calcineurin catalytic subunit (Cna1) from *C. gattii* R265, *C. gattii* WM276, and *C. neoformans* H99. Amino acid identity and multiple sequence alignments are depicted using ClustalW software (<u>http://npsa-pbil.ibcp.fr/cgi-bin/npsa\_automat.pl?page=npsa\_clustalw.html</u>). (A) The % identity shared between the full-length proteins is shown in red. (B) The conserved and divergent amino acids are indicated with yellow shading and red rectangle, respectively. The catalytic domain, calcineurin regulatory subunit (Cnb) binding, calmodulin (CaM) binding, and autoinhibitory domains are indicated with gray, green, red, and blue underlining, respectively. The amino acids of the *C. gattii* R265 Cna1 protein are numbered.