GcbC	REHANAQESATRGATTIAQLIDADVLRTVELYDLTLQGLIAAAQRDDLKDVS-
Pf101_2295	SRERALEEVDVHGLNLTQALVTYSEGIVRQSSALLLGLVERLETEGSGPVQI
Pf101 2297	RSVFASARDSVTNLARATAQHAEDTIRQVDVLTAGLAERVEGDGLQNLDV
Pf101_3800	QIEQSRRQDLANAQVSSANLTRAMAQQAEDTFLAADLVMTSLVDWVQEDGYGAAQK
-	::* ::
GcbC	PQIRHLALFDRSTTARFKGDILLLDKHGEVIADSSRVDPLPGNFADRDYFLAHAFNRDTG
Pf101_2295	QRISSLIDRQEPLMPQLSG-ITIYDSQGRWLMSSNRPIPAGANSSDRAYFIHHRDDPSPE
Pf101_2297	ARIHKLLVQQSKIMPQLHG-LFIYGPDGHWIVTDKEVTPETANNADRDYFQYHRTHEDRR
Pf101_3800	PRLQRTFARRVQQLEQLHG-MFLFDREGQWVITSFPDLPRGNGVADREYFKFHQQNVSGV
_	.: .:*::. * : . * .:** ** .
GcbC	MFISRPFKPRCDCDDADQWRISFSRRISSNTGEFLGVAVASMKLDYFDQLFNSLDIGIDS
Pf101_2295	TFIGPPIQSRTNQEWVITVSRRFNDARGEFAGVVAVTLGIENFLRLFGKIDVGQEG
Pf101_2297	VRIGQVVESRSTHDLIIPISRRLNNPDGSFAGVLLGTVKVSYFVDYYGDFRIDDKG
Pf101_3800	AHIGPAIRSRENGEWIIPISKRVNDRAGNFQGVLLAGIKMSYFDKFFKSFSLDDNG
_	** : **.* *.* ** : :. * : .: :
GcbC	$\tt TLNIINNDGILLAQKPYLQSDSIGKSFAARPNVVRILRDSSGNGSFNSISSMDHQQRLYT$
Pf101_2295	AIGLSYTDGTLLVRYPFREQD-MGRNFSKSPIYAKYLVDHS-VGTASFTSSLDGVERLYA
Pf101_2297	ALVLAMRDGTILVRRPFITSV-VGKSLANSEIFKTYLPNAN-QGIVQIRAVVDDTERLYG
Pf101_3800	TMFLGMTDGTLLARRPFDESL-IGTSLAKGEIYQKLLPNAS-AGTAMIDSVVDGVTRLYG
	:::: ** :* *: . :* .:: * : . * : :* ***
GcbC	YSRVGNLPLTVIVALSSEEVFGAWR
Pf101_2295	FRKSDRLPLITTVALGKREALAAWRTEA
Pf101_2297	YRALTTYPLVVEAGLSRDSIVAPWRQ-
Pf101_3800	YRQLESYPLVVAASSSRDTILQGWYDR-
	: ** *

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3 Fig. S6. CLUSTAL alignment of the amino acid sequence of the CACHE domains of GcbC,

4 **Pfl01_2295, and Pfl01_2297.** The red amino acids indicate the conserved residues of the RXYF

5 motif. The residues highlighted in blue are proposed to make up the putative citrate-binding

6 pocket of the CACHE domain of GcbC. The RXYF motif and residues R139 and R162 of GcbC are

7 conserved in the CACHE domains of Pfl01_2295, Pfl01_2297, and Pfl01_3800.

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