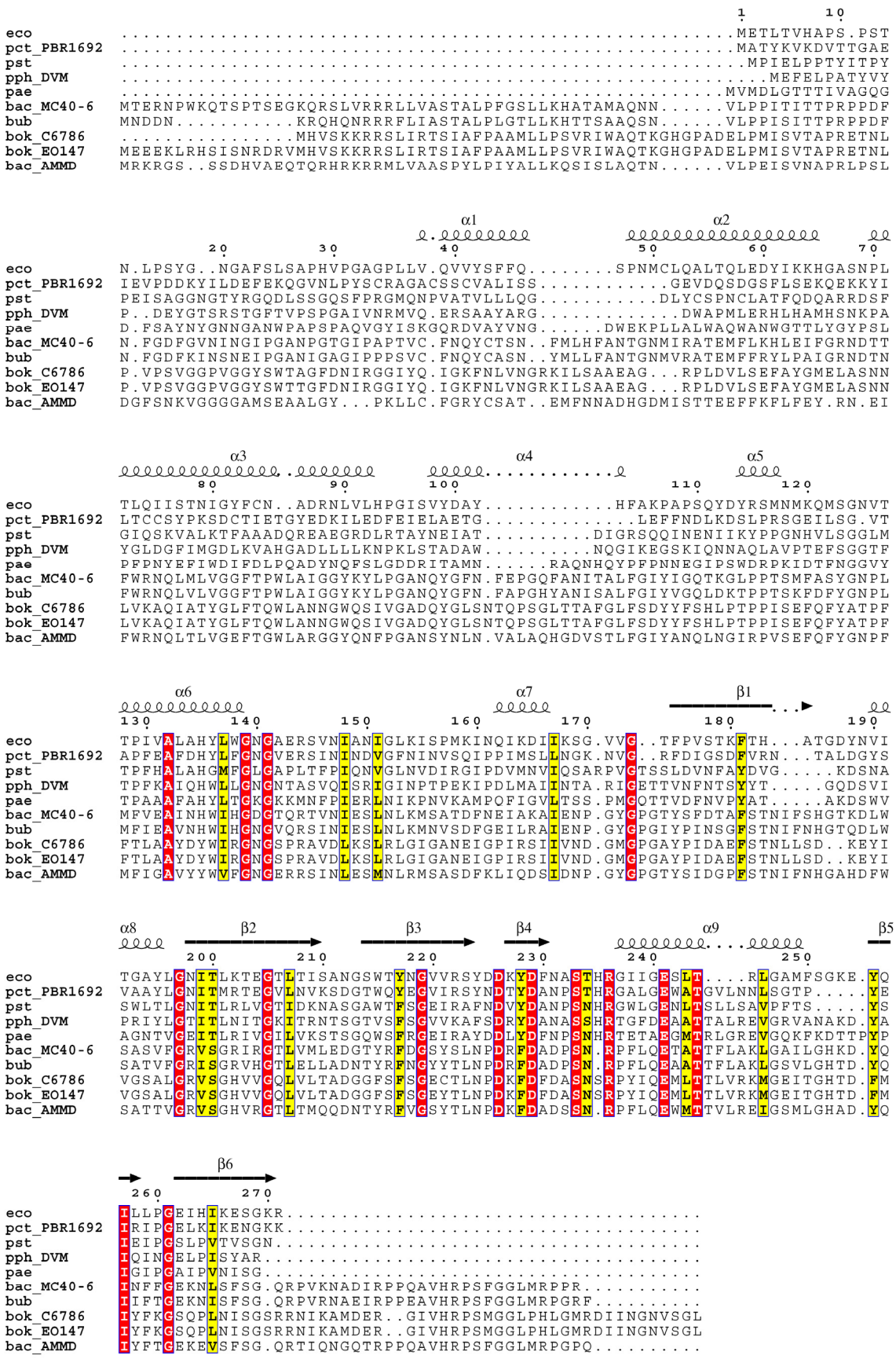
eco
pct_PBR1692
pst
pph_DVM
pae
bac_MC40-6
bub
bok_C6786
bok_EO147
bac_AMMD
α1
α2
α3
α4
α5
α6
α7
β1
α8
β2
β3
β4
α9
β5
β6

FIG. S1 Comparison of the *E. coli* Cma sequence with Cma-like sequences of partially incomplete and unassigned genomes of the following strains: eco: colicin M activity protein Cma [*Escherichia coli*]; pct_PBR1692: hypothetical protein PcarbP_02847 [*Pectobacterium carotovorum subsp. brasiliensis* PBR1692]; pst: bacteriocin, putative [*Pseudomonas syringae pv. tomato* str. DC3000]; pph_DVM: Cma [*Pseudomonas* phage DVM-2008]; pae: hypothetical protein EXA13 [*Pseudomonas aeruginosa*]; bac_MC40-6: hypothetical protein BamMC406_0333 [*Burkholderia ambifaria* MC40-6]; bub: hypothetical protein BuboB_20394 [*Burkholderia ubonensis* Bu]; bok_C6786: hypothetical protein BoklC_29925 [*Burkholderia oklahomensis* C6786]; bok_EO147: hypothetical protein BoklE_30981 [*Burkholderia oklahomensis* EO147]; bac_AMMD: hypothetical protein Bamb_0324 [*B. ambifaria* AMMD]. Abbreviations were adapted according to http://www.genome.jp/kegg/. Amino acids that occur in all sequences are shaded red, and those that have similar properties are shaded yellow.

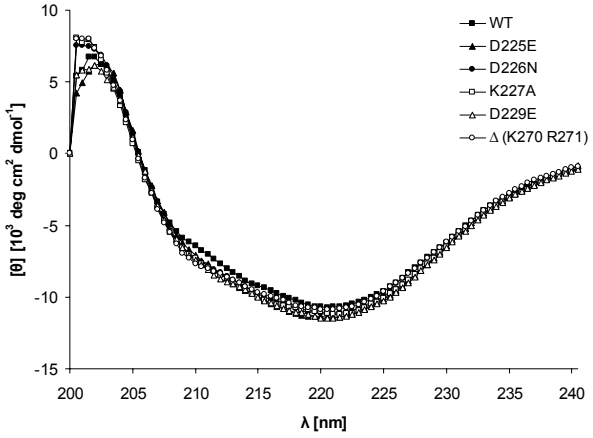

FIG. S2 CD spectra of the wild-type and mutant Cma proteins as indicated.

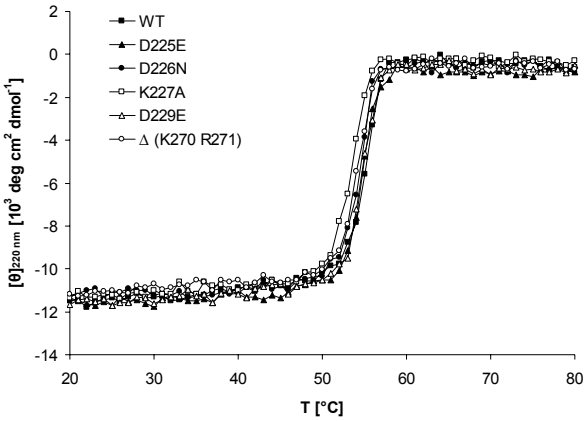

FIG. S3 Temperature-dependent denaturation of Cma (WT) and mutant Cma proteins as indicated.

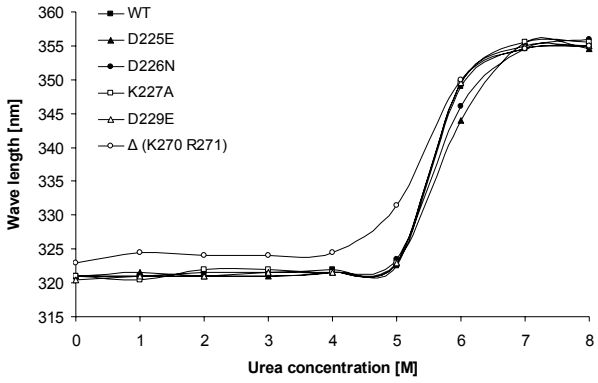

FIG. S4 Denaturation of Cma (WT) and mutant Cma proteins by various concentrations of urea. The shift in the fluorescence peak was determined.

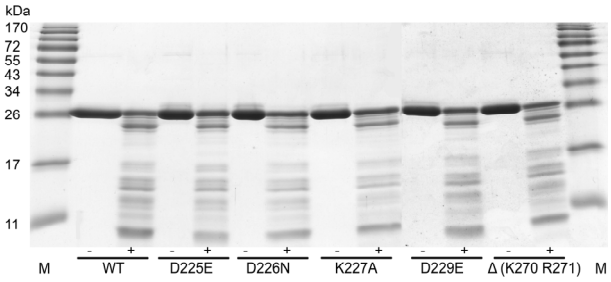

FIG. S5 SDS-PAGE of Cma (WT) and mutant Cma proteins purified by Ni-NTA agarose chromatography. +, incubation with proteinase K; -, no incubation with proteinase K.