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Clarisse Roblin, Steve Chiumento, Olivier Bornet, Matthieu Nouailler, Christina S. Müller, et al.. The unusual structure of Ruminococcin C1 antimicrobial peptide confers clinical properties. Proceedings of the National Academy of Sciences of the United States of America, 2020, 120 (13), pp.e2302405120. 10.1073/pnas.2302405120 . hal-02920462

HAL Id: hal-02920462

<https://hal.science/hal-02920462>

Submitted on 8 Dec 2020

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The unusual structure of Ruminococcin C1 antimicrobial peptide confers clinical properties

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Radical SAM enzyme, RiPP, sactipeptide, *Ruminococcus gnavus*, antibiotic

37 The emergence of superbugs developing resistance to antibiotics and the resurgence of microbial
38 infections have led scientists to start an antimicrobial arms race. In this context, we have previously
39 identified an active RiPP, the Ruminococcin C1, naturally produced by *Ruminococcus gnavus* E1,
40 a symbiont of the healthy human intestinal microbiota. This RiPP, subclassified as a sactipeptide,
41 requires the host digestive system to become active against pathogenic Clostridia and multidrug
42 resistant strains. Here, we report its unique compact structure on the basis of four intramolecular
43 thioether bridges with reversed stereochemistry introduced post-translationally by a specific
44 radical-SAM sactisynthase. This structure confers to the Ruminococcin C1 important clinical
45 properties including stability to digestive conditions and physicochemical treatments, a higher
46 affinity for bacteria than simulated intestinal epithelium, a valuable activity at therapeutic doses on
47 a range of clinical pathogens, mediated by energy resources disruption and finally safety for human
48 gut tissues.

49

50 **Significance**

51 Since the discovery of penicillin, humans have widely developed and used antibiotics to protect
52 themselves from microbial infections. However, the intensive use of these compounds has led to
53 the emergence of pathogens resistant to all classes of antibiotics. This major public health threat
54 has led scientists to find new molecules with different structures and modes of action to overcome
55 resistance phenomena. A promising alternative concerns bacteriocins secreted by certain bacteria.
56 Of a peptidic nature, their ribosomal synthesis differentiates them from conventional antibiotics.
57 The recently identified RumC1 antimicrobial peptide presents a remarkable bactericidal activity for
58 multi-drug resistant strains. Added to this efficacy, RumC1 is not toxic against a number of human
59 cell lines and is safe for human gut tissues.

60

61

62 INTRODUCTION

63 Ribosomally synthesized and Post-translationally modified Peptides (RiPPs) are an important
64 group of compounds that have stimulated research interest, notably as natural antimicrobial agents
65 with bacteriocins (1). During RiPPs biogenesis, a precursor peptide composed of at least a leader
66 and a core sequence is synthesized by the ribosome. The core peptide is modified by tailoring
67 enzymes and then the leader sequence is cleaved by one or two peptidases to produce the final
68 active product (1–4). Among the RiPPs, sactipeptides (Sulfur-to- α carbon thioether cross-
69 linked peptides) are a subgroup that has emerged in recent years (5–7). Despite spectacular soaring
70 made with genomic tools, the sactipeptide subclass is currently limited to only seven members.
71 They include subtilosin A (SboA) (8, 9), thurincin H (10), the sporulation killing factor (SkfA) (11),
72 thuricin CD that consists of two peptides, Trn- α and Trn- β (12), thuricin Z or huazacin (13, 14) and
73 the recently characterized Ruminococcin C1 (RumC1) (15, 16).

74 The precise mechanistic details of sactipeptide cross-link formation are not fully understood.
75 However, from a chemical point of view, the thioether bonds in these natural products are distinct
76 from those of the well-studied lanthipeptides, such as nisin, in which they are formed between a
77 Cys residue and a β -carbon of a dehydrated Thr/Ser residue (17). In contrast to the two-step redox
78 neutral mechanism used for the maturation of lanthipeptides, radical-SAM sactisynthase enzymes
79 introduce chemically equivalent thioether bonds by a one-step radical-based mechanism (5–7). The
80 enzymes within this superfamily contain the canonical CysX₃CysX₂Cys motif, that binds the
81 radical-SAM [4Fe-4S]^{2+/1+} cluster (referred to as the RS cluster), in which the fourth, unique iron,
82 is used to bind S-adenosylmethionine (SAM) cofactor (18). In its reduced state, the [4Fe-4S]¹⁺
83 cluster catalyzes the reductive cleavage of SAM to generate a 5'-deoxyadenosyl radical (5'-Ado•).
84 This radical abstracts a H- atom from the cognate substrate to initiate catalysis (18). In the case of
85 the characterized radical-SAM enzymes involved in the sactipeptide biosynthesis, H-atom
86 abstraction was shown to occur from the α -carbon of the acceptor residue (5–7). A survey of
87 available structural and functional data indicate that all radical-SAM enzymes involved in the
88 sactipeptides biosynthesis contain a C-terminal extension appended to the radical-SAM domain
89 called SPASM/Twitch domain that houses additional [4Fe-4S] clusters (19, 20). In contrast to the
90 Twitch domains, which bind only one additional cluster, SPASM domains present a conserved
91 cysteine-rich motif that coordinates two additional iron-sulfur clusters. The role of these clusters
92 remains to be clarified, but it was suggested that they possibly interact with the substrate during
93 catalysis or may also be implicated in electrons transfer (5–7, 21).

94 Among the seven sactipeptides reported to date, four are structurally characterized
95 (SboA, thurincin H, Trn- α and Trn- β) and all of them have been purified from the genus

96 *Bacillus*. SboA is a cyclic peptide with three thioether bridges involving two phenylalanines and
97 one threonine. Trn- α , Trn- β and thurincin H are not cyclic, they present three and four thioether
98 bridges, respectively. One common feature of SboA, Trn- α , Trn- β and thurincin H is that they all
99 present Cys residues in the N-terminal half and the corresponding partners at the C-terminal part, a
100 property that folds the peptide in a single hairpin-shaped form with the hydrophobic residues facing
101 outwards as showed by the available structures (8–10, 12, 22). Sequence analysis of the last
102 identified sactipeptide, namely RumC1, suggests a new fold. Indeed, one pair of cysteines is located
103 at the N-terminal part of the sequence while the other one is in the C-terminal end (Fig. 1A). Recent
104 data on the characterization of mature RumC1 by mass spectrometry, strongly suggests that the
105 thioether network folds the peptide in a double hairpin like structure that differs from the currently
106 reported ones (16). Furthermore, sactipeptides and by extension antimicrobial peptides (including
107 RiPPs but not only) have emerged as a potential trove of new weapons and alternatives to
108 conventional antibiotics to fight multidrug-resistant (MDR) bacteria. However, their clinical use
109 remains a challenge due to high cost of production, sensitivity to physiological or manufacturing
110 conditions, as well as toxicity for human tissues (23, 24). In this context, we previously showed
111 that RumC1 has a potent activity against Gram positive bacteria and is harmless for human cells
112 (16). Obviously, the next step was to study RumC1 in a clinical context and to address the above-
113 mentioned reasons that prevent antimicrobial peptides from being considered for pharmaceutical
114 development.

115 In this work, we sought to determine the three-dimensional structure of RumC1. The rapid
116 and large-scale production of ^{13}C - and ^{15}N -labelled mature RumC1, by heterologous expression in
117 *Escherichia coli* (16, 25), allowed extensive nuclear magnetic resonance (NMR) analyses to solve
118 the structure of RumC1 and to propose the thioether network stereochemistry. In the meantime,
119 combined EPR and Mössbauer spectroscopies enabled us to characterize the Fe-S clusters in
120 RumMc1 sactisynthase. Finally, we point out that the fold of RumC1 confers resistance to physical,
121 chemical and digestive constraints, features essential for consideration in pharmaceuticals. The
122 clinical properties of RumC1 also covers activity against clinical pathogens, including resistant
123 strains, maintained in a mammalian environment and mediated through energy resources depletion,
124 without any impact to human tissues.

125

126 **Results**

127 **RumC1 sactipeptide displays a double hairpin-like structure.** The two-dimensional [^1H , ^{15}N]
128 HSQC spectrum of RumC1 is well-resolved with 39 peptide amide peaks out of 42 expected, thus
129 attesting for the folding of the protein (fig. S1). No NH peaks were observed for residues C26, G27

130 and N28, probably due to fast amide exchange with the solvent and/or high flexibility of the region.
 131 We assigned the backbone carbon, nitrogen and proton resonances using a combined strategy of
 132 sequential residue correlations based on HNCACB, CBCA(CO)NH, HNCA, HN(CO)CA, HNCO,
 133 HN(CA)CO triple resonance experiments, and through-space nOe connectivities using 2D [¹H, ¹H]
 134 NOESY, 3D [¹H, ¹⁵N, ¹H] and 3D [¹H, ¹³C, ¹H] NOESY experiments. NMR studies of Subtilisin
 135 A, Thuricin CD and Thurincin H, by Vederas *et. al.* have shown that cysteine sulfur to α -carbon
 136 thioether linkages induce a 10 to 15 ppm downfield shift for the α -carbon atoms of bridged residues
 137 (8–10, 12, 22). Moreover, through-space nOe interactions were observed between the β -protons of
 138 cysteines and the amide proton (NH) of modified residues (8–10, 12, 22). In the same manner, we
 139 have demonstrated that RumC1 contains four sulfur to α -carbon thioether cross-links between Cys3
 140 and Asn16, Cys5 and Ala12, Cys22 and Lys42, and Cys26 and Arg34 (16). Since there are four
 141 thioether bridges, each can adopt one of the two possible configurations at the α -carbon atom (L or
 142 D). Consequently, 16 stereoisomers must be considered to establish the three-dimensional structure
 143 of RumC1. Calculations for all 16 stereoisomers were carried out using the CYANA software and
 144 seven rounds performed on each stereoisomer using the same NMR restraints file (26). The
 145 structural statistics and constraint violations (table S1) allowed to identify the stereoisomer with the
 146 D stereochemistry at Ala12 (α -S), Asn16 (α -S), Arg34 (α -S) and Lys42 (α -S) as a representative
 147 structure given: i) the absence of thioether bridge constraint violations, ii) the great number of nOe
 148 connectivities used in the structure calculation, iii) the lowest average target function value and a
 149 low root mean square deviation (*rmsd*). To improve the structure of the DDDD stereoisomer, an
 150 additional refinement step by returning to the NOESY spectra to eliminate the ambiguities found
 151 during the structure calculation by the CYANA software was added. The resulting structural
 152 statistics of the 20 conformers for the DDDD isomer of RumC1 are summarized in table S2. The
 153 backbones of the 20 lowest target function value conformers for the DDDD isomer of RumC1
 154 superimpose quite well with a *rmsd* value of 0.81 Å for the backbone (Fig. 1B). The three-
 155 dimensional structure of RumC1 is thus composed on both sides by two α -helices and in the middle
 156 by a 2-stranded parallel β -sheet fragment and the whole stiffened by four cysteine sulfur to α -
 157 carbon thioether cross-links (Fig. 1C).
 158 The electrostatic surface potentials present an overall positive charge (Fig. 1D) and the surface
 159 hydrophobicity of the DDDD stereoisomer shows a majority of hydrophilic residues (Fig. 1E). The
 160 compact three-dimensional solution structure of RumC1 reveals a new sactipeptide fold and by
 161 extension a new antimicrobial peptide fold (fig. S2A). Four sulfur to α -carbon thioether bridges
 162 with a DDDD stereochemistry have been already reported for thurincin H (10). However, the

163 presence of an additional 2-stranded parallel β -sheet fragment in the middle of RumC1 induces a
164 new fold, thus resulting in a different location of the thioether crosslinks (fig. S2, B-E) (9, 10, 22).

165
166 **Expression, purification and characterization of the RumMc1 sactisynthase.** RumMc1 is
167 predicted to contain accessory Fe-S clusters, in addition to the RS cluster, thus we decided to co-
168 express the *rumMc1* gene with the pDB1282 plasmid, which encodes for a set of proteins involved
169 in iron-sulfur cluster biogenesis (IscS, IscU, IscA, HscB, HscA and Fdx) (27). After the final step
170 of anaerobic purification, the purity was evaluated by SDS-PAGE to be over 95% (fig. S3). As
171 expected, the holo-RumMc1 protein was dark brown in color and the iron titration revealed, on
172 average, ten metal centers per monomer. In good agreement, the UV-vis spectrum of holo-RumMc1
173 suggests the presence of [4Fe-4S] clusters (Fig. 2A, solid line). Mössbauer spectroscopy on ^{57}Fe -
174 enriched oxidized holo-RumMc1 was then used to deeply investigate the nature of the Fe-S clusters.
175 The experimental spectrum recorded at $T = 77\text{ K}$ (dashed line) could be simulated (red line) with
176 three components **1**, **2** and **3** in a 2:1:1 ratio (Fig. 2B). **1** and **2** are characterized by similar isomer
177 shifts (δ) with $\delta = 0.42\text{ mms}^{-1}$ for **1** and $\delta = 0.44\text{ mms}^{-1}$ for **2** while the quadrupole splitting (ΔE_q)
178 varies with $\Delta E_q = 0.98\text{ mms}^{-1}$ for **1** and $\Delta E_q = 1.30\text{ mms}^{-1}$ for **2**. These values are in a typical range
179 for $\text{Fe}^{2.5+}$ ions in a diamagnetic $[\text{4Fe-4S}]^{2+}$ cluster (28–30). This is supported by simulations of the
180 spectra recorded at $T = 4.2\text{ K}$ in external fields of $B = 0.1\text{ T}$ and $B = 5\text{ T}$ (fig. S4, A and B) based
181 on the spin Hamilton formalism assuming a total spin of $S = 0$. The 2:1 ratio suggests that holo-
182 RumMc1 contains three $[\text{4Fe-4S}]^{2+}$ clusters. This is supported by the sequence alignment of
183 RumMc1 with other related proteins that contain conserved cysteine residues localized at the C-
184 terminal half of the protein (fig. S5). Hence, we can conclude that **1** represents 8 $\text{Fe}^{2.5+}$ ions in the
185 same tetrahedral sulfur environment belonging to two $[\text{4Fe-4S}]^{2+}$ clusters while **2** corresponds to
186 four indistinguishable $\text{Fe}^{2.5+}$ ions present in the single $[\text{4Fe-4S}]^{2+}$ cluster supposed to contain the
187 SAM-binding iron site (RS-cluster). The difference in ΔE_q between **1** and **2** points to a slightly
188 different distribution of electron density. **3** is characterized by $\delta = 0.33\text{ mms}^{-1}$ and $\Delta E_q = 0.49\text{ mms}^{-1}$
189 typical for Fe^{3+} high spin ($S = 5/2$) in a tetrahedral sulfur environment (28). This component was
190 adequately simulated (fig. S4A, with an external magnetic field) by combining contributions from
191 three distinct, but antiferromagnetically coupled Fe^{3+} centers, thus resulting in a global $S = 1/2$ spin
192 state as described for a paramagnetic $[\text{3Fe-4S}]^{1+}$ cluster (31, 32). The respective hyperfine
193 parameters are characteristic for $[\text{3Fe-4S}]^{1+}$ clusters (fig. S4B) (31, 32). Upon addition of dithionite
194 on the holo-RumMc1, the absorption decreased over the entire 310-420 nm range as expected for
195 the conversion of the $S = 0$ $[\text{4Fe-4S}]^{2+}$ chromophore to the $S = 1/2$ $[\text{4Fe-4S}]^{1+}$ level (Fig. 2A, dashed
196 line). This reduced form has been investigated by X-band EPR spectroscopy in order to gain

insights into the individual features of the three [4Fe-4S] clusters involved. The experimental EPR spectrum of holo-RumMc1 is extremely rich, suggesting the presence of multiple $S = 1/2$ [4Fe-4S]¹⁺ clusters (fig. 2C, black line). It was satisfactorily simulated considering the three following sets of g-tensors [2.034, 1.913, 1.870] (**A**), [2.050, 1.937, 1.902] (**B**) and [2.074, 1.932, 1.885] (**C**) (Fig. 2, C and E). Addition of the natural SAM cofactor then induced a substantial change in the spectrum that was well simulated with four sets of g-tensors [2.034, 1.910, 1.860] (**A**), [2.049, 1.937, 1.904] (**B**), [2.073, 1.932, 1.885] (**C**) and [2.076, 1.930, 1.852] (**A'**) instead of three (Fig. 2, D and E). As the contribution of **A** has to be lowered to achieve a reliable simulation, these experiments support that **A** originates from the RS cluster while **B** and **C** rely to two additional clusters. The new component **A'** was assigned to the amount of the RS cluster, which is bond to the SAM as previously described (33).

Efficient maturation of RumC1: both the leader and the core sequences are crucial. Here we sought to gain insights into the features of RumC1 that are required for its efficient maturation by RumMc1. It is established that the post-translational modification of RiPPs is an event that is dependent on the presence of the leader peptide (2). For example, in the case of the sactipeptide subclass, Marahiel and co-workers have shown that AlbA failed to transform a variant of the SboA peptide without its leader sequence in a mature sactipeptide (34). We investigated the maturation of RumC1 by the way of an *in vitro* assay in the presence of RumMc1, the SAM cofactor and dithionite as an external electron source. These experiments were performed with a full-length RumC1 precursor peptide, a leader less variant of 44 amino acids (RumC1-44) and a third condition in which the leader sequence and the core peptide were dissociated but both present in the solution (RumC1-44-LS). The reaction mixtures were analyzed by LC-MS to detect the formation of thioether bonds within the three substrates (fig. S6). Since the full maturation of RumC1 leads to the formation of four thioether bonds, the percentages of maturation (fig. S6A) account for the species that present a loss of 8 Da in mass compared to the unmodified substrate. The data clearly indicate that only the RumC1 peptide is fully modified, both RumC1-44 and RumC1-44-LS led to less than one and ten percent of species with four thioether linkages, respectively (fig. S6, A and B). It has to be noted that attempts to yield mature peptides from the latter two substrates lead mainly to a mixture of peptides harboring partial maturation with 2 and 3 thioether bonds (fig. S6, C and D). In good agreement with the lack of maturation of RumC1-44 during the *in vitro* enzymatic assay, we also observed that no mature peptide is obtained when this leader less form of RumC1 is produced *in vivo* using the heterologous expression and maturation protocol in *E. coli* (fig. S7A).

In contrast to the sactipeptides identified so far, the thioether connectivity in RumC1 folds the peptide in a double hairpin like structure. Sequence alignments of the five RumC isoforms shows a strictly conserved Gly18/Pro19 motif in the loop region between the two hairpins (16). We therefore sought to determine whether this motif is necessary for inducing a turn in the sequence and allowing the peptide maturation by RumMc1. For this, we replaced the Gly18/Pro19 motif by Ala18/Ala19. LC-MS analysis of the heterologously expressed Ala18/Ala19 RumC1 variant clearly demonstrate the lack of maturation thus suggesting that the loop alteration in RumC1 may disturb substrate-enzyme interactions that are crucial for the formation of the thioether network (fig. S7B). As reported by Grove and coworkers for CteA (21), these results suggest that the binding of RumC1 by RumMc1 involves determinants from both the leader and the core sequences.

The compact structure confers a high stability to RumC1. Studies have proven the potent activity of sactipeptides (12, 35), however there is a lack of evidence showing that they possess the physiochemical properties necessary for *in vivo* administration and, from an applied point of view, for pharmaceutical development (35). Consequently, we assayed the tolerance of RumC1 to such properties. RumC1 showed no loss of activity when exposed to acidic or basic pH from 2 to 11 (Fig. 3A). Furthermore, RumC1 was resistant to 70 and 100°C for up to 1 hour and more than 15 minutes respectively, meaning that RumC1 possesses the intrinsic thermal resistance that are required for drug formulation processes (Fig. 3B). Because of their sensitivities to enzymatic digestion or to physiological salts concentrations and blood enzymes, the administration of antimicrobial peptides by oral route and/or systemic injection is limited. Interestingly, the activity of RumC1 wasn't impaired by salts concentrations higher than 150 mM for NaCl and 2 mM for MgCl₂ (Fig. 3C), which are considered as physiological saline conditions. Likewise, incubation in human serum at 37°C up to 24 hours did not affect the activity of RumC1 (Fig. 3D). RumC1 was finally treated with pepsin at pH 2.5 for 2 hours at 37°C, and with pancreatin at pH 6.5 for 5 hours at 37°C in order to mimic the human gastric and intestinal compartments, respectively. RumC1 showed no loss of activity and its integrity was revealed by MS analysis after these treatments whereas the lanthipeptide nisin used as a positive control for pancreatin activity showed reduced antimicrobial potency (Fig. 3E, fig. S8, A and B). Pepsin activity was confirmed as well by hydrolysis of Bovine Serum Albumine (BSA) (fig. S8A). Therefore, the thioether network leading to a compact structure of RumC1 confers to the sactipeptide high resistance to physico-chemical treatments and to the physiological but harsh conditions encountered in blood or in the digestive tract after systemic or oral administration.

264 **RumC1 is able to act on a simulated infected intestinal epithelium.** Many studies on
265 antimicrobial peptides show their direct activity on bacterial cultures, without considering their
266 efficiency in a mammalian environment, such as an infected epithelium. Indeed, antimicrobial
267 peptides can act on bacteria but can also insert into eukaryotic cells or merely bind to their surface
268 (24, 36), which could cause a partial loss of activity against extracellular pathogens. On the
269 contrary, some peptides have higher affinity for bacterial cells than host cells (37). Therefore, we
270 assayed the potency of RumC1 against *Bacillus cereus*, an aerotolerant human intestinal
271 opportunistic pathogen, on simulated gut epitheliums using Caco2 and T84 cells as models of
272 human small intestinal and colonic epithelium, respectively. *B. cereus* was able to grow on
273 untreated monolayers of Caco2 and T84 whereas treatment with RumC1 was effective to clear the
274 infection (fig. S9). The MIC of RumC1 against *B. cereus* was measured in the eukaryotic cell line
275 culture medium in the presence or the absence of human intestinal cells. The MIC value did not
276 increase in the presence of intestinal cells when RumC1 was added 30 min before, concomitantly
277 or 30 min after the bacterial cells (Fig. 4A). Indeed, no loss of activity was detected as well when
278 *B. cereus* was allowed to colonize the epithelium for 30 min before adding RumC1 (Fig. 4A).
279 Therefore, it appears that RumC1 has a preferential affinity for bacterial cells rather than host cells.
280 Finally, these results suggest that the physiological environment of the two cell lines did not affect
281 significantly the activity of RumC1.

282
283 **RumC1 displays a potent activity against Gram-positive pathogenic clinical isolates.** We
284 previously showed that RumC1 is active against a broad range of Gram-positive bacteria including
285 resistant and multi-resistant strains (16), but focusing only on collection strains. In order to evaluate
286 the potentiality of RumC1 being considered for pharmaceutical development, we investigated its
287 activity against Gram-positive strains isolated in a clinical context from humans or animals (i.e.
288 broiler chickens). As RumC1 was first identified for its anti- *Clostridium perfringens* activity (16,
289 38, 39), we measured for the first time the MIC of the sactipeptide against a large panel of *C.*
290 *perfringens* clinical isolates (Fig. 4B). RumC1 was active under the micromolar range (between 0.4
291 and 0.8 μ M) on all the ten strains tested. In comparison with the reference molecules, usually used
292 to eradicate *C. perfringens*, RumC1 showed a higher activity than metronidazole (12 to 23 μ M) and
293 an activity similar to vancomycin (0.2 to 0.4 μ M). Interestingly, in a livestock context, RumC1 was
294 not only active against the CP24 *C. perfringens* strain isolated from a healthy broiler chicken, but
295 also against strains isolated from animals suffering from dysbiosis or necrotic enteritis, respectively
296 CP56 and CP60 (40). In addition, RumC was also active against *C. perfringens* strains isolated from
297 humans suffering from bacteremia ($n=6$) (Fig. 4B).

298 Then, we studied the effect of RumC1 on another main intestinal pathogen from the
299 *Clostridium* genus, *Clostridium difficile*. RumC1 showed activity against collection and clinical
300 strains of *C. difficile* with lower MIC (0.3 to 0.6 μ M) than two of the most common antibiotics used
301 for *C. difficile* intestinal infections (CDI), i.e. metronidazole (1.5 μ M) and vancomycin (0.3 to 0.7
302 μ M) (Fig. 4B). Moreover, RumC1 is also efficient at the micromolar range against other intestinal
303 pathogens (clinical and collection strains) of main importance such as *Listeria monocytogenes*, *B.*
304 *cereus*, *Enterococcus faecalis* and *Enterococcus faecium* including strains resistant to amoxicillin
305 and/or vancomycin (Fig. 4B). Beside its activity against pathogens causing gut infections, RumC1
306 is also active against a clinical *Streptococcus pneumoniae* strain at a low MIC (0.3 μ M), a pathogen
307 responsible of multiple types of infection (including respiratory tract infection, meningitis and
308 septicemia) (Fig. 4B).

309
310 **The killing mechanism of RumC1 involves energy resource shortage.** Unlike many bacteriocins
311 RumC1 does not have a pore forming action (16), we therefore investigated its effects on the main
312 macromolecules synthesis pathways usually targeted by antibiotics. *C. perfringens* cells were
313 exposed to RumC1 and the synthesis of DNA, RNA, proteins and peptidoglycan were followed by
314 measuring the incorporation of radio-labelled precursors. Remarkably, RumC1 was able to inhibit
315 the synthesis pathways of the four macromolecules with efficacies similar to conventional
316 antibiotics targeting each of these pathways (Fig. 5A). As these synthesis pathways are all energy-
317 dependent, we assayed the potency of RumC1 to break such energy resources. Thus, we measured
318 by bioluminescent assay the ATP released by *C. perfringens* cells in the extracellular medium, and
319 then lysed cells to derive the intracellular ATP content (Fig 5B). Upon treatment with RumC1 for
320 15 min, outer ATP was not increased compared to cells untreated whereas inner ATP decreased in
321 a dose-dependent manner. Treatment with nisin, a pore-forming bacteriocin led to drastic increase
322 of outer ATP whereas metronidazole does not impact ATP synthesis pathway. Since the synthesis
323 of DNA, RNA, proteins and peptidoglycan accounts for the consumption of approximately 70 %
324 of the total ATP content of bacteria, their observed inhibition is likely linked to ATP depletion and
325 therefore the specificity of RumC1 could be related to an inhibition of the ATP synthesis pathway
326 (41).

327
328 **Integrity of human tissues treated with RumC1.** We previously reported that RumC1 was a safe
329 new antimicrobial peptide because of its lack of *in vitro* toxicity on gastric and intestinal cell lines
330 culture (16). To further characterize the safety of RumC1, we assayed the toxicity of the sactipeptide
331 *ex vivo*, directly on human ileocecal tissues. Intestinal explants were isolated from unaffected area

of ileocecal resection from two patients diagnosed with intestinal carcinoma and were incubated with RumC1 at 100 μ M or the detergent CTAB at 300 μ M for 4 hours. Control and RumC1 exposed human intestinal explants displayed normal tissue organization with normal crypt and villosity lengths and no sign of epithelial desquamation or erosion, in accordance with data we obtained previously *in vitro* on human intestinal cell lines. Conversely, exposure to CTAB, used as positive control of tissue damages, caused important lesions to the human intestinal epithelium with cell desquamation and shortening of the crypts and villousities (Fig. 6).

Discussion

In this study, we elucidated the three-dimensional structure of mature Ruminococcin C1 from *Ruminococcus gnavus* E1. NMR experiments clearly showed that the thioether network of RumC1, involving four sulfur to α -carbon bridges, folds the peptide into a double hairpin-like motif, which differs from the currently reported structures within the sactipeptide family. By extension, the fold not described so far includes two-stranded parallel β -sheet into the core enclosed between two parallel α -helices. In contrast to a recent report by Berteau *et al.*, where the residues involved in the thioether bridges were identified to be L-configured, after hydrolysis and derivatization (15), here we found that the stereoisomers that fits best with the NMR data featured D-configurations at Ala12, Asn16, Arg34 and Lys42. RumC1 has a global positive charge at physiological pH and displays a constrained and rigid backbone structure that presents a mostly hydrophilic surface unlike sactipeptides with known structure presenting mostly hydrophobic surface. These sactipeptides, like most of the bacteriocins that target Gram-positive strains, have a pore-forming mode of action. Despite an overall cationic charge, RumC1 is unable to insert into lipids extracts most likely due to its hydrophilic surface and exerts probably an intracellular mode of action reaching one or more specific targets by active transport.

The double hairpin-like structure of RumC1 provides stability to pH and high-temperatures, which could facilitate pharmaceutical manufacturing processes. We also showed that RumC1 is resistant to digestive proteolytic conditions, most likely because the sites of cleavage are protected by the four thioether bonds and the tridimensional folding of the peptide. Many RiPPs including sactipeptides, such as Subtilisin A and Thuricin CD, are not resistant to both pepsin and pancreatic proteases (42, 43), implying that the original folding of RumC1 offers additional protection. Moreover, RumC1 is also resistant to physiological salts conditions as well as to human serum, which can both be detrimental for an exogenous compound. Based on these considerations, we followed our investigations of RumC1 in a preclinical context. The first step was to ensure that RumC1 could cure infections in the mammalian environment. Therefore, we treated with RumC1

a *B. cereus* infected simulated epitheliums. RumC1 remained active at very low doses, exactly at the same level as the MIC obtained in the absence of eukaryotic cells. This observation confirms the stronger affinity of RumC1 for bacterial versus host cells, and the specific primary function of RumC1 as antibiotic compound. Then we checked that RumC1 has potent activity on Gram-positive clinical pathogens and not only on collections strains. RumC1 showed strong activity under the micromolar range toward *Clostridia* pathogens from both human and animal origins. The measured MICs are equivalent to vancomycin, one of the reference antibiotics used in therapy against these pathogens, and lower than metronidazole, another reference antibiotic known to generate resistance (16). Therefore, the use of RumC1 to treat infections caused by *C. perfringens* or *C. difficile* should be considered. Indeed, from a livestock point of view, *C. perfringens* can cause necrotic enteritis, which is one of the most common infection in broiler chickens with mortality rates as high as 50% and resulting in dehydration, lesions on intestinal mucosa or other organs like the liver, spleen, heart or kidneys (44). On the other hand, *C. difficile* is a major human pathogen causing nosocomial infections, community-associated diarrhea and is responsible of 250,000 intestinal infections per year in the US, associated with a mortality rate of 15 to 20%. In 2019, *C. difficile* has been classified by the Centre for Diseases Control and Prevention as an urgent threat for which new antimicrobials are needed (45, 46). In the same line, RumC1 is active against amoxicillin and vancomycin resistant *E. faecium*, registered on all priority lists of human pathogens for which new antimicrobials are urgently needed. It is registered by the CDC as a serious concern that requires prompt action and by the WHO on the “antibiotic-resistant priority pathogens” as high concern. *E. faecium* is also pointed by the Infectious Diseases Society of America (IDSA) across the “ESKAPE pathogens” list of bacteria, which includes *Enterococcus faecium*, *Staphylococcus aureus*, *Klebsiella pneumoniae*, *Acinetobacter baumannii*, *Pseudomonas aeruginosa* and *Enterobacter* spp., (47) for its ability to escape the effects of the commonly used antibiotics through evolutionarily developed mechanisms of resistance (48). *E. faecium*, characterized by drug resistance mechanisms, commonly causes life-threatening nosocomial infections amongst critically ill and immunocompromised individuals. Consequently, it is important to note that RumC1 is particularly active against this pathogen with a MIC of 1,2 μ M, thus it could be considered as a potential therapeutic solution. In the case of *S. pneumoniae*, with a prevalence of 1.2 million of infections per year in the US, leading to its inclusion into the CDC and the WHO lists of priority pathogens, the use of RumC1 with a MIC of 300 nM may also be relevant. It should be noted that RumC1 is a broad-spectrum anti-Gram-positive molecule directed against resistant anaerobic and aerobic clinical pathogens, which is rare in the antibiotics market with a few exceptions such as vancomycin, thus enhancing its clinical potential. Moreover, we showed that RumC1 inhibits the

400 synthesis of macromolecules including DNA, RNA, proteins or peptidoglycan and the production
401 of ATP. At this stage, since the main biosynthetic pathways are inhibited, it is conceivable that
402 RumC1 applies its antimicrobial activity intracellularly through a non-specific mechanism, or
403 conversely, targeting specifically ATP synthases and thus disrupting all necessary energy resources,
404 such as bedaquiline, the only antibiotic currently on the market targeting ATP synthases but used
405 only for the treatment of infections caused by *Mycobacterium* (49). Otherwise, we have previously
406 identified that the phenotype induced by RumC1 treatment resembles the one induced by
407 metronidazole in *C. perfringens* (16). However, we have shown here that metronidazole only
408 inhibits DNA synthesis and, to a lesser extent, protein synthesis. Metronidazole is known to impact
409 DNA synthesis and repair systems, and most likely inhibits the activity of the strictly ATP-
410 dependent ribonucleotide reductase by modulating the redox state of cells, but its precise
411 mechanism remains elusive (50). Here we suggest that the phenotypic similarities induced by
412 RumC1 and metronidazole might arise from a DNA synthesis inhibition and possibly other
413 common events, although they certainly do not share the same mechanism. Therefore, further in-
414 depth investigations are needed to resolve the potentially unique intracellular mode of action of
415 RumC1. Finally, we followed our preclinical studies by assessing the safety of RumC1 on gut
416 tissues directly sourced from patients. RumC1 did not induce epithelial lesions at a dose about a
417 hundred times higher than the effective antimicrobial dose. This observation could be expected as
418 humans have been exposed to RumC1 through evolution as this peptide is produced by a symbiotic
419 bacterium present in the gut microbiota of healthy adults. Overall, RumC1 encompass properties
420 essential for a drug candidate to cure intestinal infections, especially since i) it can be administrated
421 by oral route, ii) it is active in the intestinal epithelium environment, iii) RumC1 shows activity at
422 therapeutic doses against clinical intestinal resistant pathogens, and finally iv) since it is safe for
423 gut tissues. Only few AMPs meet all the conditions that are necessary for reaching the marketing
424 step, i.e. respecting the conditions of stability, presenting activity under physiological conditions
425 (including in the presence of eukaryotic cells), owning antimicrobial effect against clinical
426 pathogens at very low doses including resistant or MDR, and finally retaining safety for human
427 cells and tissues. It is interesting to note that RumC1 fulfils all these conditions, except one
428 remaining bottleneck for the industrial scale use, which concerns the cost of production. RumC-
429 like synthetic molecule development could be addressed to solve this concern and highlight the
430 great potential of this original sactipeptide.

431

432 **Materials and Methods**

Detailed descriptions of materials and methods, including expression, purification of (¹³C, ¹⁵N)-labelled mature RumC1, NMR studies, structure calculations, EPR and Mössbauer analyses of RumMc1, stability assays of RumC1 and MIC determinations are given in *SI Appendix*.

Supporting Information

Supplementary figures Fig. S1 to Fig. S9 as well as Tables S1 and S2 are provided in *SI Appendix*.

Data Availability

All data needed to evaluate the conclusions in the paper are present in the paper and the *SI Appendix*. All of the peak lists and the complete ¹H, ¹³C and ¹⁵N backbone and side chain chemical shift assignments of RumC1 have been deposited into the Biological Magnetic Resonance Databank (<http://www.bmrb.wisc.edu>) under ascension code 50027. Coordinates of the twenty conformations of DDDD stereoisomer of RumC1 have been deposited into the PDB under ascension code 6T33.

ACKNOWLEDGMENTS. We would like to thank Pr. Richard Ducatelle and Pr. Filip Van Immerseel from UGent for providing us with clinical isolates of *C. perfringens* from broiler chickens. We would also like to thank Pr. Lhoussine Touqui for scientific advising. Finally, we would like to thank the people from the AVB platform (iSm2 CNRS UMR 7313, Marseille). This study was supported by grants from the French National Agency for Research (“Agence Nationale de la Recherche”) through the “Projet de Recherche Collaboratif” (*RUMBA project*, ANR-15-CE21-0020), the “Investissement d’Avenir Infrastructures Nationales en Biologie et Santé” programme (*ProFI project*, ANR-10-INBS-08) and partial financial support from the Labex ARCANÉ and CBH-EUR-GS (ANR-17-EURE-0003). We are grateful to Adisseo France company and the Association Nationale Recherche Technologie (ANRT) for funding the doctoral fellowship of C.R. entitled “Bacteriocins RumC, a novel antimicrobial peptide family as alternative to conventional antibiotics.” This grant numbered *Convention Industrielle de Formation par la Recherche* (CIFRE) no. 2016/0657 runs from 1 March 2017 to 1 March 2020. VS and CSM. acknowledge the support of the German Science Foundation (DFG) within SPP 1927 (SCHU 1251/17-1, 2).

Author contributions: CR, SC, KJ and CB performed the *in vitro* assays for RumC1, RumMc1 and were involved in interpreting the data and writing the manuscript; OB and MN performed the RumC1 structural analysis by RMN; CSM and VS performed the Mössbauer analyses on RumMc1 and wrote the corresponding parts; ST and LLP performed the EPR analysis on RumMc1; SKJ and

YC performed nanoLC-MS/MS characterizations; BDLV, PS, EDP, MM and CN performed the surgical biopsy, the human explant treatment, the cytotoxicity assays and the microscopy analysis; HO, NV and LP were involved in biosynthetic pathways and ATP assays; OI performed the peptide chemical synthesis; TG, MF and ED were involved in study design; PP, JP, MA, FG, ML and VD conceptualized the study, designed experiments, interpreted the data and wrote the manuscript.

Competing interests: The authors declare that they have no competing interests.

References

1. P. G. Arnison, *et al.*, Ribosomally synthesized and post-translationally modified peptide natural products: overview and recommendations for a universal nomenclature. *Nat. Prod. Rep.* **30**, 108–160 (2013).
2. T. J. Oman, W. A. van der Donk, Follow the leader: the use of leader peptides to guide natural product biosynthesis. *Nat. Chem. Biol.* **6**, 9–18 (2010).
3. G. A. Hudson, D. A. Mitchell, RiPP antibiotics: biosynthesis and engineering potential. *Curr. Opin. Microbiol.* **45**, 61–69 (2018).
4. J. R. Chekan, C. Ongpipattanakul, S. K. Nair, Steric complementarity directs sequence promiscuous leader binding in RiPP biosynthesis. *Proc. Natl. Acad. Sci.* **116**, 24049–24055 (2019).
5. N. Mahanta, G. A. Hudson, D. A. Mitchell, Radical S-Adenosylmethionine Enzymes Involved in RiPP Biosynthesis. *Biochemistry* **56**, 5229–5244 (2017).
6. A. Benjdia, C. Balty, O. Berteau, Radical SAM Enzymes in the Biosynthesis of Ribosomally Synthesized and Post-translationally Modified Peptides (RiPPs). *Front. Chem.* **5**, 87 (2017).
7. L. Flühe, M. A. Marahiel, Radical S-adenosylmethionine enzyme catalyzed thioether bond formation in sactipeptide biosynthesis. *Curr. Opin. Chem. Biol.* **17**, 605–612 (2013).
8. K. Kawulka, *et al.*, Structure of Subtilosin A, an Antimicrobial Peptide from *Bacillus subtilis* with Unusual Posttranslational Modifications Linking Cysteine Sulfurs to α -Carbons of Phenylalanine and Threonine. *J. Am. Chem. Soc.* **125**, 4726–4727 (2003).
9. K. E. Kawulka, *et al.*, Structure of subtilosin A, a cyclic antimicrobial peptide from *Bacillus subtilis* with unusual sulfur to alpha-carbon cross-links: formation and reduction of alpha-thio-alpha-amino acid derivatives. *Biochemistry* **43**, 3385–3395 (2004).
10. C. S. Sit, M. J. van Belkum, R. T. McKay, R. W. Worobo, J. C. Vederas, The 3D Solution Structure of Thurincin H, a Bacteriocin with Four Sulfur to α -Carbon Crosslinks. *Angew. Chem. Int. Ed.* **50**, 8718–8721 (2011).
11. W.-T. Liu, *et al.*, Imaging mass spectrometry of intraspecies metabolic exchange revealed the cannibalistic factors of *Bacillus subtilis*. *Proc. Natl. Acad. Sci.* **107**, 16286–16290 (2010).
12. M. C. Rea, *et al.*, Thuricin CD, a posttranslationally modified bacteriocin with a narrow spectrum of activity against *Clostridium difficile*. *Proc. Natl. Acad. Sci. U. S. A.* **107**, 9352–9357 (2010).
13. T. Mo, *et al.*, Thuricin Z: A Narrow-Spectrum Sactibiotic that Targets the Cell Membrane. *Angew. Chem. Int. Ed Engl.* **58**, 18793–18797 (2019).

- 505 14. G. A. Hudson, *et al.*, Bioinformatic Mapping of Radical S-Adenosylmethionine-Dependent Ribosomally
506 Synthesized and Post-Translationally Modified Peptides Identifies New C α , C β , and C γ -Linked Thioether-
507 Containing Peptides. *J. Am. Chem. Soc.* **141**, 8228–8238 (2019).
- 508 15. C. Balty, *et al.*, Ruminococcin C, an anti-clostridial sactipeptide produced by a prominent member of the human
509 microbiota *Ruminococcus gnavus*. *J. Biol. Chem.* **294**, 14512–14525 (2019).
- 510 16. S. Chiumento, *et al.*, Ruminococcin C, a promising antibiotic produced by a human gut symbiont. *Sci. Adv.* **5**,
511 eaaw9969 (2019).
- 512 17. P. J. Knerr, W. A. van der Donk, Discovery, biosynthesis, and engineering of lantipeptides. *Annu. Rev.*
513 *Biochem.* **81**, 479–505 (2012).
- 514 18. J. B. Broderick, B. R. Duffus, K. S. Duschene, E. M. Shepard, Radical S-Adenosylmethionine Enzymes. *Chem.*
515 *Rev.* **114**, 4229–4317 (2014).
- 516 19. T. A. J. Grell, P. J. Goldman, C. L. Drennan, SPASM and Twitch Domains in S -Adenosylmethionine (SAM)
517 Radical Enzymes. *J. Biol. Chem.* **290**, 3964–3971 (2015).
- 518 20. J. A. Latham, I. Barr, J. P. Klinman, At the confluence of ribosomally synthesized peptide modification and
519 radical S-adenosylmethionine (SAM) enzymology. *J. Biol. Chem.* **292**, 16397–16405 (2017).
- 520 21. T. L. Grove, *et al.*, Structural Insights into Thioether Bond Formation in the Biosynthesis of Sactipeptides. *J.*
521 *Am. Chem. Soc.* **139**, 11734–11744 (2017).
- 522 22. C. S. Sit, R. T. McKay, C. Hill, R. P. Ross, J. C. Vederas, The 3D structure of thuricin CD, a two-component
523 bacteriocin with cysteine sulfur to α -carbon cross-links. *J. Am. Chem. Soc.* **133**, 7680–7683 (2011).
- 524 23. M. Mahlapuu, J. Håkansson, L. Ringstad, C. Björn, Antimicrobial Peptides: An Emerging Category of
525 Therapeutic Agents. *Front. Cell. Infect. Microbiol.* **6** (2016).
- 526 24. W. Aoki, M. Ueda, Characterization of Antimicrobial Peptides toward the Development of Novel Antibiotics.
527 *Pharm. Basel Switz.* **6**, 1055–1081 (2013).
- 528 25. P. M. Himes, S. E. Allen, S. Hwang, A. A. Bowers, Production of Sactipeptides in Escherichia coli: Probing
529 the Substrate Promiscuity of Subtilisin A Biosynthesis. *ACS Chem. Biol.* **11**, 1737–1744 (2016).
- 530 26. P. Güntert, C. Mumenthaler, K. Wüthrich, Torsion angle dynamics for NMR structure calculation with the new
531 program DYANA. *J. Mol. Biol.* **273**, 283–298 (1997).
- 532 27. R. M. Cicchillo, *et al.*, Lipoyl synthase requires two equivalents of S-adenosyl-L-methionine to synthesize one
533 equivalent of lipoic acid. *Biochemistry* **43**, 6378–6386 (2004).
- 534 28. M.-E. Pandelia, N. D. Lanz, S. J. Booker, C. Krebs, Mössbauer spectroscopy of Fe/S proteins. *Biochim.*
535 *Biophys. Acta* **1853**, 1395–1405 (2015).
- 536 29. P. Middleton, D. P. E. Dickson, C. E. Johnson, J. D. Rush, Interpretation of the Mössbauer Spectra of the Four-
537 Iron Ferredoxin from *Bacillus stearothermophilus*. *Eur. J. Biochem.* **88**, 135–141 (1978).
- 538 30. G. Layer, *et al.*, Radical S-Adenosylmethionine Enzyme Coproporphyrinogen III Oxidase HemN. *J. Biol.*
539 *Chem.* **280**, 29038–29046 (2005).
- 540 31. B. H. Huynh, *et al.*, On the active sites of the [NiFe] hydrogenase from *Desulfovibrio gigas*. Mössbauer and
541 redox-titration studies. *J. Biol. Chem.* **262**, 795–800 (1987).
- 542 32. M. Teixeira, *et al.*, Redox intermediates of *Desulfovibrio gigas* [NiFe] hydrogenase generated under hydrogen.
543 Mössbauer and EPR characterization of the metal centers. *J. Biol. Chem.* **264**, 16435–16450 (1989).

544 33. N. A. Bruender, J. Wilcoxon, R. D. Britt, V. Bandarian, Biochemical and Spectroscopic Characterization of a
545 Radical S-Adenosyl-L-methionine Enzyme Involved in the Formation of a Peptide Thioether Cross-Link.
546 *Biochemistry* **55**, 2122–2134 (2016).

547 34. L. Flöhe, *et al.*, The radical SAM enzyme AlbA catalyzes thioether bond formation in subtilisin A. *Nat. Chem.*
548 *Biol.* **8**, 350–357 (2012).

549 35. H. Mathur, M. C. Rea, P. D. Cotter, C. Hill, R. P. Ross, The sactibiotic subclass of bacteriocins: an update.
550 *Curr. Protein Pept. Sci.* **16**, 549–558 (2015).

551 36. K. Takeshima, A. Chikushi, K.-K. Lee, S. Yonehara, K. Matsuzaki, Translocation of Analogues of the
552 Antimicrobial Peptides Magainin and Buforin across Human Cell Membranes. *J. Biol. Chem.* **278**, 1310–1315
553 (2003).

554 37. M. M. Welling, A. Paulusma-Annema, H. S. Balter, E. K. J. Pauwels, P. H. Nibbering, Technetium-99m
555 labelled antimicrobial peptides discriminate between bacterial infections and sterile inflammations. *Eur. J.*
556 *Nucl. Med.* **27**, 292–301 (2000).

557 38. F. Ramare, *et al.*, Trypsin-dependent production of an antibacterial substance by a human *Peptostreptococcus*
558 strain in gnotobiotic rats and in vitro. *Appl. Environ. Microbiol.* **59**, 2876–2883 (1993).

559 39. E. H. Crost, *et al.*, Ruminococcin C, a new anti-*Clostridium perfringens* bacteriocin produced in the gut by the
560 commensal bacterium *Ruminococcus gnavus* E1. *Biochimie* **93**, 1487–1494 (2011).

561 40. A. R. Gholamiandekhordi, R. Ducatelle, M. Heyndrickx, F. Haesebrouck, F. Van Immerseel, Molecular and
562 phenotypical characterization of *Clostridium perfringens* isolates from poultry flocks with different disease
563 status. *Vet. Microbiol.* **113**, 143–152 (2006).

564 41. J. M. Stokes, A. J. Lopatkin, M. A. Lobritz, J. J. Collins, Bacterial Metabolism and Antibiotic Efficacy. *Cell*
565 *Metab.* **30**, 251–259 (2019).

566 42. K. E. Sutyak, R. E. Wirawan, A. A. Aroutcheva, M. L. Chikindas, Isolation of the *Bacillus subtilis* antimicrobial
567 peptide subtilisin from the dairy product-derived *Bacillus amyloliquefaciens*. *J. Appl. Microbiol.* **104**, 1067–
568 1074 (2008).

569 43. M. C. Rea, *et al.*, Bioavailability of the anti-clostridial bacteriocin thuricin CD in gastrointestinal tract.
570 *Microbiology*, **160**, 439–445 (2014).

571 44. F. V. Immerseel, *et al.*, *Clostridium perfringens* in poultry: an emerging threat for animal and public health.
572 *Avian Pathol.* **33**, 537–549 (2004).

573 45. , Antibiotic Resistance Threats in the United States, 2019. 148 (2019).

574 46. W. K. Smits, D. Lyras, D. B. Lacy, M. H. Wilcox, E. J. Kuijper, *Clostridium difficile* infection. *Nat. Rev. Dis.*
575 *Primer* **2**, 16020 (2016).

576 47. L. B. Rice, Progress and Challenges in Implementing the Research on ESKAPE Pathogens. *Infect. Control*
577 *Hosp. Epidemiol.* **31**, S7–S10 (2010).

578 48. V. Cattoir, J.-C. Giard, Antibiotic resistance in *Enterococcus faecium* clinical isolates. *Expert Rev. Anti Infect.*
579 *Ther.* **12**, 239–248 (2014).

580 49. K. Andries, *et al.*, A Diarylquinoline Drug Active on the ATP Synthase of *Mycobacterium tuberculosis*. *Science*
581 **307**, 223–227 (2005).

582 50. S. A. Dingsdag, N. Hunter, Metronidazole: an update on metabolism, structure–cytotoxicity and resistance
583 mechanisms. *J. Antimicrob. Chemother.* **73**, 265–279 (2018).

585 **Figure legends**

586 **Fig. 1. Sequence and three-dimensional structure of Ruminococcin C1.** (A) Sequence of
587 RumC1 containing leader peptide (*italics*) and core peptide (RumC1-44), cysteine residues are
588 underlined. (B) Backbone overlay of the 20 lowest target function value conformers for the DDDD
589 stereoisomer of RumC1. (C) Cartoon backbone representation of the three-dimensional solution
590 structure of RumC1 with the D stereochemistry at Ala12 (α -S), Asn16 (α -S), Arg34 (α -S) and Lys42
591 (α -S). Cysteine sulfur to α -carbon thioether cross-links are colored in orange and the position are
592 indicated. (D) Electrostatic surface potential of RumC1, where blue indicates positive charge and
593 red indicates negative charge. (E) Surface hydrophobicity of RumC1, where yellow represents
594 hydrophobic residues and white represents hydrophilic residues.

595 **Fig. 2. Spectroscopic characterizations of holo-RumMc1.** (A) UV-vis spectrum of holo-
596 RumMc1 in the absence (solid trace) or the presence of dithionite (dashed trace). (B) Mössbauer
597 spectrum of holo-RumMc1 taken at T = 77 K with the simulation (red solid line) representing the
598 sum of the subcomponents **1**, **2** and **3** (black lines). **1** and **2** are simulated in a ratio of 2:1 and
599 represent two diamagnetic $[4\text{Fe}4\text{S}]^{2+}$ clusters. One $[4\text{Fe}4\text{S}]^{2+}$ cluster is supposed to bind SAM. **3**
600 was assigned to Fe^{3+} ions present in a $[3\text{Fe}4\text{S}]^{1+}$ cluster in a S = 1/2 state. The respective Mössbauer
601 parameters obtained from the simulation of the spectra at 77 K are summarized below the spectrum.
602 (C) X-band CW EPR spectra of dithionite-reduced holo-RumMc1. The black line represents the
603 experimental spectrum, while the red trace is the simulated spectrum by using three components A,
604 B and C. (D) X-band CW EPR spectra of dithionite-reduced holo-RumMc1 in the presence of SAM.
605 The black trace represents the experimental spectrum, while the red trace is the simulated spectrum
606 by using four components A, B, C and A'. (E) g-values of components A, B, C and A' used to
607 simulate the experimental EPR spectra.

608 **Fig. 3. Stability of RumC1.** (A) RumC1 was exposed to a range of pH for 1 hour, (B) to high
609 temperatures up to 1 hour, (C) to human serum up to 24 hours, before measuring its MIC. (D) MIC
610 of RumC1 was determined in MH medium supplemented with NaCl or MgCl_2 . (A to D) All MICs
611 were determined against *C. perfringens*. Residual antimicrobial activity was calculated based on
612 the MIC of untreated RumC1. (E) Stability of RumC1 in conditions mimicking the GI tract. MIC
613 of RumC1 against *C. perfringens* was determined after exposure to digestive enzymes. Nisin was
614 used as a positive control of pancreatin activity. Residual antimicrobial activity was calculated
615 based on the MIC of untreated bacteriocins. ^a Residual antimicrobial activity were measured in this
616 study. ^b Published by Jarvis and Mahoney, 1969.

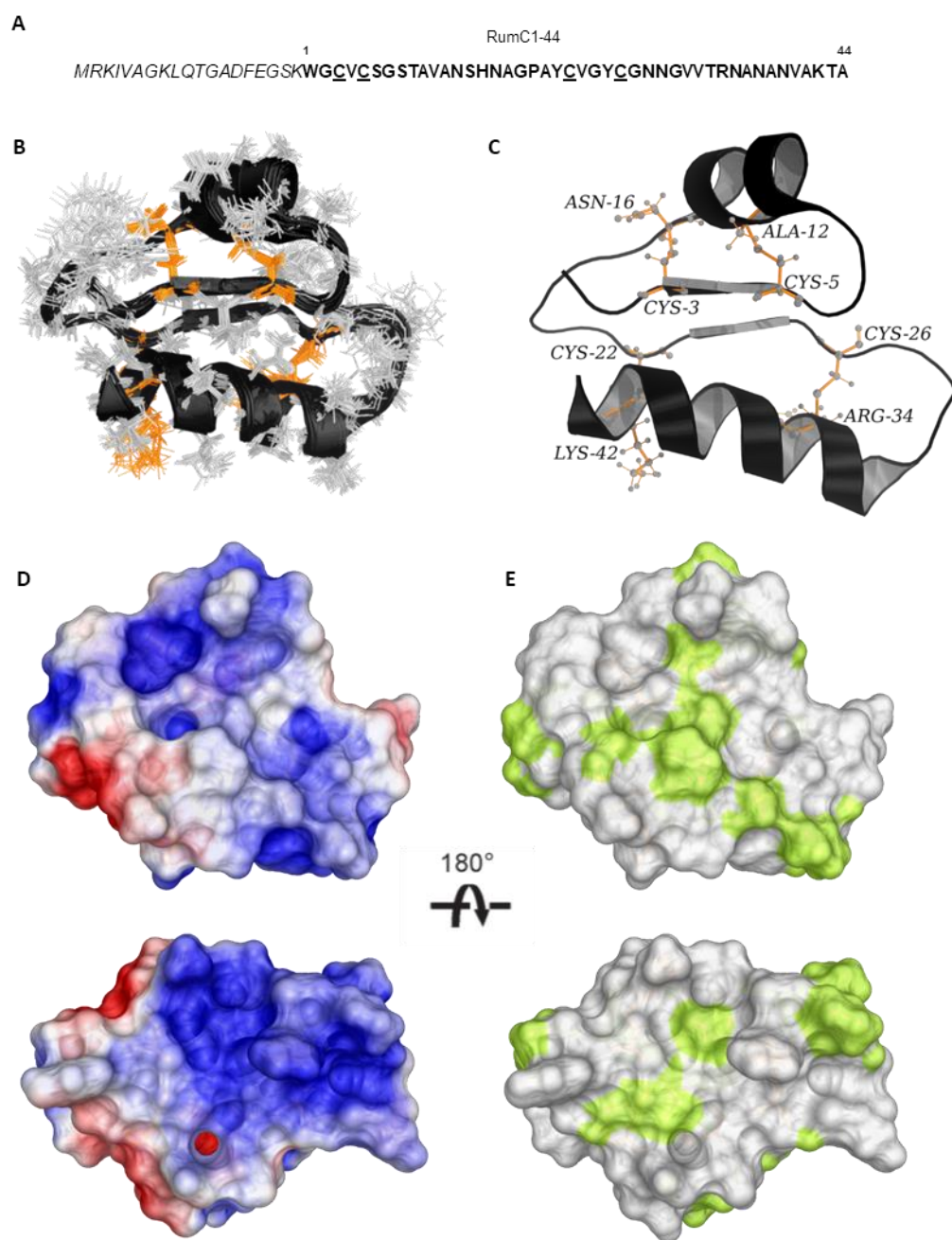
617 **Fig. 4. Antimicrobial activity of RumC1.** (A) Activity assays of RumC1 on *Bacillus cereus* grown
618 in eukaryotic cell culture medium in the absence or the presence of a simulated intestinal

epithelium. Small and colic intestine compartments were simulated by Caco2 and T84 culture cells monolayer respectively, whereas RumC1 was added before (30 min), concomitantly and after infection (30 min) with 5×10^5 CFU/mL *B. cereus* culture. **(B)** Activity spectrum of RumC1 against laboratory and clinical Gram-positive pathogens. Collection strains and clinical isolates are indicated. The table includes MIC of conventional antibiotics commonly used for clinical treatment and considered here as references (i.e. metronidazole, vancomycin and amoxicillin). Acquired resistance to antibiotics were determined following the EUCAST 2019 clinical breakpoint tables and are indicated by "R", whereas "i.r." refers to "intrinsic resistance", and * to the laboratory isolate references.

Fig. 5. Antibacterial mode of action of RumC1. (A, B) Cells of *C. perfringens* in early log phase were either treated with RumC1, control antibiotics, metronidazole, nisin or left untreated. Each experiment was done in independent triplicates. **(A)** After 15 min of treatment at 5xMIC, *C. perfringens* cells were incubated with radio-labelled precursors of DNA, RNA, proteins and peptidoglycan for 45 min. The synthesis of each pathway was measured by radioactivity counts. Gemifloxacin, rifampicin, tetracycline and vancomycin were used as controls antibiotics for the inhibition of DNA, RNA, proteins and peptidoglycan, respectively. Radio-labelled precursor incorporation is expressed as a percentage of maximum incorporation determined with the untreated condition. **(B)** After 15 min of treatment, the ATP present in the extracellular media (outer ATP) was measured by bioluminescence, then cells were lysed and the ATP content in the extracellular media was measured again. The inner ATP content was deduced from the difference between ATP content in the extracellular media before and after cell lysis. Cells were treated with 2.5x, 5x and 10xMIC for each condition. Relative Light Units (RLU) are expressed as percentages normalized by the value of the inner ATP content of untreated cells.

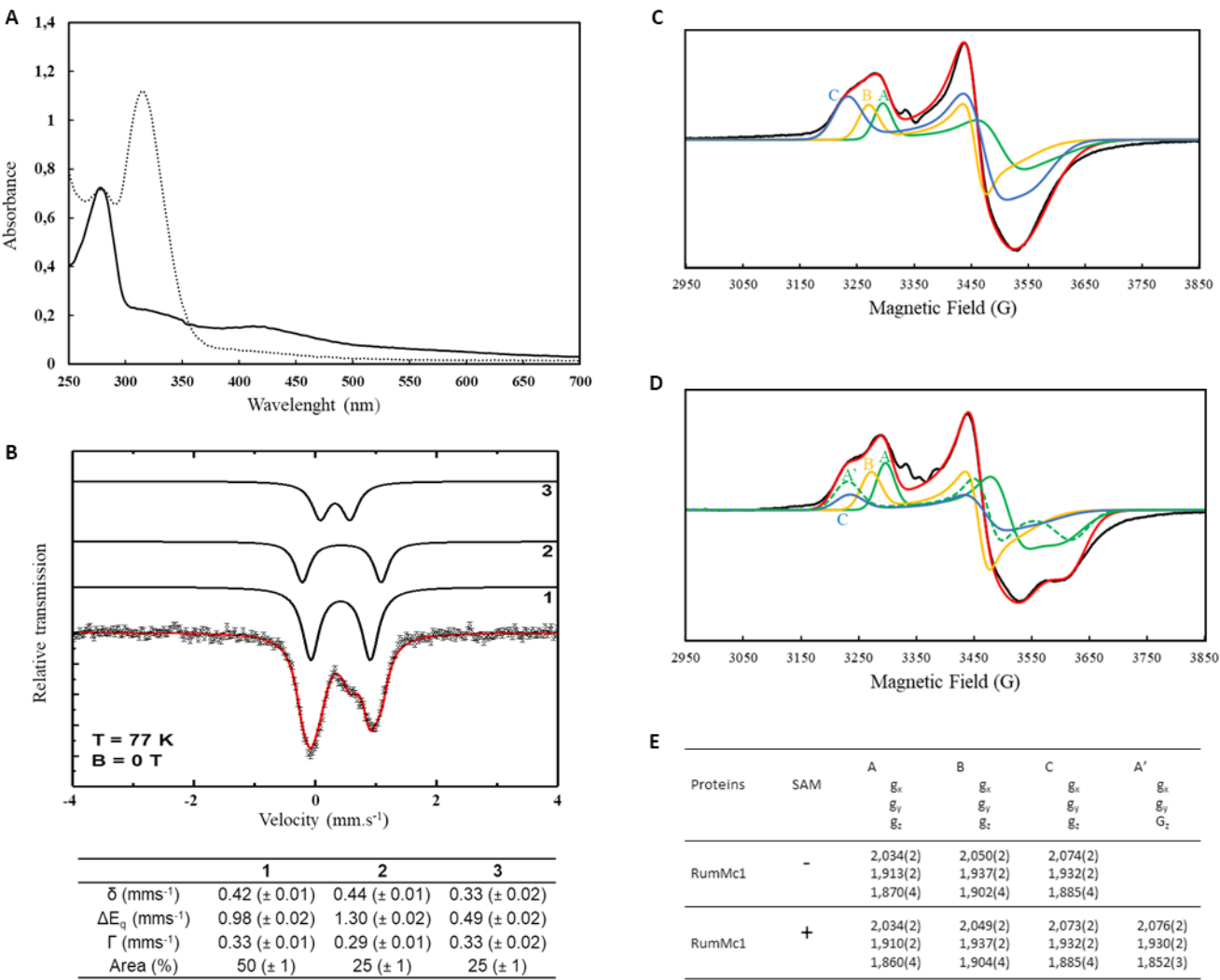
Fig. 6. Histological analysis of human intestinal tissue treated with RumC1. Human intestinal explants were left untreated or treated with RumC1 (100 μ M) or CTAB (300 μ M) for 4 h before H&E staining and microscopic observations as described in the Materials and Methods section. Images are representative of overall observed effects. Scale bar = 50 μ m.

647 Figure 1
648



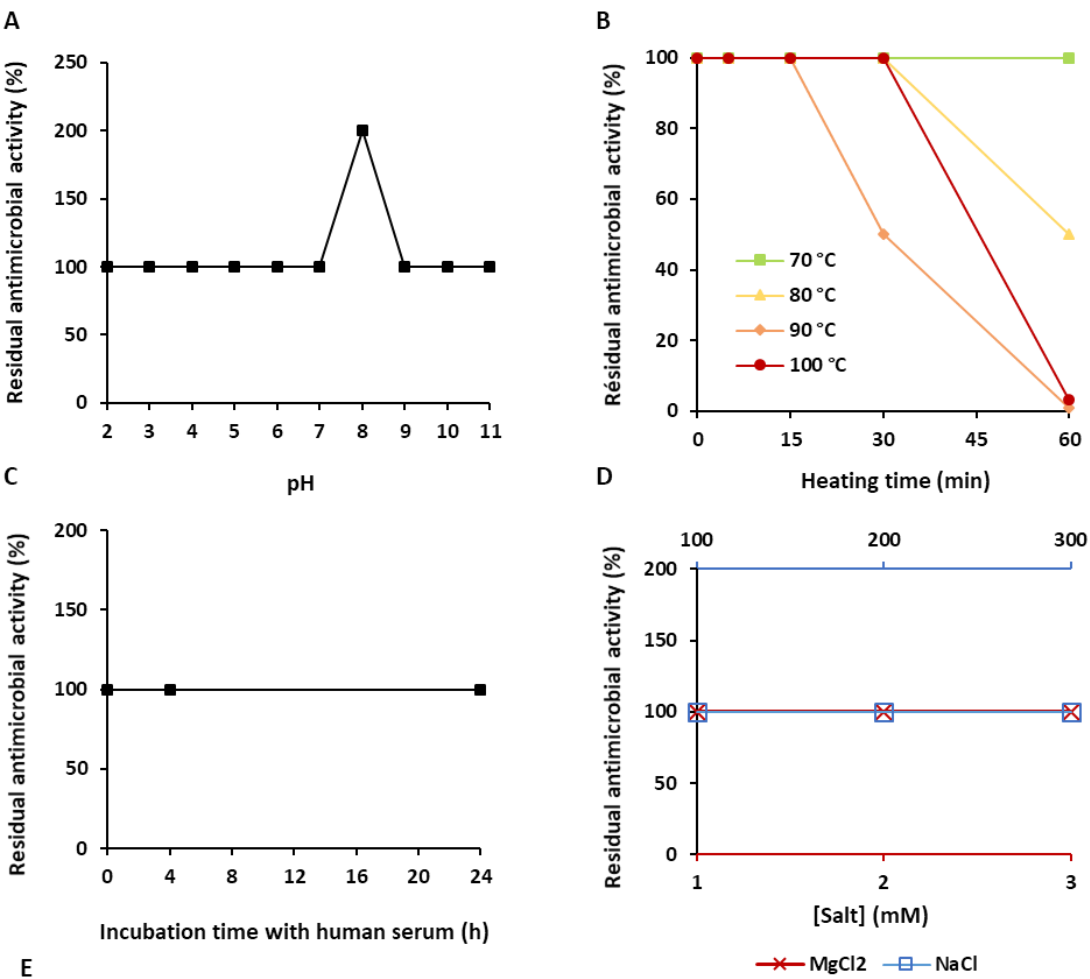
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651 Figure 2
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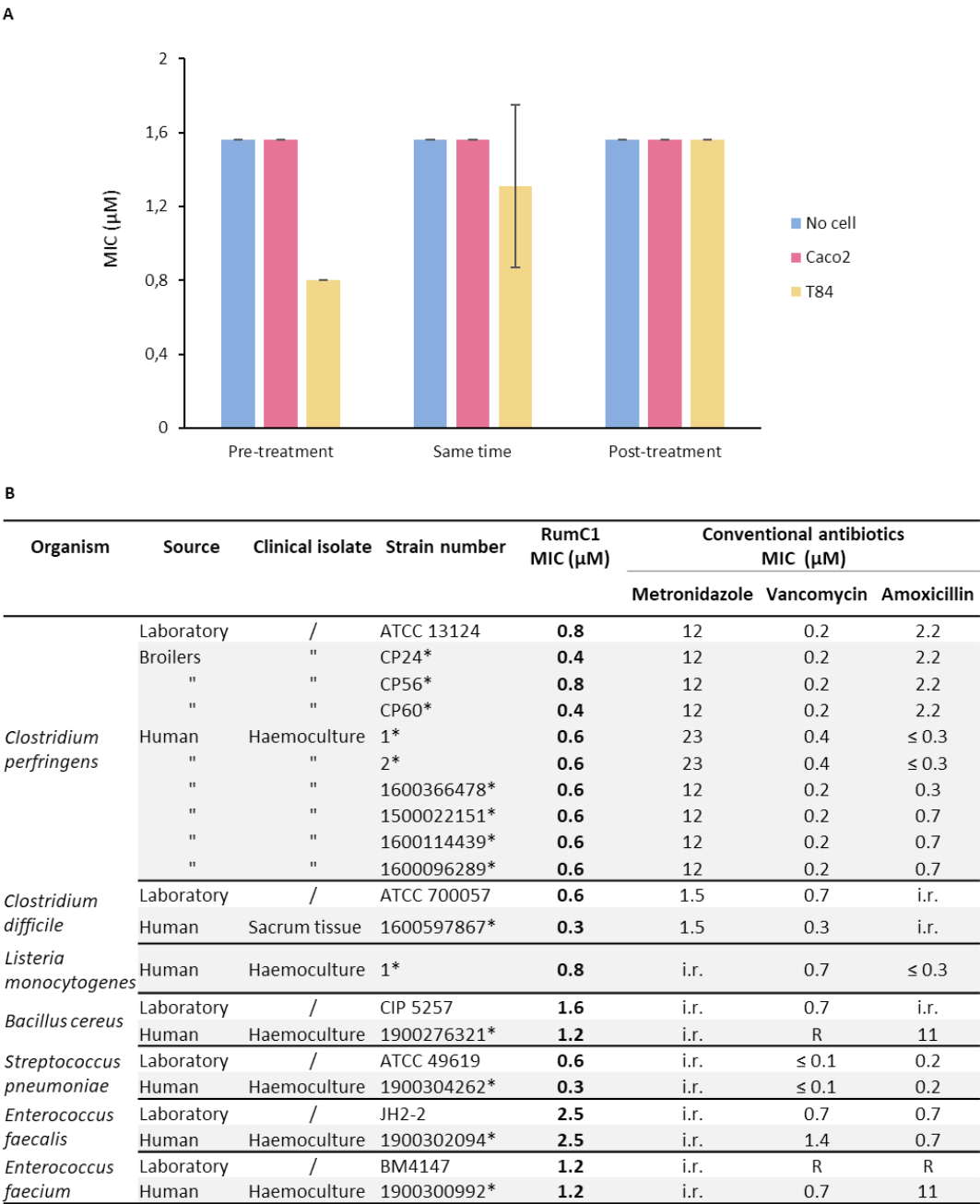
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655 Figure 3
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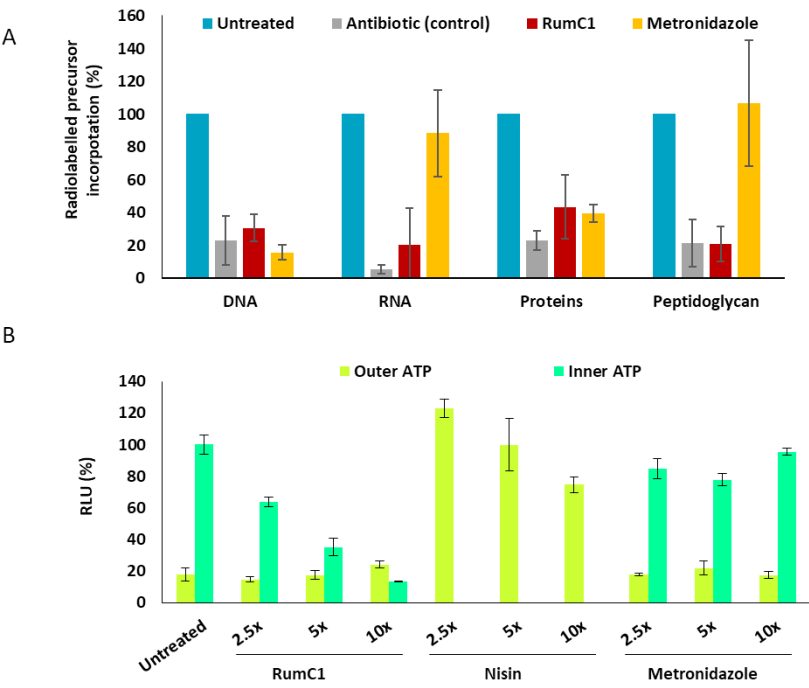
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659 Figure 4
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663 Figure 5

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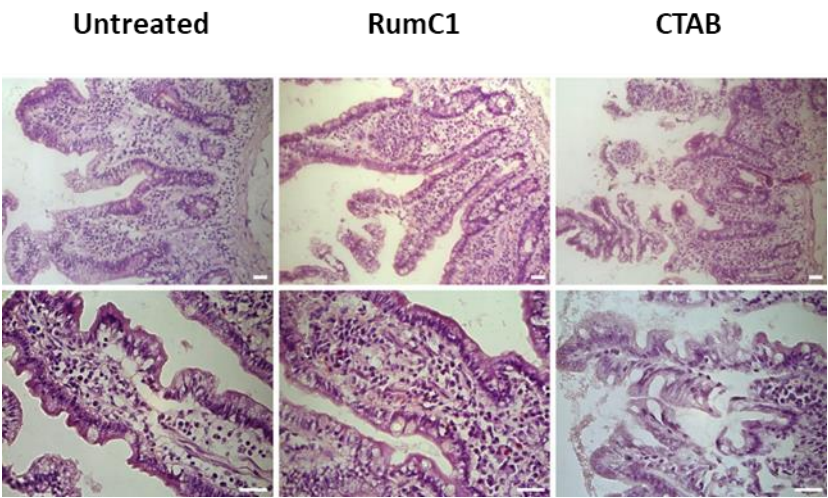


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667 Figure 6

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Supporting Information for

The unusual structure of Ruminococcin C1 antimicrobial peptide confers clinical properties

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This PDF file includes:

Figures S1 to S9

Tables S1 and S2

SI Materials and Methods

SI References

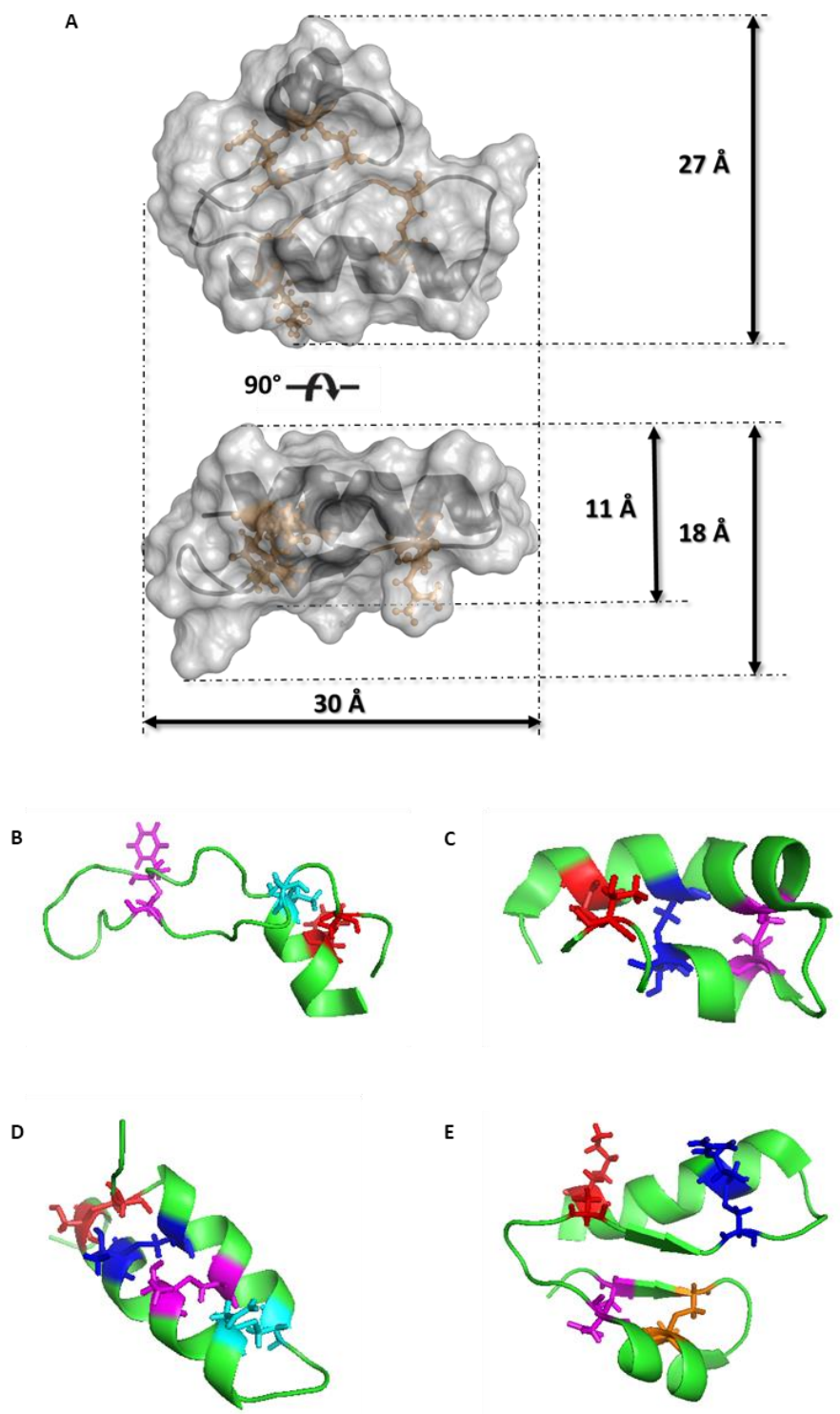


Fig. S2. Dimensions of the NMR structure of RumC1. Comparison of sactipeptides structures. (A) Dimensions of the NMR structure of the DDDD stereoisomer of RumC1. NMR Structures of: **(B)** Subtilisin A, **(C)** Thuricin CD, **(D)** Thurincin H and **(E)** RumC1. Stereoisomers at the α -carbons are LDD, LLD, DDDD and DDDD for subtilisin A, thuricin CD, thurincin H and RumC1, respectively. The Protein Data Bank codes for Subtilisin A, Thuricin CD, Thurincin H and RumC1 are 1PXQ, 2L9X, 2LBZ and 6T33, respectively.

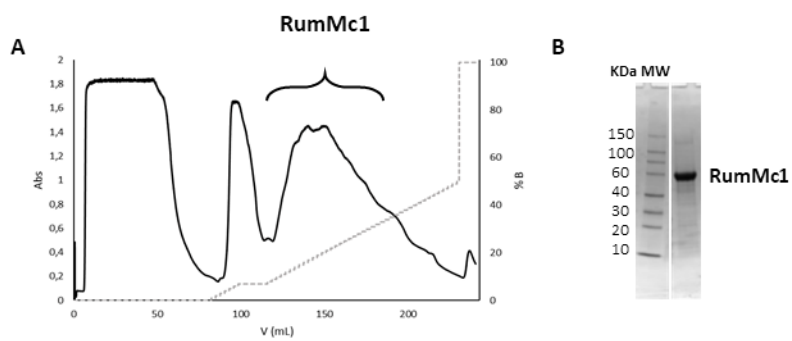
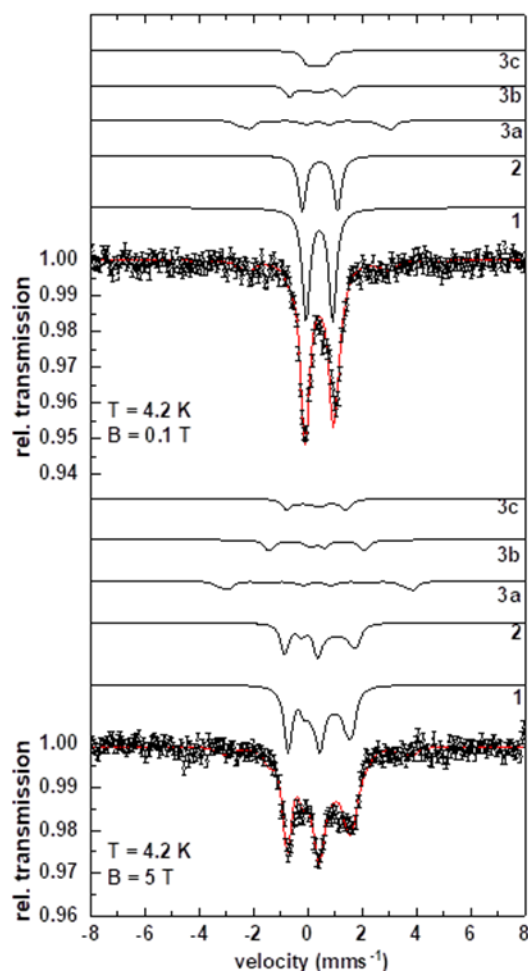


Fig. S3. Anaerobic purification of RumMc1. **(A)** FPLC chromatogram of overexpressed RumMc1 on a nickel-charge IMAC column. %B is the % of a 50 mM HEPES, pH 7,5, 300 mM NaCl, 500 mM imidazole buffer solution. **(B)** SDS-PAGE analysis of purified RumMc1

A



B

| | 1 | 2 | 3a | 3b | 3c |
|-------------------------|---------------------|---------------------|-------------------------|-------------------------|----------------------------|
| δ (mm/s) | 0.42 (± 0.02) | 0.44 (± 0.02) | 0.33 (± 0.03) | 0.33 (± 0.03) | 0.33 (± 0.03) |
| ΔE_Q (mm/s) | 0.98 (± 0.02) | 1.30 (± 0.02) | 0.49 (± 0.03) | 0.49 (± 0.03) | 0.49 (± 0.03) |
| Γ (mm/s) | 0.35 (± 0.02) | 0.33 (± 0.02) | 0.33 (± 0.03) | 0.33 (± 0.03) | 0.33 (± 0.03) |
| η | 1 (-0.4) | 1 (-0.4) | 0 (+0.5) | 0 (+0.5) | 0 (+0.5) |
| $A_{xyz}/\mu_N g_N$ (T) | (0/0/0) | (0/0/0) | (36/28/32) ¹ | (11/11/11) ¹ | (2.5/2.5/2.5) ¹ |
| Area (%) | 50 | 25 | 8.33 | 8.33 | 8.33 |

Fig. S4. Field dependent spectra of RumMc1. (A) Mössbauer spectra of RumMc1 with the simulation (red solid line) representing the sum of the subcomponents 1, 2 and 3 (black lines). Component 1 and 2 are simulated in a ratio of 2:1 and represent two diamagnetic $[4\text{Fe}_4\text{S}]^{2+}$ clusters. Component 3 is divided into three subcomponents 3a, 3b and 3c that represent three Fe^{3+} high spin ions antiferromagnetically coupled to a total spin of $S = 1/2$ as present in a $[3\text{Fe}_4\text{S}]^{1+}$ cluster. (B) Mössbauer parameters obtained from the simulation of the field dependent spectra of RumMc1. ¹ Values for $A_{xyz}/\mu_N g_N$ were taken from B. H. Huynh *et al.* (1).

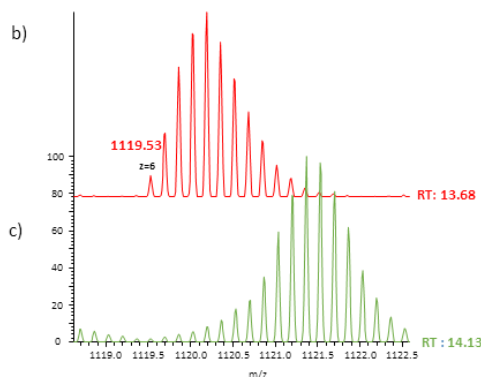
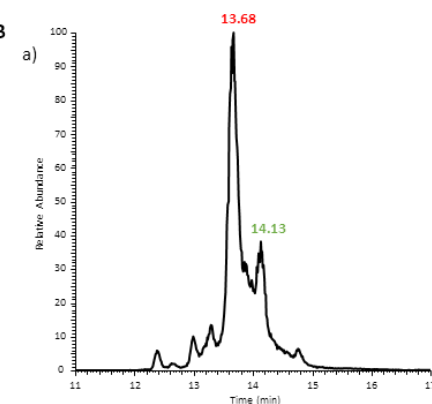
| | | |
|--------|--|-----|
| AlbA | FPMP LHATFELTHR C NLK C AH C YLESSPEALGTVSIEQ-----FKKTADMLFDN--GVL | 167 |
| anSMe | MPPLSLLIKPASSG C NLK C TY C FYHSLSDNRNVKSYGIMRDEVLES MVKRV LNEANGHCS | 60 |
| RumMc1 | RYDLQQVILELTE Q CNMR C RY C IYNEHNEG YRNFSPKAMTW DVAKRAVEYARDNSGDKVA | 169 |
| | : **::* :* . . : * | |
| AlbA | ---NWVDDFGRGRDIVHPTKDAEQHRKFMEYEQHVIDEFKDLIPII-----P-YERKRAAN C GA | 346 |
| anSMe | LFDFWYEDFLNGNRV-----SIRYFDGLL---ETILLGKSS----- S C ---GMNGT C T- | 263 |
| RumMc1 | AIEGWALARDLEEED-----PKSYVAGIV---ADKLVR IHNRRQTQEP C KDLRRNG C CIP | 395 |
| | * . * :: : | |
| AlbA | GWKSIVISPFGEVR P C ALFP-KEFSLGNIFHDSYESIFNSPLVHKLWQAQAPRFSEHCMKDK C PFSG | 412 |
| anSMe | --CQFVVESDGSV P C DFYVLDKWRLGNIQDMTMKELFETNKNHEFIKL---SFKVHEE C KK C KWFR | 324 |
| RumMc1 | GNRRVYVKTDGKFLL C EKTG-DAPDIGNVFEGADLEKIKKYYIEEY-----DEKSITR C NE C WARN | 455 |
| | . :: *.. * . : ** : . : . : . . : . : * | |
| AlbA | Y C G G C YLKGLNSNKY-----HRKNI C SWAKNEQL-----EDVVQLI----- | 448 |
| anSMe | ---L C KGGRRCRDSKEDSALELNYY C QSYK-----EFFEY-----AFPRLINVANNIK-- | 370 |
| RumMc1 | L C G L C YAACYEAEIDME---RKEKV C GAHRYATKGELISYYSILEEKPEVIEEIDAVPYY | 513 |
| | * : * : | |
| | ::: | |

Fig. S5. Alignment of selected radical-SAM enzymes with RumMc1. Alignment of anSME (anaerobic Sulfatase Maturing Enzyme), AlbA, and RumMc1. Conserved residues are marked “*” and cysteine residues are highlighted in green.

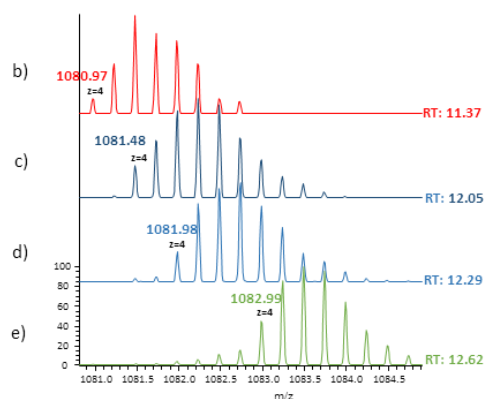
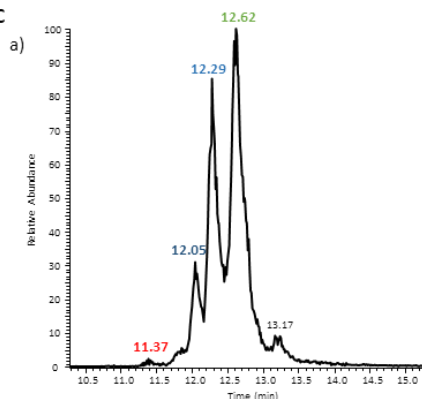
A

| | RumC1 | RumC1-44 | RumC1-44-LS |
|--------------|-------|----------|-------------|
| % maturation | 90% | < 1% | < 10% |

B



C



D

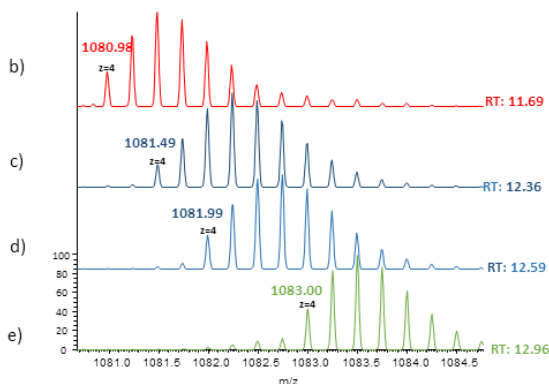
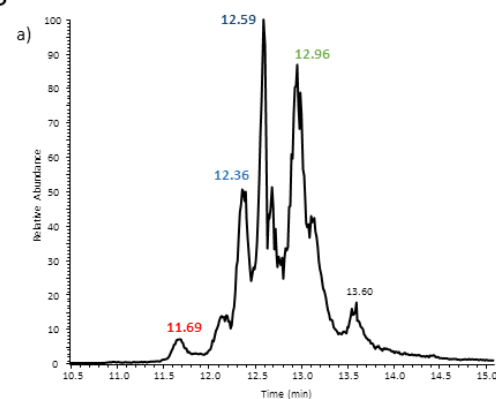
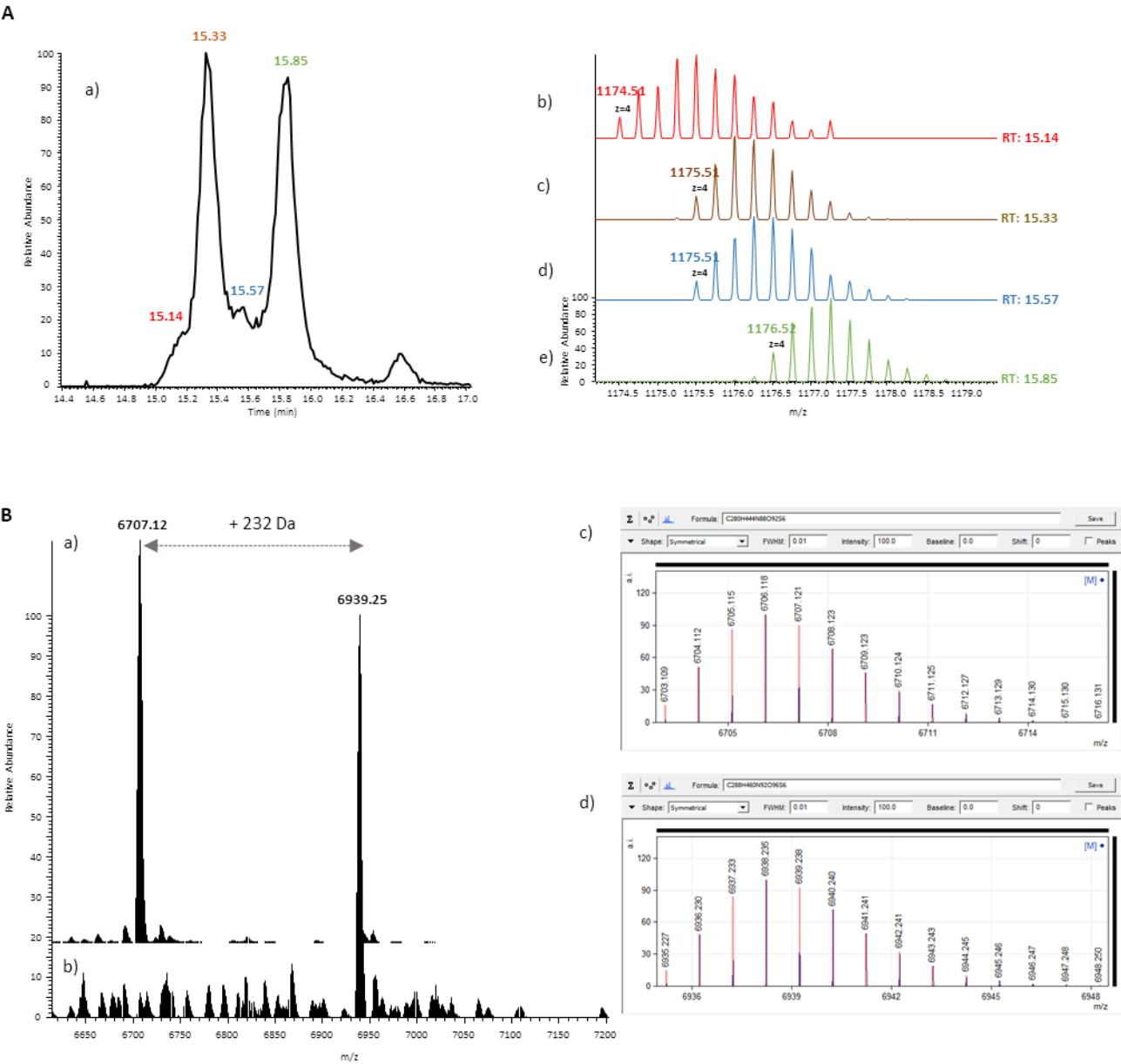


Fig. S6. LC-MS analyses of leader peptide-dependent maturation of RumC1. (A) Percentage of the full maturation for the different constructions. (B) Maturation of RumC1: (a) LC-MS trace of *in vitro* matured RumC1. Zoom-in spectra at RT = 13.68 (b) and RT = 14.13 (c) for m/z corresponding to RumC1. (b) A major ion $[M+6H]^{6+} = 1119.5$ Da corresponds to the fully matured form containing 4 thioether bonds. (c) A mixture of unmaturation forms containing no, one or two disulfide bonds are observed. (C) Maturation of RumC1-44: (a) LC-MS trace of *in vitro* matured RumC1-44. Zoom-in spectra at RT = 11.37 (b), RT = 12.05 (c), RT = 12.29 (d), and RT = 12.62 (e) for m/z corresponding to RumC1-44. (b) A major ion $[M+4H]^{4+} = 1081$ Da corresponds to the fully matured form containing 4 thioether bonds. (c) A major ion $[M+4H]^{4+} = 1081.5$ Da corresponds to a species containing 3 thioether bridges. (d) A major ion $[M+4H]^{4+} = 1082$ Da corresponds to a species with 2 thioether bridges. (e) A major ion $[M+4H]^{4+} = 1083$ Da corresponds to the non matured form of RumC1-44. (D) Maturation of RumC1-44-LS: (a) LC-MS trace of *in vitro* matured RumC1-44-LS. Zoom-in spectra at RT = 11.69 (b), RT = 12.36 (c), RT = 12.59 (d), and RT = 12.96 (e) for m/z corresponding to RumC1-44-LS. (b) A major ion $[M+4H]^{4+} = 1081$ Da corresponds to the fully matured form containing 4 thioether bonds. (c) A major ion $[M+4H]^{4+} = 1081.5$ Da corresponds to a species containing 3 thioether bridges. (d) A major ion $[M+4H]^{4+} = 1082$ Da corresponds to a species with 2 thioether bridges. (e) A major ion $[M+4H]^{4+} = 1083$ Da corresponds to the non matured form of RumC1-44-LS.



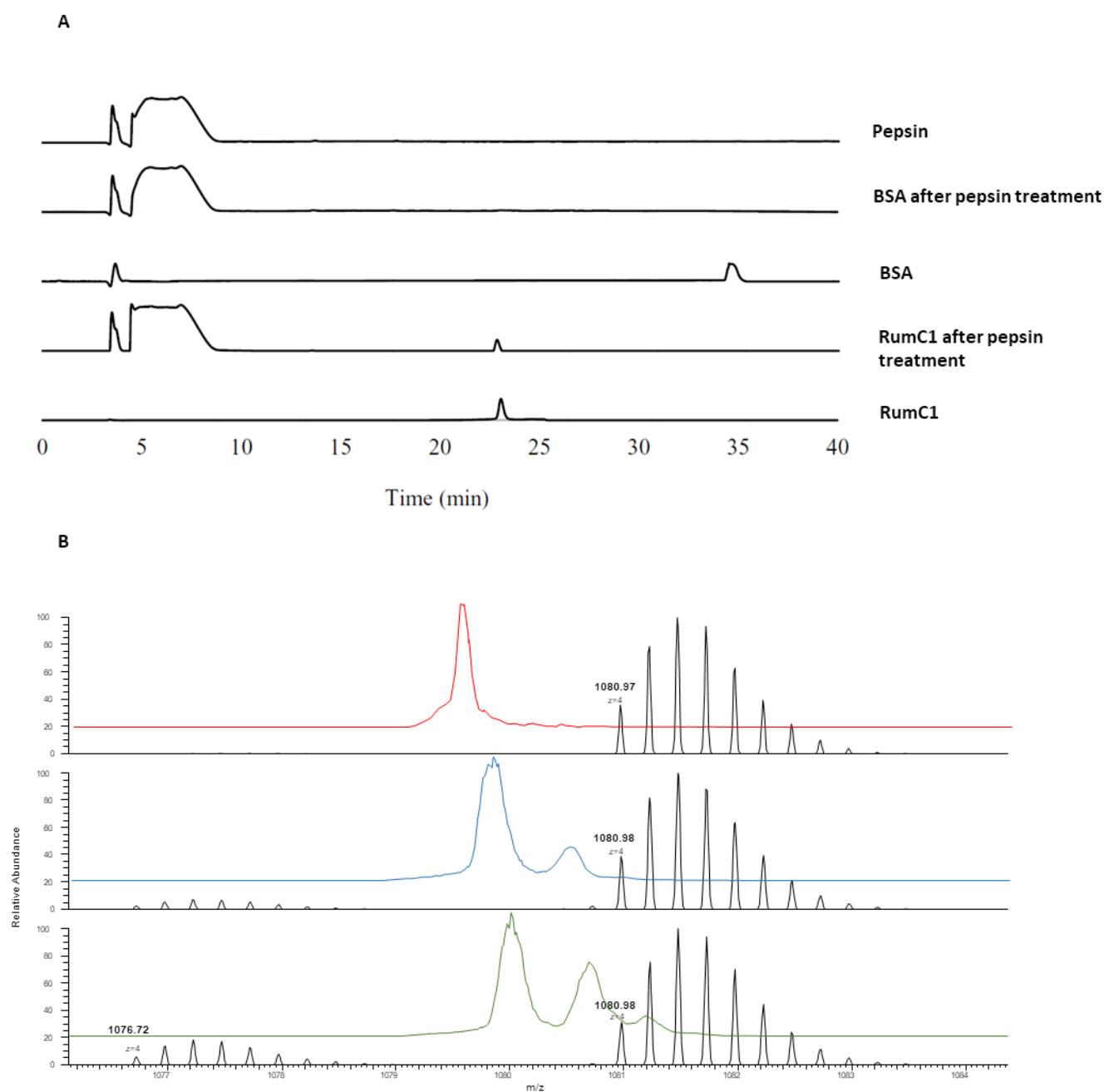


Fig. S8. Chromatographic and spectroscopic analyses to evaluate RumC1 integrity. (A) Chromatogram of RP-C18-HPLC of RumC1, or BSA used as control, treated with pepsin and in conditions simulating the stomach (pH 2,5 37°C 2h). (B) LC-MS profiles and MS spectra of RumC1 (top, red) submitted to pepsin (middle, blue) or pancreatic conditions (bottom, green). No change on RumC1 was observed after digestion except the presence of a light amino loss species due to heating (-NH₃).

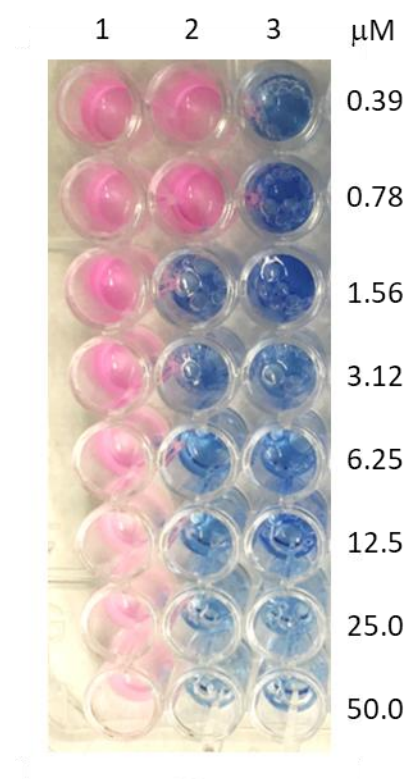


Fig. S9. Evaluation of RumC1 activity on simulated intestinal epithelium infected by *Bacillus cereus*. After 24h of incubation, suspension of *B. cereus* grown on Caco-2 and T84 cells were transferred to new 96 well plates free of eukaryotic cells. Resazurin was added to determine the viability of the bacterial cells. Briefly, resazurin is a blue dye that is reduced in pink resorufin in the presence of metabolically active cells. An example of untreated *B. cereus* grown on Caco-2 cells is shown in column 1, whereas the column 2 corresponds to *B. cereus* grown on Caco-2 cells with increasing concentrations of RumC1 and column 3 represents uninfected and untreated Caco-2 cells.

Table S1. Comparison of statistics generated by the 16 stereoisomers of RumC1. Assigned NOEs represent total number of off-diagonal NOE assignments used by CYANA to perform the structure calculation.

| Table entry | Isomers | Thioether bond violations | Assigned NOEs | RMSD (Angstroms) | CYANA average target function value |
|-------------|---------|---------------------------|---------------|------------------|-------------------------------------|
| 1 | LLLL | 3 | 374 | 2.5 ± 0.4 | 0.7 |
| 2 | LLLD | 3 | 385 | 1.9 ± 0.8 | 2.0 |
| 3 | LLDL | 2 | 400 | 1.3 ± 0.5 | 1.3 |
| 4 | LLDD | 2 | 371 | 2.7 ± 0.4 | 3.8 |
| 5 | LDLL | 3 | 399 | 1.4 ± 0.5 | 1.2 |
| 6 | LDLD | 4 | 404 | 1.2 ± 0.3 | 1.5 |
| 7 | LDDL | 3 | 398 | 1.1 ± 0.3 | 0.7 |
| 8 | LDDD | 1 | 399 | 1.4 ± 0.2 | 0.6 |
| 9 | DLLL | 3 | 405 | 1.6 ± 0.3 | 1.1 |
| 10 | DLLD | 4 | 430 | 1.5 ± 0.2 | 0.7 |
| 11 | DLDL | 8 | 406 | 2.3 ± 0.4 | 2.9 |
| 12 | DLDD | 6 | 377 | 2.5 ± 0.6 | 5.3 |
| 13 | DDLL | 3 | 405 | 1.5 ± 0.5 | 1.3 |
| 14 | DDL D | 2 | 404 | 1.3 ± 0.2 | 0.7 |
| 15 | DDDL | 1 | 394 | 1.2 ± 0.2 | 0.3 |
| 16 | DDDD | 0 | 417 | 0.9 ± 0.2 | 0.1 |

Table S2. Structure calculation statistics for the DDDD stereoisomer of RumC1. Statistics for structure calculation refers to all the twenty structures.

| Final NMR restraints in the DDDD structure calculation | | |
|--|---------------|------------------------|
| Short-range ($ i - j = 1$) | 317 | |
| Medium-range ($1 < i - j < 5$) | 99 | |
| Long-range ($ i - j \geq 5$) | 80 | |
| Total nOe distance restraints | 496 | |
| Hydrogen bonds | 50 | |
| Thioether Bridge distance restraints | 8 | |
| Dihedral angle restraints | 46 | |
| Total restraints | 600 | 13.6 restraints/residu |
| Residual violations | | |
| CYANA target function | 0.36 +/- 1.08 | |
| NOE upper distance constrain violation | | |
| Number > 0.1 Å in at least 1 structure | 7 | |
| Dihedral angle constrain violations | | |
| Number > 0.1° | 0 | |
| Van der Waals violations | | |
| Number > 0.1 Å | 0 | |
| Average structural RMSD to the mean coordinates (Å) | | |
| All backbone atoms | 0.81 +/- 0.50 | |
| All heavy atoms | 1.19 +/- 0.54 | |
| Ramachandran statistics, % of all residues | | |
| Most favored regions | 84.1 | |
| Additional allowed regions | 15.4 | |
| Generously allowed regions | 0.4 | |
| Disallowed regions | 0 | |

SI Materials and Methods

Heterologous expression and purification of (^{13}C , ^{15}N)-labelled mature RumC1. A synthetic plasmid containing the *E. coli* codon-optimized gene of *R. gnavus* E1 encoding RumMc1 (pET-15b-*rumMc1*, ampicillin-resistant) was obtained from Genscript. Plasmids pET-15b-*rumMc1*, pETM-40-*rumC1* and psuf (chloramphenicol-resistant) containing *sufABCDSE* genes were used to transform competent *E. coli* BL21 (DE3) cells for expression. The resulting strain was grown in 3 L of M9 medium containing kan (50 $\mu\text{g/mL}$), amp (100 $\mu\text{g/mL}$), chl (34 $\mu\text{g/mL}$), vitamin B1 (0.5 $\mu\text{g/mL}$), MgSO_4 (1 mM), FeCl_3 (50 μM) and glucose (4 mg/mL) at 37 °C. At an optical density (OD_{600}) of 0.25, cells were harvested by centrifugation (4,000 rpm for 20 min at 4°C). The cells were resuspended in 1 L of labeled minimal medium (Na_2HPO_4 6 g/L, KH_2PO_4 3 g/L, $^{15}\text{NH}_4\text{Cl}$ 1 g/L) containing kan (50 $\mu\text{g/mL}$), amp (100 $\mu\text{g/mL}$), chl (34 $\mu\text{g/mL}$), vitamin B1 (0.5 $\mu\text{g/mL}$), MgSO_4 (1 mM), FeCl_3 (50 μM) and labeled glucose- ^{13}C (4 mg/mL). The culture was grown at 25°C to an optical density (OD_{600}) of 0.8. FeCl_3 (100 μM) and L-cysteine (300 μM) were then added and the culture was induced with 1 mM IPTG. The cells were grown for 15h under stirring and then were harvested by centrifugation (4,000 rpm for 20 min at 4°C). Labelled MBP-RumC1 was purified as described for the MBP-RumC1 (2). (^{13}C , ^{15}N)-labelled mature RumC1 was obtained after cleavage of the MBP tag by using TEV and purified as previously reported (2). Leader peptide cleavage was performed with trypsin as described by Chiumento *et al.*, (2). Briefly, labelled RumC1 was treated with TPCK (N-tosyl-L-phenylalanine chloromethyl ketone)-treated trypsin (Sigma-Aldrich) for 1 hour at 37°C at a molar ratio of 200:1 (RumC1:trypsin). Then RumC1 was purified using RP-C18-HPLC with the following gradient: 10 min at 22% followed by 12 min from 22 to 38% of 90% ACN and 0.1% TFA, on a preparative column (250 mm by 21.2 mm; Phenomenex, Jupiter, 15 μm , 300 Å).

NMR spectroscopy of RumC1. The NMR sample used for sequential assignment of ^{13}C - ^{15}N -labeled RumC1 was approximately 0.2 mM in 10 mM phosphate buffer, 90% H_2O /10% D_2O at pH 6.8. All NMR data were collected at 27°C using a Bruker Avance III 600 MHz NMR spectrometer equipped with a TCI 5 mm cryoprobe. The following datasets were performed; 2D: [^{15}N , ^1H] HSQC and [^{13}C , ^1H] HSQC; 3D: [^1H , ^{15}N , ^{13}C] HNCACB, CBCA(CO)NH, HNCA, HN(CO)CA, HNCO, HN(CA)CO, ^{13}C -TOCSY-HSQC (spin lock of 80 ms) and (H)CCH-TOCSY. Backbone resonances were assigned from triple resonance spectra and were extended to give side chain assignments using (H)CCH-TOCSY and ^{13}C -TOCSY-HSQC. ^1H assignments for aromatic side chains and asparagines side chain amides were made using 2D [^1H , ^1H] TOCSY and NOESY (mixing time of

150 ms) spectra. Spectra were processed with Topspin 3.5 and analyzed with CcpNmr Analysis software (3). All of the peak lists and the complete ^1H , ^{13}C and ^{15}N backbone and side chain chemical shift assignments have been deposited into the Biological Magnetic Resonance Databank (<http://www.bmrb.wisc.edu>) under ascension code 50027.

Structure Calculations. For the structure calculations, a 2D [^1H , ^1H] NOESY was acquired with a mixing time of 150 ms, using a 2 mM unlabeled RumC1 sample in 10 mM phosphate buffer, 90% H_2O / 10% D_2O , pH 6.8 at 27°C, performed on the Bruker Avance III 600 MHz spectrometer. The structures of the 16 stereoisomers were calculated with CYANA 2.1 (4), using NOE restraints measured from the 2D [^1H , ^1H] NOESY, 3D [^1H , ^{15}N , ^1H] NOESY, 3D [^1H , ^{13}C , ^1H] NOESY experiments and angle restraints obtained from the TALOS+ server (5). The NOEs were calibrated within CYANA according to their intensities. The same nOe peaks list and angle restraints were used for the structure calculations of each stereoisomer, following the same procedure as previously described by John Vederas and co-workers (6–8). Twenty lowest target function value conformations were generated for each of the 16 stereoisomers. Coordinates of the twenty conformations of DDDD stereoisomer of RumC1 have been deposited into the Protein Data Bank under ascension code 6T33.

Expression of RumMc1. We obtained a commercially supplied codon-optimized synthetic plasmid of *Ruminococcus gnavus* RumMc1 (pET-28a-*rumMc1*, kanamycin-resistant) from Genscript. Vectors pET-28a-*rumMc1* and pDB1282 (ampicillin-resistant), which carries the *isc* operon required for proper assembly of the Fe-S clusters in RumMc1, were subsequently co-transformed into chemically-competent BL21 (DE3) *E. coli* cells. A 500 mL sterile culture erlenmeyer containing 100 mL Luria Bertani medium (LB) supplemented with kan (50 $\mu\text{g}/\text{mL}$), amp (100 $\mu\text{g}/\text{mL}$) was inoculated with a single colony of BL21 (DE3) cells carrying pET-28a-*rumMc1* and pDB1282. The 100 mL culture was grown overnight at 37 °C, 200 rpm and used to inoculate 10 liters M9 minimal medium on a fermenter. The minimal medium was prepared by supplementing M9 Minimal Salts (Sigma) with a final concentration of 20 mM glucose, 2 mM MgSO_4 , 50 $\mu\text{g}/\text{mL}$ kan, 100 $\mu\text{g}/\text{mL}$ amp) and 50 μM FeCl_3 . The fermenter culture was grown at 37 °C, 200 rpm to an $\text{OD}_{600\text{ nm}} \sim 0.3\text{--}0.4$ and then supplemented with a final concentration of 50 μM FeCl_3 , 300 μM L-Cys, and 13.3 mM L-arabinose. At an (OD_{600}) of 1.2, the culture was cooled at 24°C, supplemented with a final concentration of 1 mM IPTG and grown for 15h under stirring. The cells were harvested by centrifugation (4,000 rpm for 20 min at 4°C).

Purification of RumMc1. The purification protocol was carried out under strictly anaerobic conditions. The cell pellet was suspended in 40 mL of buffer A (50 mM HEPES, pH 7.5, 300 mM NaCl), sonicated and lysate clarified by centrifugation at 40,000 rpm at 4 °C for 40 min. The supernatant was collected and passed over nickel-charge IMAC column (HisTrap™ HP 5mL GE Healthcare). Columns were washed with 4 volumes of buffer A. RumMc1 was eluted from nickel-charge IMAC columns with a gradient of 0-50% of buffer B (50 mM HEPES, pH 7.5, 300 mM NaCl, 500 mM imidazole). Fractions containing RumMc1 were pooled and concentrated in a 30,000 MWCO filter in an Amicon® Ultra centrifugal filter devices. To eliminate imidazole and salts, sample was passed on NAP™ Column, NAP-25 equilibrated in buffer C (HEPES 50mM, NaCl 100 mM pH 7.5). Anaerobic UV-visible spectra were recorded on an Uvikon XL100 spectrophotometer (Bio-Tek instruments) connected by optical fibers to the cuvette holder in the anaerobic chamber. The protein concentration was estimated by UV-visible spectroscopy by using an extinction coefficient at 280 nm of 73266 M⁻¹.cm⁻¹. Iron content of RumMc1 samples were measured according to the Fish method (ref). The calibration curve was obtained by measuring iron standards with iron content from 2 to 30 nmol.

Site directed mutagenesis of *rumC1* and heterologous expression of RumC1 variant. Site directed mutagenesis of the *MBP-rumC1* construct was performed to produce the Ala18/Ala19 variant of RumC1. Mutagenesis was done by following the instructions from the Q5 Site-Directed Mutagenesis Kit (New England BioLabs®). The NEBaseChanger tool was used to generate the 2 primer sequences (5'-CCATAACGCGGCTGCGGCGTACTGCG, 5'-CTGTTCGCAACCGCGGTG) and annealing temperatures. Template plasmids were digested using DpnI and were transformed into competent Top10 cells. The mutant plasmids were recovered from cells by using the Wizard® Plus SV Minipreps DNA Purification System (Promega). Production and purification of RumC1-Ala18/Ala19 variant were performed as previously described for RumC1 (2).

Leader-peptide chemical synthesis

Chemicals

The N-fluorenylmethoxycarbonyl (Fmoc)-protected amino acids, rink amide MBHA resin (100 - 200 mesh) and 2-(1H-Benzotriazole-1-yl)-1,1,3,3-tetramethyluronium hexafluorophosphate (HBTU) were obtained from Novabiochem; N,N-diisopropylethylamine (DIEA), trifluoroacetic acid (TFA), anisole, thioanisole, 1,2-ethanedithiol, acetic anhydride, piperidine and triethylamine (TEA) were from Sigma-Aldrich. All the other chemicals and solvents (N,N-dimethylformamide

(DMF), diethyl ether, dichloromethane (DCM), acetonitrile (ACN) and N-methyl-2-pyrrolidone (NMP) were from different commercial sources (highest available grade) and used without further purification.

Peptide synthesis

The leader sequence of RumC1 peptide ($\text{H}_2\text{N-MRKIVAGKLQTGADFEGSK-NH}_2$) was prepared by solid phase peptide synthesis in an Initiator⁺ Alstra automated microwave assisted synthesizer (Biotage). The peptide was assembled on a rink amide MBHA resin (0.25 mmol scale, 0.59 mmol/g) using standard Fmoc methodologies (9). Namely, the amino acids (4 equiv) were coupled using HBTU (3.9 equiv) as coupling agent, DIEA as base (8 equiv) and DMF as solvent. The removal of the Fmoc protecting groups was always done by treating the resin with 20% piperidine in DMF solution. After assembling, the peptide was manually deprotected and cleaved from the resin by treatment with the mixture TFA/thioanisole/anisole/1,2-ethanedithiol (%v/v = 90:5:3:2) for 2 h at room temperature and under nitrogen. The resin was filtered out and rinsed with TFA. The filtrate and rinses were combined, reduced under a nitrogen stream and slowly added to cold diethyl ether with magnetic stirring to precipitate the crude peptide. The suspension was transferred to a centrifuge to recover the peptide which was washed with cold diethyl ether and centrifuged again. This step was repeated several times and finally the crude peptide was dissolved in the minimum amount of water and lyophilized. The crude peptide was purified by preparative reversed-phase HPLC in a Phenomenex Jupiter column (250 mm \times 21.20 mm, 15 μm , 300 Å) using solvent A (99.9% water/0.1 % TFA) and solvent B (90% ACN/9.9% water/0.1 % TFA). The leader sequence of RumC1 peptide was eluted with a linear gradient from 15% to 35% B in 30 min at a flow rate of 10 mL/min (R_t = 14 min). Its purity was checked by analytical reversed-phase HPLC (Phenomenex Jupiter column, 250 mm \times 4.6 mm, 15 μm , 300 Å) and it was greater than 95%. The peptide was characterized by Electrospray Ionization-Mass spectrometry (ESI-MS) in positive mode using a Waters Synapt G2 HDMS (Manchester, UK) equipped with an ESI source employing the following parameters: ESI capillary voltage: +2.8 kV; extraction cone voltage: +20 V; desolvation gas (N_2) flow: 100 L.h^{-1} ; source temperature: 35 °C. Sample solutions were introduced in the ionization source at a 10 $\mu\text{L.min}^{-1}$ flow rate using a syringe pump.

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In Vitro Enzyme Assay. The *in vitro* enzymatic assays were performed in 100 μl of 100 mM HEPES, pH 7.5, in the presence of 100 μM of the desired peptide substrate, 25 μM of RumMc1 protein, 0.25 mM SAM and 1 mM dithionite. The assays were carried out at 37 °C during 3h under anaerobic conditions. The reactions were stopped by air exposure and were flash frozen in liquid nitrogen.

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EPR and Mössbauer spectroscopies. EPR and Mössbauer samples (400 μM) were prepared and flash frozen under anaerobic conditions. When needed, cluster reduction was achieved in 1 hour by addition of 10 mM dithionite. Samples in the presence of SAM were prepared with 3 mM SAM. EPR spectra were recorded on a Bruker EMX spectrometer operating at X-band frequency equipped with an Oxford instrument ESR 900 flow cryostat. Spectra were recorded with a microwave frequency 9.65 GHz under saturated (10K, 39dB, modulation amplitude 10 G) and non-saturated (6K, 13dB, modulation amplitude 10 G) conditions for the $g = 2$ region. Simulations were performed using Easy Spin toolbox for matLAB. Mössbauer spectra were recorded in transmission mode with a conventional Mössbauer spectrometer which was operated in the constant acceleration mode in conjunction with a multi-channel analyzer in the time-scale mode (WissEl GmbH). The spectrometer was calibrated against α -iron at room temperature. Experiments at 77 K were conducted using a flow cryostat (Optistat^{DN}, Oxford Instruments). Field-dependent Mössbauer spectra were obtained with a helium closed-cycle cryostat (CRYO Industries of America, Inc.) equipped with a superconducting magnet (10). The magnetic field was aligned parallel to the γ -ray beam. The spectral data were transferred from the multi-channel analyzer to a PC for further analysis employing the public domain program Vinda (11) running on an Excel 2003[®] platform. Analysis of the spectra was performed by least-squares fits using Lorentzian line shapes with the linewidth Γ . Field-dependent spectra were simulated by means of the spin Hamilton formalism (12).

Nano-LC–MS/MS Analyses. RumC1 samples were generally injected at a concentration of 0.1 μM . Samples were diluted in 5% (v/v) acetonitrile and 0.1% (v/v) trifluoroacetic acid and analysed by online nano-LC–MS/MS (NCS HPLC, Dionex, and Qexactive HF, Thermo Fisher Scientific). Peptides were sampled on a 300 $\mu\text{m} \times 5$ mm PepMap C18 precolumn and separated on a 75 $\mu\text{m} \times 250$ mm C18 column (PepMap, Dionex). The nano-LC method consisted of a 40 min gradient at a flow rate of 300 nL/min, and MS and MS/MS data were acquired using Xcalibur (Thermo Fisher Scientific). In order to improve the quality of the MS/MS spectra we performed parallel reaction monitoring (PRM) experiments to characterize RumC1 species. According to our previous characterization of RumC1 (Chiumento et al., 2019), we decided to focus these analyses on the highest m/z ions for the long (with leader peptide) and short (without leader peptide) peptides (respectively $m/z = 1120$ (6^+) and $m/z = 1083$ (4^+)). The m/z window was open at 4 units in order to consider modified species. The collision energy was set to 27.

897 The MS interpretations were done on the basis of previously annotated spectra and specific
898 fragmentation pattern of thioether bridges using HCD (2). Mascot (version 2.6) was also used for
899 the confirmation of the modifications, as previously described (2).

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901 **Stability assays.** Stability of RumC1 was evaluated after incubation varying pH, temperatures, and
902 in human serum. RumC1 was incubated in phosphate-buffered saline (PBS) at pH range from 2 to
903 11 at a volume ratio of 1:1 for 1 hour at room temperature. In a second assay RumC1 was incubated
904 at temperatures of 70, 80, 90 and 100 °C for 5, 15, 30 or 60 minutes before being cooled on ice.
905 Finally, RumC1 was incubated in human serum (Sigma Aldrich) at a volume ratio of 1:1 for 4 or
906 24 hours at 37°C with stirring (180 rpm). After each of this treatment, Minimal Inhibitory
907 Concentrations (MIC) were determined against *Clostridium perfringens* ATCC13124 in Brain
908 Heart Infusion broth supplemented with yeast extract (5 g/L) and hemin (5 mg/L) (BHI-YH) as
909 described (2). MIC of untreated RumC1 was used to set the maximum of antimicrobial activity and
910 calculate the residual activity of each treated RumC1. Stability and activity of RumC1 was also
911 measured in physiological and higher concentration of salts: MIC of RumC1 was determined as
912 above but the BHI-YH medium was replaced with Mueller Hinton (MH) broth supplemented in
913 either NaCl at 100, 200, and 300 mM or in MgCl₂ at 1, 2 and 3 mM. For the stability to salts assays,
914 MIC of untreated RumC1 in MH broth was used as the maximum of antimicrobial activity.

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916 **Simulated gastro-intestinal digestion of RumC1.** RumC1 was treated with pepsin (Sigma-
917 Aldrich) with a molecular ratio of 1:2.5 (RumC1:pepsin) at 37°C in sodium acetate 50 mM pH 2.5
918 for 2 hours with stirring (180 rpm) to mimic the digestive conditions occurring in the human
919 stomach. To stop the enzymatic reaction of pepsin, NaHCO₃ 1M was added until pH 7 was reached.
920 To simulate the intestinal compartment, RumC1 was incubated with pancreatin (Sigma-Aldrich)
921 with a molecular ratio of 1:5 (RumC1:pancreatin) at 37°C in sodium acetate 50 mM pH 6.5 for 5
922 hours with stirring (180 rpm). Then Phenylmethanesulfonyl fluoride (PMSF, Sigma-Aldrich) was
923 added to a final concentration of 0.1 mM to inhibit the action of pancreatin. MIC of treated RumC1
924 was determined against *C. perfringens* ATCC13124 in BHI-YH as described (2) after controlling
925 that the enzymes in the above conditions without RumC1 showed no anti-*C. perfringens* activity.
926 MIC of untreated RumC1 was used to set the maximum of antimicrobial activity and calculate the
927 residual activity of each treated RumC1. Furthermore, RumC1 was detected by RP-C18-HPLC
928 using an analytical column Jupiter 15-µm C18 300 Å (250 mm by 21.2 mm; Phenomenex). Elution
929 was performed at 1 ml/min with a 0 to 40% linear gradient of 90% ACN and 0.1% TFA for 30 min.
930 Finally, mass spectrometry analysis were conducted to compare the molecular masses of digested

RumC1 and untreated RumC1. As it has been reported that the bacteriocin nisin is digested by pancreatin but not by pepsin (13), nisin (from Sigma-Aldrich) was used as a positive control of the enzymatic activity of pancreatin only. To validate pepsin activity, Bovine Albumine Serum (BSA, Sigma-Aldrich) was used as a positive control.

Antimicrobial activity on human intestinal epithelium models. Caco-2 (ATCC HTB-37) and T84 (ATCC CCL-248) cells were being used as models of small intestinal and colonic epithelial cells, respectively. Cells were cultured in Dulbecco's modified essential medium (DMEM) supplemented with 10 % foetal calf serum (FCS), 1 % L-glutamine and 1 % Streptomycin-Penicillin antibiotics (all from Invitrogen). Cells were routinely seeded and grown onto 25 cm² flasks maintained in a 5 % CO₂ incubator at 37 °C. To test the influence of human intestinal epithelial cells on RumC1 activity, cells grown on 25 cm² flasks were detached using trypsin–EDTA solution (from Thermo Fisher Scientific), counted using Mallasez counting chamber and seeded into 96-well cell culture plates (Greiner bio-one) at approximately 10⁴ cells per well. Cells were grown for 7-10 days until differentiation. The culture medium was then replaced twice with DMEM supplemented with 10% FCS but free of phenol red and of antibiotics 24h and 48h to make sure any trace of antibiotics was removed prior to the infection with *B. cereus*. A suspension of *B. cereus* DSM31 was prepared in the same media at a final concentration of 5.10⁵ CFU/mL and added or not to Caco-2 and T84 monolayers. RumC1 was added 30 min before or at the same time or after the bacterial cells. Microplates were incubated for 24h at 37°C with 5% CO₂. Minimum inhibitory concentration (MIC) was defined as the lowest concentration of peptide that inhibited the growth of bacteria. Independent triplicate were made and sterility and growth controls were prepared for each assay.

MIC determination. Strains tested were acquired from commercial collections (the American Type Culture Collection (ATCC), www.atcc.org; the Collection de l'Institut Pasteur (CIP), www.pasteur.fr), from a laboratory collection (Centre National de Référence de la résistance aux antibiotiques, www.cnr-resistance-antibiotiques.fr) or from clinical sampling. *C. perfringens* CP24, 56, 60 were isolated from chickens and provided by UGent (14). Human clinical strains were mostly isolated from bloodstream infections, and in bone and joint infection at the University hospital of Besançon (France). The MIC were determined by broth microdilution for fastidious organisms (*Streptococcus pneumoniae*, *Listeria monocytogenes*, and *Bacillus cereus*), and non-fastidious organisms (*Enterococcus* species) by independent triplicates according to the EUCAST 2019 recommendations except for the Clostridia (15). Briefly, a bacterial suspension of Clostridia

was grown in anaerobic conditions (in a Trexler-type anaerobic chamber without stirring) and adjusted in MH broth supplemented with 5% lysed horse blood and 20 mg/L β -nicotinamide adenine dinucleotide at 5.10^6 UCF/mL. Ninety microliters of cell suspension were transferred in a sterile F-bottom polypropylene 96-well microplates. Thus, ten microliters of sterile RumC1 or antibiotics used as control from 100 to 0.1 μ M by two-fold serial dilutions were added to the bacterial suspension to obtain a final concentration of 5.10^5 CFU/mL. Microplates were incubated 48h at 37°C in anaerobic conditions. MIC was defined as the lowest concentration of peptide that inhibited the growth of bacteria after 48h incubation at 37°C. Sterility and growth controls were prepared for each assay.

Macromolecules synthesis studies. *C. perfringens* ATCC 13124 was grown in BHI-YH broth (2) in airtight jars in the presence of anerobic atmosphere generation bags (Sigma-Aldrich) without stirring at 37°C until OD_{600 nm} reached 0.2. Then RumC1 or metronidazole or antibiotics with known mechanisms of action were added at 5xMIC. The antibiotics gemifloxacin, rifampicin, tetracycline and vancomycin were used as controls for the inhibition of DNA, RNA, protein and peptidoglycan synthesis, respectively. After 15 min of incubation at 37°C in anaerobic conditions, samples were labelled with [methyl-3H]thymidine or [5,6-3H]uridine or L-[4,5-3H(N)]-leucine or D-[1-3H] HCl glucosamine (all from Hartmann Analytic) at 10 μ Ci/mL to follow the synthesis of DNA, RNA, proteins and peptidoglycan respectively. After 45 min of incubation at 37°C in anaerobic conditions, bacterial cells were lysed and the macromolecules were precipitated with ice cold trichloroacetic acid (TCA, Sigma-Aldrich) at a final concentration of 20%; samples were kept on ice for an hour. Then the precipitates were filtered on Whatman glass microfiber filters pre-soaked in ice cold TCA 5%. After washing the filters with ice cold TCA 5% twice and then ice cold absolute ethanol once, they were soaked in 10 mL of scintillation liquid (Ultima Gold, PerkinElmer). Radioactivity was measured by liquid scintillation counting (TriCarb2800, PerkinElmer). As each condition displayed different growth rates, the radioactivity counts were normalized by the OD_{600 nm} of the samples. Results were expressed as a percentage of total macromolecule synthesis that was measured for each macromolecule with untreated cells. All experiments were done in independent triplicates.

ATP bioluminescent assays. *C. perfringens* ATCC 13124 was grown in BHI-YH broth (2) in anaerobic conditions (in a Trexler-type anaerobic chamber without stirring) at 37°C until OD_{600 nm} reached 0.4. Then *C. perfringens* cells were distributed in white polystyrene Nunc™ 96-well plate (ThermoFisher Scientific) and RumC1, metronidazole or nisin were added at 2.5, 5 or 10xMIC.

999 After 15 min of incubation in the same conditions, 100 μ L of cells were mixed with 10 μ L of
1000 luciferin-luciferase reagent (Yelen Analytics) prepared in IMI-Yelen Buffer (Yelen Analytics). The
1001 mix was homogenized and incubated 30 s before reading of the emitted photon using a microplate
1002 reader (Synergy Mx, BioTek). Then, 10 μ L of lysis reagent (Yelen Analytics) was added to the
1003 mixture, homogenized and incubated 1 min before a new reading of the emitted photon. The
1004 intensity of the bioluminescent light was expressed as relative light units (RLU) which is
1005 proportional to extracellular ATP concentration (16). The inner ATP concentration was derived
1006 from the difference in ATP concentration in the extracellular media before and after cell lysis.
1007 Results were expressed as a percentage of total inner ATP concentration that was measured with
1008 untreated cells. All experiments were done in independent triplicates.

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1010 ***Ex-vivo* evaluation of the RumC1 innocuity using human intestinal explants.** In order to
1011 evaluate the innocuity of RumC1 peptide for the human gut, *ex-vivo* experiments were performed
1012 using human explants as previously described (17). Human intestinal tissues, corresponding to
1013 ileocecal area, were obtained from patients undergoing surgery at the unit of gastrointestinal
1014 surgery, Hospital Laveran (Marseille, France), according to a collaborative “clinical transfer”
1015 project. The procedure was approved by the French ethic committee (CODECOH n° DC-2019-
1016 3402). All patients agreed for the use of their tissues for research purposes. Diagnoses leading to
1017 surgery were intestinal carcinoma. Samples were taken from macroscopically unaffected area as
1018 identified by the surgeons. After resection, the tissues were placed in ice-cold oxygenated sterile
1019 DMEM solution containing 1% (w/v) streptomycin/penicillin solution and 50 μ g/mL gentamycin
1020 and were directly transferred to the laboratory within 15 min. Intestinal tissues were extensively
1021 washed and maintained in ice-cold culture media. Tissues were cleaned under binocular microscope
1022 from vascular vessels and conjunctive tissue using forceps. Intestinal explants (diameter of 0.5 cm²)
1023 were then isolated from the cleaned resections using surgical punch, the complete procedure being
1024 complete in less than 2 h after the resections were obtained from the surgery unit. Finally, the
1025 explants were washed 3 times with culture media without antibiotics and transferred into 24-well
1026 plates before being incubated at 37°C during 4 h with RumC1 peptide diluted in DMEM media at
1027 100 μ M. In parallel, explants were left untreated (negative controls) or were incubated with the 300
1028 μ M of detergent cetyl trimethylammonium bromide (CTAB) used as positive control of tissue
1029 damages. After incubation, the explants were collected, washed three times with PBS²⁺ and fixed
1030 overnight at 4°C with PFA diluted at 4% (v/v) in PBS. The next day, intestinal explants were
1031 washed twice with PBS and included in inclusion medium (TFM - EMS), in transverse position to
1032 allow cutting respecting the crypt-villus axis using cryostat (Leica CM3050). Four sections of 5

1033 μm thickness were obtained per explant and each section being separated from the next by 100 μm
1034 in order to cover all the tissue. Explants were then stained using hematoxylin and eosin (H&E)
1035 staining protocol. Briefly, samples were incubated for 8 min in hematoxylin (from Sigma-Aldrich)
1036 and then allowed to stain by incubation with water for 2 min. Then explants were incubated for 1
1037 min in eosin (from Sigma-Aldrich) and then in water for 1 min. This was followed by incubation
1038 of explants with ethanol at concentration of 70% then 95% and finally 100% for 2 min each. After
1039 blotting excess ethanol, intestinal explants were incubated for 15 min with xylene and mounted
1040 with coverslip using Eukitt mounting media (EMS, Hatfield, PA, USA). Finally, explants were left
1041 overnight to dry before examination of tissue organization under the microscope (Leitz DMRB
1042 microscope (Leica) equipped with Leica DFC 450C camera) (18).

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1044 SI References

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- 1046 1. B. H. Huynh, *et al.*, On the active sites of the [NiFe] hydrogenase from *Desulfovibrio gigas*.
1047 Mössbauer and redox-titration studies. *J. Biol. Chem.* **262**, 795–800 (1987).
- 1048 2. S. Chiumento, *et al.*, Ruminococcin C, a promising antibiotic produced by a human gut
1049 symbiont. *Sci. Adv.* **5**, eaaw9969 (2019).
- 1050 3. W. F. Vranken, *et al.*, The CCPN data model for NMR spectroscopy: development of a
1051 software pipeline. *Proteins* **59**, 687–696 (2005).
- 1052 4. P. Güntert, C. Mumenthaler, K. Wüthrich, Torsion angle dynamics for NMR structure
1053 calculation with the new program DYANA. *J. Mol. Biol.* **273**, 283–298 (1997).
- 1054 5. G. Cornilescu, F. Delaglio, A. Bax, Protein backbone angle restraints from searching a
1055 database for chemical shift and sequence homology. *J. Biomol. NMR* **13**, 289–302 (1999).
- 1056 6. K. E. Kawulka, *et al.*, Structure of subtilisin A, a cyclic antimicrobial peptide from *Bacillus*
1057 *subtilis* with unusual sulfur to alpha-carbon cross-links: formation and reduction of alpha-
1058 thio-alpha-amino acid derivatives. *Biochemistry* **43**, 3385–3395 (2004).
- 1059 7. C. S. Sit, M. J. van Belkum, R. T. McKay, R. W. Worobo, J. C. Vederas, The 3D Solution
1060 Structure of Thurincin H, a Bacteriocin with Four Sulfur to α -Carbon Crosslinks. *Angew.*
1061 *Chem. Int. Ed.* **50**, 8718–8721 (2011).
- 1062 8. C. S. Sit, R. T. McKay, C. Hill, R. P. Ross, J. C. Vederas, The 3D structure of thuricin CD,
1063 a two-component bacteriocin with cysteine sulfur to α -carbon cross-links. *J. Am. Chem. Soc.*
1064 **133**, 7680–7683 (2011).
- 1065 9. W. C. Chan, P. D. White, Eds., *Fmoc solid phase peptide synthesis: a practical approach*
1066 (Oxford University Press, 2000).
- 1067 10. A. Janoschka, G. Svenconis, V. Schünemann, A closed cycle-cryostat for high-field
1068 Mössbauer spectroscopy. *J. Phys. Conf. Ser.* **217**, 012005 (2010).
- 1069 11. H. P. Gunnlaugsson, Spreadsheet based analysis of Mössbauer spectra. *Hyperfine Interact.*
1070 **237**, 79 (2016).
- 1071 12. V. Schünemann, H. Winkler, Structure and dynamics of biomolecules studied by Mössbauer
1072 spectroscopy. *Rep. Prog. Phys.* **63**, 263–353 (2000).
- 1073 13. B. Jarvis, R. R. Mahoney, Inactivation of Nisin by Alpha-Chymotrypsin. *J. Dairy Sci.* **52**,
1074 1448–1450 (1969).
- 1075 14. A. R. Gholamiandekhordi, R. Ducatelle, M. Heyndrickx, F. Haesebrouck, F. Van Immerseel,
1076 Molecular and phenotypical characterization of *Clostridium perfringens* isolates from
1077 poultry flocks with different disease status. *Vet. Microbiol.* **113**, 143–152 (2006).
- 1078 15. , v_9.0_Breakpoint_Tables.pdf (December 12, 2019).

1079 16. E. W. Chappelle, G. V. Levin, Use of the firefly bioluminescent reaction for rapid detection
1080 and counting of bacteria. *Biochem. Med.* **2**, 41–52 (1968).

1081 17. E. H. Ajandouz, *et al.*, Hydrolytic Fate of 3/15-Acetyldeoxynivalenol in Humans: Specific
1082 Deacetylation by the Small Intestine and Liver Revealed Using in Vitro and ex Vivo
1083 Approaches. *Toxins* **8** (2016).

1084 18. H. Olleik, *et al.*, Temporin-SHa and Its Analogs as Potential Candidates for the Treatment
1085 of *Helicobacter pylori*. *Biomolecules* **9**, 598 (2019).

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