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Research Article

Outer membrane translocation of pyocins via the copper regulated TonB-dependent transporter CrtA

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Pseudomonas aeruginosa is a common cause of serious hospital-acquired infections, the leading proven cause of mortality in people with cystic fibrosis and is associated with high levels of antimicrobial resistance. Pyocins are narrow-spectrum protein antibiotics produced by *P. aeruginosa* that kill strains of the same species and have the potential to be developed as therapeutics targeting multi-drug resistant isolates. We have identified two novel pyocins designated SX1 and SX2. Pyocin SX1 is a metal-dependent DNase while pyocin SX2 kills cells through inhibition of protein synthesis. Mapping the uptake pathways of SX1 and SX2 shows these pyocins utilize a combination of the common polysaccharide antigen (CPA) and a previously uncharacterized TonB-dependent transporter (TBDT) PA0434 to traverse the outer membrane. In addition, TonB1 and FtsH are required by both pyocins to energize their transport into cells and catalyze their translocation across the inner membrane, respectively. Expression of *PA0434* was found to be specifically regulated by copper availability and we have designated PA0434 as Copper Responsive Transporter A, or CrtA. To our knowledge these are the first S-type pyocins described that utilize a TBDT that is not involved in iron uptake.

Introduction

Pseudomonas aeruginosa is a major cause of serious hospital-acquired infections with treatment frequently complicated by high levels of antibiotic resistance with broad-resistance to β-lactams, aminoglycosides and fluoroquinolones and growing resistance to carbapenems observed globally [1]. The World Health Organization (WHO) lists *P. aeruginosa* in the highest threat level of 'critical' for bacterial pathogens for which new antibiotics are urgently required [2].

Protein bacteriocins, such as pyocins, are narrow-spectrum antibiotics that kill bacteria closely related to the producing strain and play a key role in colonization and competition in bacterial communities [3,4]. One potential advantage of utilizing bacteriocins as therapeutic antibiotics is the ability to target a specific pathogen while avoiding collateral damage to the microbiota. This approach may enable antibiotic therapy without common complications associated with broad-spectrum antibiotics, such *Clostridium difficile* infection and domination of the microbiota with broadly drug-resistant pathogens that may subsequently disseminate to cause serious systemic infection [5–7]. In addition, there is growing concern that alteration of the microbiota, including that induced by the use of broad-spectrum antibiotics, may increase the risk of developing a range of chronic inflammatory diseases [8].

P. aeruginosa can produce a diverse range of pyocins. The soluble or S-type pyocins are multi-domain proteins produced by *P. aeruginosa* to kill strains of the same species. S-type pyocins share basic characteristics including homologous cytotoxic domains with the well-studied colicins of *E. coli* [9]. Most characterized pyocins display a nuclease activity which targets DNA (S1, S2, S3, S8, Sn and AP41), rRNA (S6) or tRNA (S4 and SD2) [10,11]. In addition, pyocin S5 is a pore-forming toxin and

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pyocin M inhibits peptidoglycan synthesis through the degradation of lipid II [12,13]. Nuclease pyocins are normally co-expressed with immunity proteins that bind tightly to the cytotoxic domain to protect the producing strain from self-intoxication [14,15].

A number of recent structural and functional studies have enabled the elucidation of a common domain structure for the S-type pyocins and have enabled domains to be assigned to specific binding partners of the target bacterial cell envelope [11,13,16]. In particular, the structure of pyocin S5 revealed an elongated structure with two structurally similar domains consisting of a kinked three-helix bundle (kTHB) N-terminal to the globular pore-forming cytotoxic domain [13]. The binding partners of the two kTHB domains of pyocin S5 were ascertained through determining the ability of truncated pyocin S5 variants with each kTHB domain deleted to bind the known cell surface targets of this pyocin, the TonB-dependent transporter (TBDT) FptA and the common polysaccharide antigen (CPA) [11,17]. For pyocin S5, the transporter binding domain is formed by the N-terminal kTHB which mediates the interaction with FptA. Similar to other identified pyocin transporters, the normal physiological role of FptA is in iron acquisition through transport of the iron-siderophore ferripyochelin across the outer membrane [17]. Interestingly, pyocin S2 also utilizes an N-terminal kTHB domain to mediate its interaction with the TBDT FpvAI [16]. The second kTHB domain of pyocin S5 binds the CPA. Interestingly, initial contact with the cell surface for multiple S-type pyocins, including S5, SD2 and S2 and the unrelated L-type pyocin L1, is through binding the CPA [11,13,18]. For pyocins S5, SD2 and S2 the CPA binding domains share high levels of sequence similarity indicating a common mechanism of CPA binding through a kTHB domain [11]. The CPA is a homopolymer of the rare deoxyhexose D-rhamnose that is not widely distributed in nature, with L-rhamnose being predominant. The CPA is therefore a useful generic receptor for diverse pyocins to target *P. aeruginosa*, enabling their accumulation on the cell surface.

Parasitization of iron uptake pathways by pyocins extends to the energization of transport by the TonB1–ExbB–ExbD complex which services a repertoire of outer membrane TBDTs to energize outer membrane transport. In the case of pyocins, this system is hijacked through the presence of an N-terminal TonB-binding motif that directly binds to the C-terminal domain of TonB1, energizing translocation directly though the lumen of the cognate TBDT [13,16]. In the case of the pore-forming pyocin S5, transport to the periplasm is sufficient for the C-terminal cytotoxic domain to insert into and depolarize the inner membrane to kill the cell. For nuclease-type pyocins, an additional inner membrane translocation domain is required to mediate transport to the cytoplasm where its nucleic acid substrate is located [19]. For pyocin G, inner membrane translocation has been shown to be dependent on both the AAA^{+}ATPase/protease FtsH and TonB1 [19].

In this study, two novel pyocins, namely SX1 and SX2, were identified and characterized. Both pyocins display potent killing activity against *P. aeruginosa* PAO1. However, only pyocin SX2 affords effective protection in a *Galleria mellonella* model of *P. aeruginosa* infection. *In vitro* experiments demonstrated that pyocin SX1 is a metal-dependent DNase. In contrast, pyocin SX2 did not show any DNase activity but inhibited protein synthesis in an *in vitro* transcription-translation assay. Mapping the uptake pathways of SX1 and SX2 shows these pyocins utilize the CPA as a cell surface receptor and a previously uncharacterized TBDT PA0434 as a translocator to cross the outer membrane. Interestingly, expression of *PA0434* was found to be regulated by copper availability hence we have designated PA0434 as Copper Responsive Transporter A, or CrtA.

Results

Discovery and domain organization of pyocins SX1 and SX2

To identify new pyocins we performed BLAST searches using the amino acid sequence of the pyocin S2 CPA binding and inner membrane translocation domains as query sequences [11,19]. Two genes encoding putative novel pyocins, designated pyocins SX1 and SX2, were identified in the genome sequences of *P. aeruginosa* LMG5031, also known as *P. aeruginosa* WH-SGI-V-07287 [20], and *P. aeruginosa* 2_1_26, respectively (Table 1). LMG 5031is a PA7-like strain isolated from the plant *Aglaonema commutatum* and *P. aeruginosa* 2_1_26 was isolated from the human gastrointestinal tract. Both putative pyocin genes are located downstream from a P-box element which is the regulatory sequence for production of many pyocins and upstream from genes encoding putative immunity proteins (Supplementary Table S1) [9].

The domain structures of pyocins SX1 and SX2 (Figure 1A) were deduced by sequence similarity with the well-characterized pyocin S2. Comparison of the SX1 and SX2 sequences with the sequence of pyocin S2, indicates high levels of sequence identity within the CPA binding domain and inner membrane translocation domains, but little identity within the transporter binding domain (Figure 1B). In addition, little sequence

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Table 1. Origin and characteristics of pyocins SX1 and SX2 and their immunity proteins

P. aeruginosa isolate	Pyocin/immunity protein	Accession number	Size	
			Amino acids	kDa
LMG5031	Pyocin SX1	KSR45004.2	684	74
	ImSX1	KSR45005.1	85	9.9
2_1_26	Pyocin SX2	EHF11209.1	696	76
	ImSX2	WP_083842350	87	10

identity between the transporter domains of pyocins SX1 or SX2 was observed with any of the characterized pyocins indicating they likely utilize a novel pyocin transporter. However, the transporter binding domains of pyocin SX1 and SX2 share 65% sequence identity indicating they may utilize the same unknown transporter. Further analysis showed that pyocin SX1 has a DNA-targeting HNH-nuclease cytotoxic domain that shares 63% amino acid identity with pyocin S2 whereas pyocin SX2 contains a pyocin G-like cytotoxic domain [19] (Figure 1B). A cytotoxic domain homologous to those of pyocin SX2 and pyocin G is present in carocin D and carocin S3 and from *P. carotovorum* and both of these bacteriocins have been reported to display DNase activity *in vitro* [21,22]. Based on the above analysis we predict that pyocins SX1 and SX2 utilize the CPA as their receptor and an unknown TonB-dependent receptor as their transporter.

In vitro and *in vivo* activity of pyocins SX1 and SX2

To determine if the putative pyocins SX1 and SX2 display killing activity against *P. aeruginosa* isolates and predicted DNase activity, we produced recombinant pyocins in complex with their cognate immunity proteins in *E. coli*. Pyocin SX1-ImSX1 and pyocin SX2-ImSX2 were isolated by Ni^{2+} affinity chromatography (via a C-terminal His_6-tag on their respective immunity proteins) and gel filtration chromatography (Figure 2A).

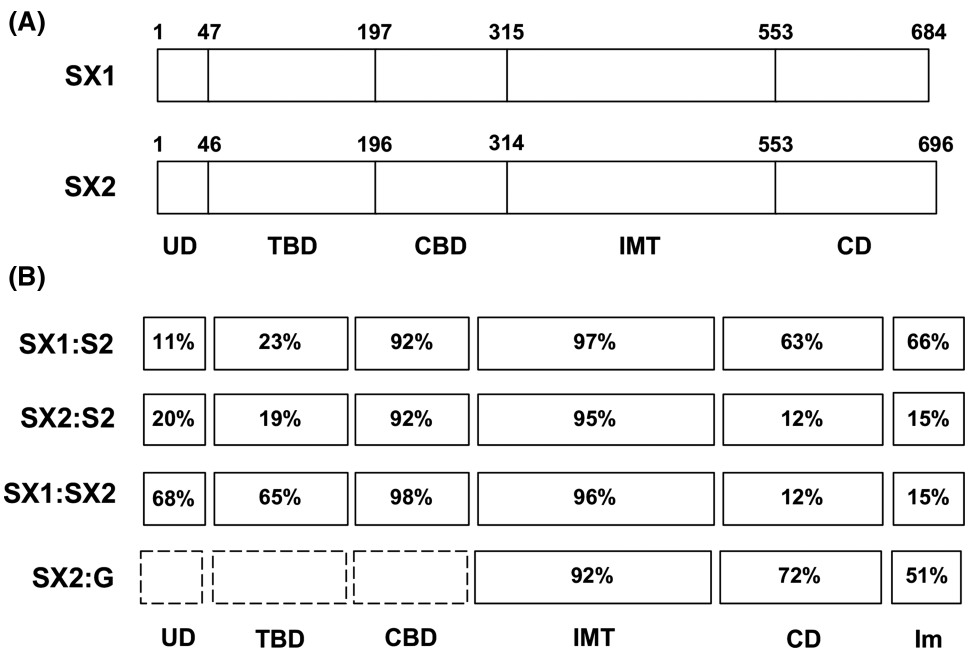

Figure 1. Amino acid sequence similarity of pyocins SX1 and SX2 with pyocins S2 and G and proposed domain architecture of pyocins SX1 and SX2.

(**A**) Percentage amino acid similarity for pyocins SX1/SX2 and their immunity protein (Im) with pyocin S2 and G. (**B**) Proposed domain architecture of pyocins SX1 and SX2 consisting of five domains including N-terminal unstructured domain (UD), transporter-binding domain (TBD), CPA-binding domain (CBD), inner membrane translocation domain (IMT) and cytotoxic domain (CD). Numbers above the boxes indicate amino acid positions.

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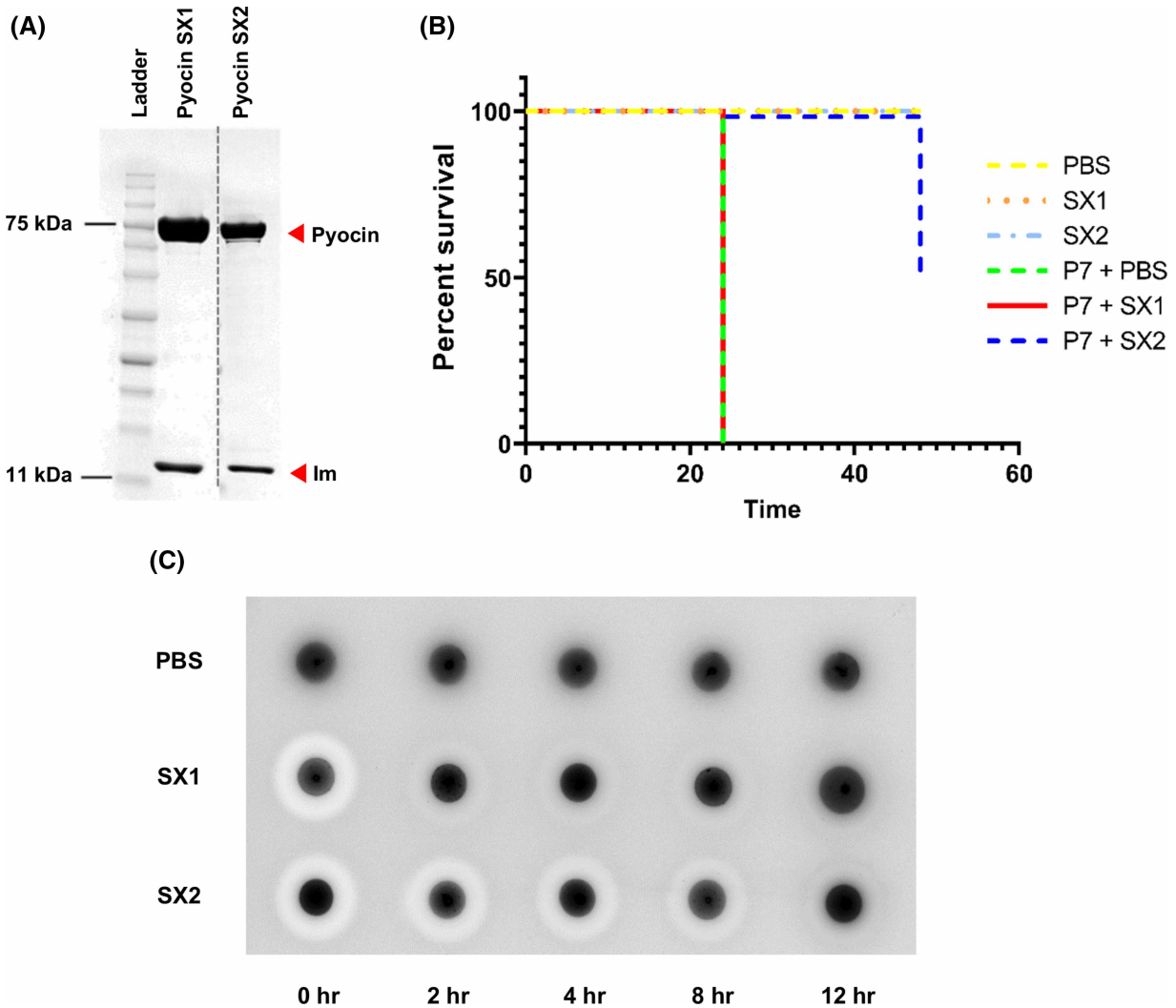

Figure 2. Purification and *in vivo* activity of pyocins SX1 and SX2.

(**A**) SDS–PAGE gel (12%) of purified pyocins SX1 and SX2 (74–76 kDa) and their immunity proteins (10 kDa). The dashed line indicates splicing of gels. (**B**) Survival plot for groups of larvae injected with PBS or pyocins alone and groups of larvae infected with *P. aeruginosa* P7 and treated with PBS or pyocins. Groups of 30 larvae were injected with ~10^4 CFU of *P. aeruginosa* P7 followed by either PBS (control), pyocin SX1 or SX2 (10 μg). The numbers of survivor were observed at 24 and 48 h after pyocin treatment. (C) Killing activity of pyocins SX1 and SX2 after injection into *G. mellonella* larvae. Groups of three larvae were injected with PBS (control) or the pyocins and were collected at different time point. Three larvae were pooled, homogenized in cold PBS and centrifuged. Five microliters of the clear fraction were spotted onto *P. aeruginosa* P7 cell lawn on a LB plate.

Both purified pyocins displayed potent killing activity against *P. aeruginosa* P7, using an overlay spot plate method on LB agar, with a minimum killing concentration of 0.051 μg/ml (0.6 nM) for SX1 and 0.457 μg/ml (5.3 nM) for SX2. Interestingly, pyocin SX2 also displayed efficacy in a *Galleria mellonella P. aeruginosa* infection model although pyocin SX1 did not (Figure 2B). Further analysis indicated that pyocin SX1 is relatively rapidly inactivated on administration to *G. mellonella* whereas SX2 retains its biological activity over an extended time period (Figure 2C).

To determine if pyocins SX1 and SX2 displayed their predicted nuclease activity against DNA, we separated the pyocins from their respective immunity proteins and tested their DNase activity in a plasmid-nicking assay. Similar to other HNH-DNase type pyocins, pyocin SX1 displayed a metal-dependent DNase activity. Pyocin SX1 was highly active in the presence of magnesium and nickel and able to completely degrade plasmid DNA, while in the presence of zinc a lower level of activity was observed (Figure 3A). In contrast, pyocin SX2 did not display DNase activity under any of the tested conditions (Figure 3B). This result is surprising given the

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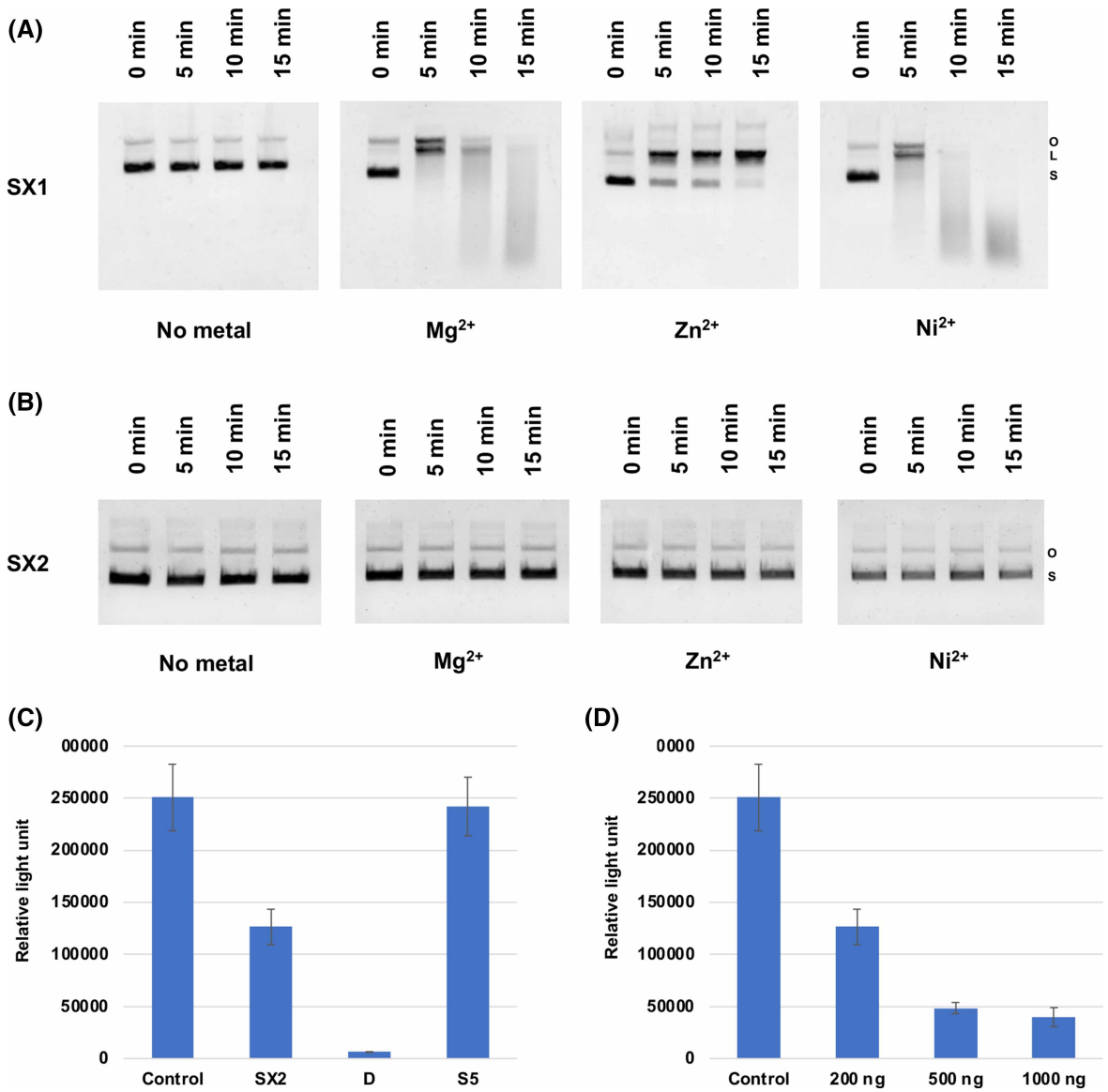

Figure 3. Molecular activities of pyocins SX1 and SX2. Plasmid nicking activity of pyocin SX1 and SX2.
One microgram of pUC18 DNA was incubated with 200 ng of pyocin SX1 (**A**) or SX2 (**B**) (immunity protein removed) in the presence different divalent metals. S, supercoiled DNA; L, linear DNA and O, open circle DNA. (**C**) *In vitro* transcription-translation of Renilla luciferase in the presence of 200 ng of different pyocins/colicin. (**D**) *In vitro* transcription-translation of Renilla luciferase in the presence of pyocin SX2 at different concentrations. The experiment was done with three replications. Error bars represent standard deviation of the mean. * indicate significant difference comparing to the untreated control (student's *t*-test, $P < 0.05$).

reported DNase activity of carocin D and carocin S3, which possess a cytotoxic domain homologous to that of pyocin SX2 [21,22]. To probe the activity of pyocin SX2 further, we tested its ability to inhibit protein synthesis in an *in vitro* transcription-translation assay. In this experiment, 200 ng of immunity protein-free pyocin SX2, colicin D, a tRNase used as a positive control, or pyocin S5, a pore-forming pyocin, used here as a negative control, were added to the transcription-translation assay. Pyocin SX2 and colicin D significantly lowered the production of the reporter protein, Renilla luciferase, by 50% and 97%, respectively, when compared with the untreated control. The negative control, pyocin S5, had little effect on luciferase production (Figure 3C). In addition, the effect on luciferase production with pyocin SX2 treatment was shown to be dose dependent

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(Figure 3D). These data indicate that the cytotoxic effect of pyocin SX2 is due to interference with either transcription or translation ultimately leading to reduced protein synthesis. However, the exact molecular target of pyocin SX2 remains unknown.

Identification of the receptor and transporter of pyocins SX1 and SX2

To date, all known S-type pyocins for which import mechanisms have been determined require a specific TBDT for translocation across the *P. aeruginosa* outer membrane. To identify the outer membrane transporter for pyocins SX1 and SX2, spontaneous resistant mutants were isolated by incubating late-stationary phase cells of *P. aeruginosa* PAO1 with pyocin SX1 or SX2 and plating on LB agar. The colonies grown after incubation were then picked and re-screened for pyocin sensitivity. In total, thirty spontaneous mutants isolated after pyocin SX1 or SX2 treatment were tested using spot tests for sensitivity against four pyocins: SX1, SX2, SD2 and L1 at 1 mg/ml. Testing against SD2 and L1 was performed to determine which isolates were likely to carry mutations that deplete or abolish CPA synthesis because both of these pyocins utilize the CPA as an outer membrane receptor [11,18]. Since both SX1 and SX2 appear to carry a CPA binding domain, it was hypothesized that mutant strains resistant or tolerant to all four pyocins were likely to be deficient in CPA production whereas mutant strains only resistant or tolerant to SX1/SX2 were putative SX1/SX2 transporter mutants.

Consistent with this strategy, genome sequencing of 4 putative CPA production mutants showed these strains carried mutations in either the *gmd* gene encoding GDP-mannose 4,6-dehydratase (GMD) or *PA5455* coding for a putative glycosyltransferase (Supplementary Table S2). Previous studies have shown that GMD is involved in CPA biosynthesis and *gmd* is located in the CPA O-antigen gene cluster together with other CPA biosynthesis genes such as *wzt* and *wzm* [23]. *PA5455* is located in a conserved gene cluster adjacent to the CPA O-antigen gene cluster. The protein produced from this gene is predicted to be a glycosyltransferase which is proposed to be involved in CPA biosynthesis and modification [24]. These data confirm that pyocins SX1 and SX2 utilize CPA as a receptor.

The genomes of four putative transporter mutants (resistant to both SX1 and SX2 but still sensitive to SD2 and L1) were sequenced and analyzed by comparing to the genome of the parent strain. All putative transporter mutants were found to carry nonsense mutations in the gene encoding the uncharacterized TBDT, PA0434. To confirm that PA0434 is the transporter for pyocins SX1 and SX2, both pyocins were tested against a *P. aeruginosa* strain (PAO1Δ*PA0434*) which contains a transposon insertion in *PA0434*. Both pyocins SX1 and SX2 were inactive against PAO1Δ*PA0434*; cell killing was restored after plasmid-based complementation indicating that PA0434 is the transporter for both pyocin SX1 and SX2 (Figure 4).

Generally, the uptake of substrates via TBDTs requires an energy-transducing TonB complex, consisting of TonB, ExbB, and ExbD proteins in the inner membrane. To determine if transport of pyocins SX1 and SX2 is Ton-dependent we tested their activity against strains lacking one of the three TonB proteins, TonB1, TonB2 or TonB3, encoded by the *P. aeruginosa* genome. TonB1 has previously been shown to play a key role in iron acquisition and although TonB2 is not required for iron acquisition, it has been shown that loss of both TonB1 and TonB2 leads to further impairment of growth under iron limiting conditions relative to the loss of TonB1 alone [25]. TonB3 has been shown to be required for twitching motility and pili assembly [25]. PAO1Δ*tonB1* was resistant to both pyocins SX1 and SX2 while PAO1Δ*tonB2* and PAO1Δ*tonB3* remained sensitive suggesting that pyocins SX1 and SX2 are TonB1 dependent (Supplementary Figure S1). In addition, previous studies have shown that an inner-membrane protein FtsH is required for killing of nuclease-type colicins as well as pyocin G. Both pyocins SX1 and SX2 were inactive against PAO1Δ*ftsH* indicating that these pyocins are also FtsH dependent (Supplementary Figure S1).

PA0434 is a copper responsive transporter

Killing by pyocins such as S5, SD2 and S2, which exploit iron-siderophore transporters, is enhanced under iron limiting conditions, where expression of the transporter is up-regulated [26]. To examine the effect of Fe(III) concentration on PA0434 expression, *P. aeruginosa* PAO1 was treated with pyocins SX1, SX2 or SD2, which utilizes the ferripyoverdine transporter FpvAI, under iron-rich (with 50 μM $FeCl_3$) and iron-limiting (with 200 μM 2,2′-bipyridine) conditions. Iron availability had little effect on sensitivity of PAO1 to pyocins SX1 and SX2 whereas sensitivity to pyocin SD2 was as expected inhibited by $FeCl_3$ and improved by bipyridine reflecting expression of the FpvAI transporter under these conditions (Supplementary Figure S2). These results suggest that the expression of PA0434 is independent of iron availability and so PA0434 likely does not play a role in iron uptake. Consistent with this, *PA0434* lacks an upstream Fur box (5′-GATAATGATAATCATTATC-3′)

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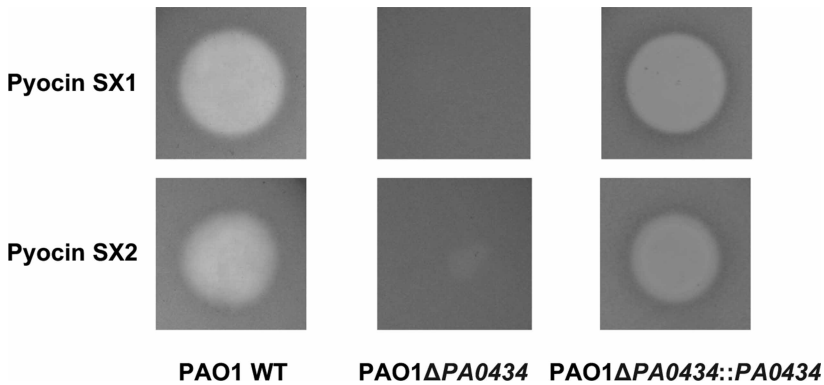

Figure 4. The TonB-dependent receptor PA0434 is required for pyocins SX1 and SX2 killing.
Five microliters of pyocin SX1 or SX2 (1 mg/ml) were spotted on to cell lawn of wild type *P. aeruginosa* PAO1 (PAO1 WT), PAO1 with transposon insertion in *PA0434* gene (PAO1Δ*PA0434*) and complement strain of PAO1Δ *PA0434* (PAO1Δ *PA0434*::*PA0434*).

which acts as the recognition sequence for the ferric uptake regulator (Fur) [27]. In *P. aeruginosa*, Fur controls both metabolism and virulence in response to iron availability including iron uptake via iron-siderophores [28]. Thus, PA0434 may be involved in the uptake of a molecule other than an iron-siderophore. To determine if pyocin sensitivity can be suppressed by other metal ions, reflecting repression of PA0434 expression, the effect of Zn(II), Mn(II), Ni(II) and Cu(II) ions on sensitivity of *P. aeruginosa* PAO1 to pyocins SX1 and SX2 was determined using the overlay spot plate assay. From the metal ions tested, only the presence of $CuSO_4$ decreased sensitivity of PAO1 to pyocins SX1 and SX2 while the addition of other metals did not (Figure 5A).

To confirm the specificity of the inhibitory effect of Cu(II), sensitivity of PAO1 to pyocins SX1 and SX2 was tested under a number of conditions. In these experiments, sensitivity to pyocins SX1 and SX2 was reduced when 1 mM $CuSO_4$ was added to the medium. Conversely, the killing activity of both pyocins was increased in the presence of triethylenetetramine (TETA), a high-affinity Cu(II) chelator (Figure 5B). $FeCl_3$, $ZnCl_2$, the Fe (III)-chelator bipyridine and the Zn(II)-chelator N,N,N′,N′-tetrakis(2-pyridylmethyl)ethylenediamine (TPEN) had little effect on the sensitivity of PAO1 to pyocins SX1 suggesting that expression of the TBDT PA0434 transporter is specifically dependent on Cu(II) availability (Figure 5C). In addition, sensitivity to pyocin SD2 was decreased by the addition of $FeCl_3$ and increased by the addition of bipyridine. The addition of $CuSO_4$ and $ZnCl_2$ did not affect sensitivity to pyocin SD2, reflecting the highly specific effect of iron availability on the expression of the iron-siderophore transporter FpvAI (Figure 5C). The killing activity of pyocin SD2 was modestly increased in the presence of TETA or TPEN. TETA and TPEN are recognized as selective copper and zinc chelators, respectively, although both chelators bind iron with a lower affinity [29,30]. Sensitivity to pyocin AP41 was not affected by the presence of any metal ions or metal ion chelators (Figure 5C). The pyocin AP41 transporter has not been identified but sensitivity to the pyocin is known to be independent of iron availability [26].

To confirm that the expression of *PA0434* gene is regulated by Cu(II), *P. aeruginosa* PAO1 was grown in liquid medium with different metals or metal-chelators for 8 h and the expression level of *PA0434* gene was determined by qPCR. The expression of *PA0434* decreased by 2.5-fold in the presence of 0.5 mM $CuSO_4$ and increased by 5.4-fold in the presence of 2 mM TETA. We also found that $FeCl_3$ and $ZnCl_2$ did not affect the expression of this gene suggesting that *PA0434* expression is specifically responsive to Cu(II) availability (Figure 6). A small increase in *PA0434* expression was observed in the presence of bipyridine and TPEN; however, the change in expression level was relatively small compared with TETA treatment (1.2- and 1.8-fold for bipyridine and TPEN, respectively). Expression of *fptA,* which is the gene coding for the outer-membrane transporter for Fe(III)-pyochelin and pyocin S5 was down-regulated in the presence of Fe(III) and up-regulated in the presence of bipyridine demonstrating the response of *fptA* expression to the presence of Fe(III). In addition, TETA and TPEN also triggered increased *fptA* expression, but at a lower level than bipyridine indicating the effect of non-specific chelation of iron by the copper and zinc chelators (Figure 6). Altogether, these results suggested that PA0434 is a Cu(II) responsive transporter and may play a role in Cu(II) transport. Thus, we named this transporter as **C**opper **R**esponsive **T**ransporter A or CrtA.

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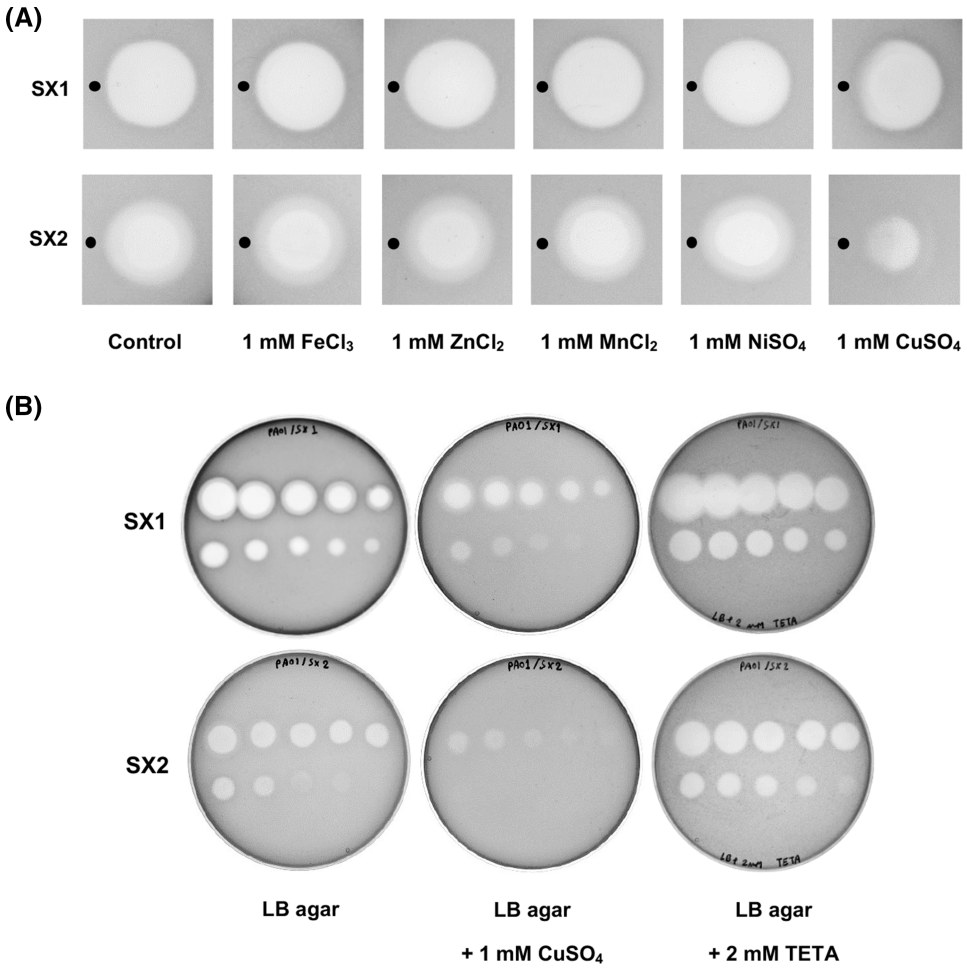

(C)

Pyocin	Treatment/ MIC (μg ml^{-1})						
	Control	1 mM $CuSO_4$	2 mM TETA	1 mM $ZnCl_2$	30 μM TPEN	1 mM $FeCl_3$	200 μM bipyridine
SX1	0.051	1.4	0.006	0.051	0.051	0.051	0.051
SD2	12.3	12.3	4.1	12.3	4.1	37	0.46
AP41	0.46	0.46	0.46	0.46	0.46	0.46	0.46

Figure 5. PA0434 expression specifically responds to Cu(II) availability.
(**A**) Overlay spot plate assay of pyocins SX1/SX2 with different metal compounds spotted adjacent to the pyocin. 5 μl of 1 mM metal solution were spotted onto LB plate overlaid with *P. aeruginosa* PAO1 alongside 5 μl of 1 mg/ml pyocin SX1 or SX2 (position of metal compound spot indicated by added black circle). The overlapping areas between $CuSO_4$ and pyocin spots showed decreased killing activity while other metals did not affect the killing zone indicating that Cu. (**B**) Overlay spot plate assay of pyocins SX1 and SX2 under normal condition (LB agar), copper-enriched conditions (LB agar + 1 mM $CuSO_4$) and copper-deficient conditions (LB agar + 2 μM TETA). (**C**) MIC of pyocins SX1, SD2 and AP41 against *P. aeruginosa* on LB agar supplemented with different metal compounds or metal-chelators. Increasing and decreasing MICs compared with the controls are highlighted in yellow, blue and gray.

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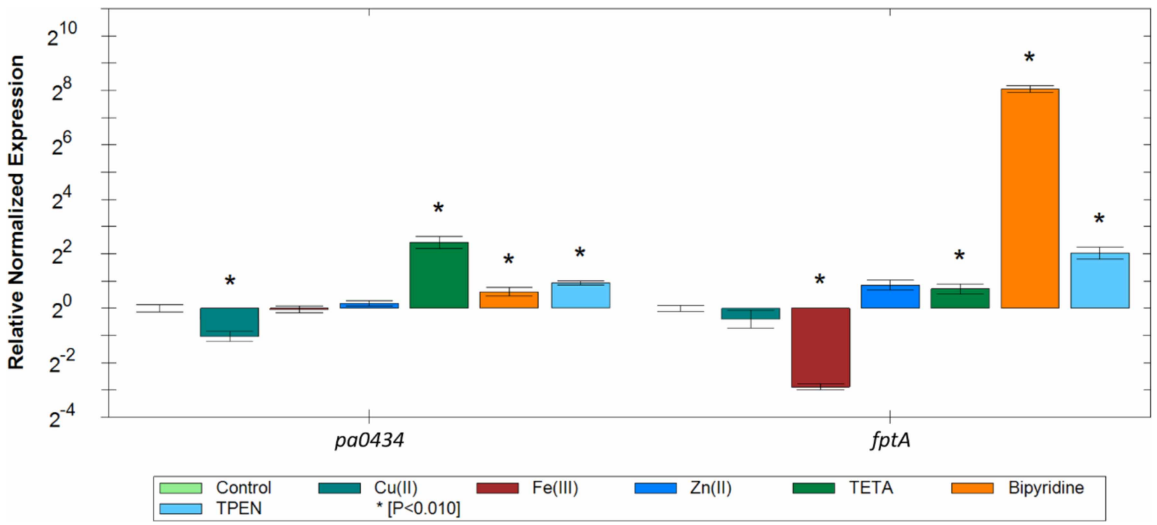

Figure 6. Analysis of the changes in the transcription of *pa0434* and *fptA* genes in *P. aeruginosa* cells grown with different metals or metal-chelators.

RT-qPCR was performed on *P. aeruginosa* PAO1 cells grown with different metals (0.5 mM $CuSO_4$, 0.5 mM $FeCl_3$ or 0.5 mM $ZnCl_2$) or metal-chelators (2 mM TETA, 200 μM bipyridine or 30 μM TPEN) for 8 h. Results are given as the relative normalized expression in a $\log_2$ scale. The data were normalized relative to the reference gene *rpsL* and are representative of three independent experiments. Error bar indicates standard error of the mean. * indicates significantly difference compared with the untreated control (*t*-test, $P < 0.010$).

Discussion

In this work, we describe the identification and characterization of two novel pyocins, SX1 and SX2. Pyocin SX1 was shown to be an active metal-dependent nuclease that targets DNA. In contrast, pyocin SX2 did not display any DNase activity but inhibited protein synthesis in an *in vitro* transcription-translation assay. This is a surprising result since carocin D and S3, which carry cytotoxic domains homologous to pyocin SX2 have been reported to display DNase activity. Well-characterized bacteriocins, including colicin E3 are known to know kill through a targeted nuclease activity against the 16S rRNA and others, such as colicin D and E5, through cleavage of specific tRNAs. Both these activities ultimately act to inhibit protein synthesis and it remains to be determined if pyocin SX2 also targets rRNA, tRNA or acts against a different component of the RNA or protein synthesis machinery.

Both pyocin SX1 and SX2 were found to utilize CPA as a cellular receptor and a novel TBDT, CrtA (PA0434) to target *P. aeruginosa* and cross the outer membrane. Interestingly, expression of CrtA was found to be regulated by the availability of copper, suggesting that in contrast with other identified pyocin transporters, which invariably target iron-containing siderophores or heme, CrtA likely plays a role in copper uptake. Based on these results and previous studies on pyocins S2, S5 and G, a model for the transport of pyocins SX1/SX2 across the *P. aeruginosa* cell envelope is proposed (Figure 7). To illustrate this mechanism, the structure of the pyocin SX2-ImSX2 complex was predicted using AlphaFold-multimer [31,32]. The predicted structure shows a highly elongated complex with the immunity protein bound to the cytotoxic domain, features typically associated with nuclease-type bacteriocins (Figure 7A). For pyocin SX2 the transporter and CPA binding domains consist of tandemly repeated kinked three-helix bundles, as is observed in pyocin S5, and these lie N-terminal to an inner membrane translocation and cytotoxic domains. The predicted structure of the cytotoxic domain shares no similarity with other bacteriocin cytotoxic domains for which the structures are known. The mechanism we propose for pyocin SX1 and SX2 (Figure 7B) is a composite of the findings of this research and current knowledge derived from a variety of bacteriocins including pyocins S2, S5, G and the nuclease-type colicins [11,13,16,19,33–35]. For pyocin SX1 and SX2, the translocation process is initiated by binding of the CPA binding domain to the CPA on the cell surface to localize the pyocin and allow the N-terminal unstructured domain and transporter binding domain to locate the PA0434 transporter (Figure 7B). Binding of pyocin SX2 to the PA0434 transporter signals for release of the TonB-box of the transporter from the membrane spanning

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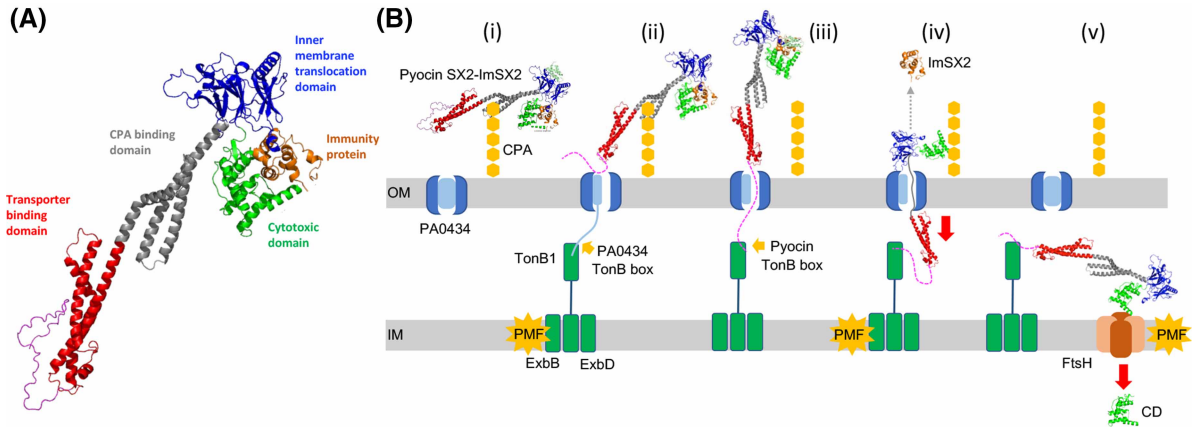

Figure 7. Predicted structure and entry mechanism of pyocin SX2.

(**A**) Predicted structure of the pyocin SX2-ImSX2 complex. (**B**) Proposed mechanism of pyocin SX2 (and SX1) translocation into *P. aeruginosa*. (i) The pyocin CBD domain (cyan) binds to CPA on the cell surface. (ii) The UD and TBD (blue) bind to PA0434 transporter and activate unfolding of the transporter's plug domain. (iii–iv) The UD passes through PA0434 barrel and presents its TonB-box in periplasm. Then, TonB1 binds to the pyocin TonB-box and imports the pyocin via PMF generated by TonB1–ExbB–ExbD complex. The immunity protein (Im) is released during the translocation. (v) The pyocin is proteolytically processed and only the cytotoxic domain (CD) is thought to be transported into cytoplasm via FtsH.

β-barrel enabling binding of this epitope to TonB1 in the periplasm. TonB1 is able to actively induce partial unfolding of the transporter plug domain by utilization of energy from the PMF transduced by the TonB1–ExbB–ExbD complex which utilizes the proton motive allowing the N-terminal to translocate through the PA0434 barrel and present its own TonB-box in the periplasm. Next, TonB1 interacts with the pyocin TonB-box and mediates pyocin translocation into the periplasm. The immunity protein is released during translocation. Finally, the pyocin molecule present in periplasm is actively transported across the inner membrane via FtsH. The pyocin is likely cleaved during translocation and only the cytotoxic domain is imported into the cytoplasm, as observed for *E. coli* colicins [34,35]. In addition, a recent study on pyocin G transportation across the inner membrane demonstrated that TonB1 is also required for pyocin G import into cytoplasm [19] (Figure 7B). TonB1 interaction may be to localize the pyocin close to the inner membrane from where the inner membrane translocation domain either interacts directly with the membrane or even with FtsH itself for transfer across the membrane and proteolytic processing [19].

CrtA is a novel pyocin transporter that has not been characterized previously. Several studies have demonstrated that *P. aeruginosa* is able to utilize different siderophores produced by other microorganisms called xenosiderophores [36]. A recent study on siderophore piracy showed that transcription of *crtA* gene is increased when *P. aeruginosa* was grown in metal-limited media, suggesting that CrtA likely plays a role in metal homeostasis [36]. Furthermore, this study also showed the induction of *crtA* gene expression by two xenosiderophores including ferric-vibriobactin and ferric-yersiniabactin produced by *Vibrio* and *Yersinia*, respectively [36]. In *P. aeruginosa*, ferric-vibriobactin is transported by a TBDT called FvbA. Even though the expression of *crtA* is induced by ferric-vibriobactin, the level of expression is relatively low when compared with the expression of *fvbA*. Moreover, *P. aeruginosa* is not able to utilize Fe(III) from ferric-yersiniabactin suggesting that ferric-vibriobactin and ferric-yersiniabactin are not the specific target for CrtA [36]. However, these xenosiderophores may share some structural characteristics with the genuine target and partially trigger the expression of *crtA* gene. In addition, a study on the uptake of siderophore-drug conjugates indicated that the overexpression of CrtA in *P. aeruginosa* PAO1 increase susceptibility to several siderophore-drug conjugates including BAL030072, MC-1 and cefiderocol [37]. Thus, the results obtained from this study and from previous reports suggest that the target of CrtA is likely to be a xenosiderophore involved in Cu(II) transport. The TBDT OprC has already been shown to be an outer membrane *P. aeruginosa* copper transporter [38,39]. However, it is clear that CrtA must function by a different mechanism to OprC which has a cysteine containing copper binding site exposed at the cell surface [38]. This binding site is not present in CrtA, which contains no cysteine residues. Interestingly, there is evidence to suggest that copper may be delivered to OprC by the copper containing protein azurin [39].

Due to the spread of MDR *P. aeruginosa*, the development of novel therapeutic approaches to treat *P. aeruginosa* infection has become essential. This work expands the repertoire of candidate pyocins for antipseudomonal therapeutic development and generates more understanding on how these proteins target and kill *P. aeruginosa*.

Materials and methods

Bacterial strains and media

P. aeruginosa and *E. coli* isolates were grown in LB medium (10 g/L tryptone, 10 g/L NaCl, 5 g/L yeast extract (pH 7.2). All strains used in this study are summarized in Supplementary Table S3. Strains were routinely grown at 37°C, with shaking at 180 rpm. Plasmids were propagated in *E. coli* DH5α (ThermoFisher Scientific, U.S.A.) and *E. coli* BL21 (DE3) pLysS (Agilent Technologies, U.S.A.) was used for the production of pyocins. Media were supplemented with ampicillin at 100 μg/ml (Sigma–Aldrich, U.S.A.), kanamycin at 50 μg/ml (Sigma–Aldrich, U.S.A.), chloramphenicol at 34 μg/ml (Sigma–Aldrich, U.S.A.) or gentamicin at 50 μg/ml (Gibco, U.S.A.) when required. Bacterial strains used in this study were stored in 50% glycerol at −80°C until used.

Cloning, expression and purification of pyocin SX1 and SX2

The annotated sequences of pyocins SX1 and SX2 (Table 1) begin at the second start codon downstream from the ribosome binding size (RBS). However, most of bacterial genes start translation at the first start codon locating at 5-10 bases downstream from the RBS. Therefore, we synthesized the pyocin genes from the first start codon located at 8 bases downstream from the RBS. Genes encoding pyocin SX1 and SX2 and associated immunity proteins, GenBank records ON716475–ON716476 [40,41] were codon optimized and synthesized (GenScript, U.S.A.) for expression in *E. coli* and introduced into the plasmid pET21a (+) (Merck, Germany) at NdeI/XhoI restriction sites to give pSX1ImSX1 and pSX2ImSX2, respectively. His_6-tag were added to the C-terminal end of the immunity proteins. The plasmids were transformed into *E. coli* BL21 (DE3) pLysS (Agilent Technologies, U.S.A.) by the heat shock method. To increase the pyocin expression level, the immunity protein genes were amplified by PCR using Phusion polymerase (New England Biolabs, U.K.) with the following primers; 5′-ACA GAT CAT ATG GAG AAG CGT ACC ATC AGC-3′ and 5′-ATC TGT CTC GAG GCC CGC TTT AAA ACC C-3′ for ImSX1, and 5′-ACA GAT CAT ATG CTG GAC CTG GAG GG-3′ and 5′-ATC TGT CTC GAG AAC AAT ACC ATA TTT CTT TTC GG-3′ for ImSX2. The PCR products were ligated into the plasmid pET24a (+) (Merck, Germany) at NdeI/XhoI restriction sites. The plasmids with the immunity protein genes were transformed into competent *E. coli* cells carrying their counterpart pyocin genes. Expression of pyocins SX1/SX2 was induced for 4 h by adding 1 mM IPTG into 5 L culture growth in LB broth at 37°C with shaking at 180 rpm (OD_{600} = 0.6). After induction, the cells were centrifuged, re-suspended in 20 mM Tris–HCl, 500 mM NaCl and 10 mM imidazole (pH 7.5) and lysed by sonication. The cell debris was removed by centrifugation at 4°C. The cell-free lysate was applied to a 5 ml His Trap™ HP column (GE Healthcare, U.S.A.) equilibrated in the same buffer. Pyocins were eluted over a 10–500 mM imidazole gradient. Fractions with target pyocin were pooled, dialyzed in 50 mM Tris–HCl and 200 mM NaCl (pH 7.5), overnight at 4°C and purified by a gel filtration HiLoad 26/600 Superdex 200 pg column (GE Healthcare, U.S.A.) using the same buffer.

Antibacterial spot assay

Eighty microliters of test strain culture (OD_{600} = 0.6) were added to 8 ml of soft agar (0.8% agar in distilled water) and poured over a LB agar plate. Five microliters of purified pyocin were spotted onto overlay plates and incubated at 37°C for 24 h. Clear zones presented after incubation indicate killing activity.

Galleria mellonella infection model

G. mellonella larvae were obtained from Livefood U.K.. *P. aeruginosa* strain P7 was grown in LB broth at 37°C until OD_{600} reach 0.6–0.7. Cells were collected by centrifugation, washed twice and diluted to OD_{600} = 0.6 in sterile PBS. To observe the protection of pyocins SX1 and SX2 against *P. aeruginosa* P7, 30 larvae were injected with 10 μl of ∼1.5×10^6 CFU/ml inoculum (100-fold dilution of OD_{600} = 0.6 bacterial suspension in PBS) into the hemocoel via the last right prolimb as previously described [42]. Larvae were kept in an incubator at 37°C for 3 h and further injected with 10 μl of pyocins at 1 mg/ml via the last left prolimb. The numbers of survivor were observed at 24 and 48 h after pyocin treatment. For determination of pyocins remaining in larvae, larvae

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were injected with 10 μl of pyocins (1 mg/ml) and incubated at 37°C. At each time point, three larvae were transferred into a 2 ml microtube containing 400 μl of ice-cold PBS. The sample was homogenized and centrifuged at 20 000***g*** for 10 min at 4°C. Five microliters of clear layer were taken and spotted onto *P. aeruginosa* P7 cell lawn on a LB plate to determine pyocin killing activity.

DNase activity assay

Immunity proteins were removed from their pyocin-immunity protein complexes by treatment with 6 M guanidine. Briefly, purified pyocin-immunity protein complex dissolved in 20 mM Tris–HCl with 10 mM imidazole (pH 7.5) was applied to a 5 ml His Trap™ HP column and the pyocin was eluted by a gradient of 0 to 6 M guanidine. Pyocins without immunity protein were dialyzed in 20 mM Tris–HCl (pH 7.5) overnight before used. DNase activity assay (50 μl) was performed in 20 mM Tris–HCl (pH 7.5) with 1 μg of pUC18 DNA and one of the following metal ions, $MgCl_2$ (10 mM), $ZnCl_2$ (10 μM) or $NiSO_4$ (10 μM). The reaction was initiated by adding 200 ng pyocin (with immunity protein removal) and incubated at 37°C for up to 15 min. The reaction was stopped by 5 mM EDTA. DNA fragments were analyzed by gel electrophoresis using 1% agarose gel.

In vitro transcription and translation assay

The effect of pyocin SX2 on protein synthesis was assessed by an *in vitro* transcription-translation assay (*E. coli* T7 S30 Extract System for Circular DNA. Promega, Germany). pRL-SV40 vector (Promega, Germany) encoding Renilla luciferase was used as a template DNA. The assay was performed at 50 μl by adding 200 ng of Im-free pyocin SX2, pyocin S5 or colicin D into the reactions and incubated at 37°C for 20 min before 4 μg of the template DNA was added. The quantity of the reporter protein was examined by measuring its enzymatic activity through the Renilla Luciferase Assay System (Promega, Germany), as per manufacturer's instruction. The light produced was measured on a Varioskan LUX microplate reader (ThermoFisher Scientific, U.S.A.). The experiment was performed with three replications. The tRNase colicin D and pore-forming pyocin S5 were used as positive and negative controls, respectively.

Identification of pyocins SX1 and SX2 transporter

P. aeruginosa PAO1 (20 independent cultures) were grown in LB broth for 48 h to obtain late-stationary-phase cultures. One milliliter of the culture was centrifuged and re-suspended in 100 μl of pyocin solutions (1 mg/ml). The suspension was incubated at 37°C for 4 h and spread onto a LB plate. Colonies emerging after 24 h were selected, streaked to single colony and verified for a resistant phenotype by spot test. Genomic DNA was isolated from overnight cultures of the wild type and mutant strains using GenElute Bacterial Genomic DNA Kits (Sigma–Aldrich, U.S.A.). Library preparation and whole genome sequencing were performed by Glasgow Polyomics, U.K. (Illumina, paired-end, 300 bp read length and 100× coverage). CLC Genomics Workbench version 7 (Qiagen, Germany) was used for analysis of the sequences. The sequences were mapped (mismatch cost of 2, insertion cost of 3, deletion cost of 3, length fraction of 0.8, similarity fraction of 0.8) to the *P. aeruginosa* PAO1 reference genome (NC_002516.2) using CLC Map Reads to Reference tool. Subsequently, mutations were identified using by CLC basic variant detection tool with default parameters. The effects of mutations on resistant phenotype against pyocins SX1/SX2 were confirmed by using spot test on mutant strains which have transposons inserted in the genes of interest. The transposon insertion mutants were obtained from Manoil Lab, University of Washington, U.S.A. [43]. A plasmid complemented strain was made to confirm that TBDT, CrtA (PA0434) is the transporter for pyocin SX1/SX2. The *PA0434* gene was amplified from *P. aeruginosa* PAO1 genomic DNA by PCR using Phusion™ High-Fidelity DNA Polymerase (ThermoFisher Scientific, U.S.A.) with the primers; 5′-ACA GAT CAT ATG AAA AAG CAC TCC ACG GCC CGC C-3′ and 5′-ATC TGT TCT AGA TCA GAA GCG CGT CTG CAC GCT CAG CTC-3′. The amplified fragment was digested with NdeI and XbaI (NEB, U.K.) and ligated into the modified pBBR1MCS-2 plasmid [44]. The pBBR1MCS-2 plasmid was modified by introducing a NdeI restriction site at the start codon of *lacZa* gene and introducing *aacC1* gene at NsiI site. The *aacC1* gene provides resistance to gentamicin which was used as a selective marker for the compliment strain. The recombinant plasmid was transformed to *P. aeruginosa* PAO1 strain PW1793, which has transposon insertion in *PA0434* gene, by electroporation. PW1793 strain was growth overnight in LB broth at 42°C without shaking. Four milliliters of the culture were centrifuged at 14 000***g*** for 1 min, washed twice and re-suspended in 25 μl of 1 mM $MgSO_4$. The cell suspension was mixed with 10 μg plasmid and transferred to a chilled 2 mm electroporation cuvette (Sigma–Aldrich, U.S.A.). The cells were subjected to electroporation treatment using a Bio-Rad Gene Pulser Xcell (Bio-Rad, U.S.A.) at 2200 kV, 600 Ω and 25 μF.

Immediately after delivery of the pulse, 975 μl of room-temperature BHI broth (Oxoid, U.K.) was added to the cell suspension without mixing and leaved at room-temperature for 5 min. The cell suspension was then incubated at 37°C with shaking at 180 rpm for 3 h and plated on a BHI agar supplemented with 50 μg/ml gentamicin. Colonies emerging after overnight incubation at 37°C were selected and confirmed by PCR and DNA sequencing (Eurofin, French).

Quantitative RT-PCR

Total RNAs were extracted and purified using RNeasy Mini kit (Qiagen) together with the RNAprotect Bacteria reagent (Qiagen), as per the manufacturer's instructions. The RNA samples were treated with DNase I (ThermoFisher Scientific, U.S.A.) and re-purified using the Monarch RNA Cleanup kit (NEB, U.K.). cDNA was synthesized from 1 μg of total RNA using the LunaScript RT SuperMix kit (NEB, U.K.) in accordance with the manufacturer's protocol. Luna Universal qPCR Master mix (NEB, U.K.) was used for qPCR according to manufacturer's recommendations (Initial denaturation 95°C, 1 min; denaturation 95°C, 15 s; extension 60°C, 30 s; 40 cycles). All reactions were prepared in a 20 μl final volume with technical duplicates and the experiments were carried out with three biological replicates. The primers used for RT-qPCR are as follow; 5′-TTC AGC TCG AAC CAG GTC AA-3′ and 5′-GTT GAG GAA GGA GGA CGG AC-3′ for *PA0434*, 5′-ACA TGG TGA TCA GCG GAG AA-3′ and 5′-CAG ATT CTG CTG TTC GAG GC-3′ for *fptA* and 5′-CAA GCG CAT GGT CGA CAA G-3′ and 5′-TAC ACG GCA TAC CTT ACG CA-3′ for *rpsL* gene. Absolute fold change was calculated as $2^{-\Delta\Delta ct}$ using *rpsL* for normalization [45,46].

Data Availability

GenBank records ON716475 [41] and ON716476 [40] contain the coding sequences for pyocin SX1 and ImSX1 from the plasmid pSX1ImSX1 and for pyocin SX2 and ImSX2 from the plasmid pSX2ImSX2, respectively.

Competing Interests

D.W. and C.K. are co-founders of Glox Therapeutics and own shares in this company. Glox develops bacteriocin based antibiotics. D.W. and C.K. are also authors on patents relating to the use of bacteriocins in treating infection.

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CRediT Author Contribution

Daniel Walker: Conceptualization, Resources, Supervision, Funding acquisition, Methodology, Writing — review and editing. **Jiraphan Premsuriya:** Conceptualization, Investigation, Writing — original draft, Writing — review and editing. **Khedidja Mosbahi:** Supervision, Writing — review and editing. **Iva Atanaskovic:** Investigation, Writing — review and editing. **Colin Kleanthous:** Funding acquisition, Writing — review and editing.

Abbreviations

CPA, common polysaccharide antigen; GMD, GDP-mannose 4,6-dehydratase; RBS, ribosome binding size; TBD, transporter-binding domain; TBDT, TonB-dependent transporter; TETA, triethylenetetramine; TPEN, N,N,N′, N′-tetrakis(2-pyridylmethyl)ethylenediamine; UD, unstructured domain.

References

1 Murray, C.J. (2022) Global burden of bacterial antimicrobial resistance in 2019: a systematic analysis. *Lancet* **399**, 629–655 https://doi.org/10.1016/S0140-6736(21)02724-0

2 WHO. (2017) *Prioritization of Pathogens to Guide Discovery, Research and Development of new Antibiotics for Drug Resistant Bacterial Infections, Including Tuberculosis*, WHO, Geneva, Switzerland

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https://doi.org/10.1042/BCJ20220552

3 Heilbronner, S., Krismer, B., Brötz-Oesterhelt, H. and Peschel, A. (2021) The microbiome-shaping roles of bacteriocins. *Nat. Rev. Microbiol.* **19**, 726–739 https://doi.org/10.1038/s41579-021-00569-w
4 Granato, E.T., Meiller-Legrand, T.A. and Foster, K.R. (2019) The evolution and ecology of bacterial warfare. *Curr. Biol.* **29**, R521–R537 https://doi.org/10.1016/j.cub.2019.04.024
5 Mullish, B.H. and Williams, H.R.T. (2018) Clostridium difficile infection and antibiotic-associated diarrhoea. *Clin. Med.* **18**, 237–241 https://doi.org/10.7861/clinmedicine.18-3-237
6 Ravi, A., Halstead, F.D., Bamford, A., Casey, A., Thomson, N.M., Van Schaik, W. et al. (2019) Loss of microbial diversity and pathogen domination of the gut microbiota in critically ill patients. *Microb. Genom.* **5**, e000293 https://doi.org/10.1099/mgen.0.000293
7 Stracy, M., Snitser, O., Yelin, I., Amer, Y., Parizade, M., Katz, R. et al. (2022) Minimizing treatment-induced emergence of antibiotic resistance in bacterial infections. *Science* **375**, 889–894 https://doi.org/10.1126/science.abg9868
8 Bernstein, C.N. (2020) Is antibiotic use a cause of IBD worldwide? *Inflamm. Bowel Dis.* **26**, 448–449 https://doi.org/10.1093/ibd/izz138
9 Michel-Briand, Y. and Baysse, C.) The pyocins of *Pseudomonas aeruginosa*. *Biochimie* **84**, 499–510 https://doi.org/10.1016/S0300-9084(02)01422-0
10 Ghequire, M.G.K. and De Mot, R. (2014) Ribosomally encoded antibacterial proteins and peptides from *Pseudomonas*. *FEMS Microbiol. Rev.* **38**, 523–568 https://doi.org/10.1111/1574-6976.12079
11 McCaughey, L.C., Josts, I., Grinter, R., White, P., Byron, O., Tucker, N.P. et al. (2016) Discovery, characterization and in vivo activity of pyocin SD2, a protein antibiotic from *Pseudomonas aeruginosa*. *Biochem. J.* **473**, 2345–2358 https://doi.org/10.1042/BCJ20160470
12 Barreteau, H., Tiouajni, M., Graille, M., Josseaume, N., Bouhss, A., Patin, D. et al. (2012) Functional and structural characterization of PaeM, a colicin M-like bacteriocin produced by *Pseudomonas aeruginosa*. *J. Biol. Chem.* **287**, 37395–37405 https://doi.org/10.1074/jbc.M112.406439
13 Behrens, H.M., Lowe, E.D., Gault, J., Housden, N.G., Kaminska, R., Weber, T.M. et al. (2020) Pyocin S5 import into *Pseudomonas aeruginosa* reveals a generic mode of bacteriocin transport. *mBio* **11**, e03230-19 https://doi.org/10.1128/mBio.03230-19
14 Kleanthous, C. and Walker, D. (2001) Immunity proteins: enzyme inhibitors that avoid the active site. *Trends Biochem. Sci.* **26**, 624–631 https://doi.org/10.1016/S0968-0004(01)01941-7
15 Joshi, A., Grinter, R., Josts, I., Chen, S., Wojdyla, J.A., Lowe, E.D. et al. (2015) Structures of the ultra-high-affinity protein-protein complexes of pyocins S2 and AP41 and their cognate immunity proteins from *Pseudomonas aeruginosa*. *J. Mol. Biol.* **427**, 2852–2866 https://doi.org/10.1016/j.jmb.2015.07.014
16 White, P., Joshi, A., Rassam, P., Housden, N.G., Kaminska, R., Goult, J.D. et al. (2017) Exploitation of an iron transporter for bacterial protein antibiotic import. *Proc. Natl Acad. Sci. U.S.A.* **114**, 12051–12056 https://doi.org/10.1073/pnas.1713741114
17 Elfarash, A., Dingemans, J., Ye, L., Hassan, A.A., Craggs, M., Reimmann, C. et al. (2014) Pore-forming pyocin S5 utilizes the FptA ferripyochelin receptor to kill *Pseudomonas aeruginosa*. *Microbiology (Reading)* **160**, 261–269 https://doi.org/10.1099/mic.0.070672-0
18 McCaughey, L.C., Grinter, R., Josts, I., Roszak, A.W., Waløen, K.I., Cogdell, R.J. et al. (2014) Lectin-Like bacteriocins from *Pseudomonas* spp. utilise D-rhamnose containing lipopolysaccharide as a cellular receptor. *PLoS Pathog.* **10**, e1003898 https://doi.org/10.1371/journal.ppat.1003898
19 Atanaskovic, I., Sharp, C., Press, C., Kaminska, R. and Kleanthous, C. (2022) Bacterial competition systems share a domain required for inner membrane transport of the bacteriocin Pyocin G from *Pseudomonas aeruginosa*. *mBio* **13**, e0339621 https://doi.org/10.1128/mbio.03396-21
20 van Belkum, A., Soriaga, L.B., LaFave, M.C., Akella, S., Veyrieras, J.B., Barbu, E.M. et al. (2015) Phylogenetic distribution of CRISPR-Cas systems in antibiotic-resistant *Pseudomonas aeruginosa*. *mBio* **6**, e01796-15 https://doi.org/10.1128/mBio.01796-15
21 Roh, E., Park, T.H., Kim, M.-I., Lee, S., Ryu, S., Oh, C.S. et al. (2010) Characterization of a new bacteriocin, carocin D, from *Pectobacterium carotovorum* subsp. carotovorum Pcc21. *Appl. Environ. Microbiol.* **76**, 7541–7549 https://doi.org/10.1128/AEM.03103-09
22 Wang, J.W., Derilo, R.C., Lagitnay, R.B.J.S., Wu, H.P., Chen, K.I. and Chuang, D.Y. (2020) Identification and characterization of the bacteriocin Carocin S3 from the multiple bacteriocin producing strain of *Pectobacterium carotovorum* subsp. carotovorum. *BMC Microbiol.* **20**, 273 https://doi.org/10.1186/s12866-020-01955-9
23 Wang, S., Hao, Y., Lam, J.S., Vlahakis, J.Z., Szarek, W.A., Vinnikova, A. et al. (2015) Biosynthesis of the common polysaccharide antigen of *Pseudomonas aeruginosa* PAO1: characterization and role of GDP-D-Rhamnose: GlcNAc/GalNAc-diphosphate-lipid α1,3-D-rhamnosyltransferase WbpZ. *J Bacteriol.* **197**, 2012–2019 https://doi.org/10.1128/JB.02590-14
24 Lam, J.S., Taylor, V.L., Islam, S.T., Hao, Y. and Kocíncová, D. (2011) Genetic and functional diversity of *Pseudomonas aeruginosa* lipopolysaccharide. *Front. Microbiol.* **2**, 118 https://doi.org/10.3389/fmicb.2011.00118
25 Shirley, M. and Lamont, I.L. (2009) Role of TonB1 in pyoverdine-mediated signaling in *Pseudomonas aeruginosa*. *J. Bacteriol.* **191**, 5634–5640 https://doi.org/10.1128/JB.00742-09
26 Six, A., Mosbahi, K., Barge, M., Kleanthous, C., Evans, T. and Walker, D. (2021) Pyocin efficacy in a murine model of *Pseudomonas aeruginosa* sepsis. *J. Antimicrob. Chemother.* **76**, 2317–2324 https://doi.org/10.1093/jac/dkab199
27 Ochsner, U.A. and Vasil, M.L. (1996) Gene repression by the ferric uptake regulator in *Pseudomonas aeruginosa*: cycle selection of iron-regulated genes. *Proc. Natl Acad. Sci. U.S.A.* **93**, 4409–4414 https://doi.org/10.1073/pnas.93.9.4409
28 Pasqua, M., Visaggio, D., Lo Sciuto, A., Genah, S., Banin, E., Visca, P. et al. (2017) Ferric uptake regulator Fur is conditionally essential in *Pseudomonas aeruginosa*. *J. Bacteriol.* **199**, e00472-17 https://doi.org/10.1128/JB.00472-17
29 Jackson, C.S. and Kodanko, J.J. (2010) Iron-binding and mobilization from ferritin by polypyridyl ligands. *Metallomics* **2**, 407–411 https://doi.org/10.1039/c003414b
30 Cooper, G.J.S. (2011) Therapeutic potential of copper chelation with triethylenetetramine in managing *Diabetes mellitus* and Alzheimers disease. *Drugs* **71**, 1281–1320 https://doi.org/10.2165/11591370-000000000-00000
31 Mirdita, M., Schütze, K., Moriwaki, Y., Heo, L., Ovchinnikov, S. and Steinegger, M. (2022) Colabfold: making protein folding accessible to all. *Nat. Methods* **19**, 679–682 https://doi.org/10.1038/s41592-022-01488-1
32 Jumper, J., Evans, R., Pritzel, A., Green, T., Figurnov, M., Ronneberger, O. et al. (2021) Highly accurate protein structure prediction with AlphaFold. *Nature* **596**, 583–589 https://doi.org/10.1038/s41586-021-03819-2
33 Atanaskovic, I., Mosbahi, K., Sharp, C., Housden, N.G., Kaminska, R., Walker, D. et al. (2020) Targeted killing of *Pseudomonas aeruginosa* by Pyocin G occurs via the hemin transporter Hur. *J. Mol. Biol.* **432**, 3869–3880 https://doi.org/10.1016/j.jmb.2020.04.020

34 Walker, D., Mosbahi, K., Vankemmelbeke, M., James, R. and Kleanthous, C. (2007) The role of electrostatics in colicin nuclease domain translocation into bacterial cells. *J. Biol. Chem.* **282**, 31389–31397 https://doi.org/10.1074/jbc.M705883200
35 Chauleau, M., Mora, L., Serba, J. and de Zamaroczy, M. (2011) FtsH-dependent processing of RNase Colicins D and E3 means that only the cytotoxic domains are imported into the cytoplasm. *J. Biol. Chem.* **286**, 29397–29407 https://doi.org/10.1074/jbc.M111.242354
36 Perraud, Q., Cantero, P., Roche, B., Gasser, V., Normant, V.P., Kuhn, L. et al. (2020) Phenotypic adaption of *Pseudomonas aeruginosa* by hacking siderophores produced by other microorganisms. *Mol. Cell. Proteomics* **19**, 589–607 https://doi.org/10.1074/mcp.RA119.001829
37 Luscher, A., Moynie, L., Auguste, P.S., Bumann, D., Mazza, L., Pletzer, D. et al. (2018) TonB-dependent receptor repertoire of *Pseudomonas aeruginosa* for uptake of siderophore-drug conjugates. *Antimicrob. Agents Chemother.* **62**, e00097-18 https://doi.org/10.1128/AAC.00097-18
38 Bhamidimarri, S.P., Young, T.R., Shanmugam, M., Soderholm, S., Basle, A., Bumann, D. et al. (2021) Acquisition of ionic copper by the bacterial outer membrane protein OprC through a novel binding site. *PLoS Biol.* **19**, e3001446 https://doi.org/10.1371/journal.pbio.3001446
39 Han, Y., Wang, T., Chen, G., Pu, Q., Liu, Q., Zhang, Y. et al. (2019) A *Pseudomonas aeruginosa* type VI secretion system regulated by CueR facilitates copper acquisition. *PLoS Pathog.* **15**, e1008198 https://doi.org/10.1371/journal.ppat.1008198
40 Expression vector pSX2-ImSX2 pyocin SX2 and pyocin immunity protein genes, complete cds
41 Expression vector pSX1-ImSX1 pyocin SX1 and pyocin immunity protein genes, complete cds
42 Smith, K., Martin, L., Rinaldi, A., Rajendran, R., Ramage, G. and Walker, D. (2012) Activity of pyocin S2 against *Pseudomonas aeruginosa* biofilms. *Antimicrob. Agents Chemother.* **56**, 1599–1601 https://doi.org/10.1128/AAC.05714-11
43 Held, K., Ramage, E., Jacobs, M., Gallagher, L. and Manoil, C. (2012) Sequence-verified two-allele transposon mutant library for *Pseudomonas aeruginosa* PAO1. *J. Bacteriol.* **194**, 6387–6389 https://doi.org/10.1128/JB.01479-12
44 Obranić, S., Babić, F. and Maravić-Vlahoviček, G. (2013) Improvement of pBBR1MCS plasmids, a very useful series of broad-host-range cloning vectors. *Plasmid* **70**, 263–267 https://doi.org/10.1016/j.plasmid.2013.04.001
45 Yoneda, K., Chikumi, H., Murata, T., Gotoh, N., Yamamoto, H., Fujiwara, H. et al. (2005) Measurement of *Pseudomonas aeruginosa* multidrug efflux pumps by quantitative real-time polymerase chain reaction. *FEMS Microbiol. Lett.* **243**, 125–131 https://doi.org/10.1016/j.femsle.2004.11.048
46 Rao, X., Huang, X., Zhou, Z. and Lin, X. (2013) An improvement of the $2^{(-\text{delta delta CT})}$ method for quantitative real-time polymerase chain reaction data analysis. *Biostat. Bioinforma. Biomath.* **3**, 71–85