Characterization of NAD salvage pathways and their role in virulence in *Streptococcus pneumoniae*

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INTRODUCTION

NAD is a necessary cofactor present in all living cells. Some bacteria cannot *de novo* synthesize NAD and must use the salvage pathway to import niacin or nicotinamide riboside via substrate importers NiaX and PnuC, respectively. Although homologues of these two importers and their substrates have been identified in other organisms, limited data exist in *Streptococcus pneumoniae*, specifically, on its effect on overall virulence. Here, we sought to characterize the substrate specificity of NiaX and PnuC in *Str. pneumoniae* TIGR4 and the contribution of these proteins to virulence of the pathogen. Although binding affinity of each importer for nicotinamide mononucleotide may overlap, we found NiaX to specifically import nicotinamide and nicotinic acid, and PnuC to be primarily responsible for nicotinamide riboside import. Furthermore, a pnuC mutant is completely attenuated during both intranasal and intratracheal infections in mice. Taken together, these findings underscore the importance of substrate salvage in pneumococcal pathogenesis and indicate that PnuC could potentially be a viable small-molecule therapeutic target to alleviate disease progression in the host.

**Abbreviation:** SOE-PCR, splicing by overhang extension method of PCR.
necessity for new bacterial targets for small-molecule therapeutics, particularly for novel targets that are essential during infection.

Because of the importance of NAD biosynthesis in bacterial physiology and the potential accessibility to the NAD salvage molecule importers on the bacterial surface, we wanted to assess their functional role in both uptake and virulence in the pneumococcus. Previous studies in Hae-
mophilus influenzae found these substrates important for survival in the blood and the PnuC pathway essential during infection (Herbert et al., 2003; Schmidt-Brauns et al., 2001). Here, by making single deletions of the NAD salvage importer genes, we have confirmed which precursors in NAD synthesis are imported by NiaX or PnuC in Str. pneumoniae and determined the effect of these mutations on virulence in murine models of pne-
mococcal infection.

METHODS

Bacterial constructs. Mutations of SP_1233 (niaX) and SP_1859 (pnuC) were created by using the splicing by overhang extension method of PCR (SOE-PCR). Briefly, 1 kb fragments upstream and downstream of the target gene were amplified and spliced to an erythromycin (Erm) resistance cassette. SOE-PCR products were subsequently transformed into the TIGR4 strain of Str. pneumoniae. Knockout mutants selected by antibiotic resistance to Erm were verified by PCR to confirm insertion of the SOE-PCR product and deletion of the target gene (Horton et al., 1990). To complement the mutant strains, the coding regions for niaX and pnuC were amplified from TIGR4 genomic DNA using primers NiaX_F/NiaX_R (GGCG CGAATTCCGAGGAGACAAACATGTCTGGTTATGTACATCAGTGC TATATGCGTACGGCTCGACATCGTACCATCTA GTGATACTTG, GATCTGGCAGTTAAACGGCGTTTTCGAACGTCA) and PnuC_F/PnuC_R (GGCCGCCCAGAATTCGGAGGACAAACATGTGTATATGC, GATCCTGCAGTTTAACGGCGTTTTCGAACGTCA) respectively; the conserved RBS (GGAGGACAAAC) was included in the forward primer to afford better expression. Amplified niaX and pnuC were then p.tagged with EcoRI/PstI and ligated with streptococcal shuttle vector pABG5 (Granok et al., 2000). The generated plasmids pABG5-niaX and pABG5-pnuC were transformed into TIGR4anieX and TIGR4ANpnuC, respectively, in standard transformation protocols. Sequence insertion in the complemented strains was confirmed using primed-specific primers.

Growth curves. Bacteria were grown at 37 °C with 5% CO2 in C+Y medium to an OD620 of 0.1, centrifuged, and resuspended in C+Y without nicotinic acid, nicotinamide, or yeast (C−Y). Bacterial strains were incubated at 37 °C with 5% CO2 for 2 h, then back-diluted to an OD620 of 0.1 in C−Y with 20% v/v glycerol and frozen for initial stock solutions. Stocks were titrated to assure equal starting bacterial numbers. Assays were performed in a CytoTect 3 cell imaging multimode reader (BioTek) using a 96-well format. Stock solutions were back-diluted 1:40 for growth curves in C+Y, C−Y, or C−Y medium supplemented with the NAD salvage substrates nicotinic acid (Sigma), nicotinamide mononucleotide (Sigma), nicotinamide (Sigma), or nicotinamide riboside (Chromadex); all growth curves were performed in quadruplicate. The OD620 of samples was read every 30 min, with a 5 s double orbital shake before each read.

Radiolabelled uptake. For uptake experiments, strains were cultured in standard C+Y to OD620 0.4 and then subjected to a 1:10 back dilution and outgrown in C−Y during labelling. Substrates utilized were nicotinic acid (14C-carbonyl; 55 mCi (1035 MBq) mmol−1), nicotinamide (14C-carbonyl; 55 mCi mmol−1) and nicotinamide β-riboside triflate salt (14C-carbonyl; 55 mCi mmol−1). All 14C-labelled substrates were purchased from American Radiolabelled Chemicals (St Louis, MO). 14C-Labelled substrates were added at a final concentration of 1 μM for nicotinamide β-riboside and nicotinic acid, and to a final concentration of 500 nM for nicotinamide, all in 1 ml volume of culture. Cultures were subsequently incubated at 37 °C for 30 min to allow uptake of the respective substrates. Cells were collected onto a 0.45 μM pore filter disc (Millipore) by vacuum filtration and the membrane was washed with 5 ml PBS, also via vacuum filtration. Dried filters were resuspended in 3 ml ScintiSafe (Fisher Scientific) and the counts min−1 of the respective samples were detected for 1 min in a Perkin Elmer liquid scintillation counter. For competition experiments, experimental conditions were identical, with the exception of the addition of 5 μM nicotinamide mononucleotide with 1 μM respective substrates. For all experiments, uptake was normalized to the counts min−1 of the parental WT TIGR4 strain, which was considered to have an uptake of 100% for all substrates.

Mouse studies. All experiments involving animals were performed with prior approval of and in accordance with guidelines of the St Jude Institutional Animal Care and Use Committee. The St Jude laboratory animal facilities have been fully accredited by the American Association for Accreditation of Laboratory Animal Care. Laboratory animals were maintained in accordance with the applicable portions of the Animal Welfare Act and the guidelines prescribed in the DHHS publication, Guide for the Care and Use of Laboratory Animals. All mice were maintained in BSL2 facilities and all experiments were done while the mice were under inhaled isoflurane (2.5%) anaesthesia. Mice were monitored daily for signs of infection. This work was approved under the IACUC protocol number 538-100013-04/12 R1.

For survival studies, cultured bacteria were grown in C+Y medium to an OD620 of 0.4 and diluted according to a previously determined standard curve. Bacteria were plated to assure that the proper amount of bacteria was added. For intranasal infections, bacteria were introduced into 6-week-old BALB/c mice (Jackson Laboratory) via intranasal administration of 105 c.f.u. bacteria in PBS (25 μl). Blood for titre determination was collected via tail snip at both 24 and 48 h post-infection. Survival data were analysed by using the Mantel-Cox log rank test in Prism 6. For intratracheal infections, mice were infected via intranasal administration with 105 c.f.u. bacteria in PBS (100 μl). For lung collection, lungs were washed twice with PBS to remove contaminating blood. The lungs were then homogenized and plated for c.f.u. titre. Blood from the chest cavity was also collected for c.f.u. titres.

Homology. All protein sequences were aligned using NCBI BLAST (Altschul et al., 1990, 1997). Sequences were analysed for overall protein identity.

RESULTS

Homology of NiaX and PnuC

Str. pneumoniae contains homologues of both NiaX and PnuC, but there is limited knowledge regarding both importers specific to the organism. Interestingly, some streptococcal species do not have any proteins that are homologous to NiaX but do share homology to pneumo-
coccal PnuC (Fig. 1a). In both cases, there is limited homology outside the respective Streptococcus genus, suggesting the proteins studied here could potentially yield different...
results from other orthologues. The solved structure of PnuC bound to nicotinamide riboside in Neisseria mucosa identified the nicotinamide riboside-binding residues, cytoplasmic gate and periplasmic gate. All but 2 of the 17 residues were identical in Str. pneumoniae; those two (T130 in TIGR4 versus N91 in N. mucosa and N203 in TIGR4 versus S168 in N. mucosa) contained functionally similar side chains (−OH) and were not directly responsible for coordinating nicotinamide riboside (Fig. 1b) (Jaehme et al., 2014).

Preparation and testing of NAD depletion medium

C+Y is a synthetic medium for growth of Str. pneumoniae (Lacks & Hotchkiss, 1960). For growth-curve testing of the NAD salvage pathway substrates, all known sources of imported precursors had to be excluded from the medium, including nicotinic acid (niacin), nicotinamide and yeast, which is a common source of nicotinic acid, nicotinamide and other molecules that the bacteria could use in the NAD salvage pathway. This medium, termed C−Y, was assessed as a growth medium for Str. pneumoniae. There was no growth of the WT TIGR4 or of the ΔniaX and ΔpnuC mutants, indicating the successful depletion of necessary NAD pathway precursors (Fig. 2). Additionally, all strains underwent equal exponential growth in the C+Y medium, signifying that the mutant strains had no initial growth defect; however, for unknown reasons, the ΔpnuC mutant seemed to undergo autolysis more rapidly than either the WT or ΔniaX mutant strains did. This effect was not attributable to pH as the culture’s pH was indistinguishable from that of WT following overnight growth (data not shown).

Substrate characterization of NAD salvage pathway importers

To assess import of the substrates of the NAD salvage pathway, C−Y was supplemented with nicotinic acid, nicotinamide, and nicotinamide riboside. In each experiment, TIGR4 and the mutants were grown in C−Y or C+Y as negative and positive controls, respectively (data not shown).

(a) Str. pneumoniae NAD salvage importer homology compared with TIGR4 isolate

<table>
<thead>
<tr>
<th>Strain</th>
<th>PnuC protein identity (%)</th>
<th>Nilax protein identity (%)</th>
<th>Gram stain</th>
</tr>
</thead>
<tbody>
<tr>
<td>Streptococcus mitis</td>
<td>98</td>
<td>96</td>
<td>+</td>
</tr>
<tr>
<td>Streptococcus oralis</td>
<td>97</td>
<td>90</td>
<td>+</td>
</tr>
<tr>
<td>Streptococcus sanguinis</td>
<td>99</td>
<td>60</td>
<td>+</td>
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<td>Streptococcus gordonii</td>
<td>75</td>
<td>No homology</td>
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<tr>
<td>Streptococcus downei</td>
<td>57</td>
<td>83</td>
<td>+</td>
</tr>
<tr>
<td>Streptococcus pyogenes</td>
<td>74</td>
<td>No homology</td>
<td>+</td>
</tr>
<tr>
<td>Haemophilus influenzae</td>
<td>30</td>
<td>41</td>
<td>+</td>
</tr>
<tr>
<td>Clostridium clariflavum</td>
<td>37</td>
<td>No homology</td>
<td>–</td>
</tr>
<tr>
<td>Neisseria mucosa</td>
<td>32</td>
<td>No homology</td>
<td>–</td>
</tr>
<tr>
<td>Enterococcus faecalis</td>
<td>31</td>
<td>42</td>
<td>+</td>
</tr>
</tbody>
</table>

(b) TIGR4 79 DWIGMICSLTG1CVFSEGRASYLFGNSVVLALQKFGYGL–VTLLITYTVMQ 137
   W+ ++TGG+CVF+SVLNFGIL+ +Y ++ YEG L L + +Q
N. mucosa 40 SWLASVANIGLVSFVVGKNSYNFLGLISVSYYSTFKLYGEMMLNLYYPQ 99
   +G W + E + + A L + W + + SV + +G+ P
TIGR4 138 PIGLVLWYIQAFK–EKQFVARKLDGKNTLYSLISVLMWAFGFIYQSGANRPRY 195
   +G W + + + A A + L + W + + SV + +G+ P
N. mucosa 100 FYGAFNWRKMALGETAEEVKNATVRQMLVVAASVVTYIEWHLHGLSALP 159
TIGR4 196 DSITATNGVQILMAYREQFWAATNFYSIYLMW--W---GE-SLOQGKLYIYLI 248
   D +T + + Q+LM YRE W N+ + I LW W GE SL + +Y+YL
N. mucosa 160 DGYTZYIQLQVLMILRYEQAWLWVNLTIWLVGWAVWFKNGETSPLLLMYVYL 219
TIGR4 249 NSVGWNYQSKAARKNT 265
   NS+ G+ W+ K+++ N. mucosa 220 NSVGYINWTKLVKHS 236

Fig. 1. PnuC and NiaX homology with known sequences and structures. (a) The TIGR4 PnuC and NiaX protein sequences were compared with other bacterial PnuC and NiaX homologues by using a BLAST search (Altschul et al., 1997); percentage identities are listed together with Gram stain results. (b) Structural alignment of TIGR4 PnuC and Neisseria mucosa PnuC (Jaehme et al., 2014), for which the structure was solved with nicotinamide riboside coordinated within the protein. Residues involved in nicotinamide riboside binding, the cytoplasmic gate, both the cytoplasmic gate and nicotinamide riboside binding, and the periplasmic gate are highlighted in red, blue, purple, and orange, respectively.
In nicotinic acid- and nicotinamide-supplemented media, the ΔpnuC mutant grew as well as TIGR4 (Fig. 3b, d) while the ΔniaX mutant showed a growth defect (Fig. 3a, c), which was restored upon complementation. This result confirmed previous predictions and in vitro data about the target of NiaX and, we believe, provided the first in vivo data supporting NiaX being the nicotinic acid/nicotinamide importer in bacteria, specifically in Str. pneumoniae (Rodionov et al., 2009; ter Beek et al., 2011).

Nicotinamide riboside was the next compound to be tested as an NAD salvage pathway substrate. The ΔpnuC mutant had poor growth in the C–Y medium supplemented with nicotinamide riboside compared with the ΔniaX mutant, which showed WT levels of growth (Fig. 3e, f), a phenotype that was restored upon complementation. This result is in agreement with previous reports that PnuC imports nicotinamide riboside into the related bacterium Streptococcus pyogenes, indicating PnuC may have similar substrate specificity amongst other streptococci (Sauer et al., 2004).

To confirm substrate transport capacity of these transporters, we measured the relative uptake of the radiolabelled substrates. Corroborating the growth-curve experiments, uptake of both nicotinamide and nicotinic acid were reduced in the ΔniaX mutant, a phenotype restored to WT levels upon complementation of niaX (Fig. 4a, b). The ΔpnuC mutant retained the capacity to import both nicotinamide and nicotinic acid (data not shown), but was severely impaired in the acquisition of nicotinamide riboside, a defect ameliorated when pnuC was complemented on a plasmid (Fig. 4c). It should be noted that greater concentrations of labelled substrates than that used in the growth-curve experiments were utilized in order to achieve sufficient label incorporation. Taken together, these data confirm the substrate specificity of these importers in the pneumococcus.

In addition to these typical substrates, we also assessed the capacity of nicotinamide mononucleotide to rescue pneumococcal growth. Import of this substrate has previously been shown to be dependent on a phosphorylase such as AphA (Salmonella) or NadN (Hae. influenzae) (Grose et al., 2005; Kemmer et al., 2001). Both the ΔniaX and the ΔpnuC mutants underwent WT growth in C–Y supplemented with nicotinamide mononucleotide (Fig. 5a), suggesting that either both proteins can import the molecule, which is modified at the cell surface and subsequently imported by either of these systems, or an additional import machinery exists. To address this unexpected finding, we assessed the capacity of exogenously added nicotinamide mononucleotide to compete with nicotinamide, nicotinic acid, and nicotinamide riboside for uptake. Interestingly, supplementation of the culture with a molar ratio of five nicotinamide mononucleotide to one of any of the other three substrates partially blocked uptake of all three of the radiolabelled substrates (Fig. 5b).

**Virulence of NAD salvage pathway importers in mice**

Because NAD is an essential cofactor, we hypothesized that the salvage pathways would be required for pneumococci to acquire NAD precursors from the mammalian host and, consequently, for their survival and pathogenicity, as seen previously with the PnuC salvage system in Hae. influenzae in vivo studies (Herbert et al., 2003). To test this, mice were intranasally infected with Str. pneumoniae (which progresses rapidly from the sinuses to the lungs and eventually traverses into the bloodstream) WT TIGR4, the ΔniaX mutant or the ΔpnuC mutant, and then mouse survival and blood titres were assessed. The virulence of the salvage pathway import mutants varied from each other, with the ΔniaX mutant having WT levels of pathogenesis and the ΔpnuC mutant being completely attenuated in the intranasal model (Fig. 6a–c). Further investigation of the ΔpnuC mutant in an intratracheal pneumonia model yielded the same attenuation phenotype as WT TIGR4, as measured by blood and lung titres (Fig. 6d, e). Taken together, these data indicate that PnuC is critical for lung colonization and bacterial virulence in mice whereas NiaX is dispensable.

**DISCUSSION**

Here, we sought to use both in vitro and in vivo techniques to confirm substrates of the NiaX and PnuC importers and assess the role of these systems during invasive pneumococcal disease. Our data confirmed that NiaX showed preference for importing nicotinic acid and nicotinamide, that PnuC specifically imported nicotinamide riboside, and that single deletions of both genes retained capacity to
import nicotinamide mononucleotide. In the process, we also have shown that the salvage pathway is essential for pneumococcal growth as the C–Y medium contains tryptophan and other components needed for traditional de novo synthesis. As the bacteria listed in Fig. 1a are pathogenic, there seems to be no connection between pathogenicity and having the salvage pathway involving NiaX or PnuC alone or involving both importers. Additionally, there seems to be no larger connection between pathogenicity in bacteria that contain de novo synthesis alone (Helicobacter pylori), both the de novo and salvage pathways (Bacillus anthracis), or an alternative de novo/salvage pathway (Francisella tularensis) (Huang et al., 2008; Sorci et al., 2009). The multitude of strategies utilized by these...
Fig. 4. Uptake of NAD salvage pathway compounds. (a) Nicotinamide, (b) nicotinic acid, (c) nicotinamide riboside. The parental TIGR4 and the ΔniaX and ΔpnuC mutants along with the complemented strains were grown in C−Y supplemented with 14C-labelled versions of their respective substrates. For ΔniaX this was 1 μM nicotinic acid or 500 nM nicotinamide, and for ΔpnuC this was 1 μM nicotinamide riboside. After incubation, cells were collected and washed, and the level of uptake was measured.

Data were normalized to counts min⁻¹ of the parental TIGR4 strain, representing 100% uptake. Data represent the mean and SE from at least three experiments. *, P<0.05 by paired student’s t-test.

Fig. 5. Nicotinamide mononucleotide rescues growth and inhibits uptake of other NAD salvage pathway components. (a) Parental TIGR4 and ΔniaX and ΔpnuC mutants were grown in C−Y with and without the addition of 10 μM nicotinamide mononucleotide. One-way ANOVA and Dunn’s multiple comparison post-test were performed using TIGR4 in the related condition as the basis of comparison (n=4) with no significant differences observed. (b) Competition for uptake was measured by supplementation of nicotinamide mononucleotide to cells grown in C−Y medium with nicotinamide, nicotinic acid, or nicotinamide riboside. Cells were incubated with a 5 : 1 molar ratio of nicotinamide mononucleotide along with the respective 14C-labelled substrates, and measured for uptake after 1 h. Data were normalized to counts min⁻¹ of the parental TIGR4 strain, representing 100% uptake. Data represent the mean and SE from three replicates.
pathogens to acquire these essential factors underscores their importance in bacterial physiology.

The nicotinamide mononucleotide data suggest either that there is an additional import system in *S. pneumoniae* or that both NiaX and PnuC are involved in import, perhaps via an extracellular protein that can modify nicotinamide mononucleotide to an importable form. There is considerable variability amongst PnuC homologues involving nicotinamide riboside binding and homology of critical residues (Jaehme *et al.*, 2014). The PnuC homologues from both *Hae. influenzae* and *Sal. typhimurium* do not import nicotinamide mononucleotide but can convert it to the form importable by PnuC (nicotinamide riboside) via NadN or AphA, respectively. The PnuC from these two organisms and from *S. pneumoniae* all contain the motif for nicotinamide mononucleotide binding. However, PnuC homologues from several other organisms do not contain the consensus binding residues (Grose *et al.*, 2014).

![Graphs showing survival and blood titres for different strains](image)

**Fig. 6.** PnuC is necessary for virulence in a mouse model. (a–c) Mice were intranasally infected with TIGR4 or the ΔpnuC or ΔniaX mutant and survival (a) and blood titres at 24 (b) and 48 h (c) were assessed. Dashed line represents limit of detection. Survival of mice infected with mutants was compared with that of those infected with WT TIGR4 by using the Mantel–Cox test; blood titre data were compared by using the Mann–Whitney test. (d, e) Mice were intratracheally infected with TIGR4 or the ΔpnuC or ΔniaX mutant, and lung (d) and blood (e) titres were assessed at 48 h. Lung and blood titre data were compared using the Mann–Whitney test and an ANOVA non-parametric test with a multiple comparison correction with the Kruskal–Wallace test. *, *P*<.01.
This observation suggests that separate classes of NAD salvage substrate importers annotated as PnuC import nicotinamide riboside and/or nicotinamide mononucleotide and that NiaX (where not enough structural information is known) imports niacin and/or nicotinamide mononucleotide as preferred substrates. This hypothesis is supported by the sequence divergence in both TIGR4 NiaX and PnuC as compared with sequences outside the genus. Such amino acid differences would likely impact the overall fold of the respective protein structures and perhaps add the ability to import nicotinamide mononucleotide directly, as observed with mutation of Salmo nella PnuC (Grose et al., 2005). Interestingly, the amino acids in Salmonella PnuC preventing this transporter from importing nicotinamide mononucleotide are not conserved in the pneumococci, indicating that the pneumococcal PnuC may be permissive for this substrate along with nicotinamide riboside. This underscores the importance of experimental confirmation of highly divergent orthologues for substrate specificity in different species.

Although it is possible for both PnuC and NiaX in Str. pneumoniae to acquire the ability to import nicotinamide mononucleotide, another possibility is the existence of an additional importer that has not been characterized. Unfortunately, to date, there are no known specific importers of nicotinamide mononucleotide in bacteria. Furthermore, Str. pneumoniae does not have an NadN or AphA homologue, which would be used to dephosphorylate nicotinamide mononucleotide to nicotinamide riboside, a form readily imported by PnuC.

On the basis of previous works, sequence homology, and our data described here, we propose the following pneumococcal pathway of NAD synthesis (Fig. 7). NiaX can import either nicotinic acid or nicotinamide, which can be deaminated to nicotinic acid by nicotinamidase PncA (SP_1583). Nicotinic acid phosphoribosyltransferase, PncB (SP_1421), adds a phosphorylated ribose to nicotinic acid to form nicotinic acid (nicotinate) mononucleotide. NadD, a nicotinamide/nicotinic acid nucleotide adenylyltransferase (SP_1747), then adds an adenine, forming nicotinic acid adenine dinucleotide. The NAD synthase NadE (SP_1420) then adds the final amide group to form NAD. NAD synthesis via nicotinamide riboside occurs in considerably fewer steps than does NAD synthesis through nicotinic acid or nicotinamide. Once imported, nicotinamide riboside is, in theory, converted to nicotinamide mononucleotide via phosphorylation by an unknown kinase, as the TIGR4 strain of Str. pneumoniae does not contain the kinase NadR (Kurnasov et al., 2002; Singh et al., 2002). Then, it is converted to NAD through NadD, which has nucleotide adenylyltransferase activity.

In addition to understanding the substrates of the salvage pathway importers, we sought to analyse their impact on virulence in two mouse infection models. Our data show the attenuation of a pneumococcal ΔpnuC mutant in a lung infection model as compared with WT. Interestingly, this result leads to speculation about the bioavailability of these metabolites in the host and to the hypothesis that nicotinamide riboside is more bioavailable than either nicotinic acid or nicotinamide, or that Str. pneumoniae is far more efficient in using nicotinamide riboside as a precursor for the NAD salvage pathway than nicotinic acid and nicotinamide, or both.

Nicotinamide riboside supplementation has been implicated in many beneficial functions in the host, including...
protection against mitochondrial myopathy (Khan et al., 2014), hearing loss (Brown et al., 2014) and obesity (Cantó et al., 2012), although these functions are not likely due to increasing NAD synthesis (Frederick et al., 2015) but may be due to general bioavailability. Although nicotinamide riboside is necessary for pathogen and host, fortunately pneumococcal PnuC and the homologous proteins of other bacteria have no sequence homology to any proteins in the animal kingdom. Thus, as has been successfully shown with Hae. influenzae (Sauer et al., 2004), PnuC could potentially be targeted therapeutically in bacterial species harbouring this pathway without mammalian consequence.

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