Antibacterial drug leads targeting isoprenoid biosynthesis

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With the rise in resistance to antibiotics such as methicillin, there is a need for new drugs. We report here the discovery and X-ray crystallographic structures of 10 chemically diverse compounds (benzoic, diketo, and phosphonic acids, as well as a bisamidine and a bisamine) that inhibit bacterial undecaprenyl diphosphate synthase, an essential enzyme involved in cell wall biosynthesis. The inhibitors bind to one or more of the four undecaprenyl diphosphate synthase inhibitor binding sites identified previously, with the most active leads binding to site 4, outside the catalytic center. The most potent leads are active against *Staphylococcus aureus* [minimal inhibitory concentration ($MIC)_{90}$ ~0.25 μg/mL], and one potently synergizes with methicillin (fractional inhibitory concentration index = 0.25) and is protective in a mouse infection model. These results provide numerous leads for antibacterial development and open up the possibility of restoring sensitivity to drugs such as methicillin, using combination therapies.

drug discovery | *in silico* high-throughput screening | peptidoglycan | protein structure

Targeting isoprenoid biosynthesis is a potentially important route for antibiotic discovery because isoprenoids are involved in the very early steps of bacterial cell-wall biosynthesis—the condensation of dimethylallyl diphosphate (DMAPP, **1**) with two molecules of isopentenyl diphosphate (IPP, **2**) to form farnesyl diphosphate (FPP, **3**), catalyzed by the enzyme farnesyl diphosphate synthase (FPPS), followed by the addition of eight more IPP molecules to form undecaprenyl diphosphate (UPP, **4**) (1, 2) (Fig. 1). Formation of **4** is catalyzed by the enzyme undecaprenyl diphosphate synthase (UPPS), and several UPPS inhibitors have been reported (3–10). UPP is then hydrolyzed to the monophosphate, which is next converted to lipid I and lipid II, leading to formation of cell wall peptidoglycan (Fig. 1) (11, 12). Antibiotics such as methicillin and vancomycin act in the latter stages of peptidoglycan formation, again as shown in Fig. 1. Here, we focus on the development of UPPS inhibitors because UPPS is an essential protein not produced by humans (13). UPPS inhibitors are predicted to synergize with the more-conventional cell-wall biosynthesis inhibitors, potentially reducing the toxicity of drugs such as vancomycin (by decreasing dosage), or restoring drug sensitivity [e.g., with methicillin-resistant *Staphylococcus aureus* (MRSA)]. The UPPS structure is unusual in that there are four known ligand binding sites (5), opening up the possibility of designing a diverse range of inhibitors.

Results and Discussion

UPPS Inhibitors. In previous work, we and others reported the discovery of several UPPS inhibitors, including bisphosphonates such as BPH-629 (**5**) (5), tetramic acids such as **6** (6), as well as diketoacids such as **7** (10) and benzoic acids such as **8** (9) (Fig. 2). Based on *in silico* high-throughput screening (9) and hit development (Fig. S1), we produced a small series of benzoic (**9**–**12**), phosphonic (**13**), and diketoacids (**14**, **15**) that had activity against UPPS (Fig. 2). In addition to these anionic species, we discovered several potent cationic inhibitors (**16**–**18**); this was unexpected from both a computational and experimental standpoint because these compounds do not mimic the (anionic) FPP substrate, and the UPPS mechanism is not thought to involve carbocation intermediates (14). We thus sought to determine how these inhibitors bind to their UPPS target, by obtaining crystal structures of **8**–**16** and **18** bound to *Escherichia coli* UPPS.

Four Inhibitor Binding Sites in UPPS. UPPS functions by sequentially adding IPP to an allylic substrate, initially FPP (15). It might reasonably be expected, then, that anionic inhibitors with lipophilic side-chains would bind to the FPP substrate site, as shown in Fig. 3*A*, yellow (PDB ID code 1X06). However, in a second structure (PDB ID code 1V7U), two FPP molecules bind, one in the substrate site and the other in a second site at the "bottom" of the protein (Fig. 3*A*, green). Moreover, with the bisphosphonate inhibitor **5**, there are actually four binding sites (sites 1–4) (5) that can be occupied (Fig. 3*B*, cyan; PDB ID code 2E98) in which the side chains in each of the four inhibitor molecules occupy the large hydrophobic center of the protein that normally accommodates the C_{55} side chain in the UPP product. With the two less-active benzoic acid inhibitors, **8** and **9**, we find that only site 3 (Fig. 3*C*; PDB ID code 3SGT) or sites 1, 2, and 3 are occupied (Fig. 3*D*; PDB ID code 3SGV), but the activity of both of these inhibitors is weak (**8**, *E. coli* UPPS, IC_{50} = 150 μM; *S. aureus* UPPS, 170 μM; **9**, *E. coli* UPPS, IC_{50} = 35 μM, *S. aureus* UPPS, 72 μM; Table S1). Full data acquisition and structure refinement details are in Table S2, and electron densities (2Fo-Fc and simulated-annealing Fo-Fc omit maps) are in Fig. S2 *A* and *B*. So, with these two benzoic acid inhibitors, binding to sites 1, 2, or 3 correlates only to weak UPPS inhibition.

Potent Benzoic Acid Inhibitors Bind to Site 4. We next determined the structures of the three potent benzoic acid inhibitors (10–12) (Fig. 2) bound to UPPS (Fig. 4 *A*–*C*). Each of these molecules contains a long hydrophobic side-chain and, on average,

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The authors declare no conflict of interest.

Data deposition: Crystallography, atomic coordinates, and structure factors have been deposited in the Protein Data Bank, www.pdb.org (PDB ID codes 3SGT, 3SGV, 3SGX, 3SH0, 4H2O, 4H38, 4H3C, 4H3A, 4H2J, 4H2M, and 4H8E).

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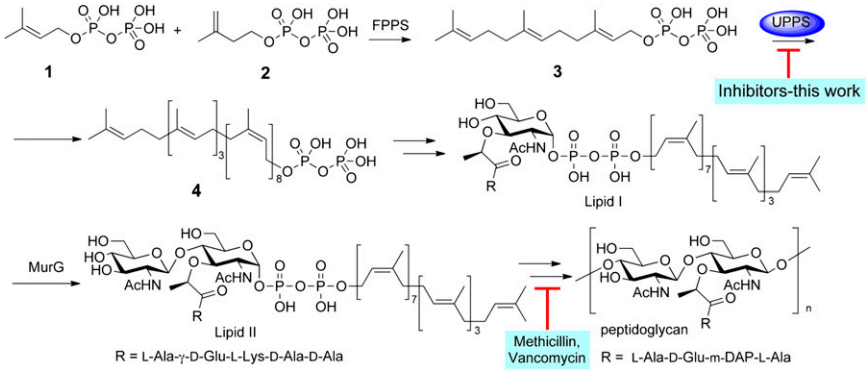

Fig. 1. Schematic outline of cell wall biosynthesis (in most bacteria) showing involvement of isoprenoid biosynthesis in the early stages of peptidoglycan formation.

the IC_{50} values against both *E. coli* and *S. aureus* UPPS are ~3 μM (Table S1). What is notable about these X-ray structures is that in each case, site 4 is occupied, together with either sites 1, 2, or 3. Full data acquisition and structure refinement details are in Table S2, and electron densities are in Fig. S2 *A* and *B*. In addition, we found that the aryl phosphonate inhibitor **13** also occupied two sites (Fig. 4*D*). However, there are two chains in one asymmetric unit, and site occupancies in the two chains are variable: the lower site-occupancy chains are shown in Fig. S2*C*. These four structures suggest that good UPPS inhibition correlates with occupancy of site 4.

Diketoacids, a Bisamidine and a Bisamine also Target Site 4. In previous work (10), we found that the diketoacid **15** had potent cell-growth inhibition activity with the following minimal inhibitory concentration $(MIC)_{90}$ values: 0.25–0.5 μg/mL against *S. aureus*; 0.5 μg/mL against *Bacillus anthracis*; 4 μg/mL against *Listeria monocytogenes* and *Enterococcus faecium*; and 1 μg/mL against *Streptococcus pyogenes*, but little toxicity toward human cell lines (>20 μM). We therefore determined the structure of **15** and a second diketoacid (**14**), bound to UPPS. As seen in Fig. 5 *A* and *B*, both diketoacids bind to site 4, with **14** also binding to site 3. The observation that **15** binds only to site 4 is of interest because this inhibitor has very good antibiotic activity (10). Plus, the occupation of site 4 in both structures is consistent with the results for the other potent anionic inhibitors (Fig. 4).

A surprising result from the *in silico* screening work (Fig. S1) was that bisamidines such as **16** had modest activity against UPPS. Moreover, the biphenyl bisamidine **17** showed potent activity against UPPS (IC_{50} = 0.1 μM) as well as a MIC_{90} of 0.25 μg/mL against *S. aureus* (USA300, MRSA strain). We also found that another dicationic species **18** was a UPPS inhibitor active against *S. aureus* (Table S1). We were unable to obtain the structure of **17** bound to UPPS, but we did obtain structures of **16** and **18** bound to UPPS.

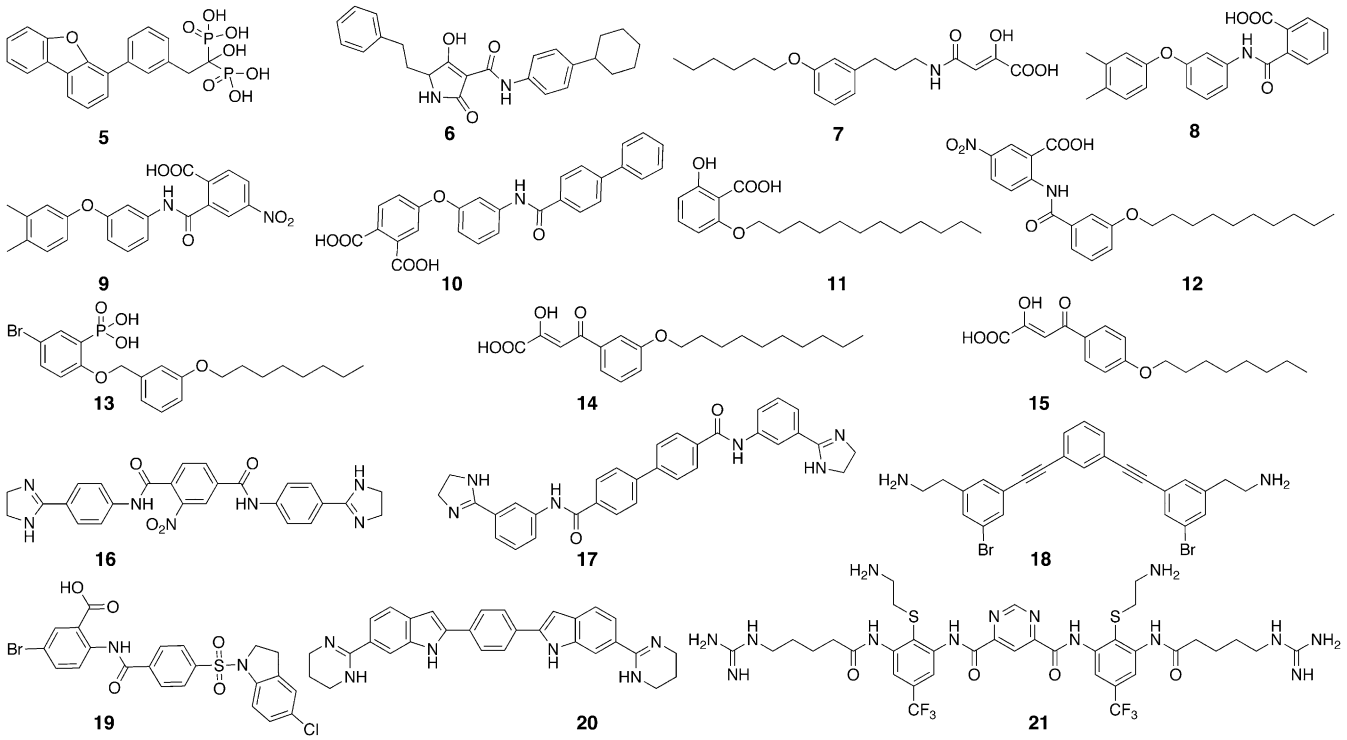

Fig. 2. Chemical structures of UPPS inhibitors and drug leads of interest.

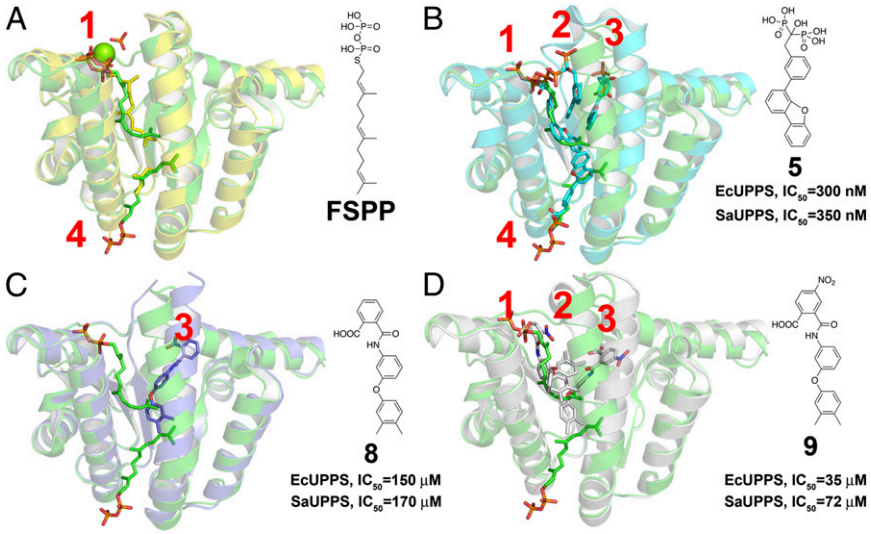

Fig. 3. X-ray structures of *E. coli* UPPS showing substrate and inhibitor binding sites. (*A*) FSPP (yellow) binds to site 1 (PDB ID code 1X06) and FPP (green) binds to sites 1 and 4 (PDB ID code 1V7U). (*B*) A bisphosphonate (**5**) binds to sites 1–4 (PDB ID code 2E98). (*C*) Benzoic acid inhibitor **8** binds to site 3 (cyan, PDB ID code 3SGT), superimposed on FPP-bound structure (green, PDB ID code 1V7U). (*D*) Benzoic acid inhibitor **9** binds to sites 1–3 (cyan, PDB ID code 3SGV), superimposed on FPP-bound structure (green, PDB ID code 1V7U). The large red numbers indicate sites 1–4.

With these two cationic inhibitors, rather than two individual molecules binding, we observe that a single molecule binds, with its polar, cationic groups located at or near the protein's surface, whereas the hydrophobic "spacer" is buried inside the protein's hydrophobic interior, (Fig. 5 *C* and *D*; PDB ID codes 4H2J and 4H2M). Though we did not succeed in crystallizing the most potent lead **17**, a similar "polar-hydrophobic-polar" binding arrangement in which the biphenyl group is buried seems very likely for this species also, and is supported by the results of computational docking, as shown in Fig. S2*D*.

Comparison of *E. coli* and *S. aureus* UPPS Structures and Their Inhibition. In this work, we determined the activity of each inhibitor against both *E. coli* UPPS and *S. aureus* UPPS, finding that there is a very good correlation ($R^2 = 0.8$) between the 14 sets of pIC_{50} ($= -\log_{10}IC_{50}$) values (Table S1; Fig. S3*A*); this is not unexpected because 18 of the top 20 residues in a SCORECONS (16) analysis of *E. coli* UPPS are present in *S. aureus* UPPS and most other bacterial UPPSs (Table S3). We were not able to determine the X-ray structures of any inhibitor bound to *S. aureus* UPPS, but we did determine the structure of the protein with a bound FPP (PDB ID code 4H8E; full data acquisition and structure refinement details are in Table S4). *S. aureus* UPPS cocrystallized with FPP in site 1, together with a SO_4^{2-} in the IPP binding site, as reported in a patent application (17). A superposition of the *S. aureus* and *E. coli* proteins is shown in Fig. S3*B*, where we find a Cα rmsd of 0.91 Å over 202 residues, indicating that both structures are very similar [in the presence of FPP/FSPP (*S-thiolo*-FPP) and either IPP or SO_4^{2-}], consistent with the pIC_{50} correlation.

Relationship to Other Inhibitors: Is UPPS a Missing Link? The structures of several of the UPPS inhibitors described here are similar to (and with **18**, the same as) those being developed as antiinfective drug leads but whose mechanisms of action are not clear. For example, the chemical structures of the benzoic acid inhibitors are similar to those of anthranilic (*ortho*-aminobenzoic) acids reported by Larsen et al. (18) and Mott et al. (19) having activity against *S. aureus*. The molecular mechanism of action of these inhibitors was initially thought to involve inhibition of translation/termination, but in later work this inhibition was not found to correlate with cell growth inhibition, and a new target (SA1575, of unknown function), as well as inhibition of cell wall biosynthesis, was reported. We find that

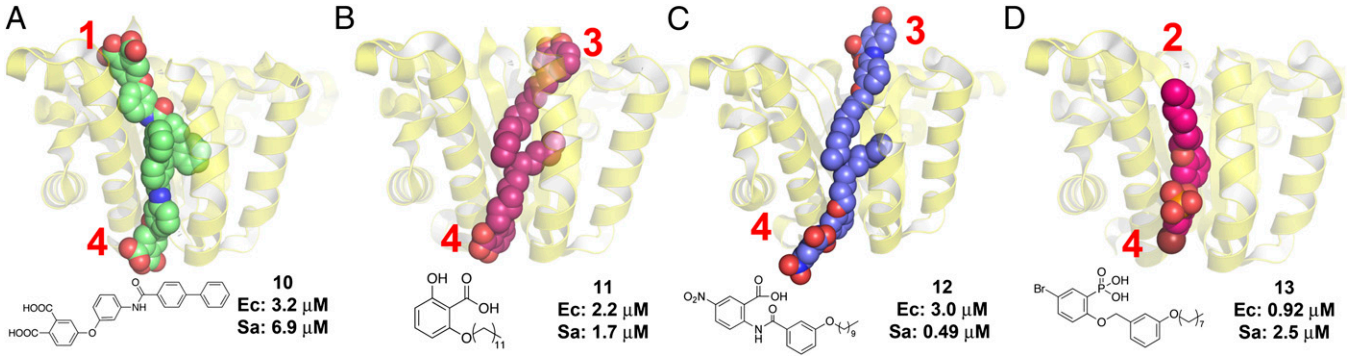

Fig. 4. Crystal structures of the more potent benzoic acids and a phosphonate inhibitor. (*A*) **10** (PDB ID code 3SGX). (*B*) **11** (PDB ID code 3SH0). (*C*) **12** (PDB ID code 4H2O). (*D*) **13** (PDB ID code 4H38). In each case, site 4 is occupied, together with either site 1, 2, or 3, indicating the likely importance of site 4 binding for good activity. The values shown are the IC_{50}s for *E. coli* UPPS inhibition (Ec) or *S. aureus* UPPS inhibition (Sa).

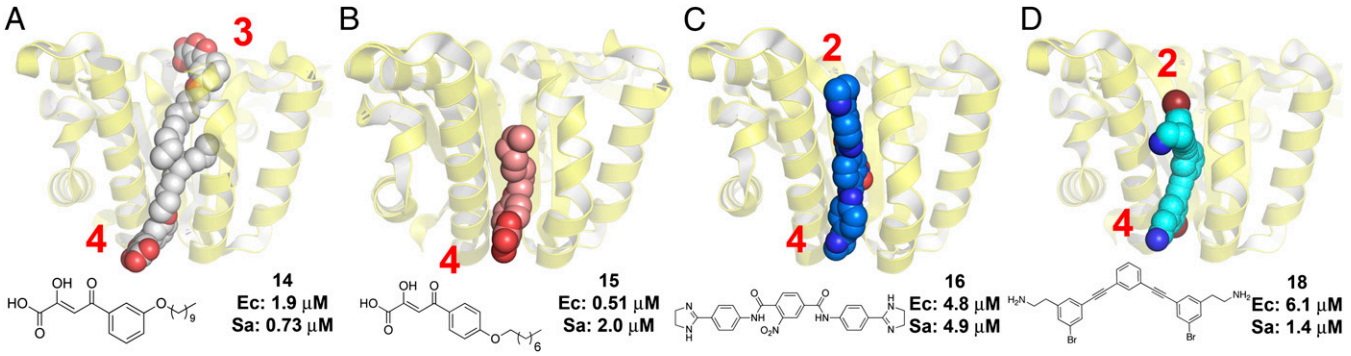

Fig. 5. Crystal structures of diketo acids and two dicationic inhibitors bound to *E. coli* UPPS. (*A*) **14** (PDB ID code 4H3C). (*B*) **15** (PDB ID code 4H3A). (*C*) **16** (PDB ID code 4H2J). (*D*) **18** (PDB ID code 4H2M). The common feature in each case is binding to site 4. The values shown are the IC_{50}s for *E. coli* UPPS inhibition (Ec) or *S. aureus* UPPS inhibition (Sa).

a pharmacophore model (Fig. 6*A*) of seven potent benzoic acid UPPS inhibitors we synthesized (Fig. S4*A*) is very similar to that obtained for *S. aureus* cell growth inhibition (Fig. 6*B*) using five structures reported by Larsen et al. (Fig. S4*B*), making UPPS inhibition one likely mechanism for these inhibitors—in particular because they are already known to inhibit cell wall biosynthesis. In addition, we found that the lead **19** reported by Larsen et al. (18) is a ~1 to 2 μM UPPS inhibitor (Table S1), consistent with a role in *S. aureus* growth inhibition.

In addition to the benzoic/anthranilic acids, there is also interest in the mechanisms of action of bisamidines, such as **20** (20, 21), as well as of other cationic species, such as **21** (22), and it has been proposed that these and related compounds could bind to the minor groove of DNA (20), or that they could alter lipid bilayer structure (23–25), as illustrated schematically in Fig. 6 *C* and *D*. Based on our crystallographic (Fig. 5 *C* and *D*) as well as enzyme inhibition results, it is clear, however, that in addition to these binding modes, polar-hydrophobic-polar inhibitors (such as **17** or **18**) can also bind to proteins, as shown in the cartoon in Fig. 6*E*, with their polar headgroups located near polar protein residues (or at the protein/water interface), whereas their hydrophobic centers are buried inside the protein target (Fig. 5 *C* and *D*).

Notably, as with the benzoic acids, bisamidines such as **20** can inhibit cell wall biosynthesis, and with **20** we find quite potent (470 nM) UPPS inhibition.* The ability to inhibit UPPS in addition to, e.g., DNA and lipid membrane targeting likely contribute to the potent activity of these compounds and, in some cases, the lack of resistance observed experimentally. In addition, it is also possible that other prenyltransferases, such as FPPS, may in some cases be targeted.

Synergy and in Vivo Results. The UPPS inhibition results suggested to us the possibility of synergistic activity with downstream cell-wall biosynthesis inhibitors, such as methicillin (Fig. 1); this is indeed the case, as shown in Fig. 7*A* in which we present the isobologram (26) for **17** + methicillin against a USA300 strain of MRSA. We observe a potent synergistic interaction with a fractional inhibitory concentration index (FICI), defined as

$$\mathrm{FICI} = \mathrm{FIC_A} + \mathrm{FIC_B} = \mathrm{MIC_{90}(AB)/MIC_{90}(A)} + \mathrm{MIC_{90}(BA)/MIC_{90}(B)},$$

where, FIC_A, FIC_B are the fractional inhibitory concentrations of drugs A and B, and MIC_{90} (AB), MIC_{90} (BA) are the MIC_{90} values of the most effective combination of A or B in the presence of B or A (27, 28). Using this method, FICI values <0.5 represent synergism; >0.5 and <1.0 represent additivity; >1 and <2 represent an indifferent effect; and ≥2 represents drug antagonism (29). An FICI = 0.25 thus represents strong synergism, opening up the probability of restoring drug sensitivity in drug-resistant strains. However, are such compounds active in in vivo models of infection?

In previous work, it has been found that, e.g., benzoic acids (such as **19**) as well as tetramic acids (such as **6**) have potent activity against bacteria; however, there have been no previous

*Opperman TJ, et al. Poster Session, 50th Interscience Conference on Antimicrobial Agents and Chemotherapy, September 12–15, 2010, Boston.

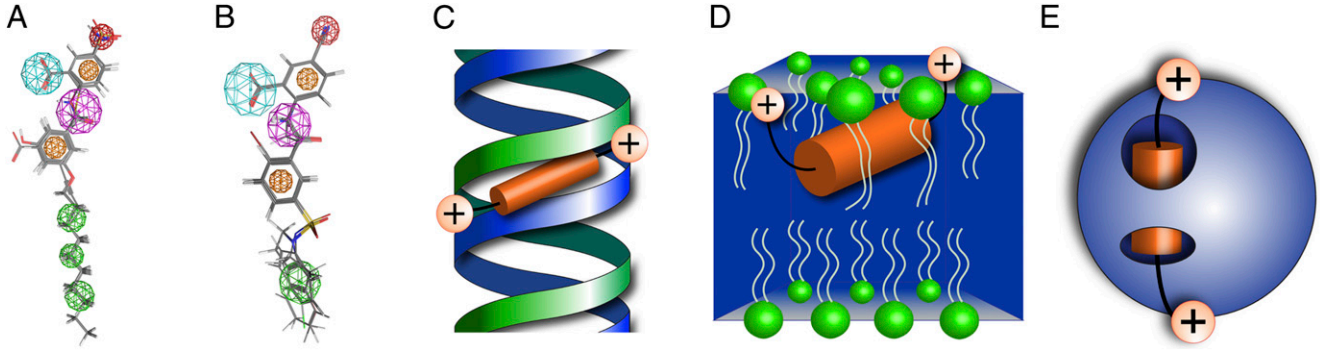

Fig. 6. UPPS as a missing link. Models and cartoons. (*A*) Pharmacophore model for UPPS inhibition by benzoic acids. (*B*) Pharmacophore model for *S. aureus* growth inhibition by benzoic acids. Common features are benzoic acid carboxylates (cyan) with electron-withdrawing *meta* substituents (red); an x–y spacer (dark pink); two aromatic features (orange); and more-distal hydrophobic features (green). (*C*) Cationic-hydrophobic-cationic inhibitor binding to DNA. (*D*) Cationic-hydrophobic-cationic inhibitor binding to anionic lipids in a membrane. (*E*) Cationic-hydrophobic-cationic inhibitor binding to a protein.

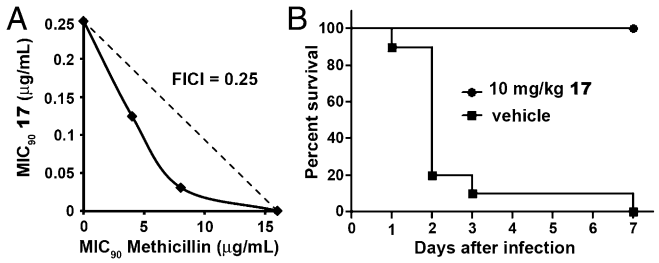

Fig. 7. In vitro synergy and in vivo results with **17**. (*A*) Isobologram for **17** + methicillin inhibition of *S. aureus* (USA300) cell growth. FICI = 0.25. (*B*) Activity of **17** in a mouse model of *S. aureus* (USA200) infection. Shown is one representative experiment repeated twice (n = 10 mice per group per experiment). No mice in the group treated once daily with 10 mg/kg of **17** (three doses total) died during either experiment.

reports of in vivo activity, due perhaps to strong binding to plasma proteins. Because **17** had potent activity against UPPS (110 nM), we tested it in a mouse model of infection using the USA200 Sanger 252 (MRSA) strain of *S. aureus*. As can be seen in Fig. 7*B*, mice treated postinfection only with vehicle control all died, whereas mice treated with **17** (20/20 total, pooled results of two experiments) survived with no apparent adverse reactions.

Computational Results: FTMap, Principal Component, and Receiver Operating Characteristic/Area Under the Curve Analyses. The results described above represent the discovery of a series of UPPS inhibitors—drug leads—some of which have potent activity in cells and a mouse infection model. From a structural perspective, the most surprising result was that the most potent inhibitors all bound to site 4, not the substrate site, site 1. In previous work on bisphosphonate UPPS inhibitors (5) we found that a wide range of bisphosphonates bound to site 1, and that enzyme inhibition and site 1 docking scores were highly correlated (5). However, with all of the nonbisphosphonate inhibitors described here, we find that binding to site 4 is the common structural denominator for ligands with high affinity. Other sites are also often occupied, with either two molecules binding, or one inhibitor spanning two sites (sites 4 and 2, with the dicationic species).

Site 4 is quite removed from the most-flexible loop region (residues 72–82) of the active site, suggesting that there may be fewer entropic costs due to constraining this loop, associated with inhibitor binding to site 4, rather than to sites 1–3, where the ligand directly contacts and restrains the loop. Site 4 is also predicted to be druggable when using the solvent-mapping program FTMap (30), as shown in Fig. 8*A*, again supporting the idea that inhibitors that bind to site 4 will be good drug leads. With the nonbisphosphonate inhibitors, we also see that the global structures are quite similar to apo UPPS (Fig. 8*B*, red), using principal component analysis (31). The bisphosphonate inhibitors (blue) and substrate (yellow)-bound structures are altered to a greater extent from the apo form than are the nonbisphosphonate structures (red), which suggests less induced-fit occurs on binding, which again will reduce any energetic costs associated with protein conformational changes upon binding.

Finally, because many of these inhibitors were the result of virtual screening, we assessed the predictive nature of each structure using a receiver operating characteristic/area under the curve (ROC/AUC) approach (32) with a 112-compound screening dataset (Fig. S5). Enrichment results are shown in Fig. 8*C* and Fig. S6. Good results (AUC = 0.768) are obtained when using the "open" structure containing **5** bound to sites 1–4, but the best result is obtained using the **15** structure (PDB ID code 4H3A), an "ajar" (Fig. 8*B*) or partially closed structure in which only site 4 is occupied (Fig. 8*C*, bottom), where AUC = 0.802. Taken together, these results strongly support the importance of developing compounds that bind to site 4 as UPPS inhibitor drug leads, and that computational models based on these structures can significantly enrich the hit rate.

Conclusions

The results we have described herein are of interest for several reasons. First, we obtained the X-ray structures of 10 UPPS inhibitors covering a diverse range of structures: benzoic acids, diketoacids, an aryl phosphonate, a bisamidine, and a bisamine. The surprising result was that both cationic as well as anionic compounds were inhibitors, the cationic species having an unusual polar-hydrophobic-polar structural motif. Second, we find evidence that occupancy of site 4 (not the FPP substrate site, site 1) correlates with the potent activity of these inhibitors, and that site 4 is predicted to be druggable. Third, we find that the cationic

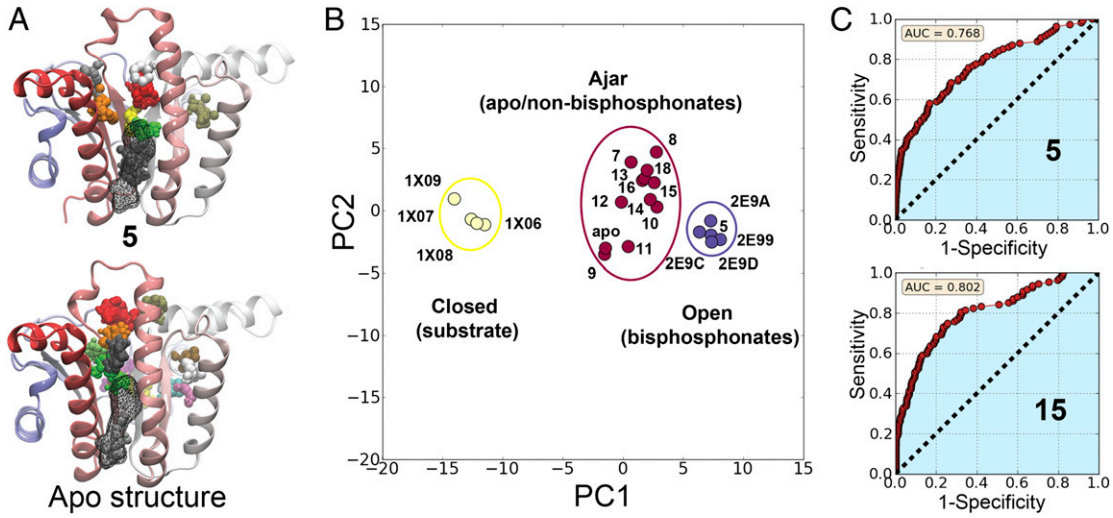

Fig. 8. Computational analysis of UPPS structural results. (*A*) FTMap computational solvent mapping of UPPS structures (PDB ID codes 2E98 and 3QAS) suggest that site 4 is druggable in either inhibitor-bound complexes or unbound. UPPS is represented as a cartoon; small probes are colored spheres; black wireframe outlines site 4. (*B*) Principal component analysis of *E. coli* UPPS structures. Substrate-bound structures (yellow) are closed (33); bisphosphonates (blue) are open (33); the apo and nonbisphosphonate structures (red) are all ajar (slightly open). (*C*) ROC/AUC analysis of most-predictive UPPS structures in terms of initial enrichment for actives under 100 μM (Fig. S6).

(bisamidine and a bisamine) inhibitors span both sites 2 and 4, with their polar groups at or near the protein/water interface, whereas their hydrophobic domains are buried. This result is of particular importance because this motif is very similar to that proposed to be important for DNA and lipid membrane binding with structurally related inhibitors, leading to the idea that such compounds may have multiple targets (including UPPS), thereby increasing potency. We also find that a closely related biphenyl analog (**17**) inhibits UPPS at ~100 nM levels, has a MIC_{90} of 0.25 μg/mL, and strongly synergistic activity (FICI = 0.25) with methicillin in an MRSA strain otherwise resistant to the antibiotic. In addition, this compound shows clear therapeutic activity in a mouse model of infection. Finally, we propose that anthranilic acids, known to be potent inhibitors of *S. aureus* growth that target cell-wall biosynthesis, also target bacterial UPPS. Taken together, these results open up additional routes to anti-infective therapies targeting bacterial isoprenoid biosynthesis, and suggest that in some cases drug leads that have been proposed to target DNA and lipid membrane structure may also target bacterial cell-wall biosynthesis via UPPS inhibition.

Methods

E. coli UPPS and *S. aureus* UPPS were expressed and purified as described previously (9). UPPS inhibition assays were carried out as described previously (5). UPPS/inhibitor crystals were obtained via soaking as described previously (5). Structure determinations and refinements were carried out basically as described previously (5), with full details given in *SI Methods*. For the 11 structures reported, the resolution was on average 1.88 Å (±0.29 Å), and R_{free} was on average 24.6% (±3.9%). Full synthesis and characterization details for all compounds investigated crystallographically are provided in *SI Methods*. In vivo experiments used female BALB/c mice infected intraperitoneally with *S. aureus* (USA200), as described in detail in *SI Methods*. Bacterial cell-growth inhibition assays were carried out as described previously (10). The care and experimental manipulation of our mice were reviewed and approved by the Institutional Animal Care and Use Committee at the University of California at San Diego.

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