

Current Topics

Pentapeptide Repeat Proteins[†]

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ABSTRACT: The pentapeptide repeat protein (PRP) family has more than 500 members in the prokaryotic and eukaryotic kingdoms. These proteins are composed of, or contain domains composed of, tandemly repeated amino acid sequences with a consensus sequence of [S,T,A,V][D,N][L,F][S,T,R][G]. The biochemical function of the vast majority of PRP family members is unknown. The three-dimensional structure of the first member of the PRP family was determined for the fluoroquinolone resistance protein (MfpA) from *Mycobacterium tuberculosis*. The structure revealed that the pentapeptide repeats encode the folding of a novel right-handed quadrilateral β -helix. MfpA binds to DNA gyrase and inhibits its activity. The rod-shaped, dimeric protein exhibits remarkable similarity in size, shape, and electrostatics to DNA.

Discovery of the Pentapeptide Repeat Family

The first protein identified with what is now recognized as the pentapeptide repeat motif was the *hglK*-encoded protein from *Anabaena* sp. strain PCC 7120 (1). This filamentous cyanobacterium is known to form heterocysts, specialized cells capable of fixing nitrogen, when reduced forms of nitrogen are unavailable. Chemical mutagenesis of the PCC 7120 strain allowed mutants to be identified that were incapable of forming the thick glycolipid outer cell

component characteristic of heterocysts. Complementation analysis revealed that the *hglK* gene could reverse the mutant phenotype and that, in the mutant strain, a mutation had introduced a stop codon at amino acid position 496 of the 727-residue protein. Starting at position 501, one observes a series of 36 uninterrupted, tandem repeats of a pentapeptide with the consensus sequence ADLSG. The amino terminus contained four possible membrane-spanning domains, suggesting that these might anchor the protein into the membrane, and that glycolipid transport or assembly into the heterocyst might be the function of the pentapeptide repeat.

Bioinformatic Approaches to Identifying Pentapeptide Repeat Proteins

The first bioinformatic approach to the genome-wide identification of pentapeptide repeat proteins was reported in 1998 by Bateman et al. (2), who searched the *Synechocystis* sp. PCC 6803 genome using a single pentapeptide repeat sequence (SLR1819 gene). This putative 331-

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amino acid protein contained 60 uninterrupted pentapeptide repeats representing 91% of the total sequence. Using this query sequence and Blast (3), 15 additional *Synechocystis* sp. PCC 6803 proteins were identified that contained between 13 and 44 tandem pentapeptide repeats. Several additional sequences were identified as being members of the pentapeptide repeat family, including the McbG gene product, known to confer resistance to the antibacterial Microcin B17 (4). A more robust approach to the identification of proteins that contain the pentapeptide repeat motif has used a Hidden Markov Model (HMM)¹ (5) and a motif that contains eight consecutive pentapeptide repeats. The Pfam (6) database (www.sanger.ac.uk/cgi-bin/Pfam) currently lists 1061 pentapeptide repeat-containing proteins (Pfam00805). Included in the database are all PRPs identified by Bateman et al. While the vast majority of these are found in prokaryotes, there are examples of proteins containing pentapeptide repeat domains in *Plasmodium falciparum*, *Anopheles gambia*, *Arabidopsis*, zebrafish, mouse, and human. Essentially all (19 of 20) eukaryotic PRP's contain 32 uninterrupted tandem pentapeptide repeats at the C-terminus of 300–390-residue proteins whose N-terminus is the cytoplasmic tetramerization domain of the voltage-gated K⁺ channel. PRPs have also been identified in bacteriophages, including mycobacteriophages. Given this broad phylogenetic distribution, it is surprising that no PRPs have been identified in any sequenced yeast genome.

Phylogenetic Categorization and Polydomain PRPs

Our bioinformatic studies indicate a wide phylogenetic distribution of PRPs. Using the PFAM Hidden Markov Model (HMM) definitions of these motifs, we used the HMMER program to scan the nonredundant (NR) sequence database (7) that currently contains approximately 2.3 million entries, and identified 1702 sequence domains that contain pentapeptide motifs. PRP motifs are highly repetitive in nature, and HMMER often locates PRP motifs multiple times in the same protein. Once redundancy is removed from the hits, we arrived at 525 currently known, unique proteins with pentapeptide motifs. These numbers can be further divided into PRPs in prokaryotic (484) and eukaryotic (41) species.

While many bacteria contain one PRP or few PRPs (see below), some microorganisms, especially the photosynthetic cyanobacteria such as *Anabaena*, have numerous chromosomally encoded PRPs. *Synechocystis* sp. strain 6803 has 16 PRPs. We can identify 40 PRPs in *Nostoc punctiforme* which range in size from 75 amino acids to >400 residues. As noted above in the case of the *Anabaena* HglK protein and the human voltage-gated potassium channel tetramerization protein, these often contain multiple domains, with the PRP domain generally found at the C-terminus of these polydomain proteins.

To explore the types and occurrence of additional domains in all 525 of the identified PRP proteins, we mapped all

Table 1: Domains Fused to Pentapeptide Repeat Proteins

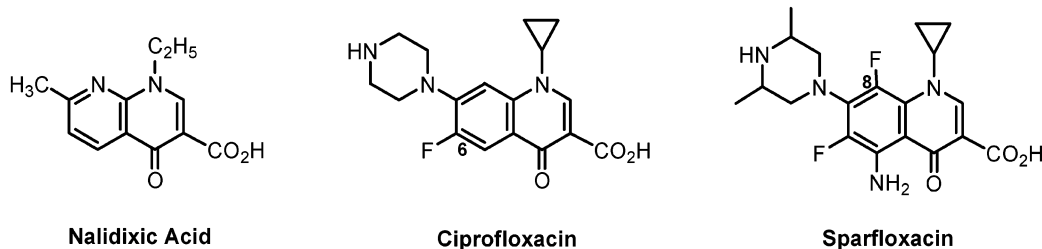
pentapeptide	pentapeptide_2
prokaryotic (172 total domains)	
WD40 β -transducin repeat (56)	PPE domain (54)
Ser/Thr protein kinase (11)	fibronectin type III (3)
tetratricopeptide_1 repeat (11)	
DNAJ domain (7)	
tetratricopeptide_2 repeat (7)	
GNAT acetyltransferase (6)	
RDD membrane-spanning (4)	
eukaryotic (21 total domains)	
K ⁺ tetramerization (19)	serine proteinase inhibitor (1)
gonadotropin-releasing hormone (1)	

the currently known 7868 Pfam (6) domain definitions using HMMER. All data are available online at <http://andes.aecom.yu.edu/prp/>. Of the 484 prokaryotic proteins containing pentapeptide motifs, 172 had at least one additional domain. The associated domains fall into 20 different types (Table 1) with the most common being WD40 domains (β -transducin repeat; coordination of multiprotein complex formation in signal transduction, transcriptional regulation, cell cycle control, and apoptosis), *Pkinase* domains (Ser/Thr protein kinases), *TPR_1* and *TPR_2* domains (tetratricopeptide repeat, role in protein–protein interactions), *DnaJ* domains (J-domains; associated with hsp70 heat shock system and mediating protein–protein interactions), *Acetyltranf_1* domains (*N*-acetyltransferase; GNAT family), RDD domains (membrane localization), and 11 other domain types with one or two representatives. These characteristic observations also hold true for the eukaryotic PRPs. These 20 extra domains are of two distinct types, the *K_tetra* (voltage-gated potassium channel tetramerization domain) and *GnRH* (gonadotropin-releasing hormone; role in reproduction) domains.

In addition to the pentapeptide repeat motif originally described by Bateman et al. (2), a second pentapeptide repeat family has been identified in the Pfam database and termed the “pentapeptide_2” family with 896 sequence domains listed in Pfam libraries. The pentapeptide_2 repeat proteins contain tandemly repeated sequences with the consensus sequence [N][T,L,I][G][S,N][G]. After redundancy is removed, 61 examples of pentapeptide_2 proteins occur in prokaryotes, with only two identified in eukaryotes. Like the original pentapeptide repeat proteins, the prokaryotic pentapeptide_2 proteins are associated with additional domains, including 54 examples of N-terminal PPE domains in mycobacterial species (unknown function; but implicated in antigenic variation in *Mycobacterium tuberculosis*) and three *fn3* domains (fibronectin type III domain; putative role in structural complexes). A single eukaryotic pentapeptide_2 protein with an associated *Kazal_2* (Kazal-type serine proteinase inhibitor) domain was identified. There is not a single instance where the two different PRP motifs occur in the same protein, nor is there any overlap of the types of additional domains associated with the two types of PRPs; the additional domains are uniquely associated with one pentapeptide repeat domain or the other. Since it is unlikely that these proteins share the same three-dimensional fold, no further discussion of the pentapeptide_2 repeat proteins will be presented.

¹ Abbreviations: PRP, pentapeptide repeat proteins; MfpA, mycobacterial fluoroquinolone resistance protein; MtMfpA, *Mycobacterium tuberculosis* mycobacterial fluoroquinolone resistance protein; HMM, Hidden Markov Model; NR, nonredundant; Qnr, quinolone resistance protein; MIC, minimum inhibitory concentration; RHQBH, right-handed quadrilateral β -helix; GNAT, Gcn5-related *N*-acetyltransferases.

Scheme 1



PRPs and Fluoroquinolone Resistance

Fluoroquinolones are synthetic derivatives of nalidixic acid and exhibit broad-spectrum and powerful antibacterial activity (Scheme 1). Prior to 1998, all mechanisms of bacterial fluoroquinolone resistance had been shown to be due to either (a) mutations in the type II topoisomerases, DNA gyrase and topoisomerase IV, that are the targets of these drugs or (b) an increased level of expression of efflux pumps that reduce the intracellular concentration of the drug. Neither of these resistance mechanisms has been shown to be transmissible between organisms. Therefore, the discovery of a plasmid-mediated, transmissible form of fluoroquinolone resistance in 1998 heralded a significant clinical concern. The 218-residue QnrA protein was originally found on a conjugative plasmid isolated from a fluoroquinolone resistant strain of *Klebsiella pneumoniae* in Alabama (8). Since then it has been found on transferable plasmids from fluoroquinolone resistant strains of *K. pneumoniae* isolated in six different states in the United States (9). Outside of the United States, *qnr* genes have been found on plasmids in fluoroquinolone resistant isolates of Enterobacteriaceae from China (10), Hong Kong (11), Korea (12), France (13), Germany (14), and Egypt (15). In some cases, the *qnr* genes were adjacent to genes that confer resistance to other antibiotics, such as sulfamethoxazole and the extended-spectrum β -lactam antibiotics within type I integrons that were apparently mobile, as they were found on an assortment of conjugative plasmids (16, 17). Thus, although several studies have found *qnr* genes in a small percentage of fluoroquinolone resistant strains in the United States (8 of 72; 9) and Europe, it appears that the *qnrA* gene is present worldwide on integrons that can integrate into a series of promiscuous plasmids within many species of Enterobacteriaceae.

The Qnr protein is a pentapeptide repeat protein (see below for a complete description). Qnr has been biochemically characterized by Jacoby et al. (18), who showed that, in vitro, the Qnr protein protects both *Escherichia coli* DNA gyrase and the *E. coli* topoisomerase IV (19) from the inhibitory effects of fluoroquinolones. More recently, these investigators have shown that Qnr competes with DNA for binding to the DNA gyrase (20), suggesting that this 218-residue PRP, consisting of 40 uninterrupted pentapeptide repeats (92% of the sequence), binds to DNA gyrase (see below). The original source of the *qnr* gene was unclear, since in all cases the G + C content (52%) of the *qnr* gene is much higher than the chromosomal G + C content of the clinical Enterobacteriaceae isolates in which it has so far been found. The origin of QnrA was recently discovered by PCR screening of 48 Gram-negative bacterial species for the presence of a *qnrA* gene (21). In *Shewanella algae*, an environmental species from marine water and freshwater, four QnrA-like proteins were

found. These four chromosomally encoded proteins (QnrA2–5) differ from each other, and from the original QnrA (now termed QnrA1), by only one to four amino acids. It is interesting that a *qnr* allele found on four different, transferable plasmids from four fluoroquinolone resistant strains of *Salmonella enterica* serotype Enteritidis in Hong Kong (11) is 100% identical to QnrA3.

Another *qnr* homologue, QnrS, which is only 59% identical to QnrA, was found on a plasmid from a broadly drug resistant strain of *Shigella flexneri* isolated in Japan (22). Transfer of the conjugative plasmid also conferred resistance to β -lactam antibiotics, but *qnrS* was not located in an integron, but rather within a putative transposon (Tn3-like) sequence, together with a TEM-1 β -lactamase gene. Another protein belonging to the Qnr family, QnrB, is only 40% identical to QnrA1, and has been found in various Enterobacteriaceae in both the United States and India (23). Genes encoding proteins similar to Qnr were recently identified in the chromosomes of three species of the Vibrionaceae family (58–66% identical to QnrA, 52–64% identical to QnrS), so it is likely that the origin of QnrS and other putative Qnr proteins may be found in the chromosomes of other Gram-negative bacteria. Interestingly, when one of the *qnr*-like genes from *Vibrio parahaemolyticus* was cloned onto a plasmid, it did not confer fluoroquinolone resistance unless cysteine 115 was mutated to a tyrosine, perhaps allowing the mutant form to bind to the gyrase (24). A recent review summarizes the rapidly changing field of Qnr function (23).

A genetic selection for fluoroquinolone resistance in the fast-growing *Mycobacterium smegmatis* identified a gene expressed on a multicopy plasmid responsible for a 2–8-fold increase in the MIC (minimum inhibitory concentration) values for ciprofloxacin and sparfloxacin (Scheme 1; 25). The gene, termed *mfpA* for mycobacterial fluoroquinolone resistance protein, encodes a 192-amino acid protein whose nearly complete open reading frame consisted of 32 uninterrupted pentapeptide repeats. The role of MfpA in fluoroquinolone resistance was confirmed by deleting the gene and demonstrating that the knockout strain was 2–4-fold more sensitive to ciprofloxacin and sparfloxacin. The 183-residue *M. tuberculosis* Rv3361 gene is 67% identical to the *M. smegmatis* MfpA protein, and contains a similar pentapeptide repeat motif.

Pentapeptide Repeat Fold

The expression and purification of the *M. tuberculosis* MfpA protein (*MtMfpA*), and its crystallization in four distinct forms, were recently reported (26). The three-dimensional structure of *MtMfpA* demonstrated that the pentapeptide repeat sequence encodes a right-handed quad-

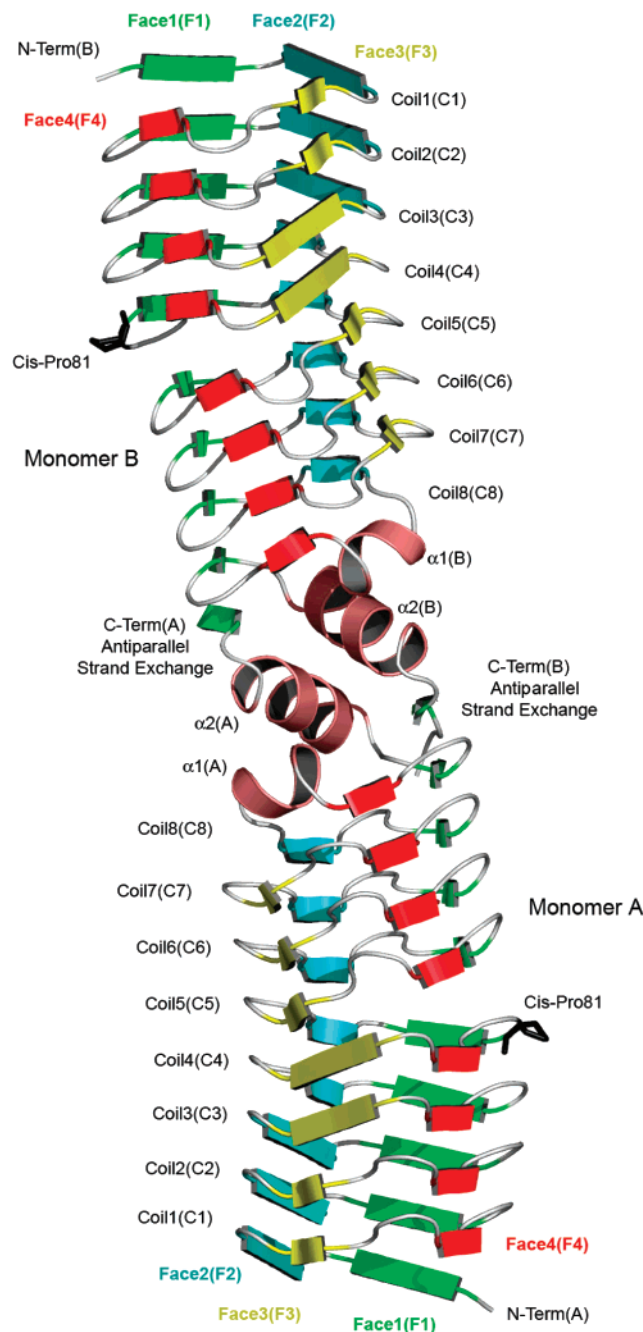


FIGURE 1: Ribbon diagram of the *M. tuberculosis* MfpA dimer. The four faces of the quadrilateral β -helix are colored green (face 1), blue (face 2), yellow (face 3), and red (face 4).

rilateral β -helix (RHQBH; Figure 1). Each pentapeptide forms one side of a nearly square repeating unit, which we have termed a coil. Each coil is composed of four pentapeptides, with 20 residues per coil, and with a rise in the helical axis of 4.8 Å per revolution. In general, the quadrilateral coils stack directly atop one another, although there is a slight left-handed twist to the helical axis. Due to this stacking and the quadrilateral nature of the coils, the protein can be designated to have four faces, termed F1–F4 (Figure 2). *MtMfpA* has eight complete coils, the first seven of which are composed exclusively of pentapeptide repeats. The eighth coil has three strands, as strand F3 is replaced by a two-turn α -helix (α 1). What would be the ninth coil has a single strand on F1, followed by a three-turn α -helix (α 2) and a β -strand that is not part of the regular coiled structure.

	Face1	Face2	Face3	Face4	
	i^{-2} i^{-1} i i^{+1} i^{+2}	i^{-2} i^{-1} i i^{+1} i^{+2}	i^{-2} i^{-1} i i^{+1} i^{+2}	i^{-2} i^{-1} i i^{+1} i^{+2}	
Coil1	Q Q W V D	C E F T G	R D F R D	E D L S R	21
Coil2	L H T E R	A M F S E	C D F S G	V N L A E	41
Coil3	S Q H R G	S A F R N	C T F E R	T T L W H	61
Coil4	S T F A Q	C S M L G	S V F V A	C R L R P	81
Coil5	L T L D D	V D F T L	A V L G G	N D L R G	101
Coil6	L N L T G	C R L R E	T S L V D	T D L R K	121
Coil7	C V L R G	A D L S G	A R T T G	A R L D D	141
Coil8	A D L R G	A T V D P	V L W R T	A S L V G	161
	A R V D V	D Q A V A	F A A A H	G L C L A	181

FIGURE 2: Structure-based sequence alignment of MfpA. Regions comprising α 1 and α 2 are shaded salmon.

MtMfpA was found to exist as a dimer in solution by ultracentrifugation (unpublished results), and in all four crystal forms a consistent dimer interface, located at the C-terminal end of the β -helix, was found. At this interface, the C-terminal α -helices form an alternating perpendicular α -helical stack (α 1– α 2– α 2′– α 1′) with a hydrophobic core at the molecular 2-fold axis. The final β -strand crosses over to the 2-fold related β -helix adding a final β -strand in an antiparallel fashion to F1. The two β -helices are coaxial, producing a highly asymmetric dimer with an axial length of 100 Å. While the main chain atoms exhibit a quadrilateral cross section, the addition of surface side chains yields a molecule with a more cylindrical appearance when viewed down the helical axis, whose diameter varies from 27 to 18 Å from the N-terminus to the dimer interface.

The individual residues of the pentapeptide are designated as follows: the conserved hydrophobic residue (Leu or Phe) at the center of pentapeptide alignments is the i residue, while the residues N-terminal to the i residue are the i^{-1} and i^{-2} residues and the residues C-terminal to the i residue are the i^{+1} and i^{+2} residues. The side chains of the i and i^{-2} residues pack in the interior of the β -helix, whereas the side chains of the remaining residues point outward and generate the surface of the protein (Figure 3). As suggested by the repeating nature of the primary sequence, the pentapeptide residues adopt similar conformations throughout the β -helix. There are two predominant main chain ϕ – ψ dihedral orientations encoded by the pentapeptide repeat which differ only in the orientation of a single peptide bond (Figure 4). In general, the pentapeptide secondary structure can be viewed as type II turns (Figure 5) composed of the i , i^{+1} , i^{+2} , and i^{-2} residues [(-120, 20), (-60, 120), (60, 20), and (-80, 160), respectively] connected by isolated β -bridges involving residue i^{-1} [(-120, 120)]. In this conformation, the carbonyl of the i th residue is hydrogen bonded to the i^{-2} amide of the following pentapeptide, and only the i^{-1} residue contributes both backbone amide nitrogens and carbonyls to intercoil hydrogen bonding. This is illustrated in the ribbon diagram in Figure 1 where the isolated β -bridges are shown as short β -strands. This ϕ – ψ composition occurs in 19 of the 30 turns in *MtMfpA* (Figure 4). In the other cases, the peptide bond between residues i and i^{+1} is rotated 90° such that both the i and i^{+1} main chain atoms participate fully in intercoil hydrogen bonding (type IV turns). These pentapeptides are illustrated in the ribbon diagram in Figure 1 as the longer β -strands and have ϕ – ψ angles for the i^{-2} , i^{-1} , i , i^{+1} , and i^{+2} residues of (-80, 160), (-120, 120), (-120, 120), (-120, 120), and (60, 20), respectively. The choice between

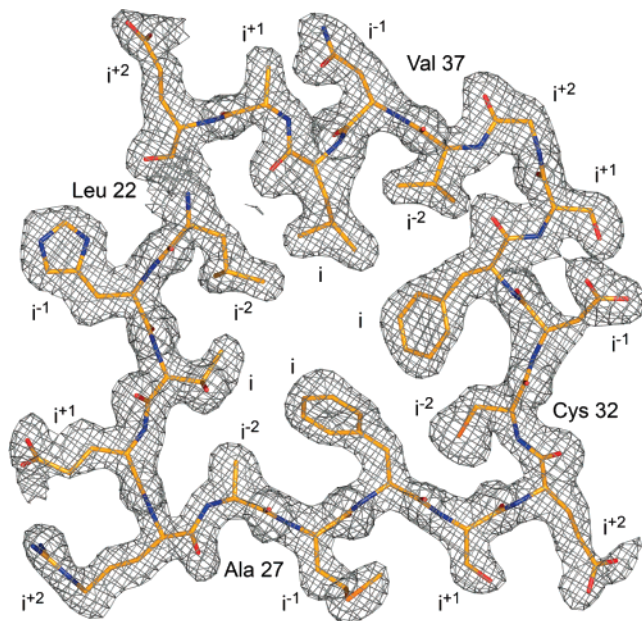


FIGURE 3: Electron density and molecular model of MfpA. Shown are $2F_o - F_c$ electron density contoured at 1σ and residues comprising the second coil.

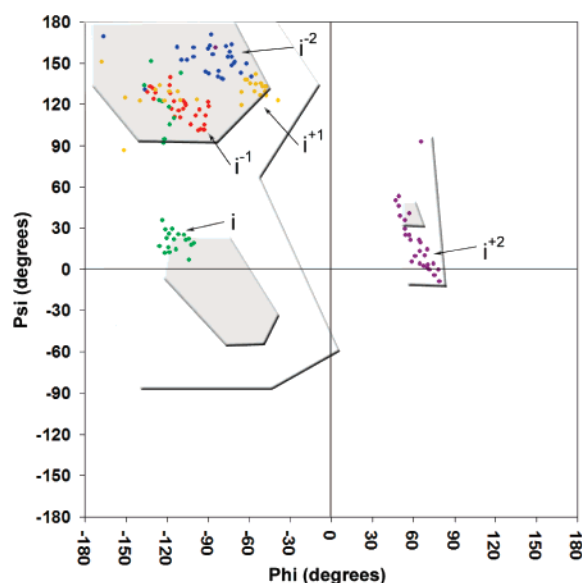


FIGURE 4: Ramachandran plot of the first 165 residues that make up the right-handed quadrilateral β -helix domain of MfpA. Pentapeptide repeat positions are colored blue (i^{-2}), red (i^{-1}), green (i), yellow (i^{+1}), and purple (i^{+2}). The most favored and additionally allowed ϕ - ψ orientations are shaded dark and light gray, respectively.

the type II and type IV turn appears to be related to the identities of the internal side chains (i^{-2} and i). The type IV turn of the pentapeptide repeat lacks the intracoil hydrogen bond of the type II turn, and yields a pentapeptide with a more extended conformation (~ 0.5 – 0.75 Å). The type IV turns, which frequently occur in the N-terminal coils, have predominately phenylalanine at the i position, and this larger side chain is accommodated by extended pentapeptides forming a larger core. In contrast, the C-terminal coils have only leucines, and all exhibit the type II turn.

Each of the residues of an individual pentapeptide exhibits a propensity for a restricted number of amino acids, with a

structure-based consensus sequence of [S,T,A,V][D,N][L,F]-[S,T,R][G]. The central i residue is the main component of the hydrophobic core of the RHQBH and is predominately either a phenylalanine or a leucine. Typically, the central hydrophobic side chain is in van der Waals contact with residue i in neighboring coils above and below both on its own face and on neighboring faces and also the i^{-2} residue of its own face and the i^{-2} residue of the next consecutive pentapeptide. Due to the equivalent nature of each of the quadrilateral sides and the distances from C α to C α of opposite faces, residue i never interacts with any of the internal residues of the opposite face. Stacks of phenylalanine residues exist internally on F2 (Phe9, -29, and -49) and F3 (Phe14, -34, -54, and -74) with similar conformations of their side chain torsion angles ($\chi_1 \sim -70^\circ$, $\chi_2 \sim -70^\circ$) (Figure 6). The aromatic ring conformation and the left-handed twist to the coil stacking are used to minimize the negative interaction between their π -electron clouds and maximize their interaction with the somewhat positive ring hydrogens in an interaction that has been described for the interaction of phenylalanines in general, and phenylalanine stacking in β -helices (27). Stacks of leucine residues of at least three leucines occur on F1 (Leu84, -104, -124, and -144) and F4 (Leu19, -39, -59, -79, -99, and -119) (Figure 7). The stacks of leucine side chains have a much wider conformational space when compared to the phenylalanine stacks and tend to assume conformations that maximize van der Waals contacts with nearby residues.

The i^{-2} residues typically are alanine, serine, threonine, or valine (18 of 33). The side chains of the i^{-2} residues project inward, participate in hydrogen bonding with main chain atoms, and form part of the hydrophobic core. In most cases, the hydroxyl groups of serine and threonine residues in the i^{-2} position hydrogen bond to the amide backbone of residue i^{-2} or the carbonyl of residue i in the turn directly below. *MtMfpA* is unique among pentapeptide repeat proteins in that residue i^{-2} is often a cysteine (7 of 33). The cysteine residues are in conformations similar to those of the serine residues at this position.

The i^{+2} residue adopts a left-handed α -helical conformation (α_L) and is typically either a glycine (11 of 32) or a polar residue (15 of 32). Glycine is the most frequent amino acid found in type II turns at this position, where a bulkier amino acid would have limited conformational flexibility due to peptide clashes with C β . Finally, the i^{-1} residue is often an asparagine or aspartate, while the i^{+1} residue is often a serine, threonine, or arginine. The structure reveals that the propensities for specific amino acids at these two positions are linked. When the carbonyl of the i residue participates in a type II turn, the amide group of the i^{+1} residue projects outward, but is shielded from possible solvation by the side chain of the i^{-1} residue. The side chains of asparagine and aspartate at the i^{-1} position are of the correct length to form a hydrogen bond with this i^{+1} amide group (Figure 4). In addition, to further stabilize this arrangement, the asparagine or aspartate residues at the i^{-1} position will also form a hydrogen bond with the i^{+1} side chain when it is a serine, or threonine or a salt link when it is an arginine.

There is a 12° kink in the helical axis midway through the β -helix. This results in the disruption of intercoil hydrogen bonding between coils 4 and 5 on F4 and coils 5 and 6 on F1. This disruption is due to a *cis*-proline (Pro81)

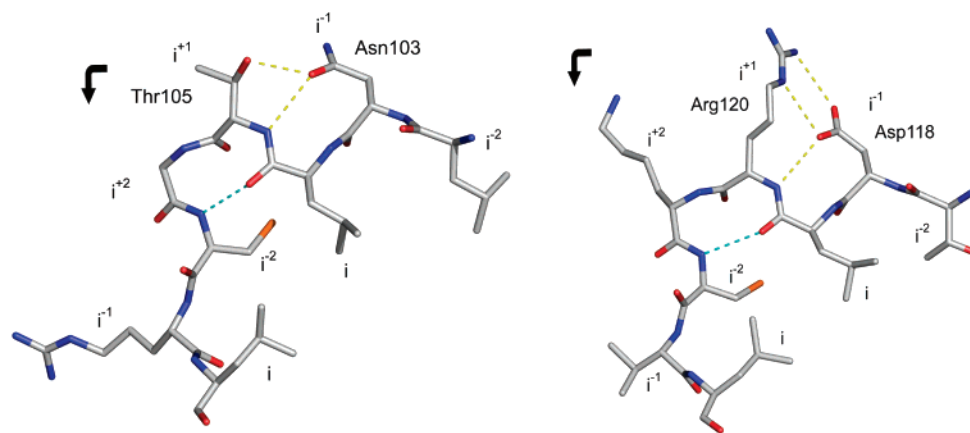


FIGURE 5: Side chain and main chain interactions of the pentapeptide repeat type II turns.

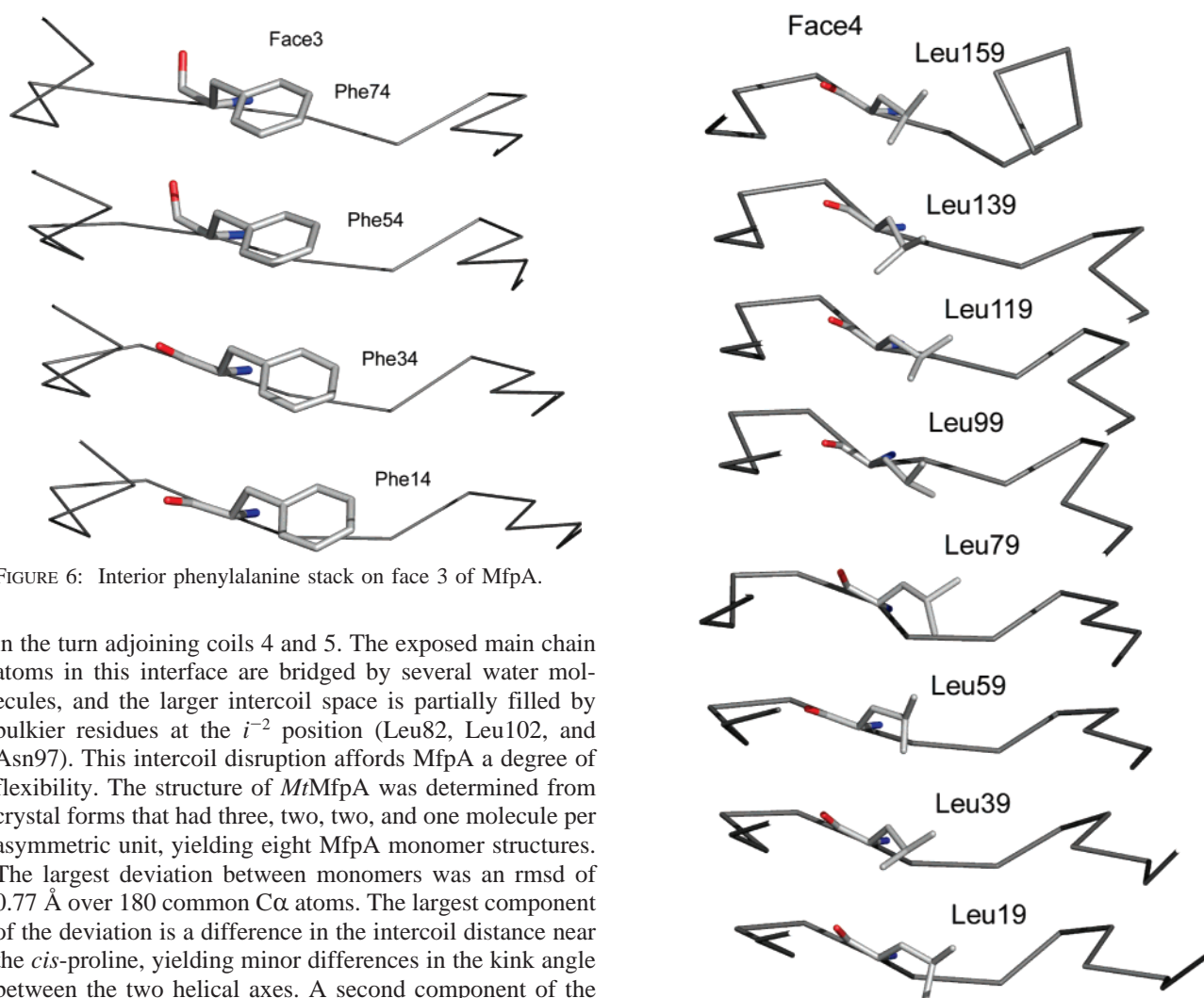


FIGURE 6: Interior phenylalanine stack on face 3 of MfpA.

in the turn adjoining coils 4 and 5. The exposed main chain atoms in this interface are bridged by several water molecules, and the larger intercoil space is partially filled by bulkier residues at the i^{-2} position (Leu82, Leu102, and Asn97). This intercoil disruption affords MfpA a degree of flexibility. The structure of *MtMfpA* was determined from crystal forms that had three, two, two, and one molecule per asymmetric unit, yielding eight MfpA monomer structures. The largest deviation between monomers was an rmsd of 0.77 Å over 180 common Cα atoms. The largest component of the deviation is a difference in the intercoil distance near the *cis*-proline, yielding minor differences in the kink angle between the two helical axes. A second component of the deviation is flexibility at the C-termini, probably because of the nature of the hydrophobic interaction between the C-terminal α-helices (unpublished data).

Because the *i* residues of opposing pentapeptides do not interact, there is unoccupied space at the core of the structure along the helical axis. Indeed, in the original analysis of pentapeptide repeat proteins by Bateman et al. (2), models of pentapeptide repeat proteins with four sides per coil were rejected due to poor packing of the internal side chains. This is why a model similar to the left-handed β-helix observed for hexapeptide repeat proteins with a triangular cross section

(28) was proposed for pentapeptide repeat proteins. The largest continuous space is within and among coils 4–6 with a volume of ~100 Å³, whose size is larger than the unoccupied space of other coils due to the kink in the helical axis at this point. Other smaller “cavities” are in the 15–30 Å³ size range. It is unclear if these internal cavities have functional consequences. The highest-resolution structure was refined to 2.0 Å; all of the refined waters are located on the

FIGURE 7: Interior leucine stack on face 4 of MfpA.

protein surface, and no water molecules are observed within these protein cavities.

Modeling the Interaction of MfpA and DNA Gyrase

DNA gyrase is involved in the negative supercoiling of DNA. The proposed mechanism of DNA gyrase involves coordinated binding of two sections of DNA, termed the T and G segments, cleavage of both strands of the G-segment, the passage of the T-segment through the cleavage point, and religation of the cleaved strands (29). Fluoroquinolones act by stabilizing the tyrosyl122–DNA–gyrase cleavage complex, preventing religation of the DNA. This results in the hydrolysis of the phospho–phenolic linkage and release of cleaved DNA. The fragmentation of the DNA is the bactericidal consequence of fluoroquinolone treatment. DNA gyrase is an $\alpha_2\beta_2$ heterotetramer. The structure of the entire $(\alpha\beta)_2$ complex has not been amenable to structure determination to date, but the structures of various subdomains of the DNA gyrase have been structurally characterized. The α -subunit is the site at which fluoroquinolones bind to form the tyrosyl–DNA–gyrase adduct. The structure of an N-terminal construct composed of residues 2–523 of the α -subunit (GyrA59) has been determined (30). GyrA59 is a dimer in the crystal structure, whose conformation is proposed to be consistent with the α_2 dimer binding the G-segment DNA. A large electropositive “patch” at the dimer interface contains the catalytic tyrosine residues and residues whose mutation are known to confer resistance to fluoroquinolones. This is the proposed binding site for the G-segment of DNA and where the tyrosyl–DNA–gyrase adduct is generated. Modeling of DNA into this electropositive region indicates that approximately 30–35 bp of B-DNA would occupy the entire length of the dimer. Interestingly, the length of 30–35 bp of B-DNA is similar to the axial length of the *MtMfpA* dimer. *MtMfpA* has a preponderance of electronegative charge over its entire surface (net charge of -10), and molecular modeling indicated that MfpA would also fit comfortably in this groove with the dimer axis of MfpA aligning with the dimer axis of GyrA59 (26). The negative charge of *MtMfpA* is projected more prevalently from face 1 and 2, so MfpA was positioned so that these faces were in closer contact with the electropositive groove of GyrA59 (Figure 8). The binding of MfpA to this surface would provide a compelling hypothesis about how MfpA can provide an organism with resistance to fluoroquinolones. Overexpression and binding of MfpA to the GyrA subunit of DNA gyrase would inhibit the binding of DNA, and block the formation of the target of fluoroquinolones, the DNA–gyrase binary complex. This would give the population of bacteria time to achieve resistance through alternative means such as mutation of GyrA or expression of drug efflux pumps. However, caution must be applied to such a model, since there are likely to be several surfaces on DNA gyrase that are involved in the capture, cleavage, transfer, religation, and release of DNA, and this involves many complex structural rearrangements. However, the general interaction of pentapeptide repeat proteins with GyrA is supported by the biochemical data. Increasing concentrations of MfpA inhibit the topoisomerase activity of DNA gyrase (26). Utilizing surface plasmon resonance, MfpA was found to interact with DNA gyrase with k_{on} and k_{off} values of $\sim 10^3 \text{ M}^{-1} \text{ s}^{-1}$ and $\sim 10^{-4} \text{ s}^{-1}$, respectively,

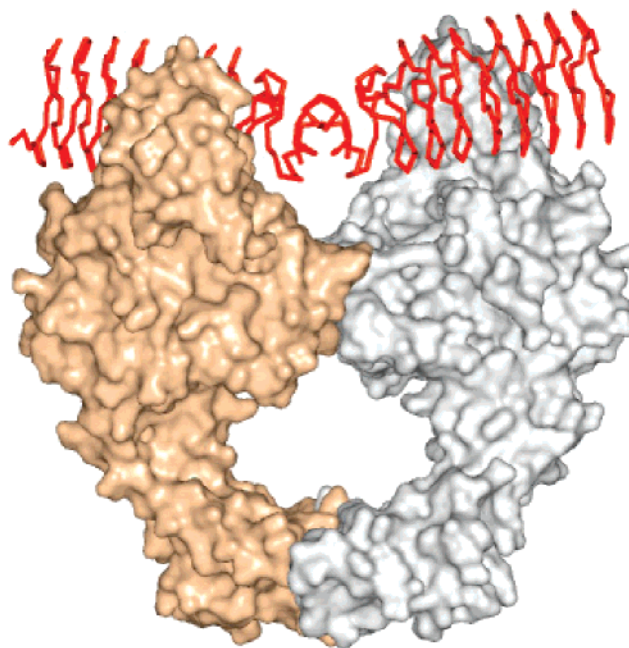


FIGURE 8: Model for the interaction of MfpA with DNA gyrase. DNA gyrase monomers are presented as silver and gold surface renderings, while the MfpA dimer is shown as a red C α trace.

allowing a K_d of 450 nM to be calculated. In addition, the QnrA protein was found to promote the release of DNA from a DNA–gyrase complex (20).

Genomic Environment and Potential Regulation

The role of *MtMfpA* in the biology of mycobacteria is unknown, but there are some indications that it could play an important role. First, the gene is present and very similar in all mycobacterial genomes (*M. tuberculosis*, *M. smegmatis*, *Mycobacterium bovis*, *Mycobacterium ulcerans*, and *Mycobacterium avium*) but appears to be present as a pseudogene in *Mycobacterium leprae*. Second, just upstream of *mfpA*, and apparently expressed as part of the same transcriptional unit, are four genes that are highly conserved in the mycobacteria. This four-gene cluster (Rv3362c–3365c; Figure 9) is found together only in the *Actinomycetes*, the family of bacteria to which the mycobacteria belong. It is presumed to be a regulatory team because the four encoded proteins are similar to other regulatory proteins. Blast searching with Rv3362c finds approximately 30 putative GTPases (31) that are all at least 50% identical to Rv3362c, and these are found only in the *Actinomycetes* family of bacteria, and are all located within conservons (see below). Rv3363c encodes a possible protein of 122 amino acids that is most similar to members of the DUF472 family (pfam05331.4) of proteins whose function is unknown. Rv3364c encodes a possible protein of 130 amino acids that is most similar to members of the Roadblock/LC7 (pfam03259.10) family of proteins, which in eukaryotes are associated with dynein, and in *Myxococcus xanthus*, with gliding motility. Rv3365c is similar to bacterial histidine kinases, is likely membrane-bound, and may serve as a sensor. However, the presumptive histidine kinases in the conservon units, such as Rv3365c, appear to form a subgroup that is distinct from most of those in two-component systems (32). The histidine residue phosphorylated in the classic

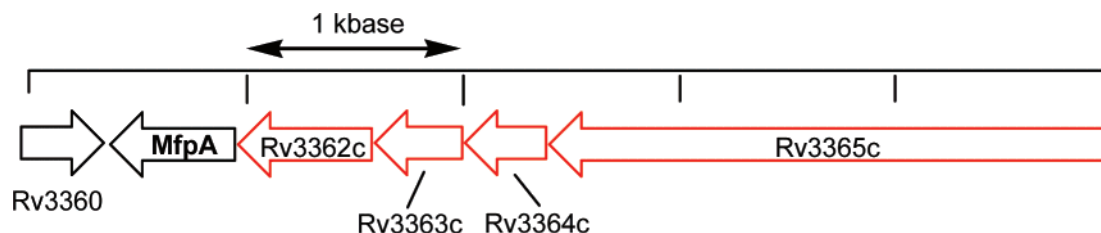


FIGURE 9: Genomic environment of *M. tuberculosis* MfpA. The four upstream genes colored red are termed the conservon in other *Actinomyces* species.

histidine kinase proteins appears to be conserved, but the surrounding amino acids in the “H-box” are different than those well conserved in the histidine kinases that are part of two-component systems.

In the chromosome of *Streptomyces coelicolor* A3(2), another actinomycete, this four-gene group is present 13 times and has been labeled a “conservon” (33, 34). The four-gene unit is also found in some other actinomycetes, with 10 representatives in *Streptomyces avermitilis*, three in different *Frankia* species, five in *Nocardia farcinica*, five in *Thermobifida fusca*, and two in *Kineococcus radiotolerans*. Other examples may appear as more actinomycete genomes are sequenced. There is only one conservon in mycobacteria, and this is the only one associated with a pentapeptide protein.

Biological Functions?

A very small fraction of the PRPs are associated with any defined biochemical function. We will first discuss those PRPs whose expression leads to drug resistance to compounds that inhibit DNA gyrase. While it is clear that MfpA inhibits DNA gyrase activity by binding to the enzyme, possibly in the same region to which the G-segment of DNA binds based on our modeling studies and the phenotype of fluoroquinolone resistance, the physiological role of the chromosomally encoded protein remains unclear. *M. tuberculosis* does not contain a second type II topoisomerase, and thus, its DNA gyrase must fulfill the roles of DNA supercoil introduction, relaxation, and decatanation. Given the long doubling time of the organism, one possible function is to prevent the relaxation of the supercoiled DNA and maintain a condensed chromosome during periods of replicative senescence. This would require that the protein’s expression be coordinated with the cell cycle. Alternatively, if its expression were constitutive, then the regulatory team of proteins found upstream of the gene, and presumably cotranscribed with the gene, would function to modulate the activity of MfpA. Whether this physiological role is shared with the functionally homologous family of Qnr proteins that are responsible for transmissible, clinical resistance to fluoroquinolones is unclear at present. The *mcbG* gene is located in an operon that includes many of the Microcin B17 biosynthetic genes, and was initially identified as an immunity factor (35). On the basis of the results with MfpA, it seems very likely that the McbG protein will adopt a similar fold and act via a similar mechanism. Like fluoroquinolones, Microcin B17 induces double-strand breaks in chromosomal DNA (36); however, resistance to Microcin B17 occurs via mutations in the *gyrB*-encoded subunit (37). This argues that Microcin B17 binds to DNA gyrase (38), or a DNA gyrase–DNA complex (39), somewhere in the *GyrB* subunit, and

that the McbG protein prevents its binding, possibly by mimicking a DNA gyrase–DNA complex.

A fourth member of the PRP family involved in resistance is the *oxrA*-encoded oxetanocin A resistance factor. *Bacillus megaterium* contains an operon that includes biosynthetic genes for oxetanocin A as well as the *oxrA* resistance locus (40). Oxetanocin A is an unusual nucleoside whose nucleotide triphosphate form powerfully inhibits viral DNA polymerases (41), human telomerase (42), and HIV reverse transcriptase (43). OxrA has been shown to confer resistance to oxetanocin A, in a manner similar to that discussed above for MicrocinB17 and the McbG resistance protein. OxrA contains only nine pentapeptide repeats in a 185-amino acid protein, suggesting an alternative mechanism of resistance.

The HglK protein was the first PRP discovered (1), and has been assigned potential functions in glycolipid transport and/or localization. The four N-terminal membrane-spanning domains suggest that the protein is membrane-associated, but the function of the pentapeptide repeat domain is unclear. The small, discontinuous cavities in the MfpA structure would require a decrease in the van der Waals volume of the *i* residues, or a small expansion of the exterior of the fold to allow for the insertion of unbranched lipids into the core. A second potential transport function for a pentapeptide repeat domain was reported for a gene in the photosynthetic cyanobacterium, *Synechocystis* sp. strain 6803, termed the *rfrA* gene, which is pronouncedly similar to HglK in overall domain organization, containing both four membrane-spanning sequences at its N-terminus and an uninterrupted tandem repeat of 12 pentapeptides. The RfrA gene was shown to be involved in the regulation of manganese uptake (44), although the authors did not suggest that RfrA itself transported manganese, but rather regulated a high-affinity transport system by an unknown mechanism. Whether the extremely high genome density of PRPs in the photosynthetic cyanobacteria, including *Synechocystis* (16 PRPs), *Gloeobacter* (18), *Anabaena* (31), and *Nostoc* (40), is related to multiple functional roles in these organisms, not associated with DNA mimicry, is unclear at present.

Finally, many PRPs are polydomain proteins with additional associated motifs, some of which are homologous to catalytic domains. The best studied is the *Synechocystis* sp. strain 6803 SpkB protein (45). Its N-terminal domain is homologous to mammalian protein Ser/Thr kinase domains. The SpkB protein is one of 13 proteins encoded in the genome of this organism with putative Ser/Thr protein kinase activity, but the only one that contains an additional associated pentapeptide repeat domain. The SpkB protein catalyzes its autophosphorylation, as well as the phosphorylation of bovine myelin basic protein, casein, and calf thymus histones. The ability of this bacterial protein to

phosphorylate mammalian proteins is highly reminiscent of bacterial aminoglycoside phosphotransferases that have been shown to phosphorylate both aminoglycoside antibiotics, conferring high-level resistance to these compounds, and mammalian proteins (46). A second example of a polydomain PRP with an N-terminal catalytic domain is the *Bacillus anthracis* PRP. In this case, the protein has an N-terminal Gcn5-related *N*-acetyltransferase (GNAT) domain similar to those found in eukaryotic histone acetyltransferases. Although this protein has not been functionally characterized to date, it is again highly reminiscent of other bacterial aminoglycoside *N*-acetyltransferases that acetylate mammalian histone proteins (47). While the role of the catalytic domains is clear in these systems, the role of the pentapeptide repeat domain is cryptic. One possibility is that the pentapeptide domain, by potentially mimicking DNA in these proteins, might target the catalytic domains to DNA-binding proteins, thus controlling the selectivity of the catalytic domains that post-translationally modify the normal bacterial proteins.

Conclusions and Perspectives

The first PRP was identified only 10 years ago, but we now know that they are broadly present in bacteria and multicellular eukaryotes. In only a handful of cases have any biochemical functions been ascribed to these proteins; however, their role in clinical resistance to fluoroquinolones and other DNA gyrase inhibitors is now clear. Whether they serve additional transport and post-translational modification functions is unclear at present. As additional structural information is obtained about how the PRP fold can accommodate peptide excursions, and how additional domains are appended, and biochemical information that defines functions and specificities of these domains becomes available, we will start to have a more complete picture of this large family of proteins.

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