

The Molecular Basis of FimT-mediated DNA Uptake during Bacterial Natural Transformation

Sebastian A.G. Braus¹, Francesca L. Short^{2,3}, Stefanie Holz^{1,#}, Matthew J.M. Stedman^{1,#},
Alvar D. Gossert^{1,4}, Manuela K. Hospenthal^{1,5,*}

¹ Institute of Molecular Biology and Biophysics, ETH Zürich, Otto-Stern-Weg 5, 8093 Zürich, Switzerland

² Monash University, Melbourne, Australia

These authors contributed equally

* Correspondence: manuela.hospenthal@mol.biol.ethz.ch

³ ORCID: 0000-0002-0025-4858

⁴ ORCID: 0000-0001-7732-495X

⁵ ORCID: 0000-0003-1175-6826

Abstract

Naturally competent bacteria encode sophisticated protein machineries for the uptake and translocation of exogenous DNA into the cell. If this DNA is integrated into the bacterial genome, the bacterium is said to be naturally transformed. Most competent bacterial species utilise type IV pili for the initial DNA uptake step. These proteinaceous cell-surface structures are composed of thousands of pilus subunits (pilins), designated as major or minor according to their relative abundance in the pilus. In this study, we show that the minor pilin FimT plays an important role in the natural transformation of *Legionella pneumophila*. We used NMR spectroscopy, *in vitro* DNA binding assays and *in vivo* transformation assays to understand the molecular basis of FimT's role in this process. FimT directly interacts with DNA via an electropositive patch, rich in arginines, several of which are well-conserved and located in FimT's conformationally flexible C-terminal tail. We also show that FimT orthologues from other γ -Proteobacteria share the ability to bind to DNA. Our functional characterisation and comprehensive bioinformatic analysis of FimT, suggest that it plays an important role for DNA uptake in a wide range of competent species.

Introduction

Competent bacteria can take up exogenous DNA, present in their environment, and integrate it into their genomes by the process of natural transformation. This is an important avenue of horizontal gene transfer (HGT), which has widespread consequences for bacterial evolution and the spread of antibiotic resistance and other pathogenicity traits. In contrast to other modes of HGT, namely transduction and conjugation, natural transformation is entirely controlled by the recipient cell that encodes all the required machinery for DNA uptake, translocation and integration¹. More than 80 bacterial species, including Gram-negative and Gram-positive organisms, have been shown to be naturally competent², yet the true prevalence of this mechanism amongst bacteria likely remains underappreciated. The Gram-negative bacterium *Legionella pneumophila* is naturally competent³, consistent with the observation that its genome bears evidence of frequent HGT and recombination events^{4–6}. Although *L. pneumophila* could be described as an accidental human pathogen, it is the aetiological agent of Legionnaire's disease, a serious and life-threatening form of pneumonia, that results from an infection of alveolar macrophages by contaminated aerosols^{7,8}.

Legionella, like most Gram-negative bacteria, are thought to utilise type IV pili (T4P) for DNA uptake^{3,9,10}, defined as the movement of DNA across the outer membrane (OM) and into the periplasmic space¹¹. However, the molecular mechanisms involved in this step remain poorly defined. T4P are extracellular proteinaceous appendages composed of thousands of

individual pilus subunits (pilins), designated as major or minor depending on their relative abundance in the pilus^{12,13}. A prevailing model suggests that T4P can bind to DNA⁹ and transport it into the cell *via* pilus retraction, which is powered by the retraction ATPase PilT^{14,15}. Pilus retraction is thought to bring the DNA into proximity with the OM and be taken up across the OM-embedded secretin channel PilQ, which is the same pore traversed by the T4P themselves^{16,17}. Once in the periplasm, ComEA binds to incoming DNA to prevent its back-diffusion by acting like a Brownian ratchet^{18,19}. Subsequently, DNA is converted into single-stranded DNA (ssDNA) and transported across the inner membrane (IM) by a putative channel called ComEC²⁰. In the cytoplasm, ssDNA is protected by single-stranded DNA binding protein (Ssb)²¹ and DNA processing protein A (DprA)²², before being integrated into the genome by homologous recombination in a RecA- and ComM-dependent manner^{23,24}.

In recent years, studies of several competent bacteria have shown that their T4P (or their pilins) can directly interact with DNA^{15,25–29}. This function was attributed to specialised minor pilins or pilin-like proteins in *Neisseria species* (ComP)^{27,28}, *Vibrio cholerae* (VC0858 and VC0859)¹⁵, and *Thermus thermophilus* (ComZ)²⁹, although a major pilin (PilA4) has also been suggested to contribute in the latter³⁰. Of these, ComP found in *Neisseria species*, is the best-characterised DNA-binding minor pilin to date. ComP displays a sequence preference for neisserial DNA containing so-called DNA uptake sequences (DUS)^{31–33} and binds to DNA through an electropositive surface patch^{27,28,34}. VC0858, VC0859 and ComZ are thought to be located at the pilus tip^{15,29}, whereas ComP has been suggested to either be incorporated throughout the pilus fibre²⁸ or at the pilus tip⁹. In addition to these proteins, the minor pilin FimT has also been implicated in natural transformation, as its loss leads to a reduction in transformation efficiency in *Acinetobacter bayly*³⁵. However, this phenotype was never followed up with further DNA-binding studies.

We set out to study DNA uptake during natural transformation in *Legionella pneumophila*. It is not known whether *Legionella*'s T4P can interact with DNA, and if so, which pilins are responsible. We tested several major and minor *Legionella* pilin candidates for their ability to bind DNA and show that FimT efficiently interacts with DNA *in vitro* and *in vivo*, and that loss of binding, just like *fimT* deletion, results in almost complete abrogation of natural transformation. We also determined the structure of FimT and show that a conserved electropositive surface patch rich in arginines is required for DNA binding. Finally, we show that FimT is not only important for natural transformation in *L. pneumophila*, but that it likely plays a role in many other bacterial species, as suggested by DNA binding studies and bioinformatic analyses. Together, our work provides the molecular basis of FimT's role in natural transformation.

Results

FimT is critical for natural transformation in *L. pneumophila* and interacts with DNA

FimT and FimU are minor type IV pilins that belong to the GspH/FimT family of proteins (Pfam: PF12019; InterPro: IPR022346), which also includes the type II secretion system (T2SS) pseudopilin GspH/XcpU. All three genes are encoded in the *L. pneumophila* genome and share an overall amino acid sequence identity of ~15–25%. *L. pneumophila* FimT (FimT_{Lp}) and FimU (FimU_{Lp}) possess all the features of typical type IV pilins, including an N-terminal signal sequence required for their targeting to the inner membrane (IM), followed by a hydrophobic transmembrane helix required for IM insertion prior to pilus assembly and proper packing into the filament structure post assembly^{12,36}. First, we tested whether FimT_{Lp} or FimU_{Lp} are required for T4P biogenesis in *L. pneumophila*. To this end, we overexpressed a Flag-tagged version of the major pilin PilA2¹⁰ and compared relative amounts of PilA2-Flag-containing T4P in fractions of surface appendages sheared from the cell surface of various *L. pneumophila* Lp02 strains, including *fimT* and *fimU* deletion strains (**Extended Data Fig. 1a**). These results indicate that T4P are still assembled and present on the cell surface when *fimT* or *fimU* are deleted. Next, to test whether FimT_{Lp} or FimU_{Lp} play a role in natural transformation in *L. pneumophila*, we performed transformation assays comparing the *fimT* and *fimU* deletion strains with the parental strain and strains harbouring deletions in genes known to be important for natural transformation (**Fig. 1a**). Deletion of *comEC*, encoding the putative IM DNA channel, *pilQ*, encoding the OM secretin, and *pilT*, encoding the retraction ATPase, resulted in undetectable levels of natural transformation in our assay. These observations are in close agreement with previous studies in *L. pneumophila*, as well as other competent Gram-negative organisms such as *V. cholerae*, where deletion of these genes resulted in severe or complete natural transformation phenotypes^{10,16}. Deletion of *fimU* did not produce a phenotype, whereas natural transformation was undetectable in the *fimT* deletion strain, as observed previously in *A. bayly*³⁵. Expression of FimT_{Lp} *in trans* from an IPTG-inducible promoter restored the transformation efficiency of our *L. pneumophila* strain to wild-type levels, showing that the transformation defect is specific to FimT_{Lp}.

We reasoned that FimT contributes to the OM DNA uptake step of natural transformation by forming a constituent part of type IV pili (T4P) able to directly bind to DNA. Therefore, we performed electrophoretic mobility shift assays (EMSA) to test whether FimT_{Lp} is able to bind to DNA *in vitro* (**Fig. 1b**). In order to produce soluble protein samples, all pilins were expressed as truncations lacking the N-terminal transmembrane helix (**Extended Data Fig. 1b**). Indeed, purified FimT_{Lp} interacted with all DNA probes tested (**Extended Data Table 4**), including ssDNA, dsDNA, linear and circular DNA molecules, whereas neither

FimU_{Lp}, nor the putative major pilin subunits (PilA1 and PilA2) showed any interaction (Fig. 1b and Extended Data Fig. 1c). These experiments suggest that the dissociation constant (K_D) of the interaction between FimT_{Lp} and 30meric DNA is in the low μ M range. In order to determine the K_D more precisely and to learn about the binding stoichiometry of this interaction, we performed isothermal titration calorimetry (ITC) utilising shorter 12meric ssDNA or dsDNA fragments (Fig. 1c). We determined a K_D of 7.0 μ M and 2.8 μ M for 12meric ssDNA and dsDNA, respectively. Interestingly, these experiments revealed that a single FimT_{Lp} binds to 12meric ssDNA, whereas two molecules can bind to the dsDNA ligand, suggesting two binding sites on opposite sides of the double helix.

The solution structure of FimT_{Lp}

We determined the solution structure of the soluble N-terminally truncated (residues 28-152, mature pilin sequence numbering) FimT_{Lp} by nuclear magnetic resonance (NMR) spectroscopy (Fig. 2a, Table 1). The structure consists of an N-terminal α -helix (α 1C) (the transmembrane portion of this helix, α 1N, has been removed in the construct), two β -sheets that complete the C-terminal globular pilin domain, and a C-terminal tail, which exhibits conformational flexibility. Both β -sheets are composed of antiparallel strands: β -sheet I is formed by β 1, β 2, β 3 and β 5, and β -sheet II by β 4, β 6 and β 7. The closest structural homologue is FimU from *Pseudomonas aeruginosa* (FimU_{Pa}) (PDB ID: 4IPU, 4IPV) (Fig. 2b). While the two structures share a common fold, there are some key differences. In the FimU_{Pa} structure, the loop between β 2 and β 3 in β -sheet I forms an additional β -hairpin (β 2' and β 2''). It is possible, however, that this additional β -hairpin of FimU_{Pa} simply represents the conformation captured in the crystal structure, as the length of the β 2- β 3 loop is similar in both proteins. In addition, the β 7 strand of β -sheet II is longer in FimU_{Pa} and it contains an additional strand (β 8)³⁷. Furthermore, FimU_{Pa} contains a disulphide bond connecting Cys127 of β 6 to the penultimate residue, Cys158, effectively stapling the C-terminal tail in place on top of β -sheet II. Such a disulphide bond is found in various major and minor pilins and the intervening sequence is known as the D-region^{36,38}. Further structures of GspH/FimT family proteins exist, including of the minor T2SS pseudopilins, GspH from *Escherichia coli* (PDB ID: 2KNQ) and its orthologue EpsH from *V. cholerae* (PDB ID: 2QV8³⁹ and 4DQ9⁴⁰), which display similar folds (Extended Data Fig. 2).

The C-terminal tail (residues 140–152) of FimT_{Lp} is unique amongst the currently determined structures of GspH/FimT family members. Different pieces of NMR data suggest significant conformational exchange, but not an entirely flexibly disordered tail. The amide resonances of residues 140–149 are very weak and those of residues 142–144 are not visible at all. We could not observe any intense long-range nuclear Overhauser effects (NOEs) for residues

140–152, which would be expected for a well-defined β -sheet conformation. T_2 relaxation measurements indicated conformational exchange on the millisecond timescale, as the T_2 values for backbone amide ^1H and ^{15}N nuclei for the C-terminal tail were approximately half the value of the structured part of the protein (**Fig. 2d, Extended Data Fig. 3**). A fully disordered C-terminal tail could however be excluded by $\{^1\text{H}\}$ - ^{15}N heteronuclear NOE measurements, as the NOE intensity for the amides in the tail was close to the theoretical value of 0.78, which is expected for amides on globular particles. Finally, the deviations of $\text{C}\alpha$ chemical shifts from random coil values clearly indicated a β -strand propensity (**Fig. 2d, Extended Data Fig. 3**). The data therefore suggest that the C-terminal amino acids have a β -strand-like backbone conformation but sample different states in the micro- to millisecond timescale. These findings are further supported by low amide proton temperature coefficients⁴¹ and increased proteolytic susceptibility of this region, compared to the rest of the structure, witnessed by disappearance of the NMR resonances of the tail after prolonged storage of samples.

FimT_{Lp} interacts with DNA via a conserved C-terminal region rich in arginines

Next, we characterised the residues of FimT_{Lp} involved in DNA binding using NMR spectroscopy (**Fig. 3a-c**). We performed binding experiments titrating increasing amounts of 12 bp dsDNA (**Extended Data Table 4**) into ^{15}N -labelled FimT_{Lp} and recorded ^{15}N , ^1H heteronuclear single-quantum correlation (2D [^{15}N , ^1H]-HSQC) spectra. Most FimT_{Lp} resonances remained unperturbed (**Fig. 3a**), which suggests that no global conformational change occurs upon DNA binding. However, a subset of resonances exhibit marked chemical shift perturbations (CSPs) (**Fig. 3a**), indicating changes in the local chemical environment resulting from direct contact with DNA or other indirect conformational changes. A plot of CSPs against the amino acid sequence is shown in **Figure 3b**, and we mapped CSPs greater than a threshold ($\Delta\text{ppm} > 1\sigma$) onto the FimT_{Lp} surface (**Fig. 3c, Extended Data Fig. 4**). The largest CSPs correspond to residues located in three adjacent loop regions in the C-terminal globular domain of the protein, the $\beta 4$ - $\beta 5$ loop (residues 103–106), the $\beta 5$ - $\beta 6$ loop (118–126) and the C-terminal tail (140–152) (**Fig. 3b**). These shifts predominantly map to an elongated surface patch connecting the C-terminal tail with the globular C-terminal domain of FimT_{Lp} (**Fig. 3c**). Most of these residues are predicted to be accessible in the context of the assembled pilus, particularly when considering the flexibility of this region (**Fig. 2d, Extended Data Fig. 3**). CSPs corresponding to residues outside this contiguous surface patch can be explained by indirect conformational changes. We attempted to further structurally characterise the DNA-bound state, with special emphasis on possible changes in the structure or dynamics of the C-terminus. However, the FimT_{Lp}-DNA complex was not stable long-term and NMR signals were generally strongly weakened upon

DNA binding, such that relaxation or triple resonance experiments did not yield spectra of sufficient quality. An analysis of evolutionary conservation of the FimT_{LP} surface revealed that many of the interacting residues are also well conserved (**Fig. 3c**). In particular, residues of the C-terminal tail show marked sequence conservation and include a number of positively charged arginines, which are often involved in protein-DNA contacts through binding to the negatively charged DNA backbone via electrostatic interactions⁴².

Interface mutations inhibit DNA binding and natural transformation *in vivo*

We conducted microscale thermophoresis/temperature-related intensity change (MST/TRIC) experiments to measure the binding of labelled 12 bp dsDNA (**Extended Data Table 4**) to purified FimT_{LP} variants (**Extended Data Fig. 1b**), in order to further understand the nature of the FimT_{LP}-DNA interaction and the importance of specific interface residues. First, we conducted experiments under different buffer conditions to test whether the affinity of the interaction between wild-type FimT_{LP} and DNA is dependent on ionic strength. Indeed, when we increased the NaCl concentration from 50 mM to 150 mM, thereby raising the ionic strength, the K_D increased from ~6.3 μ M to ~70.1 μ M (**Fig. 4a**). This is consistent with a non-sequence specific protein-DNA interaction, which is electrostatically driven. Furthermore, the K_D determined at a NaCl concentration of 50 mM agrees very well with the affinities determined from the ITC experiments (K_D of 2.8 μ M) (**Fig. 1c**), as well as our NMR binding studies (K_D of ~8 μ M) (**Extended Data Fig. 5**), which were all conducted in the same buffer. Next, we used MST/TRIC to test the importance of several charged residues at the DNA binding interface identified by our NMR analyses (**Fig. 4b**). We substituted arginine or lysine residues for glutamine in the three loop regions we identified to be important for binding. As expected, the loss of a single charged residue (e.g. K103 in the β 4- β 5 loop; R119 in the β 5- β 6 loop; R143, R146 or R148 in the C-terminal tail) only led to a small reduction in the affinity (~1.4–4 fold). However, the combined loss of two (R146/R148) or three (R143/R146/R148) charged residues next to each other on the FimT_{LP} surface was more detrimental to binding, resulting in a ~10 fold or ~45 fold reduction in affinity, respectively. Lastly, we tested what effect these binding mutations have on natural transformation *in vivo* (**Fig. 4c**). These data show that mutations of single charged residues reduce *Legionella*'s transformability by ~30-600 fold, whereas the double and triple mutants completely abrogate DNA uptake in our assay and thus phenocopy the effect observed upon *fimT* deletion (**Fig. 1a**). These results further support a model in which FimT_{LP} contributes to natural transformation in *Legionella* by virtue of its ability to interact with DNA in the context of a DNA uptake pilus.

FimT of other Gram-negative bacteria also interacts with DNA

Given that FimT, and the residues involved in DNA binding identified in FimT_{Lp}, appear to be conserved, we wondered whether FimT orthologues from other bacteria are also capable of binding DNA. We expressed and purified FimT and FimU from the human pathogen *P. aeruginosa* and the plant pathogen *Xanthomonas campestris* (both γ -Proteobacteria) and performed EMSAs to assess DNA binding *in vitro* (**Fig. 5a**). Interestingly, FimT from both species binds to DNA and the affinity appears to be within the same order of magnitude as *L. pneumophila* FimT. On the other hand, FimU does not interact with DNA, except for the *X. campestris* homologue, which shows very weak binding at very high FimU concentrations. Since both FimT orthologues (FimT_{Pa} and FimT_{Xc}) likely share structural similarities to FimT_{Lp}, we tested whether they are capable of restoring natural transformability in a *L. pneumophila* *fimT* deletion strain. The FimT orthologues were ectopically expressed either as wild-type full-length proteins or as chimeric proteins. The chimeric constructs replaced the flexible C-terminal tail region (lacking a disulphide bond) of FimT_{Lp} with the *bona fide* D-region of the FimT orthologues (**Fig. 5b**). The expression of full-length FimT_{Pa} and FimT_{Xc} did not restore natural transformation. Intriguingly, when we replaced the flexible C-terminal tail of FimT_{Lp} with the D-region of FimT_{Pa}, natural transformation levels were restored to near wild-type levels. Together, these results indicate that DNA binding by FimT is not unique to *L. pneumophila* and that FimT may be important for DNA uptake in a wide range of competent species.

We then used genomic context and sequence information from the four FimT orthologs known to either bind to DNA or contribute to competence (from *L. pneumophila*, *X. campestris*, *P. aeruginosa* and *A. baylyi*) to explore the distribution and conservation of this protein (see Methods). First, we looked at the genetic location and organisation of FimT and FimU in *Legionella* and other bacteria (**Extended Data Fig. 6**). In *L. pneumophila*, *fimU* (*lpg0632*) is encoded in a minor pilin operon upstream of *pilV* (*lpg0631*), *pilW* (*lpg0630*), *pilX* (*lpg0629*), *pilY1* (*lpg0628*) and *pilE* (*lpg0627*). In contrast, *fimT* (*lpg1428*) appears as an 'orphan' gene, encoded elsewhere in the genome, and seemingly distant from genes encoding other type IV pilins, components of the T4P machinery or genes with known functions in natural transformation. Interestingly, while FimT in other species could be found either as an orphan, or adjacent to other minor pilin-related genes, the location of FimU was conserved, and this pattern was seen in a broader collection of homologues as well as the functionally-characterised representatives. We then retrieved a diverse set of homologues of FimT_{Lp} and classified them according to genomic location and sequence similarity to exclude sequences that were likely to be FimU proteins. We found that FimT is conserved in all sequenced *Legionella* species, and homologues are found in a wide variety of

γ -Proteobacteria from various phylogenetic orders, with representatives of the Xanthomonadales, Alteromonadales and Pseudomonadales being particularly common (**Fig. 5c**). The pairwise sequence identity was 40-50% between FimTs from *Legionella pneumophila* and other *Legionella* species, and ~25% (median) between *L. pneumophila* FimT and those from more distantly related bacteria. Around half of the FimT homologues are located in proximity (within 5 kb) to other minor pilin locus components. FimU is also present in many bacterial species, albeit not all species encode both genes. Phylogenetic analysis of FimT homologues showed that these proteins largely clustered with others from the same order and sharing the same locus type, indicating that *fimT* is likely to be vertically inherited. The best conserved regions of FimT include the N-terminal helix, important for pilus biogenesis (IM insertion, assembly and structural packing), and the C-terminal region (**Fig. 5d**). This region of conservation includes many of the residues we have identified to be important for DNA binding and thus natural transformation (**Fig. 3c, d**). Indeed, it appears as though these DNA binding residues can be identified in proteins with as little as 18% overall amino acid sequence identity with FimT_{Lp}. Taken together, FimT homologues share an overall fold and a conserved DNA-binding motif near the C-terminus of the protein, and can be found in diverse genomic locations within diverse proteobacterial species.

Discussion

Natural transformation is an important mode of horizontal gene transfer with widespread consequences for bacterial evolution. Furthermore, the spread of pathogenicity traits and antibiotic resistance genes leads to the emergence of increasingly virulent and difficult to treat bacterial strains. The first step of this process involves DNA uptake mediated by T4P⁹, which has only been studied in a handful of competent species. The minor type IV pilin FimT, but not the closely related FimU, from *A. baylyi* was previously implicated in natural transformation³⁵, yet its mechanism remained obscure. Here, we characterised FimT from the naturally competent human pathogen *L. pneumophila* (FimT_{Lp}) and revealed the molecular mechanisms underlying its role in natural transformation.

We hypothesised that FimT_{Lp} is involved in DNA uptake by binding to extracellular DNA in the context of T4P and showed that *Legionella* strains lacking *fimT* display a marked reduction in transformation efficiency (**Fig. 1a**). Indeed, purified FimT_{Lp} interacted with DNA *in vitro*, regardless of the nature of DNA probe tested (**Fig. 1b, Extended Data Fig. 1c**). Furthermore, we determined the structure of FimT_{Lp} by NMR spectroscopy (**Fig. 2**) and mapped its DNA interaction surface by chemical shift perturbation experiments (**Fig. 3**). This binding surface consists of several positively charged residues, some of which are highly conserved, located primarily in two loop regions (the β 4- β 5 and β 5- β 6 loops) and the

C-terminal tail (**Fig. 3b, c**). The importance of key residues for DNA binding and natural transformation was confirmed by *in vitro* DNA binding assays and *in vivo* transformation assays (**Fig. 4b, c**). Although our ITC experiments (**Fig. 1c**) indicate a 2:1 (FimT_{Lp}:DNA) binding mode, we do not think this is physiologically relevant in the context of the T4P.

Our structure of FimT_{Lp} shares the same overall fold as the closely related T4P minor pilin FimU_{Pa}, and the T2SS minor pseudopilins GspH_{Ec} and EpsH_{Vc}, albeit with some key differences (**Fig. 2, Extended Data Fig. 2**). In place of the last β -strand ($\beta 8$), part of β -sheet II in all other currently determined FimT/GspH family structures, FimT_{Lp} contains a conformationally flexible C-terminal tail (**Extended Data Fig. 3**). In our NMR studies, the heteronuclear $\{^1\text{H}\}$ - ^{15}N NOE data and C α chemical shifts for the C-terminal residues are indicative of a β -strand conformation, while the T₂ transverse relaxation times for backbone amide ^1H and ^{15}N nuclei, increased line broadening and the absence of H-bonds indicate a less well-structured conformation. A plausible interpretation of these results is that this region can exchange between a β -strand and a less-structured conformation on a millisecond timescale. The flexibility of this region is further supported by its increased proteolytic susceptibility. FimT_{Lp}, as well as all FimT homologues from the order Legionellales, lack the D-region defining disulphide bond present in many major and minor pilins, including other FimT and FimU homologues (**Fig. 5d**). Therefore, it is likely that disulphide bond-containing FimT orthologues do not possess a conformationally flexible C-terminal tail. The structure of GspH_{Ec} was also determined in solution by NMR spectroscopy, yet it possesses a clearly defined and complete four-stranded β -sheet II region. This suggests that this region, also shared by FimU_{Pa} and EpsH_{Vc}, is not simply a result of crystal lattice effects and thus further highlights FimT_{Lp}'s unique C-terminal tail (**Fig. 2, Extended Data Fig. 2**).

FimU and GspH/EpsH have been suggested to serve as adaptors in T4P and T2SS pseudopili, respectively, linking the tip subunits to the remainder of the filament structure composed of the major pilin subunit^{43–45}. Whereas minor pilins in general have been suggested to play a role in pilus priming/pilus biogenesis^{37,45}, the deletion of FimU, but not FimT affected pilus biogenesis in *P. aeruginosa* and *Pseudomonas syringae*^{46,47}. Furthermore, FimU, but not FimT of *P. aeruginosa* has been shown to play a role in bacterial twitching motility⁴⁸. In *A. baylyi* on the other hand, both proteins showed near wild-type levels of twitching, but FimT appeared to play a role in natural transformation³⁵. Orthologues of the GspH pseudopilin are critical components of the T2SS and may play a role in binding to T2SS protein substrates⁴⁹. To this end, the crystal structure of the *V. cholerae* orthologue EpsH revealed an extended and disordered $\beta 4$ - $\beta 5$ loop (**Extended Data Fig. 2d**), which has

been proposed to play a role in substrate binding⁴⁰. Interestingly, we have identified this same loop to contribute to FimT_{Lp}-DNA binding (**Fig. 3b**). Therefore it appears that, although sharing a common evolutionary origin⁵⁰, FimT/GspH family proteins have become functionally diverged and specialised for the binding of different macromolecular substrates^{51,52}. In the case of FimT_{Lp}, a surface patch rich in arginines enables it to function in DNA uptake during natural transformation.

The currently best-characterised DNA binding minor pilin is ComP^{27,28,34}. While ComP homologues seem to be restricted to species of the family *Neisseriaceae*²⁷, FimT homologues are present in diverse γ -Proteobacteria and some Hydrophilales (**Fig. 5c**). Both proteins share a conserved type IV pilin core structure, including the N-terminal helix and a four-stranded antiparallel β -sheet, but differ substantially in their C-terminal regions. In the case of ComP, this region is characterised by its so-called DD-region containing two disulphide bonds²⁷ (**Extended Data Fig. 7**). By contrast, FimT contains a second three-stranded antiparallel β -sheet followed by its conformationally flexible C-terminal tail and contains no disulphide bonds. In both proteins, important DNA binding residues are located near the C-terminus, which would be exposed to the solvent in the context of a fully assembled pilus²⁸. Interestingly, competent *Neisseriaceae* species preferentially take up DNA sequences from related species^{31–33}. This has been attributed to ComP's increased binding affinity towards DUS-sequences, which are DNA sequences that are highly enriched in their own genomes²⁷. It was proposed that ComP engages DNA *via* an initial electrostatic attraction, followed by ComP's $\alpha 1$ - $\beta 1$, $\beta 1$ - $\beta 2$, DD-region binding to successive grooves of the dsDNA to achieve specificity²⁸. In contrast, no sequence selectivity has been reported for *L. pneumophila*³, which is consistent with the electrostatic binding mode of FimT_{Lp}. In addition to FimT_{Lp} and ComP, other type IV pilins or pilin-like proteins that contribute to T4P DNA binding include ComZ and PilA4 from *T. thermophilus*^{29,30} and VC0858 and VC0859 from *V. cholerae*¹⁵. Once again, positively charged lysine and/or arginine residues likely contribute to DNA binding in all these proteins.

Lastly, we showed that other FimT orthologues, including FimT of the human pathogen *P. aeruginosa* and the plant pathogen *X. campestris*, are also capable of DNA binding (**Fig. 5a**). These experiments showed that FimT orthologues, whether they contain or lack the D-region defining disulphide bond, are capable of DNA binding. This was demonstrated even more strikingly by the FimT chimera, where the fusion of FimT_{Lp} with FimT_{Pa} introduced a non-native disulphide bond into the *Legionella* system, yet resulted in a functional protein *in vivo* capable of supporting natural transformation (**Fig. 5b**). In addition, our bioinformatic

analyses showed that FimT is present across a wide range of γ -Proteobacteria and that the DNA-binding C-terminal region is well-conserved on a sequence level (**Fig. 5d**). In particular, our alignments of high-confidence FimTs revealed a conserved GRxR motif (where x is often, but not always, a hydrophobic residue) at their C-terminus (**Fig. 5d**). In FimT_{Lp} these two arginines correspond to R146 and R148, which we showed contribute to DNA binding *in vitro* and *in vivo* (**Fig. 4b, c**). This motif is less well defined or only partially present in FimU orthologues and those we tested in this study do not bind DNA *in vitro* (**Fig. 5a**). Interestingly, a similar C-terminal motif can also be found in the pilins that assemble into the Com pili of Gram-positive organisms, which have been implicated in DNA uptake during natural transformation^{53–55}. It remains to be investigated, whether this motif also contributes to DNA binding and natural transformation in those proteins.

In summary, this study provides a comprehensive analysis of the molecular mechanisms underpinning FimT's interaction with DNA and demonstrated its pivotal role during natural transformation of the human pathogen *L. pneumophila*. Furthermore, we analysed FimT orthologues from other naturally competent and pathogenic γ -Proteobacteria, which together with our thorough bioinformatic analysis, suggests that FimT is a key player in the natural transformation of a wide range of bacteria.

Methods

Bacterial strains and growth conditions

L. pneumophila Lp02 (laboratory strain derived from *L. pneumophila* Philadelphia-1) was cultured in ACES [N-(2-acetamido)-2-aminoethanesulfonic acid]-buffered yeast extract (AYE) liquid medium or on ACES-buffered charcoal yeast extract (CYE) solid medium, supplemented with 100 µg/mL streptomycin and 100 µg/mL thymidine. When appropriate, chloramphenicol and kanamycin were added at 5 µg/mL and 15 µg/mL, respectively. For the construction of knockout Lp02 strains, the relevant genes and 1000 bp of upstream and downstream regions were first cloned into the pSR47S suicide plasmid (derivative of pSR47⁵⁶). Following deletion of the gene of interest from the plasmid, the modification was introduced onto the Lp02 chromosome by triparental conjugation and subsequent selection as described previously^{57,58}. All strains were verified by colony PCR and DNA sequencing (Microsynth) and are listed in **Extended Data Table 2**.

Plasmids

All protein expression constructs were generated using the pOPINS or pOPINB vectors^{59,60} carrying an N-terminal His₆-SUMO or His₆ tag, respectively. Constructs for *in vivo* studies were generated using pMMB207C⁶¹, by cloning the relevant genes downstream of the *P_{tac}* promoter. DNA fragments were amplified from *L. pneumophila* (RefSeq NC_002942.5) genomic DNA by PCR using CloneAmp HiFi PCR premix (Takara) and the relevant primers. For FimT and FimU orthologues from *P. aeruginosa* PAO1 (RefSeq NC_002516.2) and *X. campestris* pv. *campestris* str. ATCC 33913 (RefSeq NC_003902.1), template DNA was first synthesised (Twist Bioscience). In-Fusion cloning and site-directed mutagenesis was carried out according to the manufacturer's guidelines (Takara). All plasmids and primers used in this study can be found in **Extended Data Table 3** and **Extended Data Table 4**, respectively. A summary of the gene locus tags of genes mentioned in this study from their respective genomes can be found in **Extended Data Table 5** and **Extended Data Table 6**.

Protein Production

Recombinant His₆-SUMO tagged proteins (FimT_{Lp}, FimU_{Lp}, FimT_{Pa}, FimU_{Pa}, FimT_{Xc}, FimU_{Xc}) and His₆-tagged proteins (PilA1, PilA2) were expressed in BL21 (DE3) or Shuffle T7 *E. coli* cells (NEB). All constructs were N-terminally truncated to remove the transmembrane helix (α1N) (**Extended Data Table 3**). Cultures were grown in Luria-Bertani (LB) media to an optical density at 600 nm (OD₆₀₀) of 0.6–0.8, induced using 0.5 mM IPTG and further incubated at 16°C for 12–18 h while shaking. Cells were lysed in 50 mM Tris-HCl pH 7.2, 1 M NaCl, 20 mM imidazole, 0.1 mg/mL lysozyme, 1 mg/mL DNase and one complete mini

EDTA-free protease inhibitor cocktail tablet (Roche), by passing the sample three times through a pressurised cell disruptor (M110-L, Microfluidics) at 12000 psi. The clarified lysate was applied to a 5 mL HisTrap HP column (Cytiva) and His₆-SUMO or His₆ tagged pilins were eluted with a linear 20–500 mM imidazole gradient. The His₆-SUMO or His₆ tag was cleaved using the catalytic domain of the human SENP1 protease or PreScission protease, respectively, while the sample was dialysed against 50 mM Tris-HCl pH 7.2, 50 mM NaCl. Protein samples were further purified by cation exchange chromatography using a 5 mL HiTrap SP HP column (Cytiva), from which pilins were eluted using a linear 50–1000 mM NaCl gradient. Lastly, the pilin samples were purified by size exclusion chromatography in 50 mM Tris-HCl pH 7.2, 50 mM NaCl using a HiLoad 16/600 Superdex 75 pg column (Cytiva). Protein samples were concentrated using Amicon Ultra-15 centrifugal filters (3 kDa molecular weight cut-off, Millipore). Reducing agent (2 mM DTT) was included in the buffers for those pilins with free cysteines. All purification steps were performed at 4°C.

NMR spectroscopy

Production of isotope-labelled FimT_{Lp}

To produce uniformly labelled FimT_{Lp}, cells were grown in M9 minimal medium containing 1 g/L ¹⁵NH₄Cl and further supplemented with 3 g/L glucose (or ¹³C₆-glucose for double labelled FimT_{Lp}), 2 mM MgSO₄, trace elements, vitamin mix and appropriate antibiotics for selection. Protein expression was induced at an OD₆₀₀ of 0.6–0.8 with 0.5 mM IPTG and cells were harvested after 20 h at 16°C. FimT_{Lp} was purified as described above.

Data acquisition and structure determination

For resonance assignments and structure determination the following spectra were recorded on a 580 μM sample of (u-¹³C,¹⁵N)-labeled FimT 28–152 in 25 mM NaPi pH 7.2, 150 mM NaCl and 10% D₂O at 298 K in a 3 mm diameter NMR tube: 3D HNCACB and 3D CBCACONH spectra⁶² were recorded on a 700 MHz AVIIIHD spectrometer equipped with a TCI cryoprobe (Bruker). The spectra consisted of 2048×50×100 complex points in the ¹H, ¹⁵N and ¹³C dimensions with respective spectral widths of 16, 34 and 64 ppm, and were recorded with 8 scans per increment resulting in 2 and 1.5 days of measurement time, respectively. A 3D HcC(aliao)H-TOCSY⁶³ was recorded on a 600 MHz AVIIIHD spectrometer equipped with a TCI cryoprobe (Bruker). The spectrum consisted of 1536×100×150 complex points in the ¹H, ¹H and ¹³C dimensions with respective spectral widths of 16, 12 and 140 ppm and was recorded with 2 scans per increment in 3 days using a recycle delay of 2 s. A time shared 3D [¹³C/¹⁵N,¹H]-HSQC NOESY (modified from⁶⁴) was recorded on a 900 MHz AVIIIHD spectrometer equipped with a TCI cryoprobe (Bruker). The spectrum consisted of 1536×100×256 complex points in the ¹H, ¹H and ¹³C/¹⁵N dimensions

with respective spectral widths of 16, 12 and 140/58 ppm and was recorded with 2 scans per increment in 3 days.

Resonance assignments were determined with the program cara (www.cara.nmr.ch, Keller R (2005), ETH Zürich) to 98.2% completeness. Signals in the NOESY spectra were subsequently automatically picked in the program analysis of the ccpnmr 2.5.1 software package⁶⁵. Peaklists and assignments were used as input for a structure calculation with cyana⁶⁶ where angle constraints were automatically generated from Cα chemical shifts.

Manual inspection of the automatically picked peak lists resulted in a set of 4595 picked NOE peaks of which 4220 were assigned in the final cyana calculation which yielded an average target function value of 0.21. The structures were finally energy minimized in the program amber20⁶⁷. Statistics for the resulting bundle of 20 conformers can be found in **Table 1**. Additional analysis of the structural bundle after the cyana calculation revealed 42 hydrogen bonds (each present in more than 6 structures) and the following Ramachandran statistics: 72.2%, 27.4% and 0.4% of residues in favoured, allowed and additionally allowed regions, respectively. All structural figures were generated using PyMOL (<https://www.pymol.org>).

DNA binding studies by NMR

To map the surface patch of FimT_{Lp} involved in DNA binding, chemical shift perturbation experiments were performed using 12 bp or 36 bp dsDNA fragments (**Extended Data Table 4**). [¹⁵N,¹H]-HSQC experiments of 80 μM ¹⁵N-labelled FimT_{Lp} at saturating concentrations of DNA were recorded. In order to use the same conditions as other assays, all protein and DNA samples for NMR binding studies were dialysed into 50 mM Tris-HCl pH 7.2, 50 mM NaCl buffer. Weighted chemical shift perturbations (CSPs), defined as $((\Delta^1\text{H}^2)^{0.5} + ((\Delta^{15}\text{N}/5)^2)^{0.5}$ (ppm), were measured by comparing spectra of unbound and bound states. The standard deviation (σ) of the chemical shift range was calculated, CSP maps were plotted in GraphPad Prism v9 and residues for which the shift change was greater than σ were mapped onto the FimT_{Lp} surface. To estimate the equilibrium dissociation constant (*K_D*) of this interaction, [¹⁵N,¹H]-HSQC experiments of 40 μM ¹⁵N-labelled FimT_{Lp} at different concentrations (0–600 μM) of DNA were recorded. For selected residues undergoing large CSPs, binding curves were plotted and fitted to a model assuming one set of binding sites using the software fitKD (four representative curves are shown in (**Extended data Fig. 5**)). The spectra were recorded on a 700 MHz AV-NEO spectrometer equipped with a TCI cryoprobe (Bruker) and consisted of 2048×128 complex points using 32 scans per increment resulting in an experiment time of 2 h.

Electrophoretic mobility shift assay

Various DNA probes were tested for interaction with purified pilin samples using an agarose gel-based electrophoretic mobility shift assay (EMSA). Short 30 bp dsDNA fragments were generated by annealing complementary strands of the appropriate length. To generate fluorescently labelled dsDNA probes, one of the two annealing strands was labelled at the 5' end with fluorescein (FAM). All oligonucleotides were obtained from Microsynth and are listed in **Extended Data Table 4**. The pTRC99A-*lpg2953-2958::Kan* (9074 bp) plasmid, left intact or linearised by a single-cutter restriction enzyme (ClaI), was used for the comparison between circular and linear dsDNA probes, respectively. All DNA probes were resuspended in or dialysed into the same buffer as the protein samples prior to the assay. DNA samples (1 µM of 30-meric ssDNA and dsDNA; 20 ng/µl for longer DNA fragments) were incubated with increasing concentrations (0-100 µM) of pilins in 50 mM Tris-HCl pH 7.2, 50 mM NaCl, 15% (v/v) glycerol in a final volume of 20 µL. These samples were incubated at 25°C for 30 min and subsequently separated by gel electrophoresis at 10 V/cm for 30 min using 0.9-2.5% (w/v) agarose gels containing SYBR Safe DNA stain (Invitrogen). DNA was visualised using UV illumination in a gel imaging system (Carestream).

Isothermal Titration Calorimetry

Isothermal titration calorimetry (ITC) experiments were carried out in duplicate on a VP-ITC microcalorimeter (MicroCal). All measurements were performed in 50 mM Tris-HCl pH 7.2, 50 mM NaCl buffer at 30°C. Following a pre-injection of 1 µL, titrations consisted of 19 consecutive 15 µL injections of 320 µM 12meric dsDNA or 350 µM ssDNA (syringe) into 30 µM FimT_{Lp} (cell) performed at 180 s or 240 s intervals, respectively. The heat of ligand dilution, obtained by injecting DNA into buffer, was subtracted from the reaction heat, and curve fitting was performed in Origin (OriginLab) using a model assuming two binding sites of equal affinity or "one set" of binding sites.

Microscale thermophoresis/temperature-related intensity change measurements

Microscale thermophoresis (MST) experiments were conducted measuring the temperature-related intensity change (TRIC) of the fluorescence signal⁶⁸. A 12 bp fluorescently labelled dsDNA probe was generated by annealing a 5' FAM-labelled and an unlabelled strand (Microsynth; **Extended Data Table 4**) and used in all MST/TRIC experiments. Equilibrium binding assays were performed in 50 mM Tris-HCl pH 7.2, 50-150 mM NaCl, 0.05% (v/v) Tween-20. Increasing concentrations of purified wild-type or mutant FimT_{Lp} samples were incubated with 100 nM of FAM-labelled 12 bp dsDNA probe at 25°C for 30 min prior to measurement. MST/TRIC measurements were performed at 20°C using a Monolith NT.115 instrument (NanoTemper) at 25% LED power and 20% MST laser power. Curve fitting was

performed with data derived from the TRIC effect. For the experiment conducted with wild-type FimT_{Lp} measured at 50 mM NaCl, the data appeared slightly biphasic in nature. This suggested the presence of two binding sites with similar, yet non-identical binding affinities. When these data were fitted with a binding model assuming two non-identical binding sites, $K_D(1)$ was indeed very similar to that obtained when fit according to two identical sites (~2.9 vs 6.3 μ M). All other binding experiments using other methods (ITC and NMR), as well as MST/TRIC experiments conducted with FimT_{Lp} mutants, did not reveal an obvious biphasic binding signature, which could be explained by insufficient resolution. Therefore, we chose to fit all data in the same manner, assuming two identical binding sites, to allow for their comparison. All MST/TRIC measurements were performed at least three times. In addition, all samples were measured twice, 30 min apart, resulting in very similar binding curves and derived dissociation constants, indicating that the binding equilibrium had been attained at the time of measurement.

Transformation assay

All transformation assays were performed with the *L. pneumophila* Lp02 strain in liquid medium at 30°C, similar to transformation assays performed by others^{10,69}. Strains were streaked onto CYE solid medium from frozen stocks and incubated at 37°C for 3-4 days. From this plate, bacteria were resuspended in a liquid starter culture (5 mL of AYE medium) and incubated at 37°C overnight while shaking at 200 rpm. The starter culture was diluted into a fresh 10 mL AYE culture (starting OD₆₀₀ of 0.02) and cultured at 30°C while shaking. Once the culture reached an OD₆₀₀ of 0.3, 1 mL was transferred into a new tube and incubated with 1 μ g of transforming DNA at 30°C for a further 24 h. The transforming DNA consisted of a 4906 bp PCR product encompassing the *L. pneumophila* genomic region spanning *lpg2953-2958*, where the *hipB* gene (*lpg2955*) is interrupted by a kanamycin resistance cassette (based on⁷⁰). This provides 2000 bp regions of homology up- and downstream of the resistance cassette. Tenfold serial dilutions of the culture were plated on selective (supplemented with 15 μ g/mL kanamycin) and non-selective CYE media. The plates were incubated at 37°C for 4-5 days and colony forming units (CFUs) were counted. The transformation efficiency corresponds to the ratio of the number of CFUs obtained on selective medium divided by the number of CFUs counted on non-selective medium. The minimum counting threshold was set at 10 colonies per plate. Transformation assays to test complementation of knockout strains with protein ectopically expressed from the pMMB207C plasmid were performed in the same manner, except for the addition of 0.5 mM IPTG during the incubation step of the bacteria with transforming DNA. Transformation assays requiring direct comparison between strains or complemented strains were performed in parallel.

Western blot detection of pilin in sheared surface fractions

Lp02 strains (parental, $\Delta fimT$ and $\Delta fimU$) harbouring pMMB207C-*pilA2-flag* were cultured at 37°C for 24 h on CYE media, additionally supplemented with 0.5 mM IPTG. Cells were resuspended in AYE media containing a complete mini EDTA-free protease inhibitor cocktail tablet (Roche) and adjusted to an OD₆₀₀ of 20. To shear appendages from the cell surface, the resuspended cells were vortexed at maximal speed for 30 s. Subsequently, the depiliated cells were pelleted by two rounds of centrifugation at 20'000 g for 20 min at 4°C. The supernatants containing surface appendages, including T4P, were transferred to new tubes and the pellets were washed twice by resuspension in 1 mL AYE followed by centrifugation at 20'000 g for 20 min at 4°C. Both pellets and supernatants were separated by SDS-PAGE. Proteins were transferred to polyvinylidene fluoride (PVDF) membranes (Amersham) and PilA2-Flag was detected using a horse radish peroxidase (HRP)-coupled primary anti-Flag antibody at a 1:2000 dilution (Sigma, cat. no. SAB4200119). Enhanced chemiluminescence (ECL) (Cytiva) was used for the detection of the protein signal in a Amercham Imager 600. PVDF membranes were stained with Ponceau S to verify even loading across all lanes.

Bioinformatic analyses

Collection of putative FimT and FimU sequences

Three sets of FimT or FimU sequences were collected as follows: 1) a FimT set was retrieved by BlastP against FimT_{Lp}, FimT_{Pa}, FimT_{Ab} and FimT_{Xc} with a 95% query coverage cutoff, 2) a FimU set was retrieved by BlastP against FimU_{Lp}, FimU_{Pa}, FimU_{Ab} and FimU_{Xc} with a 95% (Pa, Ab, Xc) or 80% (Lp) query coverage cutoff, 3) a diverse FimT/U set was retrieved by a PSI-blast⁷¹ search against FimT_{Lp}, with >95% query coverage and e-value >0.005 cutoffs applied at each iteration, and the search continued for 8 iterations. To limit redundancy in the results all searches were conducted against the refseq_select protein database which, for prokaryotes, contains only sequences from representative and reference genomes. The FimT and FimU sets were used for initial gene neighbourhood analyses beyond the four functionally characterised representatives (**Extended Data Fig. 6**), while the diverse set was used for phylogenetic analysis and to define conserved regions.

Gene neighbourhood analysis

The gene neighbourhood of each *fimT* and *fimU* was examined using custom Biopython⁷² scripts and NCBI resources as follows 1) source genome(s) for each protein entry were identified from the Identical Protein Groups (IPG) resource (this was necessary because many of the blast results were non-redundant entries comprising multiple identical proteins), 2) the genome region corresponding to the gene of interest and 5000 bp up- and

downstream was downloaded from the nucleotide database for one representative of each IPG (if <5000 bp flanking up- and downstream sequence was available the entry was excluded from further analysis), and 3) coding sequences in the neighbouring region were extracted as multifasta and searched against the Pfam⁷³ database of domain profiles using HMMER⁷⁴ (hmm scan function, e-value threshold 0.0001). *fimT* or *fimU* genes were classified as orphans or minor pilin locus components based on the presence of one or more of the Pfam domains PilC, PilX, PilX_N and PilW in the flanking region. The presence of just one of these domains was defined as indicating a minor pilin locus, to account for the possibility that proteins only weakly matching the relevant Pfam domain would be missed, or that relevant proteins may be found >5000 bp away. NCBI scripts used in this study are available at https://github.com/francesca-short/NCBI_scripts.

Generation of high-confidence FimT set and phylogenetic analysis

Because FimT is a GspH-domain protein and shares overall structural similarity with the type IV minor pilin FimU and the T2SS protein GspH, putative homologues from the diverse FimT/U set were filtered based on their gene neighbourhood to exclude likely *fimU* genes and generate a subset of high-confidence putative *fimT* genes for further analyses. As 100% of genes in the FimU set were located in minor pilin operons, orphan genes within the diverse FimT/U set were presumed to encode genuine FimT proteins, and these sequences were aligned along with FimT_{Lp}, FimT_{Pa}, FimT_{Ab} and FimT_{Xc} and used to generate a FimT HMM profile using HMMER⁷⁴ (hmmbuild function). A FimU HMM profile was generated from sequence set 2 (FimU homologues), following alignment with MUSCLE and removal of entries showing >80% amino acid identity to another entry. Each sequence from the diverse FimT/U set was scanned against both the FimU and FimT sequence HMMs and reported as a likely FimT if its match score to the FimT profile was >20 points greater than its match to the FimU profile. In this way, a set of 196 putative FimT protein sequences was obtained. FimT protein sequences were aligned using MUSCLE⁷⁵ with default (high-accuracy) settings, and the alignment was visualised and manually improved using JalView⁷⁶. The FimT alignment was processed using TrimAL⁷⁷ to remove low-quality positions and uninformative sequences (parameters: -strictplus -resoverlap 0.8 -seqoverlap 75). A maximum-likelihood phylogenetic tree of the FimT homologues was constructed using IQtree⁷⁸ with the substitution model LG+F+R5⁷⁹ and ultrafast bootstrapping⁸⁰. The phylogenetic tree and associated metadata was viewed using iTol⁸¹. The tree was midpoint-rooted and branches with less than 50% bootstrap support removed. Gene neighbourhood diagrams for selected FimT homologues were generated using Clinker⁸². The FimT motif diagram was generated using WebLogo⁸³.

Data availability

The data that support the findings of this study are available from the corresponding author upon reasonable request. NMR spectra and corresponding model coordinates have been deposited in the **BioMag Resonance Data Bank (BMRB: XXX)** and Protein Data Bank (**PDB ID: XXXX**), respectively.

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Author Contributions

SAGB cloned constructs, created *Legionella* strains, purified proteins, performed DNA binding studies, transformation assays, Western blots and analysed results. FLS designed and performed all bioinformatic analyses. SH constructed FimT chimera constructs and performed the corresponding transformation assays. MJMS purified proteins and performed ITC experiments. ADG performed and analysed all NMR-related experiments with help from SAGB. MKH designed and supervised the study, made figures and wrote the manuscript with help from all authors.

Competing Interests Statement

The authors declare no competing interests.

Figures

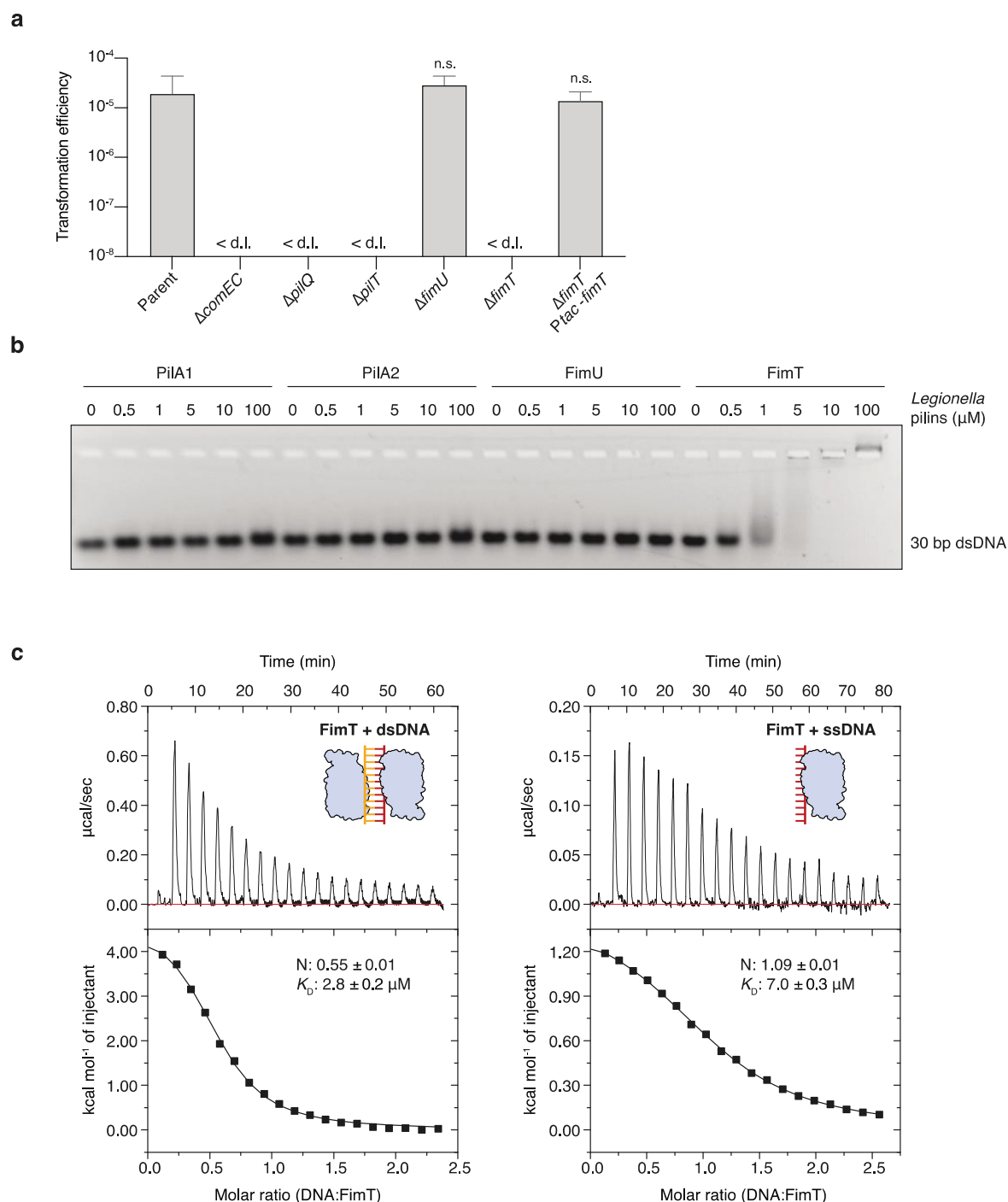


Figure 1: FimT is critical for the transformation of *L. pneumophila* and binds to DNA

a, Natural transformation efficiencies of the parental *L. pneumophila* Lp02 strain and Lp02 strains harbouring deletions of genes known to play a role in transformation compared to the *fimU* and *fimT* deletion strains. The $\Delta fimT$ strain was complemented by ectopic expression of wild-type FimT, under the control of an IPTG-inducible promoter. The mean transformation efficiencies of three independent biological replicates is shown (error bars represent

standard deviation [SD]). <d.l., below detection limit (d.l.) (average d.l. = $2.0 \times 10^{-8} \pm 8.2$
 $\times 10^{-9}$). Statistical significances of transformation differences were determined on log-
transformed⁸⁴ data using an unpaired t-test with Welch's correction. n.s., not statistically
significant ($p > 0.05$). **b**, *In vitro* DNA binding of purified *L. pneumophila* PilA1, PilA2, FimU
and FimT assessed by an EMSA. A 30 bp dsDNA fragment (1 μ M) was incubated with
increasing concentrations of purified pilins (0–100 μ M) and resolved by agarose gel
electrophoresis. **c**, ITC binding studies of wild-type FimT binding to 12meric dsDNA (right)
and ssDNA (left). In both cases, DNA (syringe) was injected into FimT (cell). Data were fitted
using the “one set” of sites model, assuming that both binding sites on the dsDNA are of
equal affinity.

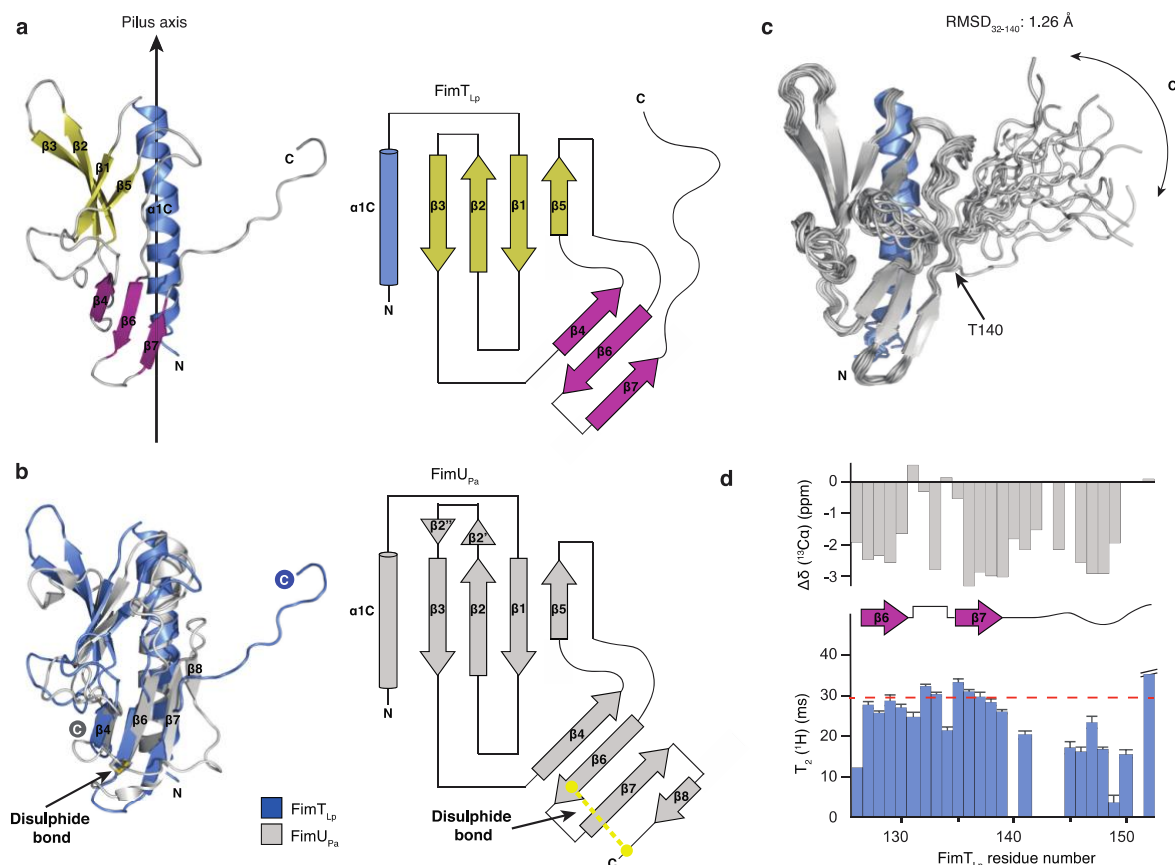


Figure 2: The structure of FimT_{Lp}

a, The solution structure of FimT_{Lp} 28-152 (state 18) in ribbon representation (left) and the corresponding topology diagram (right). Secondary structure elements are indicated: truncated N-terminal α -helix ($\alpha 1\text{C}$) (blue), β -sheet I formed by $\beta 1$, $\beta 2$, $\beta 3$ and $\beta 5$ (yellow), and β -sheet II formed by $\beta 4$, $\beta 6$ and $\beta 7$ (magenta). A vertical arrow indicates the pilus axis from the cell surface towards the pilus tip. **b**, Structure alignment of FimT_{Lp} (blue) and FimU_{Pa} (grey; PDB ID: 4IPV) (left) and the topology diagram of FimU_{Pa} (right). The disulphide bond of FimU_{Pa} is indicated in stick representation with sulphur atoms in yellow. **c**, Superimposed 20 lowest energy structures calculated by NMR spectroscopy. An arrow indicates the conformational flexibility of the C-terminal tail (140-152). The pairwise backbone root-mean-square deviation (RMSD) for the structured region (residues 32 to 140) is 1.26 Å. N- and C-termini are indicated in each panel. **d**, C α chemical shift values (top) and $T_2(^1\text{H})$ transverse relaxation data (bottom), encompassing the last 27 residues of FimT_{Lp}. Secondary structural elements are indicated and error bars represent the fitting errors of the respective exponential decay curves.

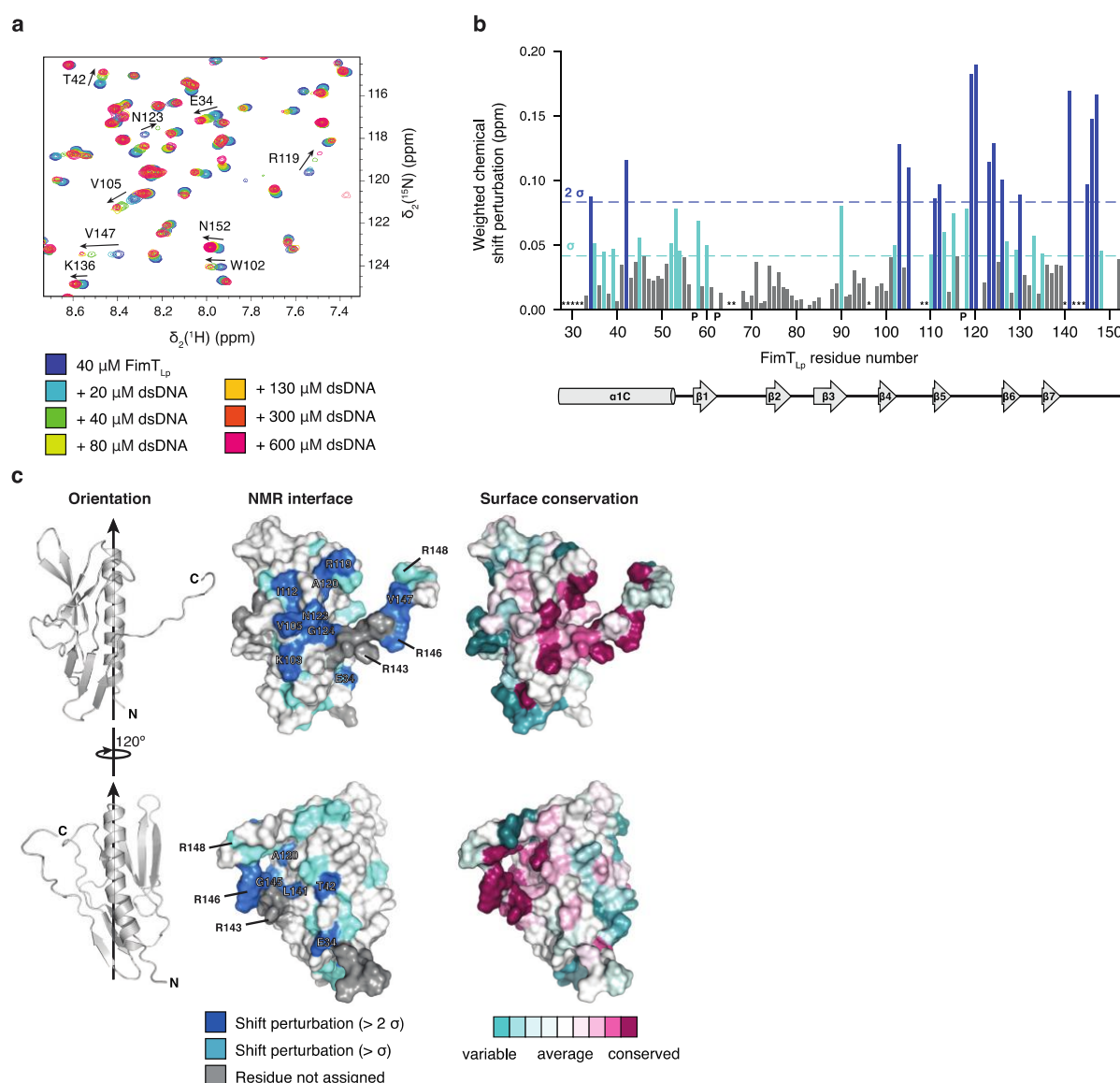


Figure 3: Identification of the DNA interaction surface of FimT_{LP}

a, Selected region of ^1H , ^{15}N -HSQC spectra showing ^{15}N -labeled FimT_{LP} alone and in presence of increasing concentrations of 12 bp dsDNA. Full spectra are in **Source Data**. **b**, Weighted CSP map generated from **a**. Residues experiencing CSPs ($\Delta\text{ppm} > 1\sigma$), light blue; residues experiencing CSPs ($\Delta\text{ppm} > 2\sigma$), dark blue; P, prolines; *, residues not assigned. **c**, Left, FimT_{LP} is shown in two orientations rotated by 120° in ribbon representation. Arrows indicate the pilus axis as in Fig. 2a. Middle, CSPs are mapped onto the surface of FimT_{LP} and coloured as in **b**. Residues producing large shifts are labelled on the molecular surface. Right, Surface residues of FimT_{LP} are coloured according to conservation (full multisequence alignment in **Source Data**). This image was generated using the ConSurf server⁸⁵.

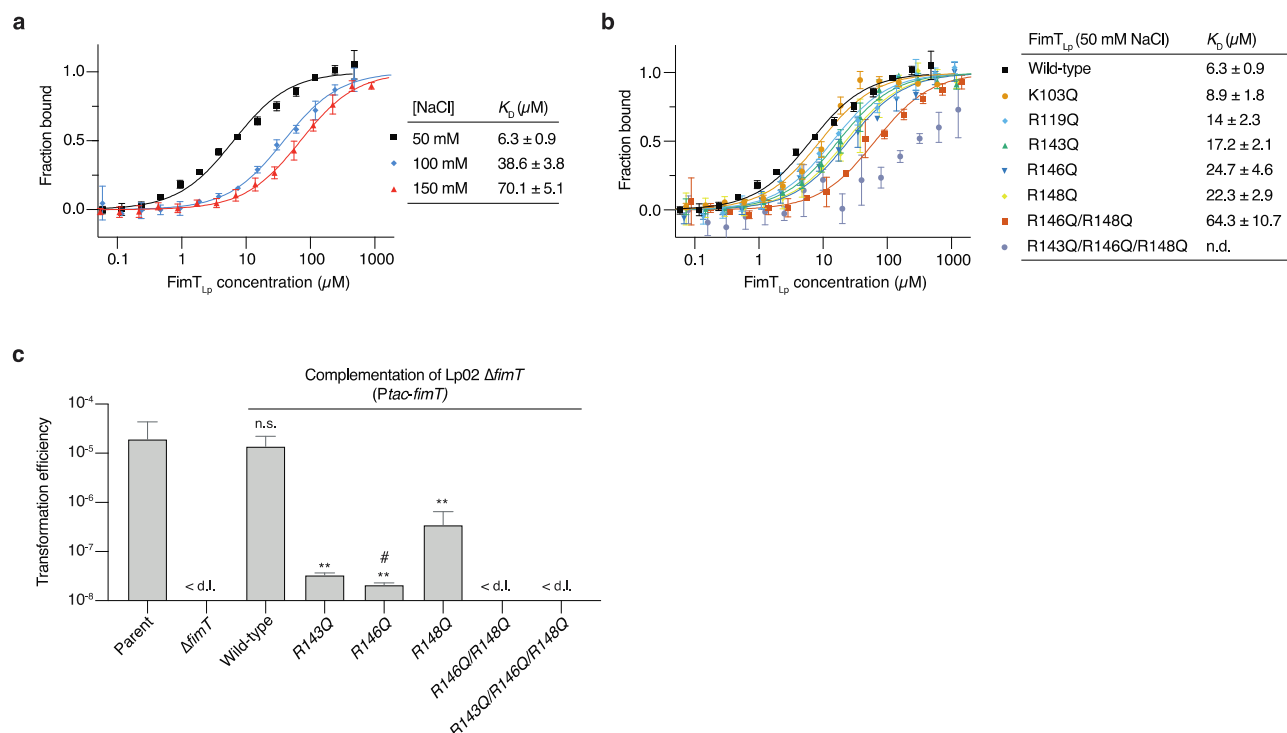
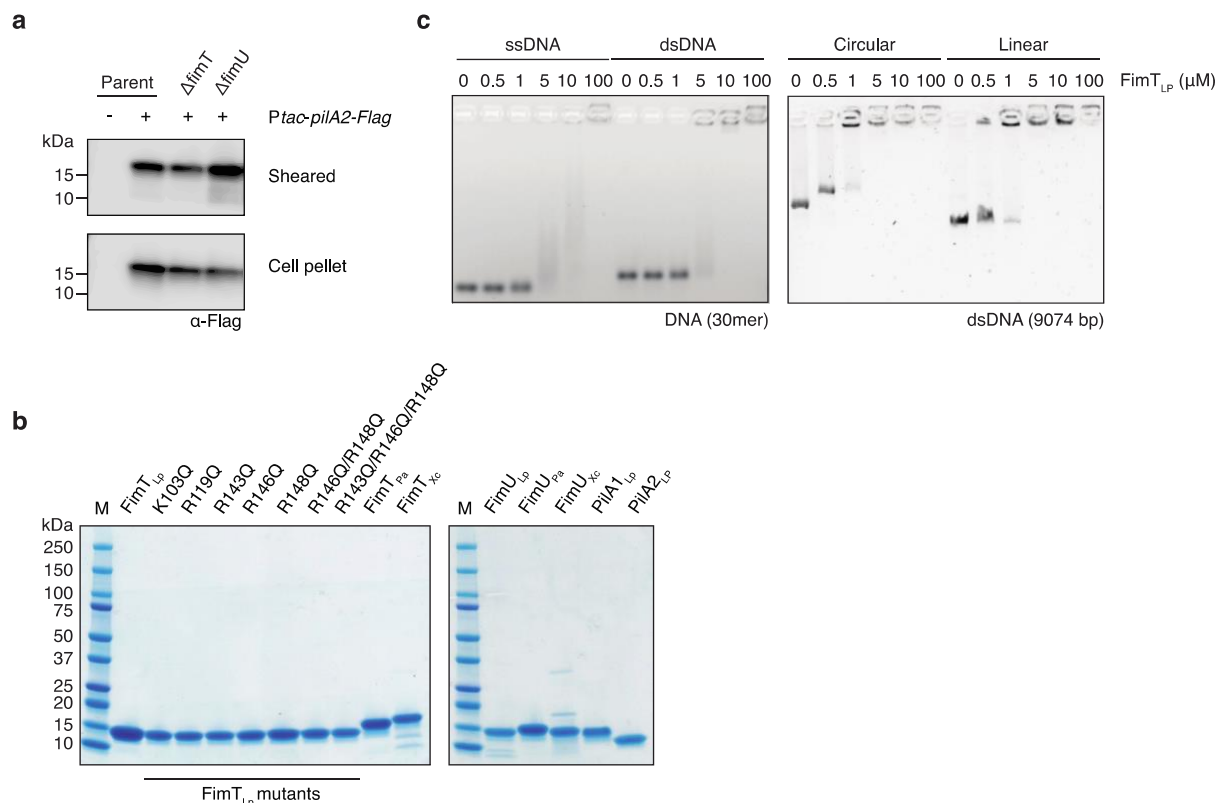


Figure 4: Characterisation of FimT_{Lp} binding to DNA *in vitro* and *in vivo*

MST/TRIC binding assay of 12 bp FAM-labelled dsDNA with **a**, wild-type FimT_{Lp} performed at increasing NaCl concentrations (ionic strength) and **b**, wild-type FimT_{Lp} compared to FimT mutants. n.d., not determined. The MST/TRIC data were fitted according to two binding sites with equal affinity. Error bars represent the mean ± SD. **c**, Natural transformation efficiencies of parental Lp02, Lp02 ΔfimT, and the Lp02 ΔfimT strain complemented by ectopic expression of wild-type and FimT_{Lp} mutants. The mean transformation efficiencies of three independent biological replicates are plotted with error bars representing the SD. <d.l., below d.l. (average d.l. = 2.0 × 10⁻⁸ ± 8.2 × 10⁻⁹); #, below d.l. in at least one replicate (average d.l. used to calculate the mean transformation efficiency). These assays were performed in parallel to those displayed in Fig. 1a, and statistical differences were determined on log-transformed data using an unpaired t-test with Welch's correction. **, p<0.01; n.s., not statistically significant (p>0.05).

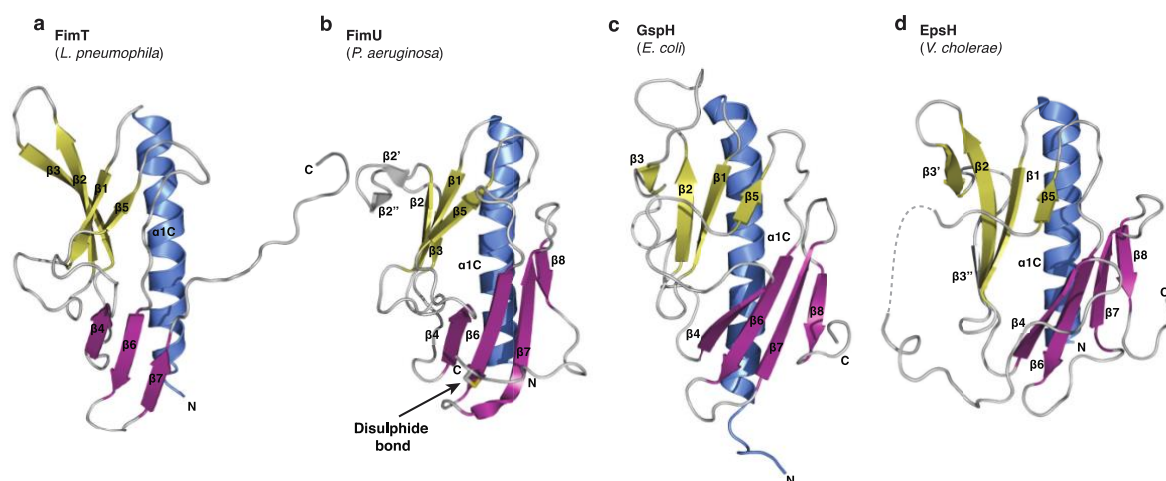
1016 *X. campestris*). The scale bar indicates the average number of substitutions per site. **d**, Top,
 1017 multisequence alignment of representative FimT orthologues across six orders (indicated by
 1018 a coloured line as in c) focusing on their C-terminal region (Lc, *Legionella cherrii*; La,
 1019 *Legionella anisa*; Fd, *Fluoribacter dumoffii*; Vg, *Ventrosimonas gracilis*; Pc, *Pseudomonas*
 1020 *chloritidismutans*; Ml, *Marinicella litoralis*; He, *Halomonas endophytica*; Xt, *Xylella*
 1021 *taiwanensis*; Sp, *Shewanella polaris*; Si, *Shewanella indica*; Eh, *Ectothiorhodospira*
 1022 *haloalkaliphile*). Residues are coloured according to sequence identity. Bottom, sequence
 1023 logo generated from the full multisequence alignment of 196 high-confidence FimTs (**Source**
 1024 **Data**).
 1025

Extended Data



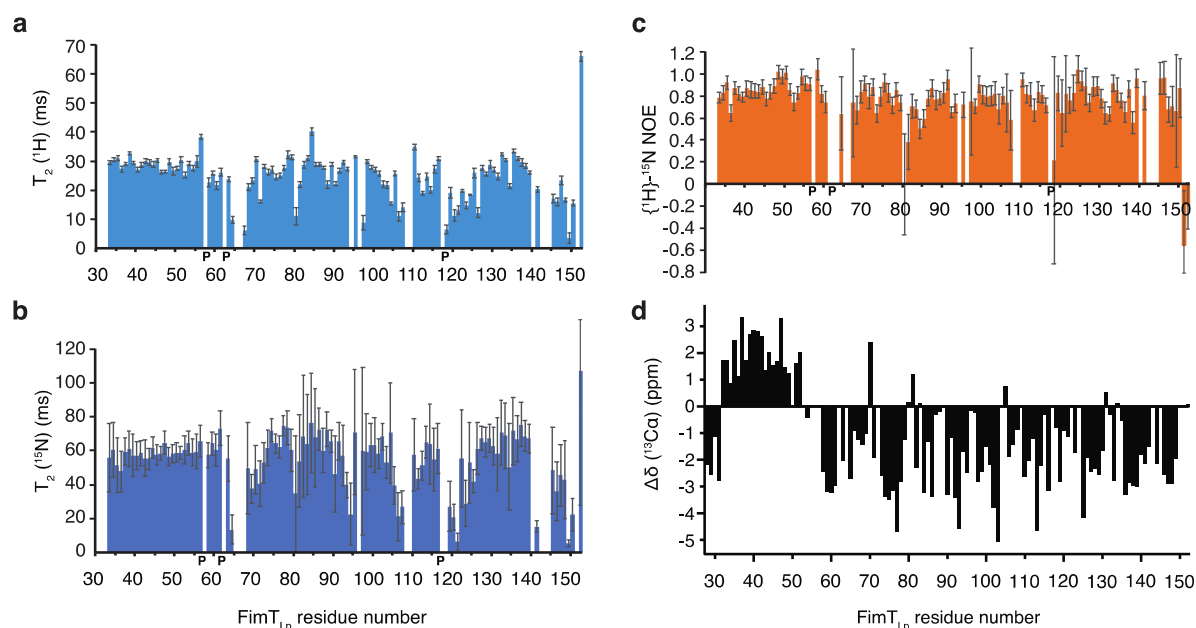
Extended Data Figure 1: Cell surface expression of PilA2-Flag, *in vitro* DNA binding of FimT_{Lp} and purified proteins utilised in this study

a, Immunodetection of ectopically expressed PilA2-Flag in various Lp02 strains using anti-Flag antibodies (**Source Data**). Sheared pili were detected in supernatants (sheared) and the whole cell lysates of depiliated cells (cell pellet). **b**, All purified N-terminally truncated pilins (construct boundaries can be found in **Extended Data Table 3**), utilised in this study, resolved by SDS-PAGE. M, marker; Lp, *L. pneumophila*; Pa, *P. aeruginosa*; Xc, *X. campestris*. **c**, EMSAs showing *in vitro* DNA binding of FimT_{Lp} to ssDNA vs dsDNA (left) and linear vs circular DNA (right). DNA probes were incubated with increasing concentrations of FimT_{Lp} and resolved by agarose gel electrophoresis.



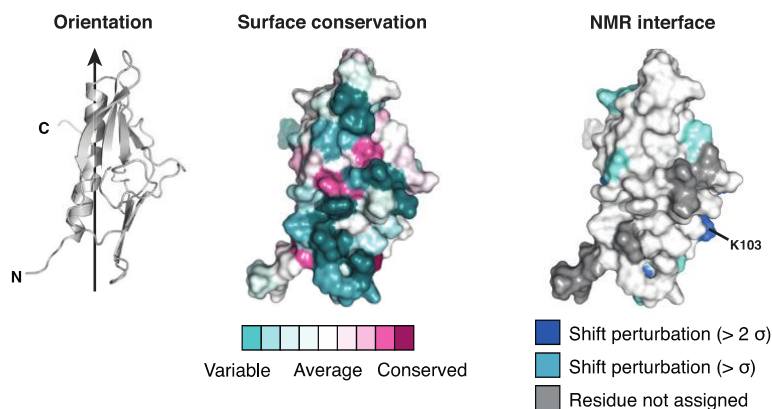
Extended Data Figure 2: Structures of GspH/FimT family members

a, The structure of FimT from *L. pneumophila* (state 18, this study); **b**, FimU from *P. aeruginosa* (PDB ID: 4IPV); **c**, GspH from *E. coli* (state 1, PDB ID: 2KNQ); and **d**, EpsH from *V. cholerae* (PDB ID: 2QV8). The FimT_{LP} and GspH_{EC} structures were determined using NMR spectroscopy, while those of FimU_{Pa} and EpsH_{Vc} are crystal structures. The disulphide bond of FimU is shown in stick representation (sulphur atoms in yellow), indicated by an arrow. The previously named $\beta 3$ and $\beta 4$ -strands of the EpsH structure¹ have been labelled as $\beta 3'$ and $\beta 3''$ for consistency of strand nomenclature across all depicted structures. All structures are shown in ribbon representation with their N-and C-termini indicated and secondary structural elements are coloured and labelled as in Fig. 2a.



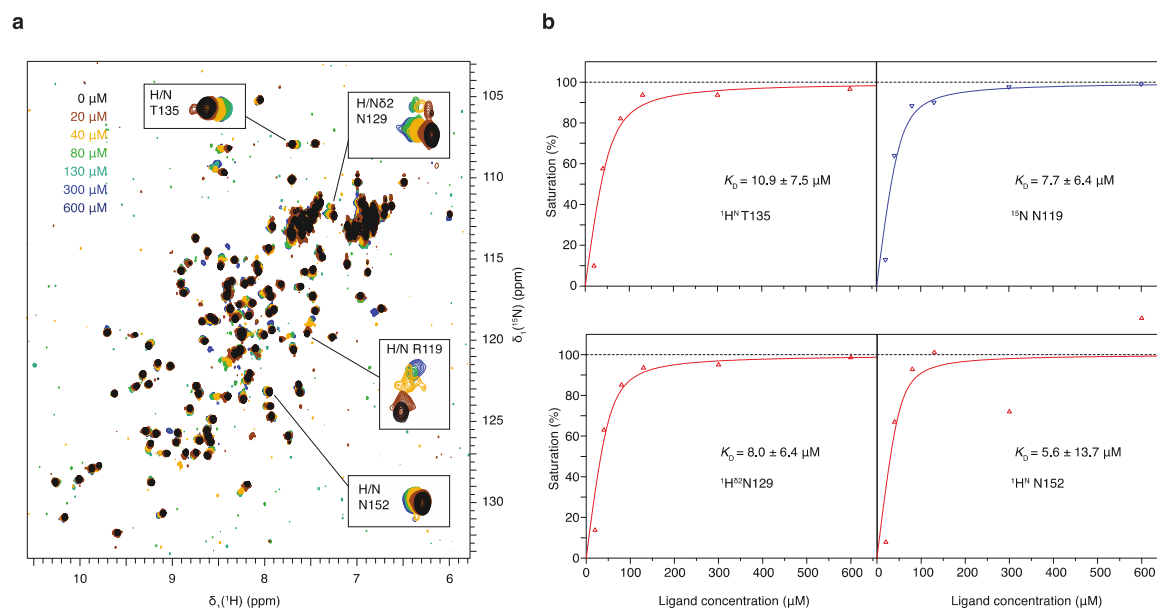
Extended Data Figure 3: Relaxation data for FimT_{Lp} indicate dynamics of the C-terminal residues 140–150 on the millisecond timescale

a, b, Backbone amide T₂ transverse relaxation data of FimT_{Lp} for ¹H (**a**) and ¹⁵N (**b**) nuclei, where amide groups of the loops and the C-terminus show significantly decreased T₂ values compared to the folded part of the domain. The low T₂ values for the C-terminal tail (signals of amides of residues 140 and 142–144 were too weak to be analysed), indicate dynamics of the C-terminal residues (140–150) on the microsecond to millisecond timescale. Proline residues are indicated with a bold letter P. Error bars represent the fitting errors of the respective exponential decay curves. **c**, Heteronuclear {¹H}-¹⁵N NOE data show that only the last two residues (151 and 152) exhibit fast dynamics on the nanosecond timescale, typical for flexibly disordered termini. Error bars reflect the error from the signal-to-noise ratio of the individual signals used for the analysis. **d**, Cα chemical shift deviation from random coil values (Δδ(¹³Cα)) indicate predominantly β-strand secondary structure for the C-terminal residues. Significant (>0.5 ppm) positive and negative deviations of ¹³Cα chemical shifts from random coil values indicate α-helical and β-strand conformations of the backbone, respectively. ¹³Cα chemical shifts are shown without smoothing, representing the raw data after calibration of the ¹³C chemical shift to 2,2-dimethyl-2-silapentane-5-sulfonate (DSS).



Extended Data Figure 4: NMR binding studies of FimT_{Lp} to DNA

Left, FimT_{Lp} is shown in ribbon representation rotated a further 120° with respect to the orientations displayed in Fig. 3c. Middle, residues experiencing chemical shift perturbations due to DNA binding are mapped onto the surface of FimT_{Lp}. Right, surface residues of FimT_{Lp} are coloured according to conservation.

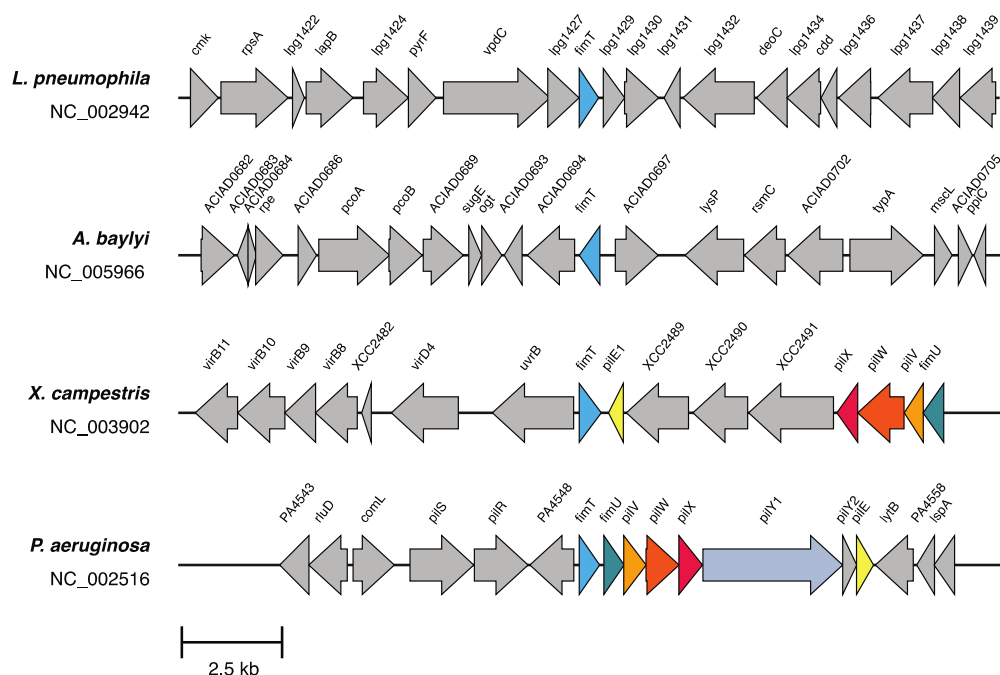


Extended Data Figure 5: Affinity determination of FimT to 12 bp dsDNA by NMR

a, DNA binding studies of FimT_{LP} performed by NMR spectroscopy. Increasing concentrations of 12 bp dsDNA (see colour code on top left in spectra overlay) were added to 40 μM of ^{15}N -labelled FimT_{LP} and the CSPs of four peaks were plotted against the ligand (12 bp DNA) concentration. **b**, For the four signals indicated in the spectra overlay, the binding curves are shown on the right-hand side, for ^1H and ^{15}N nuclei in red and blue triangles, respectively. The data were fitted assuming two identical binding sites (solid lines) and averaged to estimate a K_D of $\sim 8 \mu\text{M}$ of the interaction.

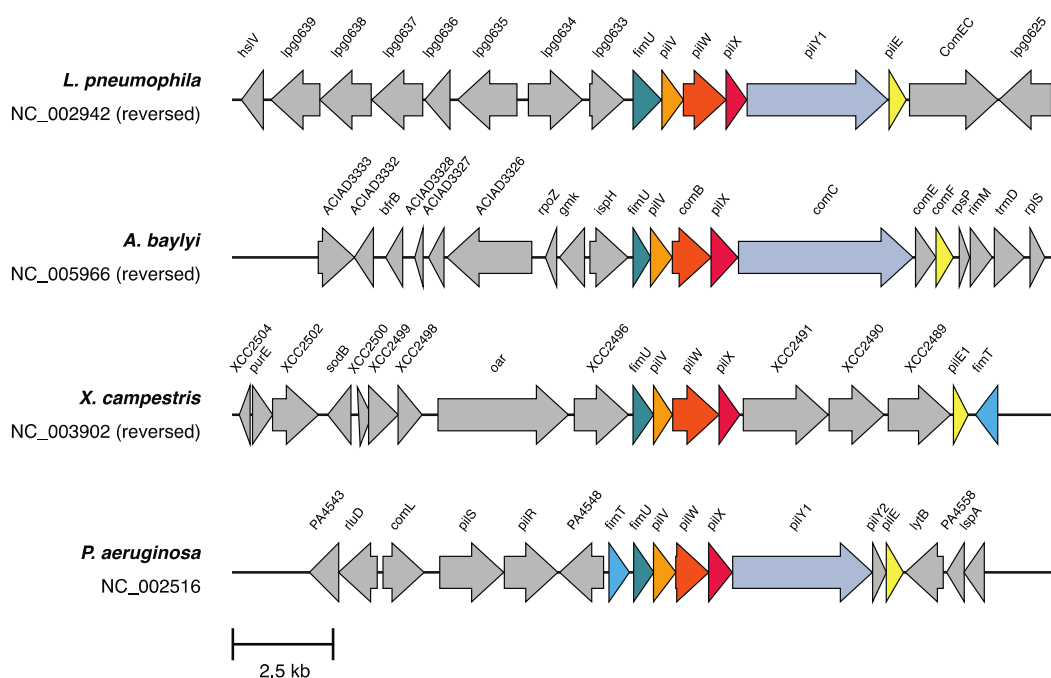
a

Gene neighbourhood: FimT



b

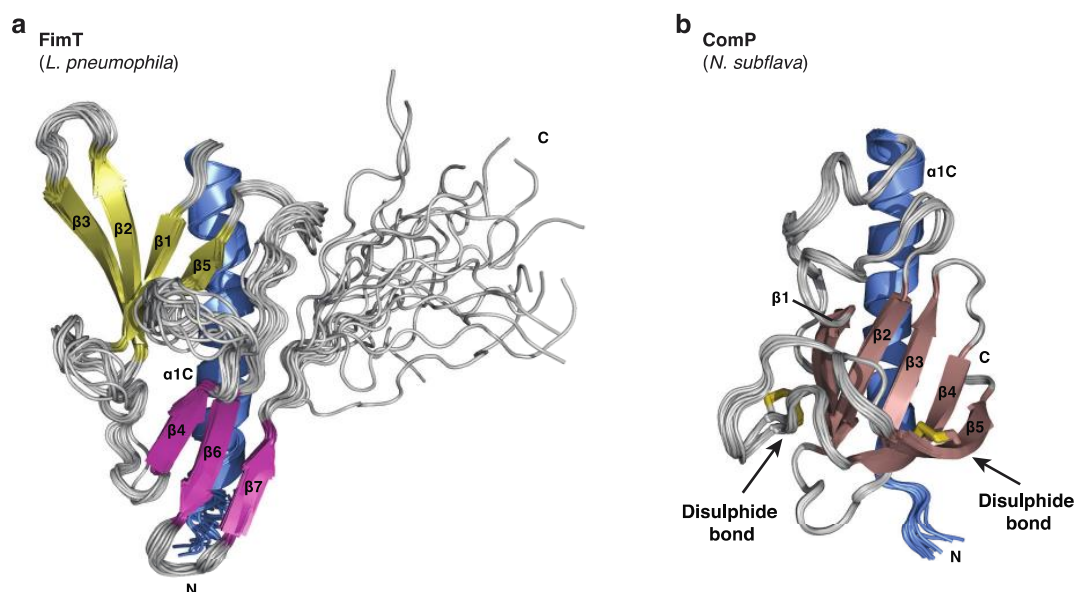
Gene neighbourhood: FimU



Extended Data Figure 6: Gene neighbourhoods of FimT and FimU

Genomic regions around FimT (a) and FimU (b) in *L. pneumophila*, *A. baylyi*, *X. campestris* and *P. aeruginosa*. Each gene is labelled with its name or locus tag (if unannotated). Genes coding for T4P homologues are colour-coded identically across the different bacterial

1100 species. Among FimT and FimU homologues collected by BlastP using the four
 1101 representative sequences, 25% of FimT sequences were located close to other minor pilin
 1102 operon components, while 100% of FimU sequences were located in minor pilin operons
 1103 (see **Source Data**).
 1104



Extended Data Figure 7: Comparison of the NMR structures of FimT and ComP

a, b, Superimposed 20 lowest energy structures calculated by NMR spectroscopy of FimT from *L. pneumophila* (**a**) and ComP from *Neisseria subflava* (PDB ID: 2NBA³) (**b**). The DD-region defining disulphide bonds of ComP are shown in stick representation (sulphur atoms in yellow) and are indicated by arrows. Both structures are shown in ribbon representation with their N-and C-termini indicated.

1114 **Extended Data Table 1 NMR and refinement statistics for FimT_{LP}**

	FimT_{LP}
NMR distance and dihedral constraints	
Distance constraints	
Total NOE	2311
Intra-residue	635
Inter-residue	1676
Sequential ($ i - j = 1$)	522
Medium-range ($ i - j < 4$)	344
Long-range ($ i - j > 5$)	810
Hydrogen bonds	-
Total dihedral angle restraints*	
Backbone	666
Other	558
Structure statistics	
Average Cyana target function	0.21 ± 0.02
Violations (mean and s.d.)**	
Distance constraints (Å)	0
Max. dihedral angle violation (°)	123.98 ± 28.54
Max. distance constraint violation (Å)	0.57 ± 0.19
Deviations from idealized geometry	
Bond lengths (Å)	0.0035 ± 0.0012
Bond angles (°)	1.377 ± 0.459
Average pairwise r.m.s. deviation*** (Å)	
Heavy	1.13 ± 0.13
Backbone	0.56 ± 0.16

1115

1116 * Dihedral angle restraints were derived from Cα chemical shifts using TALOS+ as
1117 implemented in cyana 3.98

1118 ** Restraints violated in 6 or more structures

1119 *** Pairwise r.m.s. deviation for structured regions (res. 32–62, 70–139) was calculated
1120 among 20 refined structures.

1121

Extended Data Table 2: Strains used in this study

Name	Relevant genotype/description	Source/Reference
<i>Escherichia coli</i>		
BL21 (DE3)	<i>E. coli</i> expression strain	NEB (cat. no. C2527H/I)
Shuffle T7	<i>E. coli</i> expression strain	NEB (cat. no. C3026J)
Stellar (HST08 strain)	<i>E. coli</i> cloning strain	Takara (cat. no. 636763/636766)
DH5α λpir	<i>E. coli</i> cloning strain: Encodes π protein for the replication of the <i>pir</i> - dependent origin of replication - <i>oriR</i> (R6K)	4,5
CR019	<i>E. coli</i> mobilizing strain: MT607 <i>E. coli</i> containing pRK600 plasmid [<i>oriR</i> (ColE1) <i>oriT</i> (RK2); CmR]	6
<i>Legionella pneumophila</i>		
Lp02 WT	Philadelphia-1 <i>rpsL hsdR thyA</i> ; SmR	7
Lp02 Δ <i>fimT</i>	Lp02 Δ <i>fimT</i> (<i>lpg1428</i>)	This study
Lp02 Δ <i>fimU</i>	Lp02 Δ <i>fimU</i> (<i>lpg0632</i>)	This study
Lp02 Δ <i>pilQ</i>	Lp02 Δ <i>pilQ</i> (<i>lpg0931</i>)	This study
Lp02 Δ <i>pilT</i>	Lp02 Δ <i>pilT</i> (<i>lpg2013</i>)	This study
Lp02 Δ <i>comEC</i>	Lp02 Δ <i>comEC</i> (<i>lpg0626</i>)	This study

1125 Extended Data Table 3: Plasmids used in this study

Name	Relevant genotype/description	Source/Reference
pMMB207C	<i>Legionella</i> expression vector derived from RSF1010: IncQ lacI ^q P _{tac} oriT Δ <i>mobA</i> ; CmR	8
pMMB207C- <i>fimT</i> _{Lp}	<i>L. pneumophila</i> wild-type <i>fimT</i>	This study
pMMB207C- <i>fimT</i> _{Lp} R143Q	pMMB207C- <i>fimT</i> _{Lp} , with <i>fimT</i> R143Q mutation	This study
pMMB207C- <i>fimT</i> _{Lp} R146Q	pMMB207C- <i>fimT</i> _{Lp} , with <i>fimT</i> R146Q mutation	This study
pMMB207C- <i>fimT</i> _{Lp} R148Q	pMMB207C- <i>fimT</i> _{Lp} , with <i>fimT</i> R148Q mutation	This study
pMMB207C- <i>fimT</i> _{Lp} R146Q, R148Q	pMMB207C- <i>fimT</i> _{Lp} , with <i>fimT</i> R146Q, R148Q mutations	This study
pMMB207C- <i>fimT</i> _{Lp} R143Q, R146Q, R148Q	pMMB207C- <i>fimT</i> _{Lp} , with <i>fimT</i> R143Q, R146Q, R148Q mutations	This study
pMMB207C- <i>pilA2</i> -flag	<i>L. pneumophila pilA2</i> (lpg1915)-flag	This study
pMMB207C- <i>fimT</i> _{Pa}	<i>Pseudomonas aeruginosa</i> PAO1 <i>fimT</i> (PA4549)	This study
pMMB207C- <i>fimT</i> _{chimera 1}	pMMB207C- <i>fimT</i> _{Lp} residues 1-128, fused to <i>fimT</i> _{Pa} residues 125-161	This study
pMMB207C- <i>fimT</i> _{Xc}	<i>Xanthomonas campestris</i> ATCC 33913 <i>fimT</i> (XCC2486)	This study
pMMB207C- <i>fimT</i> _{chimera 2}	pMMB207C- <i>fimT</i> _{Lp} residues 1-128, fused to <i>fimT</i> _{Xc} residues 138-172	This study
pSR47S	Suicide plasmid: oriR(R6K) oriT(RP4) <i>sacB</i> ; KanR	Vogel, J. P., et al. (unpublished data) 9
pSR47S- <i>fimT</i>	<i>L. pneumophila fimT</i> gene with 1000 bp up- and downstream sequence (homology regions)	This study
pSR47S- <i>fimU</i>	<i>L. pneumophila fimU</i> gene with 1000 bp up- and downstream sequence (homology regions)	This study
pSR47S- <i>pilQ</i>	<i>L. pneumophila pilQ</i> gene with 1000 bp up- and downstream sequence (homology regions)	This study
pSR47S- <i>pilT</i>	<i>L. pneumophila pilT</i> gene with 1000 bp up- and downstream sequence (homology regions)	This study
pSR47S- <i>comEC</i>	<i>L. pneumophila comEC</i> gene with 1000 bp up- and downstream sequence (homology regions)	This study
pSR47S-Δ <i>fimT</i>	pSR47S- <i>fimT</i> , with <i>fimT</i> deletion	This study
pSR47S-Δ <i>fimU</i>	pSR47S- <i>fimU</i> , with <i>fimU</i> deletion (52 nt left intact at 5' end of gene)	This study
pSR47S-Δ <i>pilQ</i>	pSR47S- <i>pilQ</i> , with <i>pilQ</i> deletion	This study
pSR47S-Δ <i>pilT</i>	pSR47S- <i>pilT</i> , with <i>pilT</i> deletion	This study
pSR47S-Δ <i>comEC</i>	pSR47S- <i>comEC</i> , with <i>comEC</i> deletion	This study
pOPINS	<i>E. coli</i> expression vector: N-terminal His ₆ -SUMO tag, T7 promoter; KanR	10
pOPINS- <i>fimT</i> _{Lp}	<i>L. pneumophila</i> wild-type <i>fimT</i> , residues 28-152	This study
pOPINS- <i>fimT</i> _{Lp} K103Q	pOPINS- <i>fimT</i> _{Lp} , with <i>fimT</i> K103Q mutation	This study
pOPINS- <i>fimT</i> _{Lp} R119Q	pOPINS- <i>fimT</i> _{Lp} , with <i>fimT</i> R119Q mutation	This study
pOPINS- <i>fimT</i> _{Lp} R143Q	pOPINS- <i>fimT</i> _{Lp} , with <i>fimT</i> R143Q mutation	This study
pOPINS- <i>fimT</i> _{Lp} R146Q	pOPINS- <i>fimT</i> _{Lp} , with <i>fimT</i> R146Q mutation	This study
pOPINS- <i>fimT</i> _{Lp} R148Q	pOPINS- <i>fimT</i> _{Lp} , with <i>fimT</i> R148Q mutation	This study
pOPINS- <i>fimT</i> _{Lp} R146Q, R148Q	pOPINS- <i>fimT</i> _{Lp} , with <i>fimT</i> R146Q, R148Q mutations	This study
pOPINS- <i>fimT</i> _{Lp} R143Q, R146Q, R148Q	pOPINS- <i>fimT</i> _{Lp} , with <i>fimT</i> R143Q, R146Q, R148Q mutations	This study
pOPINS- <i>fimU</i> _{Lp}	<i>L. pneumophila fimU</i> , residues 28-167	This study
pOPINS- <i>fimT</i> _{Pa}	<i>Pseudomonas aeruginosa</i> PAO1 <i>fimT</i> (PA4549), residues 28-161	This study
pOPINS- <i>fimU</i> _{Pa}	<i>P. aeruginosa</i> PAO1 <i>fimU</i> (PA4550), residues 28-159	This study

pOPINS- <i>fimT</i> _{Xc}	<i>Xanthomonas campestris</i> ATCC 33913 <i>fimT</i> (XCC2486), residues 28-172	This study
pOPINS- <i>fimU</i> _{Xc}	<i>X. campestris</i> ATCC 33913 <i>fimU</i> (XCC2495), residues 28-163	This study
pOPINB	<i>E. coli</i> expression vector: N-terminal His ₆ -tag, T7 promoter; KanR	11
pOPINB- <i>pilA1</i> _{Lp}	<i>L. pneumophila pilA1</i> (<i>lpg1914</i>), residues 25-132	This study
pOPINB- <i>pilA2</i> _{Lp}	<i>L. pneumophila pilA2</i> , residues 25-131	This study
pTRC99A	<i>Ptc oriR</i> (pBR322); AmpR	12
pTRC99A- <i>lpg2953-2958::Kan</i>	<i>L. pneumophila</i> genomic region spanning <i>lpg2953-2958</i> . The <i>hipB</i> gene (<i>lpg2955</i>) is interrupted by kanamycin cassette, KanR	This study

1126
1127
1128

1129 Extended Data Table 4: Oligonucleotides used in this study

Name	Sequence (5' to 3')	Construct
<i>Cloning</i>		
pMMB207_lin_F	aattcgagctcggtaccgg	pMMB207C
pMMB207_lin_R	ctgttcctgtgtgaaattgtatccgc	
fimT _{Lp} _pMMB207C_F	tcacacaggaaacagatgcggctcaattgatgaaaataacaggattt ac	pMMB207C- <i>fimT</i> _{Lp}
fimT _{Lp} _pMMB207C_R	taccgagctcgaattttaattaccccctaccctaaccctgcc	
fimT _{Lp} R143Q_ pMMB207C_F	ccctaaccctgccaagctgatttaaagtaaccacaac	pMMB207C- <i>fimT</i> _{Lp} R143Q
fimT _{Lp} R143Q_ pMMB207C_R	gggtactttaaatcagcttggcagggttagggtag	
fimT _{Lp} R146Q_ pMMB207C_F	ctggccaggttagggtaggggtaattaaaattcg	pMMB207C- <i>fimT</i> _{Lp} R146Q
fimT _{Lp} R146Q_ pMMB207C_R	taccctaacctggccaagcctatttaaagtaaccacaac	
fimT _{Lp} R148Q_ pMMB207C_F	cagggttcaggtaggggtaattaaaattcgagctc	pMMB207C- <i>fimT</i> _{Lp} R148Q
fimT _{Lp} R148Q_ pMMB207C_R	cccctacctgaacctgccaagcctatttaaag	
fimT _{Lp} R146QR148Q_ pMMB207C_F	ctggccaggttcaggtaggggtaattaaaattcg	pMMB207C- <i>fimT</i> _{Lp} R146Q, R148Q
fimT _{Lp} R146QR148Q_ pMMB207C_R	cctacctgaacctggccaagcctatttaaagtaac	
fimT _{Lp} R143QR146QR148Q_ pMMB207C_F	gccaggttcaggtaggggtaattaaaattcgagctc	pMMB207C- <i>fimT</i> _{Lp} R143Q, R146Q, R148Q
fimT _{Lp} R143QR146QR148Q_ pMMB207C_R	ctacctgaacctggccaagctgatttaaagtaaccacaacttttcattg	
pilA2 _{Lp} -flag_ pMMB207C_F	tcacacaggaaacagatggagatggcatgagacaaaagggttttac	pMMB207C- <i>pilA2</i> - flag
pilA2 _{Lp} -flag_ pMMB207C_R	atcgctctttagtctgtgtcgaactggcaggtc	
fimT _{Pa} _pMMB207C_F	tcacacaggaaacagatggcgaagggtcgagagagc	pMMB207C- <i>fimT</i> _{Pa}
fimT _{Pa} _pMMB207C_R	taccgagctcgaatttcatccggaagtgtgcatagctc	
fimT _{Pa} _125_pMMB207C_ F	ggtaaatttatttgtgcggaaggcataccgttgc	pMMB207C- <i>fimT</i> _{chimera 1}
fimT _{Lp} _138_pMMB207C_ R	caaaataaattaccattactcatcgacgattcg	
<i>fimT</i> _{Xc} _pMMB207C_F	tcacacaggaaacagatgcagacaggacctcagtcacc	pMMB207C- <i>fimT</i> _{Xc}
<i>fimT</i> _{Xc} _pMMB207C_R	taccgagctcgaatttattgtctgctgcaggtgcc	
<i>fimT</i> _{Xc} _138_pMMB207C_ F	ggtaaatttatttgtgcacccagtcagagcgagtg	pMMB207C- <i>fimT</i> _{chimera 2}
fimT _{Lp} _138_pMMB207C_ R	caaaataaattaccattactcatcgacgattcg	
pSR47S_lin_F	ggatccccggggtgcaggaattcg	pSR47S
pSR47S_lin_R	ccactagttctagagcgccgcc	
fimT_HR_pSR47S_F	ggccgctctagaactagtgtggcaaatgggatttaggtctccctcaatg	pSR47S- <i>fimT</i>
fimT_HR_pSR47S_R	cctgcagcccggggatccataaatgcctcagacaagctgacctctcc	
fimU_HR_pSR47S_F	ggccgctctagaactagtggccaacacatcactacctgttgagcattgc c	pSR47S- <i>fimU</i>
fimU_HR_pSR47S_R	tcctgcagcccgggggtcccaatcactattgatgattgcccttgttggt g	
pilQ_HR_pSR47S_F	ggccgctctagaactagtgttgaaaaaagcaacatcaggcagc	pSR47S- <i>pilQ</i>
pilQ_HR_pSR47S_R	tcctgcagcccggggatccatcgaaacatcaacctcgccataaag	
pilT_HR_pSR47S_F	ggccgctctagaactagtgttatcgtaatgagtcgaatattttcttacta atgc	pSR47S- <i>pilT</i>

pilT_HR_pSR47S_R	tcctgcagcccgggggatccccgttacaataacacgtaattttaccaatt atgc	
comEC_HR_pSR47S_F	ggccgctctagaactagtggtttatccacaaacattatcactgccact g	pSR47S-comEC
comEC_HR_pSR47S_R	tcctgcagcccgggggatccactctgcttgaaggtatcccagg	
ΔfimT_HR_pSR47S_F	tcttaattataagcaatggttttcataaagagg	pSR47S-ΔfimT
ΔfimT_HR_pSR47S_R	ccattgcttataatttaagacatctacaaaattttatgatgaagataagatg cg	
ΔfimU_HR_pSR47S_F	agcattatccctattgtttgatcgaacccac	pSR47S-ΔfimU
ΔfimU_HR_pSR47S_R	caaacaatagggataatgctaacaacacccggccaagcagtc	
ΔpilQ_HR_pSR47S_F	tcaagattggactaattttatctcattaataaagataaaaaacattaattta atagc	pSR47S-ΔpilQ
ΔpilQ_HR_pSR47S_R	ttagtccaatcttgagcctcactcctgc	
ΔpilT_HR_pSR47S_F	atacacatgacttgtgaaaaagacccaaggtc	pSR47S-ΔpilT
ΔpilT_HR_pSR47S_R	acaagtcattgtgtatactctataattcccgc	
ΔcomEC_HR_pSR47S_F	atggattggctgacccatgttatatctaagc	pSR47S-ΔcomEC
ΔcomEC_HR_pSR47S_R	ggtcagccaatccatttcaaattaagttggactttcc	
pOPINS_lin_F	taaagcttctagaccatttaaaccaccac	pOPINS
pOPINS_lin_R	accaccgatctgttcgcgat	
fimT _{Lp} _28_pOPINS_F	atcgcgacagatcggtggtatataaaaataatgagagagaaacatta gttaatatataaaaaacagccattc	pOPINS-fimT _{Lp}
fimT _{Lp} _152_pOPINS_R	aaatggtctagaaagctttattaattaccccctaccctaaccctgcc	
fimT _{Lp} K103Q_pOPINS_F	tggaatattaattggcagggcgtagattcaaaccatag	pOPINS-fimT _{Lp} K103Q
fimT _{Lp} K103Q_pOPINS_R	tacgcctgccaattaatattccaggaattagaactcc	
fimT _{Lp} R119Q_pOPINS_F	ccaatattccgaatcaggcgatgagtaattgtaaatttatttg	pOPINS-fimT _{Lp} R119Q
fimT _{Lp} R119Q_pOPINS_R	catcgctgattcggaatattgatatataaattctatggttgaatc	
fimT _{Lp} R143Q_pOPINS_F	ggttactttaaatcagcttggcagggtagggtag	pOPINS-fimT _{Lp} R143Q
fimT _{Lp} R143Q_pOPINS_R	ccctaaccctgccaagctgatttaaagtaaccacaac	
fimT _{Lp} R146Q_pOPINS_F	gcttgccaggttagggtaggggtaattaataaag	pOPINS-fimT _{Lp} R146Q
fimT _{Lp} R146Q_pOPINS_R	cctaacctggccaagcctatttaaagtaaccacaac	
fimT _{Lp} R148Q_pOPINS_F	caggggtcaggttaggggtaattaataaagctttctagac	pOPINS-fimT _{Lp} R148Q
fimT _{Lp} R148Q_pOPINS_R	cccctacctgaaccctgccaagcctatttaaagtaac	
fimT _{Lp} R146QR148Q_pOPINS_F	cttgccaggttcaggttaggggtaattaataaagc	pOPINS-fimT _{Lp} R146Q, R148Q
fimT _{Lp} R146QR148Q_pOPINS_R	ccctacctgaaccctggccaagcctatttaaagtaac	
fimT _{Lp} R143QR146QR148Q_pOPINS_F	ggccaggttcaggttaggggtaattaataaagctttctag	pOPINS-fimT _{Lp} R143Q, R146Q, R148Q
fimT _{Lp} R143QR146QR148Q_pOPINS_R	tacctgaaccctggccaagctgatttaaagtaaccac	
fimU _{Lp} _28_pOPINS_F	atcgcgacagatcggtggtattttgaatagccgttgactcaaacattg ac	pOPINS-fimU _{Lp}
fimU _{Lp} _167_pOPINS_R	atggtctagaaagctttattaagggcagttcaaagctccattattcc	
fimT _{Pa} _28_pOPINS_F	atcgcgacagatcggtggtctggacggcaatcgcgagc	pOPINS-fimT _{Pa}
fimT _{Pa} _161_pOPINS_R	aaatggtctagaaagctttatcatccggaagtgtgcatagctc	
fimU _{Pa} _28_pOPINS_F	atcgcgacagatcggtggtctgacagaacgcaacgaactgcag	pOPINS-fimU _{Pa}
fimU _{Pa} _159_pOPINS_R	aaatggtctagaaagctttatcaatagcatgactggggcgc	
fimT _{Xc} _28_pOPINS_F	atcgcgacagatcggtggtatcgagcggcagcggttg	pOPINS-fimT _{Xc}
fimT _{Xc} _172_pOPINS_R	aaatggtctagaaagctttattatgtctgcgaggtgccgg	
fimU _{Xc} _28_pOPINS_F	atcgcgacagatcggtggtattcggtcgaatcgcgctgttac	pOPINS-fimU _{Xc}
fimU _{Xc} _163_pOPINS_R	aaatggtctagaaagctttatcattgacagttatcctttctactctgacttcg	
pOPINB_lin_F	agcagcggtctggaagtctgtttcag	pOPINB
pOPINB_lin_R	atggtctagaaagcttta	
pilA1 _{Lp} _25_pOPINB_F	aagttctgttcagggcccgaggactataccatcagagcac	pOPINB-pilA1 _{Lp}
pilA1 _{Lp} _132_pOPINB_R	atggtctagaaagctttattaagggcggcagtagg	

pilA2 _{Lp} _28_pOPINB_F	aagttctgttcagggcccgcaagattacacaatacgagctcg	pOPINB- <i>pilA2_{Lp}</i>
pilA2 _{Lp} _131_pOPINB_R	atggctagaaaagctttattatggctgcaactggcag	
pTRC99A_lin_F	gtgtctagagtcgacctgcaggcat	pTRC99A
pTRC99A_lin_R	gaacacaccagagatatctggcagaattc	
Lpg2953_F	atctctgggtgttcggatagattatgcgagaggtctattgaagattctctg actatg	pTRC99A- <i>lpg2953-2958::Kan</i> Amplification of transforming DNA
Lpg2958_R	gtcgactctagacacagacatggcctggaaacgttggtggg	
KanR_lin_F	cattcaaatatgtatccgctcatga	pTRC99A- <i>lpg2953-2958::Kan</i>
KanR_lin_R	cggggctctgacgctcagt	
pTRC99A_lpg2953_F	atacatatttgaatgcacgaatttctattctttggcc	pTRC99A- <i>lpg2953-2958::Kan</i>
pTRC99A_lpg2958_R	gagcgtcagaccccggttggcagttttctcttca	
<i>DNA-binding assays*</i>		
FAM-12mer	# gttcgcaacgaa	MST/TRIC
12mer	gttcgcaacgaa	NMR titrations/ITC
FAM-30mer	# ttaaataggcttggcagggttagggtaggg	EMSA
30mer	ttaaataggcttggcagggttagggtaggg	EMSA

* The complementary strand for dsDNA probes is not shown. Only one of the two strands is fluorescein (FAM)-labelled.

Indicates the position of the FAM label.

Extended Data Table 5: Gene locus tags of *fimT* and *fimU* genes from previous and recently updated genomes

	<i>L. pneumophila</i> Philadelphia 1 (old)*	<i>L. pneumophila</i> Philadelphia 1 (new)	<i>X. campestris</i> ATCC 33913 (old)*	<i>X. campestris</i> ATCC 33913 (new)	<i>A. baylyi</i> ADP1 (old)	<i>A. baylyi</i> ADP1 (new)
RefSeq	NC_002942.5	NC_002942	NC_003902.1	NC_003902	NC_005966.1	NC_005966
Release date	2014	2021	2014	2021	2015	2020
<i>fimT</i>	<i>lpg1428</i>	LPG_RS07155	XCC2486	XCC_RS12930	ACIAD0695	ACIAD_RS03200
<i>fimU</i>	<i>lpg0632</i>	LPG_RS03130	XCC2495	XCC_RS12975	ACIAD3321	ACIAD_RS15030

* In this study we have referred to the old locus tags throughout.

Extended Data Table 6: Gene locus tags of selected genes from this study from previous and recently updated genomes

	<i>L. pneumophila</i> Philadelphia 1 (old)*	<i>L. pneumophila</i> Philadelphia 1 (new)
RefSeq	NC_002942.5	NC_002942
Release date	2014	2021
<i>pilQ</i>	<i>lpg0931</i>	LPG_RS04620
<i>pilT</i>	<i>lpg2013</i>	LPG_RS10105
<i>comEC</i>	<i>lpg0626</i>	LPG_RS03100
<i>pilA1</i>	<i>lpg1914</i>	LPG_RS09600
<i>pilA2</i>	<i>lpg1915</i>	LPG_RS09605
<i>hipB</i>	<i>lpg2955</i>	LPG_RS14950
<i>pilV</i>	<i>lpg0631</i>	LPG_RS03125
<i>pilW</i>	<i>lpg0630</i>	LPG_RS03120
<i>pilX</i>	<i>lpg0629</i>	LPG_RS03115
<i>pilY1</i>	<i>lpg0628</i>	LPG_RS03110
<i>pilE</i>	<i>lpg0627</i>	LPG_RS03105

* In this study we have referred to the old locus tags throughout.

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