Bacterial histone HBb from *Bdellovibrio bacteriovorus* compacts DNA by bending

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Abstract

Histones are essential for genome compaction and transcription regulation in eukaryotes, where they assemble into octamers to form the nucleosome core. In contrast, archaeal histones assemble into dimers that form hypernucleosomes upon DNA binding. Although histone homologs have recently been identified in bacteria, their DNA-binding characteristics remain largely unexplored. Our study reveals that the bacterial histone HBb is indispensable for the survival of *Bdellovibrio bacteriovorus*, suggesting critical roles in DNA organization and gene regulation. We also elucidate the crystal structure of the HBb dimer at 1.06 Å resolution and employ various biophysico-chemical approaches to show its ability to bind and compact DNA in a sequence-independent manner. This binding induces DNA bending, similar to that observed with bacterial HU/IHF family proteins. Finally, using DNA affinity purification and sequencing, we reveal that HBb binds along the entire genomic DNA of *B. bacteriovorus* without sequence specificity. These unique DNA-binding properties of bacterial histones, distinct from their archaeal and eukaryotic counterparts, highlight the diverse roles that histones can play in DNA organization across the domains of life.

Author Summary

Histones, traditionally known for organizing and regulating DNA in eukaryotes and archaea, have recently been discovered in bacteria, opening up a new frontier in our understanding of genome organization across the domains of life. Our study investigates the largely unexplored DNA-binding properties of bacterial histones, focusing on HBb in *Bdellovibrio bacteriovorus*. We reveal that HBb is essential for bacterial survival and exhibits DNA-binding akin to the bacterial nucleoid-associated HU/IHF family proteins. Contrary to eukaryotic and archaeal histones that wrap DNA, HBb bends DNA without sequence specificity. This work not only broadens our understanding of DNA organization across different life forms but also suggests that bacterial histones may have diverse roles in genome organization, distinct from their eukaryotic and archaeal counterparts.

Introduction

Histones, a class of highly conserved DNA-binding proteins, are predominantly found in eukaryotes and archaea. These proteins share a characteristic “histone fold”, comprising three α-helices connected by two short strap loops (1, 2). In eukaryotes, the four core histones—H2A, H2B, H3, and H4—assemble into an octamer that wraps around approximately 146 base pairs of double-stranded DNA, forming the nucleosome, the fundamental unit of chromatin (1-3). A unique feature of eukaryotic histones is their unstructured N-terminal tails, which serve as hotspots for post-translational modifications and play pivotal roles in various cellular processes, including transcriptional regulation, DNA repair, replication, and condensation (4, 5).

The first archaeal histone homologs, HMfA and HMfB, were identified in the hyperthermophilic archaeon *Methanothermus fervidus* (6). These homologs assemble into dimers that further oligomerize into elongated, nucleosome-like structures, termed hypernucleosomes, upon DNA binding (7-9). Subsequent research has identified one or more histone variants in the majority of archaeal lineages (10-16), including the Asgard superphylum, which comprises the closest prokaryotic relatives of eukaryotes (8, 17). Archaeal histones can assemble into both homo- and hetero-oligomers and exhibit varying sizes, with some even possessing N- or C-terminal tails akin to eukaryotic histones (8, 18). Additionally, archaeal histone-DNA complexes display a wide variety of histone-oligomerization states. These states are influenced by lateral dimer-dimer interactions and stacking interactions (19), which are not consistently conserved across species. The widespread occurrence and diversity of archaeal histones suggest distinct roles in genome organization and regulation (14, 17, 20, 21).

Notably, histones are also encoded within viral genomes (22, 23). Phylogenetically, viral histones are currently positioned between eukaryotic and archaeal histones (24). While many characterized viral nucleosomal histones structurally resemble eukaryotic nucleosome-like structures (25, 26), some stack into larger complexes that lack linker DNA, resembling archaeal hypernucleosomes (27).

Historically, it was widely assumed that bacteria lack histone homologs, and any observed instances were thought to have been acquired through horizontal gene transfer (28, 29). Instead of histones, bacteria were believed to rely on a multitude of small architectural proteins termed nucleoid-associated proteins (NAPs) (30). These NAPs are sometimes, albeit misleadingly, referred to as “histone-like proteins”. However, NAPs are evolutionarily distinct from histones. Their similarities lie in their abundance, basic nature, and DNA-binding properties. While histones are conserved among eukaryotes, no single NAP is found in all prokaryotes. Despite this broad diversity, NAPs in various prokaryotes

perform similar architectural functions by bending DNA, bridging DNA segments, and forming filaments on the DNA (30).

To shed light on the origins of histones and nucleosome-based DNA packaging and regulation, we recently conducted a comprehensive search for bacterial histones and discovered about 600 histone homologs in various bacterial classes, including Actinomycetes, Aquificae, Bdellovibrionia, Cyanophyceae, and Spirochaetia (31). Interestingly, these bacterial histones often co-exist with NAPs, whose structural and functional properties have been extensively studied. NAPs contribute to the local and global structuring of genomes and regulate DNA-associated proteins, including those involved in transcription. Bacterial histones can be categorized into pseudodimeric histones, which consist of two consecutive histone domains on a single chain, and single histone fold proteins with only one domain. Importantly, many bacterial histones contain conserved residues essential for DNA binding in eukaryotic and archaeal histones (Fig. 1A), suggesting that bacterial histones may also bind DNA (31).

In this study, we present the crystal structure and biochemical characterization of the histone homolog HBb from the predatory Gram-negative bacterium *Bdellovibrio bacteriovorus*. Our findings demonstrate that the single histone fold protein HBb forms a homodimer and has the ability to bind and compact DNA. Furthermore, we establish that HBb is essential for maintaining bacterial viability. Our results corroborate many of the observations reported in a recent study by Warnecke and co-workers (32), while providing strong evidence for different DNA structuring properties of HBb, suggesting a generic role in global genome organization.

Materials and methods

Detailed information is provided in the *SI Appendix,* under *Material and Methods.*

Bacterial strains and cultivation

Genes encoding HBb (*BD_RS00255,* old locus tag: *Bd0055*) and HMfB (GenBank accession number M34778.1) were cloned for recombinant protein expression in *E. coli*. *B. bacteriovorus* HD100 (DSM 50701, DSMZ) was cultured to construct a chromosomal *BD_RS00255* deletion strain using *E. coli* Top10 as prey cells.

Cloning, plasmids and synthetic DNA

Plasmids pETHis1a (33) and pET28a were used as expression vectors for HBb and HMfb protein production, respectively. For chromosomal deletion of *BD_RS00255* in *B. bacteriovorus*, the suicide vector pT18mobSacB (Addgene plasmid # 72648;

http://n2t.net/addgene:72648; RRID:Addgene_72648) was used. Synthetic oligonucleotides (Merck) used in this study are listed in Table S1.

Deletion of *BD_RS00255*

Attempts to delete *BD_RS00255* in *B. bacteriovorus* HD100 were conducted as previously described, with slight modifications (34, 35).

Protein expression and purification

HBb, HMfB, and FLAG-HBb were recombinantly expressed in *E. coli* Mutant56(DE3) (36) and purified to homogeneity using affinity and size-exclusion chromatography.

Circular dichroism (CD) spectroscopy

CD spectroscopy was performed to analyze the secondary structure and thermal stability of purified HBb protein using a Jasco J-810 spectrometer (JASCO).

Size exclusion chromatography coupled with multi-angle light scattering (SEC-MALS)

SEC-MALS was performed to measure the mass of purified HBb in solution, using a 1260 Infinity II HPLC system (Agilent) coupled to a miniDAWN TREOS and Optilab T-rEX refractive index detector (Wyatt Technology).

Crystallization, data collection, and structure determination

Crystallization trials of HBb were set up in 96-well sitting-drop vapor-diffusion plates using commercially available screens. Data were collected at beamline X10SA of the Swiss Light Source (Villigen, Switzerland). Detailed methods for data processing and structure determination are described in detail in *SI Appendix.* The structure has been deposited in the PDB under accession code 8CMP.

Microscale thermophoresis (MST)

The DNA binding affinities of HBb to the 80 bp (9, 37) and 80 bp-GC50 oligonucleotides were measured using the Monolith NT.115 instrument (NanoTemper Technologies). MST data were analyzed using the associated MO.Control software.

DNA binding analysis

Binding of HBb and HMfb to DNA was comparatively analyzed using various assays, including Electrophoretic Mobility Shift Assay (EMSA), Micrococcal Nuclease (MNase) digestion assay, DNA topology assay, Ligase-mediated circularization assay, and Tethered Particle Motion (TPM) experiments.

DNA affinity purification sequencing (DAP-seq)

Preparation of fragmented DNA libraries from genomic DNA of *B. bacteriovorus* HD100, subsequent DNA Affinity Purification, and next-generation sequencing were conducted as previously described, with some modifications (38). Data were processed with the nf-core/chipseq (version 2.0.0) pipeline (39), under Nextflow (version 23.04.2).

Modeling of the HBb-DNA complex

Molecular dynamics (MD) simulations of binding of the HBb dimer to DNA were performed using a structural model of an HBb dimer generated based on the crystal structure of HBb (PDB entry 8CMP) and an AlphaFold2 (AF2) prediction (40). Methods and software used for MD simulations are described in detail in the *SI Appendix, Material and Methods.*

Results

Structure of the histone HBb from *B. bacteriovorus*

The majority of bacterial histone homologs that we have identified in a recent bioinformatics analysis originate either from sparsely characterized bacteria of marine origin or from environmental samples (31). The predatory bacterium *B. bacteriovorus* represents one of the few organisms identified in the analysis that is both culturable in the lab and amenable to genetic manipulation. For these reasons, we selected the histone protein HBb of *B. bacteriovorus* (UniProt entry Q6MRM1) for comprehensive functional and structural characterization.

We overexpressed HBb recombinantly in *Escherichia coli* and purified the protein to homogeneity. Its purity was confirmed through SDS-PAGE, which displayed a single band corresponding to a molecular weight of 10 kDa, in line with the theoretical molecular weight of 7 kDa (Fig. 1B). BN-PAGE separation yielded two bands (Fig. 1B), suggesting the presence of diverse oligomers. Nonetheless, SEC-MALS analysis showed only a major peak with a molecular weight of 14 ± 0.4 kDa, indicating a dimer (Fig. 1C). CD spectroscopy indicated HBb to be an α-helical protein with flexible regions that cooperatively unfolds when heated, exhibiting a melting temperature of 51.6°C (Fig. 1C).

Within a few days, crystallization trials with purified HBb yielded crystals that diffracted to atomic resolution. The best dataset could be processed to a resolution of 1.06 Å and the structure solved by molecular replacement using the archaeal histone HMk (PDB entry 1F1E) as a search model. Except for the first three and last three amino acids, the full chain is clearly resolved in the electron density map. The asymmetric unit contains a single chain of HBb, forming a dimer through crystallographic symmetry. HBb exhibits a characteristic dimeric histone fold, with monomers consisting of three α-helices (α1, α2, α3) connected by

two loops (l1 and l2) (Fig. 1D). In each monomer, the longer central helix α2 is flanked at both ends by the shorter helices α1 and α3. Dimerization occurs through the antiparallel alignment of the central α2-helices of the two monomers at an angle of approximately 25°. The dimer is stabilized primarily by hydrophobic contacts along the interface, involving residues L31, I35, and L38 in α2, as well as contributions from α1 (e.g. V11) and α3 (e.g. I59).

In contrast to the archaeal histone HMfB, the α2-helix of HBb is one turn shorter, and α3 comprises only a single helical turn (Fig. 1D). Like HMfB, HBb features a conserved intramolecular salt bridge, known as the RD clamp, involving residues R51 and D58 (Fig. 1A, D). In HBb, this motif is augmented by D49, which forms an additional salt bridge with R51, potentially stabilizing the conserved KT motif in loop l2. This KT motif in HMfB is known to be involved in DNA interactions. Four of the six DNA-binding residues in HMfB, including K52 and T53, are conserved in HBb (Fig. 1A), indicating a potential for DNA binding.

HBb binds and bends DNA *in vitro*

We investigated the potential interaction of HBb with DNA using an EMSA with an 80 bp DNA fragment that has a high affinity for HMfB (9, 37). We observed a band shift, indicative of HBb-DNA complex formation. This was markedly different from the well-defined protein-DNA bands formed by hypernucleosomal histones, such as HMfB (Fig. 2A). The HBb-DNA complexes appeared as smeared bands, suggesting varied conformations, stoichiometries, or potential protein dissociation. We quantified the binding affinity of HBb to the 80 bp DNA fragment and a DNA fragment of random sequence with a GC content of 50% (80 bp-GC50) using MST (Fig. 2B and Table S3). Our results showed that HBb binds nonspecifically to DNA, with an affinity in the lower micromolar range, comparable to HMfB (41-43).

To estimate the size of the DNA binding site of HBb, we performed another EMSA using a DNA ladder (Fig. 2C). Stable HBb-DNA complexes were observed with fragments equal to or larger than 35 bp. Although no band shift was observed for the 20 bp and 25 bp fragments, these fragments appear blurred, suggesting that HBb forms unstable complexes with these smaller fragments. In this EMSA ladder assay, HMfB binds to fragments larger than 35 bp, in agreement with previous EMSAs performed on small substrates.

Next, we conducted TPM experiments with a linear 685 bp DNA fragment to determine the extent to which HBb alters DNA conformation upon binding. TPM is a single-molecule technique that allows for real-time observation of DNA-protein interactions. In this method, a DNA molecule is tethered at its ends on a bead and a glass surface, respectively, and the motion of the bead serves as a proxy for the conformational state of the DNA. TPM detects conformational changes of the DNA molecule as a function of the protein concentration,

measured by the change in root mean square (RMS) displacement of the bound bead. Proteins that compact the DNA reduce the distance between the ends of the DNA, which is measured as a decrease in RMS. In the presence of HBb, the RMS values decrease significantly and reach saturation at ≈110 nm (Fig. 3A). This value is comparable to the TPM values we measured previously for other DNA-bending proteins, such as *E. coli* HU and *Sulfolobus solfataricus* Sul7 and Cren7 (44, 45). However, it is higher than the values reported for the archaeal hypernucleosome-forming histones HMfA and HMfB (19), strongly suggesting that HBb bends DNA rather than wrapping it.

We further characterized the DNA binding properties of HBb by performing well-established assays, including MNase digestion, DNA topology, and ligase-mediated circularization assays (46-49). In the MNase digestion assay, MNase is used to digest DNA that is not protected by bound proteins. Unlike the positive control HMfB, which tightly packs DNA and protects multiples of 30 bp fragments from endo-exonuclease digestion (11), the binding of HBb to DNA, similar to NAPs (50, 51), offered no such protective effect (Fig. 3B). In the DNA topology assay, we analyzed whether the binding of HBb alters the geometry of DNA. Such changes affect the supercoiling state of DNA in the presence of Topoisomerase I and can be visualized by separation of the DNA in an agarose gel. Here, both HBb and HMfB constrain supercoils in a concentration-dependent manner (Fig. 3C). Using a ligase-mediated circularization assay, we next examined whether this change in DNA geometry results from DNA bending. DNA-bending proteins effectively render small DNA fragments more flexible, thus promoting the formation of small circular DNA during a ligation reaction. The unambiguous identification of circular DNA is possible by treatment of the ligation product with T5 exonuclease, followed by separation through gel electrophoresis. In the assay, fewer linear fragments and more 240 bp circles formed upon addition of increasing amounts of HBb to 240 bp linear DNA and T4 DNA ligase, indicative of DNA bending induced by HBb (Fig. 3D).

MD simulations support DNA bending model

To validate our hypothesis that HBb functions as a DNA-bending histone dimer, we turned to MD simulations. For the initial setup, we replaced an H3-H4 dimer in the nucleosome crystal structure (PDB entry 1AOI) with our HBb dimer structure and truncated the DNA to a length of 40 bp. We then performed several short 10 ns simulations to reach an initial stable state where the DNA is tightly wrapped around the HBb dimer (Fig. 4A). This initial state served as the starting point for two subsequent simulations, each lasting 500 ns of MD simulation time, for a total of 1 μs. During both 500 ns runs, the DNA remained tightly bound to HBb and did not dissociate (Fig. 4B). The major residues involved in DNA binding were identified as S9, K12, K16, N22, S24, K52, T53, and R57 (Fig. 4C). These residues interact with the DNA

backbone and are conserved in related bacterial histones from Bdellovibrionota, Elusimicrobiota, Spirochaetota, Planctomycetota, Myxococcota, and Chlamydiota (Fig. 1A) (52).

Nonspecific binding of HBb to the *B. bacteriovorus* chromosome is essential for viability

The bacterium *B. bacteriovorus* is a well-studied model organism with a predatory life cycle. To further understand the functional significance of HBb, we aimed to replace the gene encoding HBb, *BD_RS00255*, with a kanamycin resistance cassette using the suicide vector pT18mobSacB. We achieved successful integration of the plasmid into the chromosome but failed to select for a second crossover event. This suggests that HBb is essential for *B. bacteriovorus* growth and corroborates recent findings (32).

In a subsequent step, we investigated whether HBb has DNA sequence specificity and possibly functions as a transcription factor. To this end, we conducted DAP-seq on a chromosomal scale, a recently developed method to identify genome-wide binding regions of DNA-binding proteins (38). We coupled purified FLAG-HBb to magnetic beads coated with FLAG antibodies and incubated them with a genomic *B. bacteriovorus* DNA library. Protein-bound DNA fragments were isolated, purified, amplified, and subjected to next-generation sequencing. We deviated from the original protocol by expressing FLAG-HBb in *E. coli* rather than in its natural host *B. bacteriovorus*, as this did not yield a sufficient amount of protein. Moreover, we incubated the magnetic beads directly with purified protein instead of cell extract to minimize the risk of nonspecific binding of *E. coli* proteins. DAP-seq analysis was performed for two independently prepared genomic DNA libraries with a fragment size of approximately 200 bp, representing two biological replicates. Samples containing only DNA incubated with anti-FLAG beads in the absence of protein served as controls. For these samples, as determined by Bioanalyzer analysis, the quantity of recovered amplified DNA was less than the amount of primer dimers formed during the amplification. Since this confirms the absence of non-specifically bound DNA, sequencing of these samples was omitted.

Plotting the raw data from DAP-seq analysis on the chromosome map of *B. bacteriovorus* shows HBb binding to both genic and intergenic regions randomly throughout the genome (Fig. 5A, B). After peak-calling analysis (as described in *Supplemental Materials and Methods*), we identified a total of 475 statistically significant HBb-binding sites for DAP-seq sample 1 and 455 for DAP-seq sample 2, respectively, distributed across the chromosome (Fig. 5A). Most of these peaks are between ~230 bp and ~660 bp in length reaching maximum lengths of 2,416 bp and 1,747 bp for DAP-seq sample 1 and 2, respectively (Fig. S1). This indicates that while HBb binds to DNA throughout the entire

genome, certain regions are notably enriched with HBb dimers, which are likely spaced along the DNA. Analysis of the peaks in relation to the GC content of the DNA fragments covered yielded a value of approximately 50%, which corresponds to the mean GC content of 50.7% of the *B. bacteriovorus* genome (53) (Fig. S2). This suggests that HBb binds DNA without preferring GC-rich or AT-rich regions. The search for special sequence motifs proved to be infeasible given the broad length distribution and random pattern of binding sites across the chromosome.

Discussion

Building on our recent discovery of bacterial histones (31), this study investigates the DNA-binding and structuring properties of the histone protein HBb in *B. bacteriovorus*. We solved the crystal structure of HBb at a resolution of 1.06 Å, which notably, makes it the first structure of a histone protein at atomic resolution; the previous structure with the highest resolution (1.48 Å) was that of histone HMfA from *M. fervidus* (PDB entry 1B67) (54). HBb features the characteristic histone fold and forms dimers. Most amino acid residues crucial for DNA binding in archaeal and eukaryotic histones are conserved in HBb. However, residues facilitating tetramerization in archaeal HMfB (17, 43) are absent (Fig. 1A), suggesting that the dimeric state observed in both the crystal structure and biophysical data likely represent the physiological oligomer.

Employing a comprehensive array of assays, we demonstrate that HBb not only binds to DNA but also alters its topology. Our findings challenge a recent model (32) that suggested high-density binding of HBb would straighten DNA without inducing compaction. This straightening effect has been previously observed in the *E. coli* NAP HU at high density (55, 56); however, the physiological relevance of these structures remains unclear. It is possible that such high-density binding of HU occurs on a local scale, driven by sequence determinants that have not yet been identified. In contrast, our data indicate that HBb binds as individual dimers along the DNA and induces compaction through DNA bending, akin to the low-density binding mode of HU. Moreover, unlike HU, we did not observe a straightened conformation of the DNA even at high HBb densities. Importantly, MNase digestion assays and TPM measurements reveal that HBb does not compact DNA through wrapping, thereby ruling out nucleosome or hypernucleosome formation, a characteristic of canonical archaeal and eukaryotic histones (8, 9, 30).

Previous studies have reported that the expression of the *BD_RS00255* gene, encoding HBb, is upregulated during the replicative growth phase of *B. bacteriovorus*, a phase closely linked to prey consumption (57). This observation is corroborated by the most recent RNA-seq experiments, which also show that *BD_RS00255* is expressed exclusively during the

replicative phase and not during the prey attack phase (Renske van Raaphorst and Géraldine Laloux, personal communication). Multiple independent attempts to disrupt the *BD_RS00255* gene have been unsuccessful, both by us and others (32), underscoring the essential role of HBb in the survival of *B. bacteriovorus*. DAP-seq analyses confirm that HBb binds to DNA across the entire genome, a pattern also observed in bacterial NAPs of the HU/IHF family. These proteins are encoded in 93% of bacterial genomes and are thought to play a role in controlling the dynamics and organization of the bacterial chromosome (58, 59).

While our study primarily focuses on the bacterial histone HBb in *B. bacteriovorus*, the evolutionary implications of our findings merit further discussion. The presence of histone-like proteins in bacteria raises compelling questions about the evolutionary trajectory leading to the intricate histone structures and DNA-compacting capabilities observed in eukaryotes. One hypothesis is that the foundational aspects of histones and their DNA-binding abilities were already in place during the time of the Last Universal Common Ancestor (LUCA). These proteins may have initially served as 'simple' NAPs and subsequently underwent a series of evolutionary adaptations, enabling them to form nucleosomes and other higher-order chromatin structures. Such adaptations could have led to a gain of function, attributed to enhanced DNA affinity and (structural) binding specificity, priming the proteins for more efficient DNA packaging, organization, and specific regulatory roles. The presence of histones in a broad spectrum of deeply-branching bacterial lineages, combined with the conservation of key amino acid residues crucial for DNA binding across bacterial, archaeal, and eukaryotic histones, lends support to this notion. However, considering the infrequent occurrence of histones in bacteria and their sequence similarity to archaeal histones, we cannot rule out the possibility that these proteins were acquired by bacteria from archaea through horizontal gene transfer events. The future availability of additional bacterial histone sequences in molecular databases, as well as comparative genomic and functional studies, could illuminate the evolutionary pathways that have shaped histones across the domains of life.

In summary, our study establishes HBb as a unique bacterial histone with distinct DNA-structuring capabilities compared to eukaryotic, archaeal, and viral histones. Its architectural properties closely resemble those of HU/IHF family proteins. While HU/IHF family proteins also exist in *B. bacteriovorus*, they are present in significantly lower quantities compared to HBb (19). This supports the notion of functional redundancy among different bacterial NAPs, particularly in their global effects on chromosome organization. The indispensability of HBb for *B. bacteriovorus* survival suggests that bacterial histones, like their archaeal and eukaryotic counterparts, play critical roles in cellular functions.

Data availability

The TPM and molecular dynamics data generated in this study are available from the 4TU repository (https://data.4tu.nl) with the DOI 10.4121/6c07e4bb-96f1-4ee0-88ef-6978bda27e5d.

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Figures

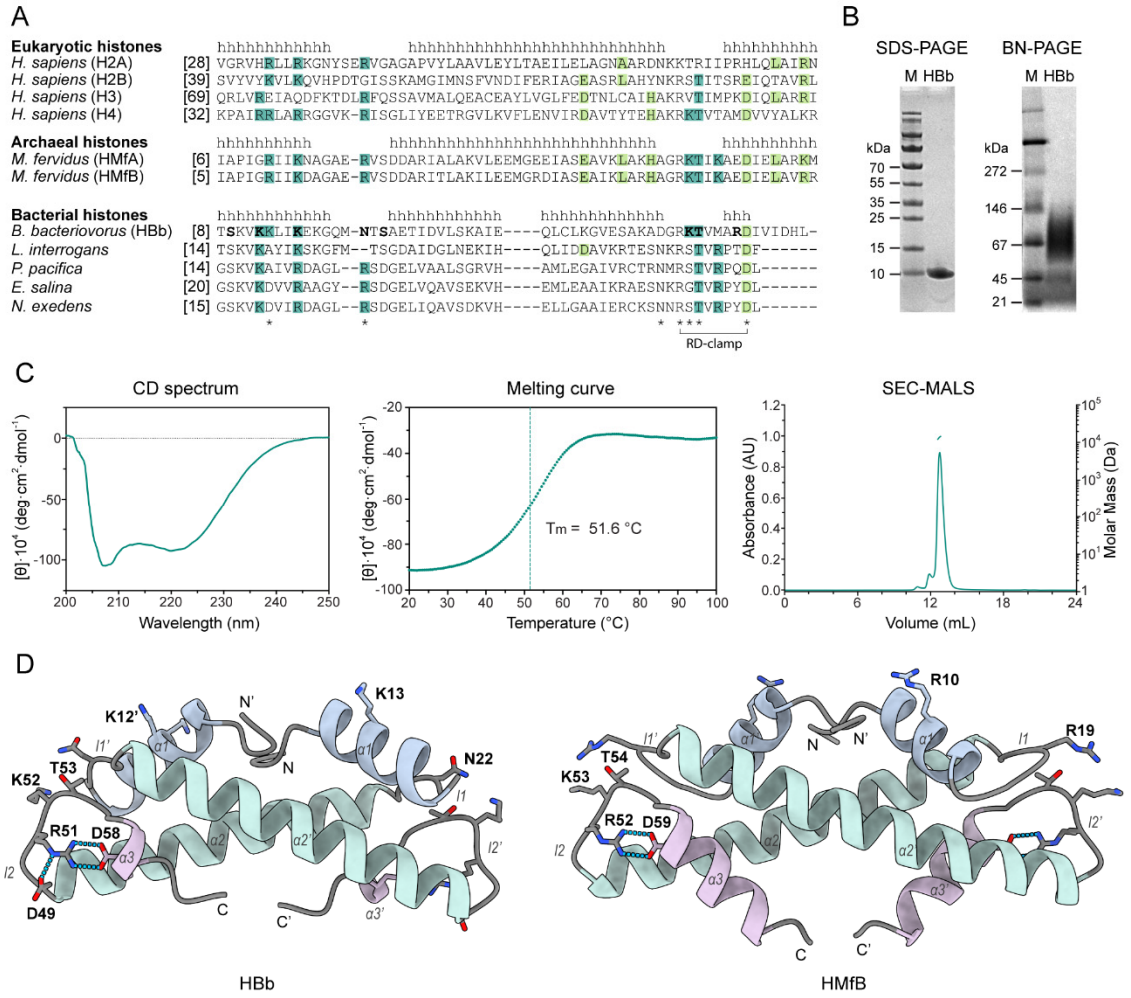

Figure 1

Biophysical and structural characterization of HBb. A. Sequence alignment of representative eukaryotic, archaeal, and bacterial histones from *Homo sapiens* (UniProtKB/Swiss-Prot entry for H2A: P04908; H2B: P62807; H3: P68431; H4: P62805), *Methanothermus fervidus* (HMfA: P48781; HMfB: P19267), *Bdellovibrio bacteriovorus* (Q6MRM1), *Leptospira interrogans* (Q8F3E8), *Plesiocystis pacifica* (A6GF99), *Enhygromyxa salina* (NCBI entry WP_052547863.1), and *Nannocystis exedens* (WP_096326703.1). α-Helices are labelled with "h" according to the crystal structures of H2A, HMfB and HBb, respectively. Conserved residues involved in DNA binding and tetramerization are highlighted in dark and light green, respectively. HBb residues involved in DNA backbone interaction according to MD simulations are in bold. Residues represented as sticks in panel D are labelled with *****. Residues R51 and D58 forming the RD clamp in HBb are connected by a bracket. **B.** SDS-PAGE and BN-PAGE showing purified HBb. **C.** Biophysical characterization of HBb by CD spectroscopy (left: single CD spectrum, middle: thermal melting curve) and SEC MALS (right) for determination of secondary structure, thermal

stability and oligomeric state. **D.** The crystal structure of HBb dimer (PDB entry 8CMP) in comparison with the crystal structure of HMfB dimer (PDB entry 1A7W). Conserved residues with roles in DNA binding or fold stabilization are depicted as sticks. Salt bridges at the RD clamp with a length of less than 3 Å are shown as cyan dashed lines.

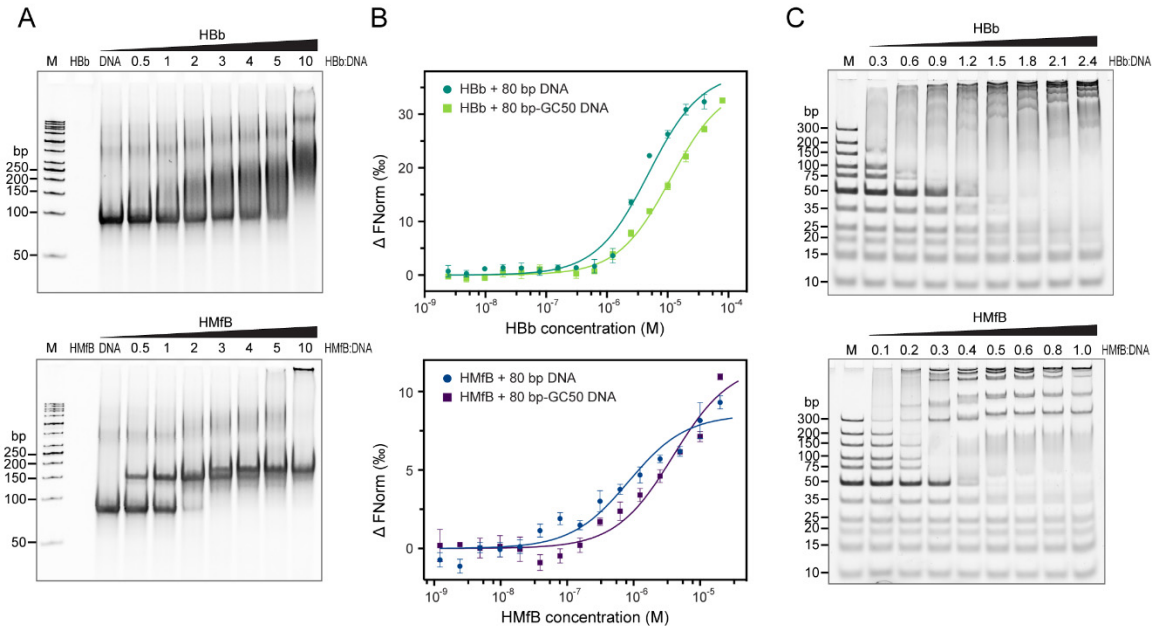

Figure 2

HBb binds DNA. A. EMSA with the 80 bp DNA fragment in the presence of HBb and HMfB as a control. The molar ratios of protein:DNA in lanes 4-10 are indicated. **B.** MST curves showing binding of HBb to the 80 bp DNA fragment and the 80 bp-GC50 DNA fragment (10 nM), as compared to HMfB. **C.** EMSA of HBb and HMfB as a control with the GeneRuler Ultra Low Range DNA Ladder (ThermoFisher Scientific). For lanes 2-9, the protein/DNA mass ratios are labelled.

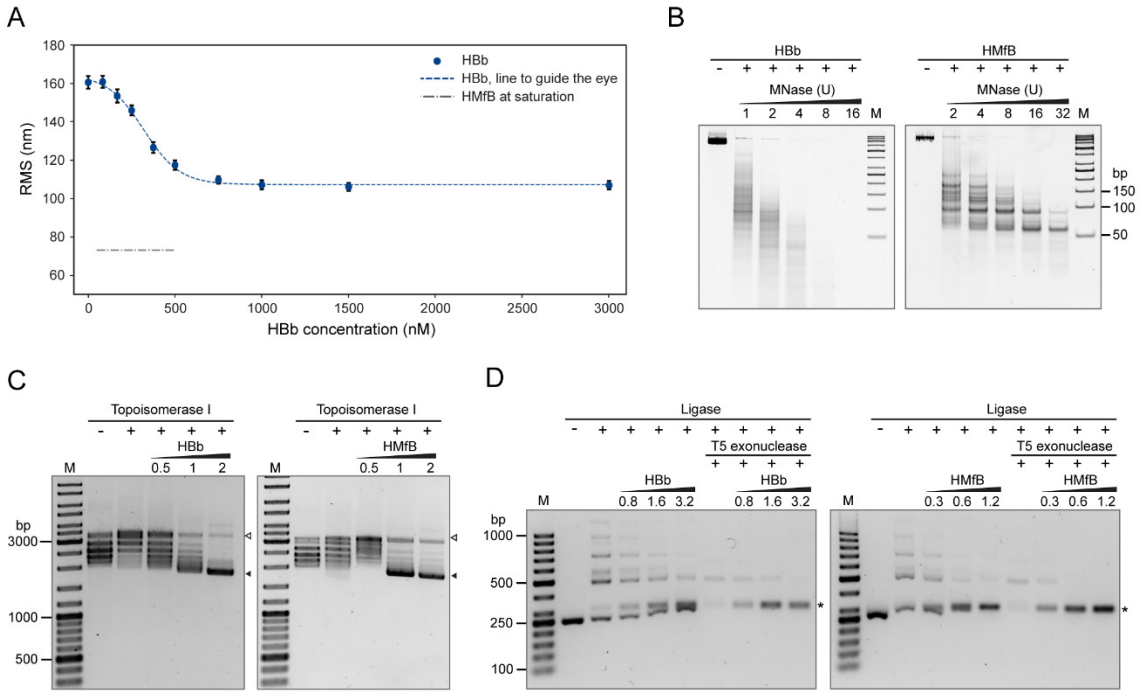

Figure 3

HBb is a DNA bender. A. TPM experiment of HBb with 685 bp DNA. All measurement points are averages of triplicate measurements, with error bars indicating standard deviations. As reference, the RMS value obtained for hypernucleosome structure formed with HMfB is shown as the gray dash-dotted line (19). **B.** MNase digestion of 685 bp DNA following incubation with HBb and HMfB. Increasing amounts of MNase in the assay are indicated in Units. **C.** DNA topology assay with relaxed pUC19 in the presence of HBb in comparison to HMfB. Protein:DNA mass ratios were labeled in the figure. The bands showing relaxed (△) and supercoiled pUC19 (▲) are marked. **D.** Ligase-mediated circularization assay of a 240 bp DNA in the presence of HBb and HMfB. Samples are shown before and after T5 exonuclease digestion. Protein:DNA mass ratios are labeled. Monomeric DNA rings are indicated (*).

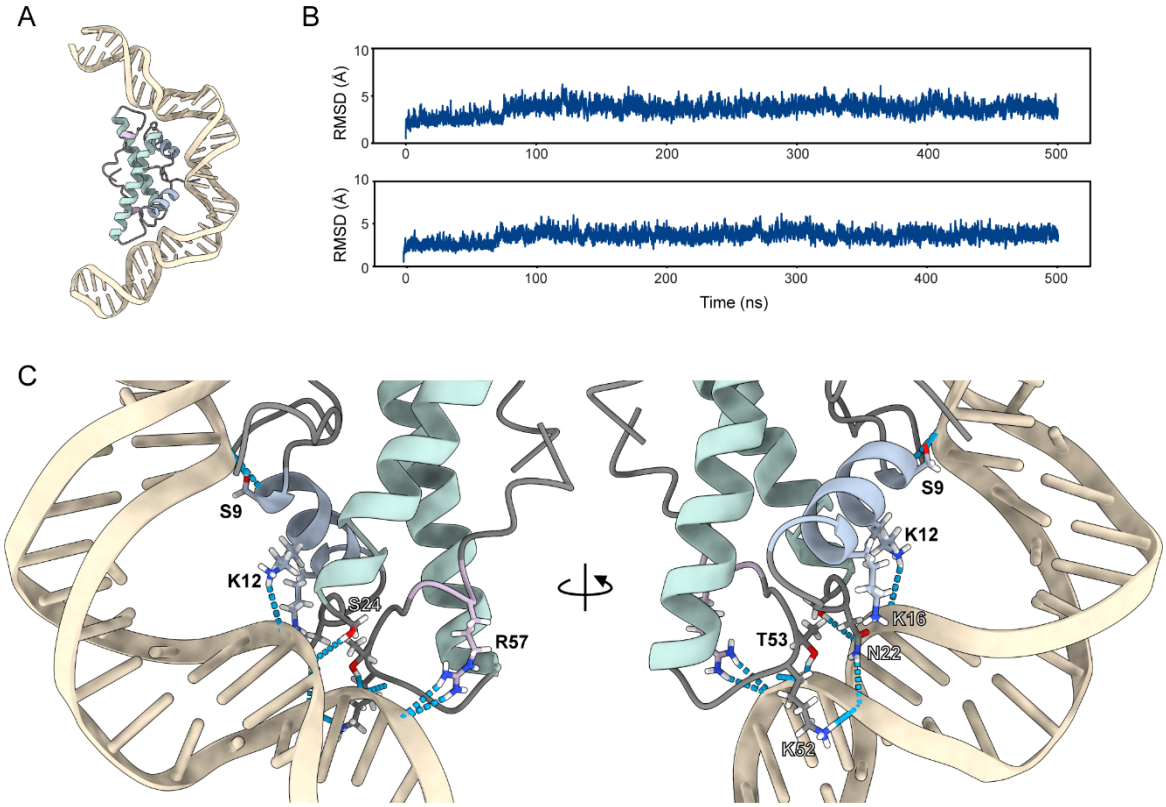

Figure 4

The HBb dimer bends DNA. A. The starting structure of HBb bound to DNA for the 500 ns MD simulations. It was generated using the H3/H4 nucleosome structure (PDB entry 1AOI) and the initial state was generated by running several short 10 ns MD simulations as described in the *SI Appendix,* under *Material and Methods*. **B.** Plot showing RMSD values of the DNA during two independent 500 ns simulations relative to the DNA in the starting structure. **C.** Cartoon representation of a section of the DNA-bound HBb structure obtained from MD simulations. The structure shown is the central structure of the most common structure cluster in the last 100 ns of one of the simulations. Residues interacting with the DNA backbone are depicted as sticks. Hydrogen bonds formed between protein and DNA are shown as cyan dashed lines.

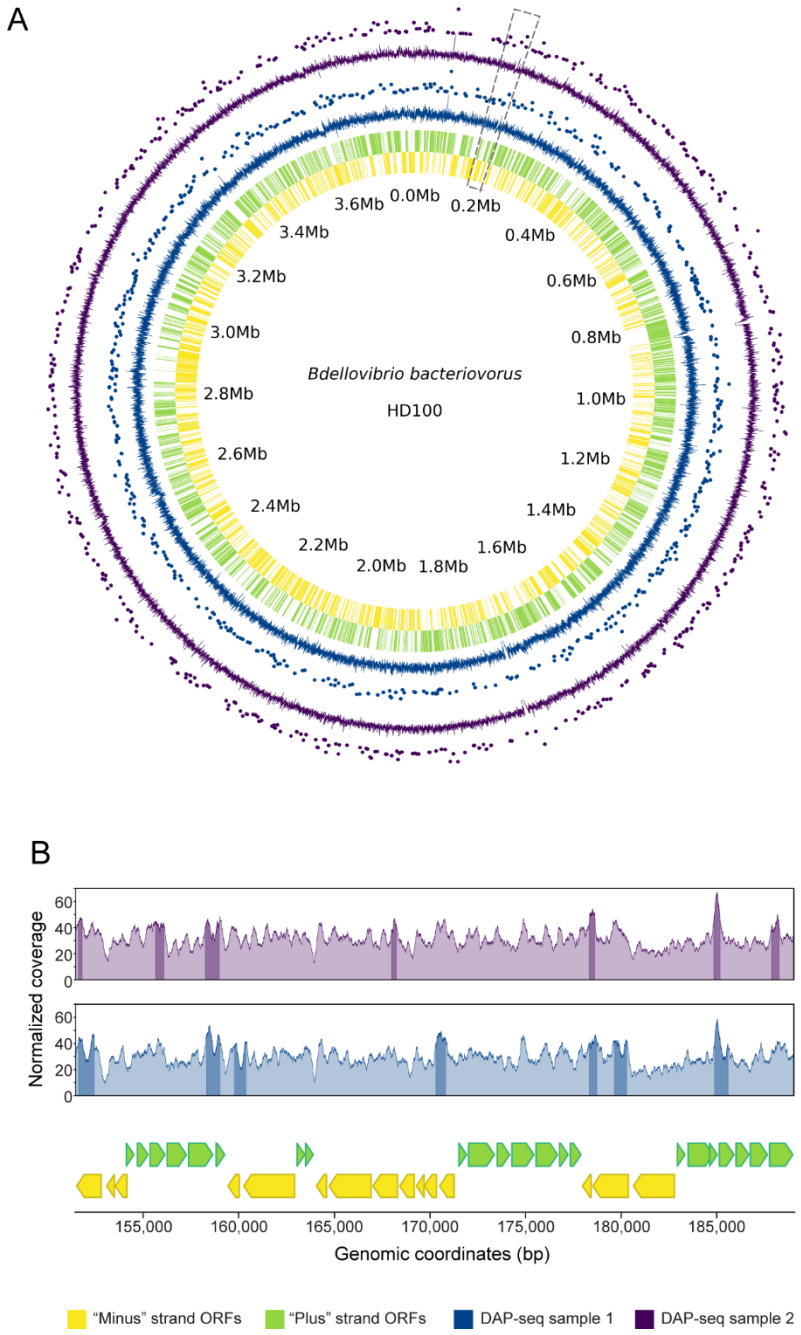

Figure 5

The HBb dimer binds DNA nonspecifically. A. DAP-seq data visualized using a circos plot of the *B. bacteriovorus* HD100 genome. The inner rugplots represent the "minus" (yellow) and "plus" (light green) strand ORFs. Each wedge represents the coordinates of a gene. Outer line plots represent the normalized read coverage values, and scatter plots above show the major peaks for the two DAP-seq samples (blue and purple). Peaks are shown as dots, where the strength of the peak signal correlates positively with the distance from the axis. The enlarged section shown in panel E is indicated by a gray dashed line. **B.** Line plots

showing the normalized read coverage values for a randomly selected section of the *B. bacteriovorus* HD100 genome encompassing the genomic region from 151,464 bp to 189,033 bp. The bottom plot shows the genomic context, and the top line plots depict the normalized read coverage values for each DAP-seq sample with the major peaks shaded darker. The color code corresponds to panel D.

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