A framework to validate fluorescently labeled DNA-binding proteins for single-molecule experiments

Graphical abstract

Highlights
- KCK tag can alter protein properties both quantitatively and qualitatively
- Electrostatic interactions between the KCK tag and DNA contribute to the artifacts
- Adding a short peptide tag to ParB protein does not lead to its in vivo changes
- Single-molecule DNA flow-stretching assay can detect protein property changes

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In brief
Introducing a short peptide such as lysine-cysteine-lysine (KCK) tag is one of the commonly used fluorescent-dye labeling strategies. Molina et al. show that single-molecule DNA flow-stretching assay is a versatile tool to detect unwanted protein property changes. Their results highlight that rigorous validations are required when studying modified proteins.

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A framework to validate fluorescently labeled DNA-binding proteins for single-molecule experiments

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SUMMARY
Due to the enhanced labeling capability of maleimide-based fluorescent probes, lysine-cysteine-lysine (KCK) tags are frequently added to proteins for visualization. In this study, we employed an in vitro single-molecule DNA flow-stretching assay as a sensitive way to assess the impact of the KCK tag on the property of DNA-binding proteins. Using Bacillus subtilis ParB as an example, we show that, although no noticeable changes were detected by in vivo fluorescence imaging and chromatin immunoprecipitation (ChIP) assays, the KCK tag substantially altered ParB’s DNA compaction rates and its response to nucleotide binding and to the presence of the specific sequence (parS) on the DNA. While it is typically assumed that short peptide tags minimally perturb protein function, our results urge researchers to carefully validate the use of tags for protein labeling. Our comprehensive analysis can be expanded and used as a guide to assess the impacts of other tags on DNA-binding proteins in single-molecule assays.

INTRODUCTION
Fluorescence-based protein visualization has played an instrumental role in single-molecule experiments.1−5 Intensive research has led to fruitful development of a variety of fluorophores and tagging methods for proteins.6−10 Regardless of the kinds of probes and labeling modalities, the main goals have remained largely unchanged: achieving adequate fluorescence labeling while minimally perturbing the properties of the proteins.

Unwanted alteration of protein properties can occur at any stage during the preparation of the labeled protein, which must be minimized to reveal the true function of the protein of interest. First, introducing additional components into a protein requires careful consideration during the protein design. The sizes of common fluorescent proteins are around 25 kD,5,11 and those of self-labeling proteins SNAP, CLIP, and Halo tags are about 20, 20, and 33 kDa, respectively.12 It has been well appreciated that large protein tags could interfere with the protein’s function and disrupt protein-protein interactions, and smaller tags are preferred.5,13 Second, fluorescent-dye labeling steps can adversely affect protein activities. For example, Bacillus subtilis structural maintenance of chromosomes (BsSMC) protein is capable of compacting flow-stretched DNA.14 We previously observed that using a centrifugal concentrator-based method to remove unreacted fluorescent dyes abolished BsSMC’s...
DNA compaction ability, whereas using a resin-based column did not.\textsuperscript{14} Third, fluorescent dyes could disrupt the proper functioning of a protein itself. Especially, it has been shown that hydrophobic fluorescent dyes have a potential to cause artifacts due to nonspecific binding.\textsuperscript{15} Lastly, fluorescently labeled proteins may malfunction in the context of experimental environments. Prominent examples were reported with quantum dot (QD)-labeled proteins. Effective diameters of commercially available functionalized QDs (“big” QDs) are in the 14–35 nm range,\textsuperscript{15,16} while “small” QDs are 9–12 nm in diameter.\textsuperscript{17,18} When the localization of AMPA receptors (AMPAR) on neurons were examined, big QD-labeled AMPARs localized differently from small QD-labeled (or 4-nm organic fluorescent-dye-labeled) AMPARs, along with difference in diffusion coefficients, possibly due to the narrow synaptic cleft size (~30 nm).\textsuperscript{19,20}

While fluorescently tagged proteins are crucial in a variety of biological studies, a challenge is the lack of predictions for how the fluorescent tags or probes will alter protein function. Thus, empirical investigations must follow. The purpose of this study is to explore the single-molecule DNA flow-stretching assay as a sensitive and efficient tool to test whether a tag alters the function of a DNA-binding protein. We chose the DNA flow-stretching approach because it has been extensively used in studying actions of DNA-binding proteins on individual DNA molecules.\textsuperscript{14,21–26} Furthermore, contrary to force-based single-molecule assays that visualize one DNA molecule at a time, single-molecule DNA flow-stretching assay allows 10–40 DNA molecules to be analyzed in each field of view, which is advantageous for subsequent statistical data analyses.

In this study, for a proof of principle, we tested the effect of lysine-cysteine-lysine (KCK) tag on \textit{B. subtilis} ParB (BsParB) proteins. We chose this tag because maleimide-conjugated fluorescent dyes have been widely used to label proteins via covalent conjugation to surface-exposed cysteines.\textsuperscript{15} However, labeling all desired cysteines with maleimide dyes is not always possible. The reaction efficiency between the thiol group on cysteine and the maleimide moiety of a fluorescent dye can be increased by flanking the cysteine with two positively charged lysine residues. It was revealed that the neighboring lysine residues decrease pKa of the cysteine residue, thereby increasing thiol-maleimide reactivity.\textsuperscript{27–30} Thus, appending the KCK tag to a protein has been a popular and extensively used method due to its superior fluorescence-labeling efficiency.\textsuperscript{23,31–37}

We chose ParB protein as our example because of its well-known \textit{in vivo} and \textit{in vitro} activities. The ParABS DNA partitioning system is a broadly conserved segregation machinery for bacterial chromosomes and plasmids. ParB binds to \textit{parS} sequences and spreads to neighboring regions\textsuperscript{38,39} to form a nucleoprotein complex, which is translocated by ParA.\textsuperscript{38,39} \textit{In vivo}, ParB spreading is evident by two approaches: fluorescence microscopy in which fluorescently tagged ParB proteins form foci in live cells and chromatin immunoprecipitation (ChIP) assays in which ParB protein associates with 10–20 kb DNA regions encompassing \textit{parS}.\textsuperscript{38,39} Importantly, it was recently discovered that ParB protein is a novel enzyme that utilizes cytidine triphosphate (CTP) to modulate ParB spreading.\textsuperscript{40–42} \textit{In vitro}, ParB’s spreading has been shown by imaging fluorescently labeled ParB proteins on doubly tethered (or doubly trapped) DNAs with protein load blocks.\textsuperscript{41,43,44} In addition, previous single-molecule DNA flow-stretching assays have reported that ParB’s DNA compaction activity \textit{in vitro} is correlated with ParB’s spreading activity \textit{in vivo}.\textsuperscript{23} Here we report that DNA compaction by ParB is artificially enhanced by KCK tags in single-molecule DNA flow-stretching assays \textit{in vitro}. Further investigation indicates that electrostatic interactions between the negatively charged DNA backbone and the positively charged KCK tag contribute at least partly to these artifacts that are not rescued even with fluorophore labeling onto the KCK tag. Contrary to the \textit{in vitro} single-molecule results, the KCK tag did not lead to any noticeable changes \textit{in vivo}. In sum, our single-molecule DNA flow-stretching assay is highly sensitive and allows the detection of the property changes in DNA-binding proteins for single-molecule experiments. Its high-throughput data production allows statistical analyses and leads to conclusions more efficiently. We propose that the DNA flow-stretching-based approaches can be used as a tool to detect property changes of DNA-binding proteins upon addition of tags or fluorescent probes.

**RESULTS**

**KCK tags increase BsParB’s DNA compaction rates \textit{in vitro}**

KCK tags are frequently used for \textit{in vivo} and \textit{in vitro} protein labeling due to their small size and the increased labeling efficiency of maleimide-fluorescence dyes.\textsuperscript{27–30} To understand whether this three-amino-acid tag has any impact on ParB proteins, we purified tagged and untagged wild-type \textit{B. subtilis} ParB (BsParB) proteins (Figure S1A) and employed single-molecule DNA flow-stretching assays with a lambda DNA substrate (Figure 1A). Since ParB has been shown to be a CTPase,\textsuperscript{45–48} our samples were treated with apyrase to remove residual nucleotides from our protein samples. Upon addition of the purified proteins, we measured the speed of DNA compaction by tracking the positions of a fluorescent QD labeled at one DNA end (Figure 1B).\textsuperscript{23} In the presence of 50 nM untagged BsParB(WT), we observed robust DNA compaction all the way to the DNA tether point in the absence of CTP as previously shown (Figures 1B and S2).\textsuperscript{23} Interestingly, both 1 mM CTP and CTP\textsubscript{7}S (a non-hydrolyzable CTP analog) dramatically inhibited DNA compaction rates, by 39-fold and 149-fold, respectively (Figures 1C and S1D, three blue bars, and Figure S3A), implying counter-productive roles of CTP binding in DNA compaction. The mechanism of CTP binding on ParB’s action is currently being investigated in a separate study. When BsParB(WT) with the KCK tag at its N terminus (hereafter “KCK-BsParB(WT)”) (Figure S1A) was subjected to the same experiment, without CTP, we observed that the lambda DNA was compacted to the tether point at a slightly slower rate (at 0.72x) than BsParB(WT) (Figures 1C and S1D, compare the first blue and red bars, and Figure S2). Conversely, in the presence of CTP or CTP\textsubscript{7}S, KCK-BsParB(WT) exhibited much higher DNA compaction rates than BsParB(WT), at 10.5-fold for CTP (Figures 1C and S1D, compare second blue and red bars) and 19.4-fold for CTP\textsubscript{7}S (Figures 1C and S1D, compare third blue
Figure 1. *In vitro* quantitative and qualitative BsParB compaction rate changes by the KCK tags

(A) Schematic of single-molecule DNA flow-stretching assays.

(B) An example of DNA compaction by 50 nM BsParB(WT) protein (top) and the definition of compaction rate (bottom).

(C and D) Lambda DNA compaction rates by 50 nM (C) wild-type (n = 30–74 from three to eight experiments) and (D) R80A mutant (n = 29–58 from three to four experiments) proteins. Numbers indicate compaction rate fold increases. Error bars: SEM.

(E) Top: Mann-Whitney test (the Wilcoxon rank-sum test) p value color scheme. Bottom: Mann-Whitney test comparisons for compaction rates by wild-type BsParB and its KCK versions.

(F) Mann-Whitney test comparisons for BsParB(R80A) and its KCK versions. (E and F) Cyan, green, and yellow boxes highlight qualitative protein property changes due to the KCK tags for visual aids. (C–F) See Tab 1 in Data S1 for detailed sample number (n) information. See also Figures S1–S3, S5, and S7.
and red bars). As seen in Figures 1C and S1D (compare the three red bars), adding the nucleotides only reduced KCK-BsParB(WT)'s DNA compaction rate by 2.7-fold for CTP and 2.5-fold for CTPyS, whereas, mentioned earlier, BsParB(WT)'s response to nucleotides was much more dramatic (Figures 1C and S1D, three blue bars) (also see Figure S3A).

We note that although the purified proteins were stored in a buffer that contains 5 mM β-mercaptoethanol, which is a reducing agent that blocks disulfide bridge formations between cysteines, the imaging experiments were conducted in buffers without reducing agents. To understand whether reducing agents could make a difference, we added 1 mM β-mercaptoethanol (Figure S3B) or 1 mM dithiothreitol (DTT) (Figure S3C) to our imaging experiments. We observed that these reducing agents resulted in nonspecific binding of QD-DNA-protein onto the sample chamber surface or the decrease of fluorescence intensity of the QD (Figures S3B and S3C). Nevertheless, in the absence of DTT, supplementing CTP still caused 2.8-fold DNA compaction rate decrease using KCK-BsParB(WT) (Figure S3D), which was the same trend observed without reducing agents (Figures 1C and S3A). Thus, the reducing agents did not alter our experimental conclusions. Due to the technical challenges of our imaging experiments in the presence of reducing agents (Figures S3B and S3C), we have performed further experiments without them.

Of note, in our experience, batch-to-batch variations in purified proteins only lead to up to 2-fold differences for DNA compaction rates. The dramatic changes in protein behavior caused by KCK tags (Figures 1C and S1D) prompted us to investigate further.

Next, we examined the effect of ParB-specific parS sequence on DNA compaction rates by inserting a parS in the middle of the lambda DNA (hereafter, “parS DNA”). We found that without any nucleotides, untagged BsParB(WT) compacted parS DNA 25% slower than it did for lambda DNA without parS (Figures S1B and S1D). In the presence of CTP or CTPyS, untagged BsParB(WT)'s compaction rate of parS DNA decreased by 16-fold and 50-fold, respectively (Figures S1B and S1D, three blue bars with lined fill pattern). The mechanism of parS on ParB’s action is currently being investigated in a separate study. Strikingly, KCK-BsParB(WT) exhibited substantial increase in the parS DNA compaction rates in the presence of CTP (4.9-fold, compare second blue and red bars with lined fill pattern) or CTPyS (7.2-fold, compare third blue and red bars with lined fill pattern) compared with untagged BsParB(WT) (Figures S1B and S1D). Thus, the KCK tag enhanced BsParB(WT)'s DNA compaction rate (compared to the untagged BsParB(WT)) when nucleotides are present on both lambda DNA and parS DNA.

Given that ParB protein’s CTP binding pocket resides at the N-terminal domain (NTD) and the NTD is implicated to be the DNA entry gate,11,42,45 we questioned if the unexpected compaction rate increases also occur when KCK is tagged at the C terminus of BsParB(WT) protein (hereafter, “BsParB(WT)-KCK”) (Figure S1A). Indeed, like KCK-BsParB(WT), BsParB(WT)-KCK also showed much faster compaction with CTP compared with BsParB(WT) (Figure 1C for the lambda DNA; Figure S1B for the parS DNA). Thus, KCK enhanced BsParB(WT)'s DNA compaction rate when appended to either terminus.

The KCK tag alters the action of BsParB R80A mutant
We next investigated whether the compaction rate change induced by the KCK tag was limited only to the wild-type BsParB. The R80A mutant of BsParB has been shown to abolish proper in vivo sporation, localization, and spreading along with in vitro lambda DNA compaction in the absence of nucleotides.23,46,47 Surprisingly, without nucleotides, although its DNA compaction rate was 18.2-fold lower than BsParB(WT) (Figure S1D, compare first blue and purple bars), BsParB(R80A) (Figure S1A) was still capable of compacting the lambda DNA (Figure 1D), contradicting a previous report (see discussion).23 Next, we wondered whether a KCK tag alters BsParB(R80A)'s action on DNA. Indeed, with lambda DNA, the compaction rates of both KCK-BsParB(R80A) and BsParB(R80A)-KCK were substantially increased for all tested nucleotides (Figures 1D and S1D). When parS DNA was used as a substrate, compaction rate increases by KCK tags (p < 0.0001) were also noted (Figures S1C and S1D). The visualized Mann-Whitney comparison charts for DNA compaction rates highlight that BsParB(R80A), KCK-BsParB(R80A), and BsParB(R80A)-KCK respond differently to different nucleotides and the presence of parS (see green and yellow boxes in Figure 1F; also see Figure S1F).

The effects of KCK tags on protein action are limited to in vitro assays but not in vivo
The different effects of KCK tags on DNA compaction in vitro prompted us to systematically test the effect of KCK tag on BsParB’s or BsParB(R80A)’s localization and spreading in vivo. We first generated eight GFP fusions to the ParB variants with KCK tags at the C or N terminus of the protein and performed fluorescence microscopy (Figure 2A). Consistent with previous findings that R80A abolishes ParB spreading,23 BsParB(WT) formed foci in the cells, while BsParB(R80A) had diffused localization on the DNA. Interestingly, KCK tags at the C or N terminus did not alter the localization of ParB(WT) or ParB(R80A) (Figure 2A). In a complementary approach, we analyzed the in vivo
spreading of ParB variants on the genome by chromatin immunoprecipitation (ChIP-seq) assays using anti-ParB antibodies (Figure 2B). We observed that BsParB(WT) spreads to an ~20-kb region surrounding the parS site, but BsParB(R80A) did not spread. These results are consistent with previously published data.23 Importantly, having a KCK tag at the C or N terminus did not affect the spreading of BsParB(WT) or BsParB(R80A). We also show that the KCK-tagged proteins have similar expression levels compared to the matched untagged controls (Figures S4A and S4B). These experiments demonstrate that the KCK tag does not affect BsParB’s functions in vivo. Thus, the effects of KCK tags on BsParB(WT) and BsParB(R80A) are specific to in vitro experiments.

Figure 2. KCK tags do not affect in vivo BsParB localization or spreading
(A) Localization of fluorescently tagged ParB(WT) and ParB(R80A) (green). The nucleoid is labeled with HBsu-mCherry (red), and phase-contrast images are shown in gray. Scale bar represents 2 μm. The imaging experiments were performed in two biological replicates, and representative images from one set of experiment are shown.
(B) ChIP-seq of wild-type and mutant ParB association with a region of the B. subtilis chromosome from 354°C14 to 360°C14 (3,960- to 4,033-kb of strain the PY79 genome). Red dotted lines indicate the positions of the four parS sites. The number of reads were normalized by the total number of reads per sample. Whereas wild-type ParB spreads several kilobases from parS sites, the R80A mutant is restricted to the immediate vicinity of each parS site. KCK tags at the N terminus or C terminus of wild-type ParB or R80A mutant do not change the property of the variants. One ChIP-seq replicate was done. See also Figure S4.

Charges on the KCK tag contribute to the in vitro protein property changes
This finding prompted us to understand the mechanism by which the KCK tag boosts the DNA compaction rate of ParB protein in vitro. One possibility for the compaction rate increase is that more BsParB proteins were recruited onto DNA due to interactions between the positively charged KCK tag and the negatively charged DNA backbone. Alternatively, the KCK tag could impact the subsequent action of the BsParB proteins, while the level of the initial protein recruitment is intact. To distinguish these two possibilities, we directly visualized the recruitment of untagged and KCK-tagged BsParB(R80A) proteins onto lambda DNA. Proteins were nonspecifically labeled with the NHS ester version of

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cyanine3 fluorescent dye, and the moment of the very first labeled protein’s arrival into the camera’s field of view was evident by increase in background intensity (Figures 3 A and 3B). In this approach, background-subtracted integrated fluorescence intensity on DNA is directly proportional to the amount of BsParB protein recruited onto the DNA. The microscopy showed that the background-subtracted integrated fluorescence intensities with KCK-BsParB(R80A) and BsParB(R80A)-KCK in the absence of CTP were higher than those with BsParB(R80A) (p < 0.0001) (Figure 3 C, compare it with Figure 1 D). A similar trend was observed using BsParB(WT), KCK-BsParB(WT), and BsParB(WT)-KCK (Figures S5 A and S5B). Thus, our data show that DNA compaction rates by BsParB protein variants are correlated with the degree of protein loading onto DNA, although our experimental approaches do not address if the KCK tags impact subsequent protein action after being recruited onto DNA.

To address whether the charge of KCK tags was the issue, we prepared recombinant wild-type and R80A mutant BsParB proteins where a negatively charged glutamic acid-cysteine-glutamic acid (ECE) tag was added to the N terminus of proteins. If electrostatic interactions between the appended tags and DNA backbone contribute to in vitro artifacts, slower compaction rates are expected with ECE-tagged BsParB proteins (hereafter “ECE-BsParB”) due to repulsive forces between negative charges. As expected, DNA compactions by ECE-BsParB(R80A) were noticeably inefficient. The compaction rates by ECE-BsParB(R80A) are significantly lower (0.001 < p < 0.01 and p < 0.0001) than those by BsParB(R80A) regardless of the presence of the parS DNA sequence and CTP (Figure 4 A). Consistent with this observation, the ECE-BsParB(WT) protein also exhibits inefficient DNA compaction compared with its BsParB(WT) counterpart in the absence of any nucleotides (Figure S6).

Next, we investigated any in vivo property changes caused by the N-terminally appended ECE tag. Fluorescence microscopy experiments show that the ECE tag neither abolishes the in vivo fluorescence foci formation with the wild-type BsParB protein nor leads to the formation of clear foci with the R80A mutant BsParB (Figure 4B). For instance, clear foci formation was observed with BsParB(WT), KCK-tagged BsParB(WT), and ECE-tagged BsParB(WT) in vivo, while the localization of BsParB(R80A), KCK-tagged BsParB(R80A), and ECE-tagged BsParB(R80A) appeared as a haze of green fluorescence in the cytoplasm. Additionally, ChIP-seq assays using anti-ParB antibodies indicate that wild-type BsParB proteins spread to ~20-kb regions around the parS site, and the R80A mutant does not spread regardless of the presence of the ECE tag (Figure 4C). All in vivo results consistently demonstrate that the KCK and ECE tags appended to BsParB proteins do not have

Figure 3. More BsParB(R80A) proteins are loaded onto flow-stretched lambda DNAs when the KCK tag is appended
(A) (Left) A representative kymograph for DNA flow-stretching experiments with fluorescently labeled BsParB protein. 30 nM KCK-BsParB(R80A) without any nucleotides. (Right) The mean background intensity was obtained for the area bound by the red square (0.96 × 0.96 μm), and the background-subtracted integrated fluorescence intensity was obtained for the area bound by the yellow box (2.4 × 14.4 μm).
(B) Time trajectories for mean background and integrated fluorescence intensities on the DNA shown in (A). The time point when the mean background intensity starts to increase is defined as t = 0. DNA flow-stretching experiments were performed with fluorescently labeled proteins.
(C) Integrated fluorescence intensities on lambda DNAs by cyanine3-labeled BsParB(R80A) (n = 51 from two experiments), KCK-BsParB(R80A) (n = 40 from two experiments), and BsParB(R80A)-KCK (n = 26 from three experiments) measured at different time points. Error bars: SEM; ****p < 0.0001. See also Figure S5.

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noticeable impacts. The effects of the tags are only limited to in vitro assays, and electrostatic interactions between charged residues on the tag and the DNA backbone are at least partly responsible for the in vitro effects.

**KCK-tagged BsParB proteins labeled with fluorescent dyes do not behave the same as the untagged protein**

In single-molecule experiments, the KCK tag is frequently included in proteins to facilitate maleimide-based labeling. As discussed above, we observed that appending a KCK tag itself caused unexpected in vitro behavior changes to BsParB proteins. We next set out to test whether a fluorescent labeling to the KCK tag could reverse the changes and make the KCK-tagged protein behave the same as the untagged protein. We chose Alexa Fluor 647 maleimide because its negative charge may neutralize the effects of positively charged KCK tag. The fluorescence signals from the QD labeled at the end of DNA and Alexa 647-labeled KCK-BsParB(WT) were separated from each other by OptoSplit II image splitter (Cairn Research) and imaged onto different fields of view on the detector. The DNA compaction rates were obtained by tracking the QD positions in real time. Figures 1C and S3A indicate that CTP addition leads to a dramatic (39-fold) and a moderate (2.7-fold) DNA compaction rate reduction for unlabelled BsParB(WT) and KCK-BsParB(WT), respectively. We used the DNA compaction rate changes between having and not having CTP as a determinant to assess if Alexa 647 maleimide-labeled KCK-BsParB(WT) can behave the same as untagged BsParB(WT). In the presence of CTP, substantial decreases of DNA compaction rate by Alexa 647-KCK-BsParB(WT) were not observed. Qualitatively, the Alexa 647-labeled KCK-BsParB(WT) protein still did not behave like unlabeled BsParB(WT). One technical challenge with this experiment was that at least 30% of QD-DNA-dye-protein nonspecifically bound to the sample chamber surface during the compaction and prevented us from accurate quantification. To further passivate the surface, we flowed in casein and bovine serum albumin (BSA) after tethering DNAs, which was a common strategy used in single-molecule imaging. Then the protein in the imaging buffer (without casein and BSA) was flowed in for single-molecule DNA flow-stretching experiments. This was done not only for Alexa 647-KCK-BsParB(WT) but also for
However, our thorough assessments of untagged and the KCK-tagged BsParB proteins by the single-molecule DNA flow-stretching assay revealed unexpected alterations in the protein recruitment level and DNA compaction rates.

The increased compaction rates shown with the KCK-tagged BsParB proteins are ascribed, at least partly, to electrostatic interactions between opposite charges on the KCK tag and DNA backbone as evidenced by the enhanced fluorescence intensity on DNA and results of the ECE-tagged BsParB. However, we note that the KCK tag affected not only quantitative compaction rates but also qualitative behaviors of the protein against different nucleotide statuses and the presence of a parS sequence. Furthermore, in the absence of CTP, the lambda DNA compaction stopped before reaching the tether point with BsParB(WT)-KCK protein, while BsParB(WT) and KCK-BsParB(WT) proteins compacted DNA all the way to the tether point (Figure S2). Therefore, it is possible that KCK tags affect BsParB protein actions after its loading onto DNAs.

Previously, the R80A mutant of BsParB protein has been shown to be incapable of compacting DNA.23,43,46 However, slow but robust DNA compaction by BsParB(R80A) protein was observed in this study. Although both studies used the same assay, in our study, we supplemented magnesium ions to our buffer as a cofactor of CTP and used apyrase during our protein purification to remove residual CTPs. Since BsParB(R80A) is deficient in CTP hydrolysis,41 it is possible that CTPs were co-purified with BsParB(R80A) in the previous study.23 Consistent with our speculation, in the absence of Mg2+ and the presence of CTP, BsParB(R80A)’s compaction rate was reduced dramatically (Figure S7), providing an explanation for the undetectable compaction by BsParB(R80A) in the previous study.

Although only the KCK-tagged BsParB proteins were tested with single-molecule DNA flow-stretching assay, our approach could be readily applicable to other DNA-binding proteins. For proteins capable of compacting DNA molecules, the DNA compaction rates of proteins containing desired tags (such as Halo, CLIP, SNAP, KCK, and sortase tags) need to be measured. DNA motion capture assay (a variant of the single-molecule DNA flow-stretching)14,21–23,51 can be also performed, and the comparison between untagged and tagged proteins will help determine the validity of the tagged protein. Once intact or minimally perturbed activity of the tagged proteins is confirmed, those tags can be labeled with a desired fluorescent dye, and the compaction rates can be measured again to detect any changes. In this case, the fluorescent dye on the protein and the QD at the end of the protein must be spectrally distinct to allow the compaction rate measurements as we did in this and other studies.14,22 Our current study with KCK-tagged BsParB proteins shows that fluorescent labeling onto cysteine in the KCK tag with a charged fluorophore does not rescue the reduced protein’s response to CTP. However, we do not rule out possibilities that for other DNA-binding proteins, or using a different fluorescent probe, the situation can be different. Our results urge researchers to thoroughly validate the use of tags and dyes for their single-molecule experiments.

In summary, deep understanding of any biological system requires both in vitro and in vivo approaches. Our study reveals...
that the addition of short peptide tags may produce misleading in vitro results despite normal functionality in vivo. Additionally, our results raise a possibility that fluorescent dyes conjugated to a DNA-binding protein result in altered in vitro protein activities due to electrostatic interactions between charges on the fluorescent probe and those on the DNA backbone. Whenever adding a small amino acid tag is desired for in vitro experiments, careful controls must be performed to ensure that this does not perturb the activity of the protein. Here we show that the highly sensitive single-molecule DNA flow-stretching assay can be used as a powerful and efficient validation tool for modified proteins.

Limitations of the study
Here, using KCK tag on BsParB protein as a model system, we evaluate single-molecule DNA flow-stretching assay as an efficient and sensitive tool to assess the impact of small tags on protein action. While this study focuses on the methodology to validate protein tagging, the mechanism of BsParB action is being investigated in a separate study. Interestingly, although the KCK tags drastically altered ParB’s activity at in vitro single-molecule level, they did not change ParB’s activity in B. subtilis live cells in any detectable way. These results imply that other cellular factors, such as the property of the cytoplasm and/or the biophysical aspects of the chromatin, make BsParB more tolerant to tagging in live cells than in the minimalist in vitro setups.

Here we have discovered and evaluated that small protein tags can lead to the change of protein property in single-molecule experiments. However, the scope of this study is limited to only BsParB protein and the KCK tags. It is desirable that other DNA-binding proteins with different fluorophore labeling platforms be investigated for future studies, such as site-specific labeling methodologies involving unnatural amino acids or aldehyde tags.

Finally, this DNA flow-stretching assay is applicable to proteins that have reasonable affinity to DNA. If the protein’s DNA-binding affinity is too low, the fluorescence background might mask the signal from the DNA-bound proteins.

STAR METHODS
Detailed methods are provided in the online version of this paper and include the following:

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  - Nonspecific fluorescence BsParB protein labeling
  - Fluorescent dye labeling on cysteine residue
  - Single-molecule assays with unlabeled proteins
  - Single-molecule assays with labeled proteins
  - Fluorescence microscopy
  - ChiP-seq
  - Immunoblot analysis
  - Plasmid construction for in vivo experiments
- Quantification and statistical analysis

Supplemental Information
Supplemental information can be found online at https://doi.org/10.1016/j.crmeth.2023.100614.

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We thank the Kim and Wang labs for discussions and support, Xheni Karaboja for assisting with ChIP-seq and microscopy experiments, Patrick Sheets for assisting with strain building, Candice Elston for providing the E. coli strain containing parS-lambda DNA, Thomas Graham for providing plasmids for BsParB wild-type and R80A mutant, Alan Grossman for strains and antibodies, and the Indiana University Center for Genomics and Bioinformatics for high-throughput sequencing. We thank Thomas Graham for reading the manuscript and providing insightful feedback. Support for this work comes from National Institutes of Health R01GM141242, R01GM143182, R01AI172822 (X.W.), and R35GM143093 (H.K.).

Author contributions
M.M. and H.K. purified proteins. M.M., B.G., B.S., and H.K. performed single-molecule experiments and analyzed data. L.E.W. constructed plasmids and strains and performed microscopy and immunoblot analysis. Z.R., Q.L., and X.W. performed ChiP-seq and analysis. X.W. designed, analyzed, and supervised the in vivo experiments. H.K. designed, analyzed data, and supervised the in vitro experiments. M.M. and L.E.W. contributed to writing the method sections of the paper. X.W. and H.K. wrote the paper with input from all authors.

Declaration of interests
The authors declare no competing interests.

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References


# STAR★METHODS

## KEY RESOURCES TABLE

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Further information and requests for resources should be directed to and will be fulfilled by the lead contact, HyeongJun Kim (hyeongjun.kim@utrgv.edu).

Bacterial strains and plasmids generated in this study are available from the corresponding authors upon request.
**Cell Reports Methods**

**Resource**

**Data and code availability**

- ChIP-seq data that support the findings of this study have been deposited in the Gene Expression Omnibus with accession no. GSE212751 (https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE212751). Next-generation sequencing samples used in this study can be found in Tab 9 in Data S1. A list of figures that have associated raw data can be found from Tabs 6 and 9 in Data S1.
- Single-molecule analysis data can be found in Tabs 1–5 in Data S1.
- The MATLAB codes used in single-molecule data are available from our previous publication. Alternatively, the codes will be available from the corresponding author (H.K.) upon request.
- Any additional information required to reanalyze the data reported in this paper is available from the lead contact upon request.

**EXPERIMENTAL MODEL AND STUDY PARTICIPANT DETAILS**

*Burkholderia subtilis* strains were derived from the prototrophic strain PY79.47 *B. subtilis* strains were generated by successive transformations of plasmids or genomic DNA. Cells were grown in defined rich Casein Hydrolysate (CH) medium at 37°C. Strains used in this study can be found in Tab 6 in Data S1 and the Key resources table.

**METHOD DETAILS**

**Plasmid constructions for in vitro assays**

Plasmids harboring coding sequences of His6-SUMO-BsParB(WT) (pTG011),23 His6-SUMO-KCK-BsParB(WT) (pTG042),23 His6-SUMO-R80A (pTG037),23 and His6-SUMO-KCK-BsParB(R80A) (pTG044)23 were generous gifts from Thomas Graham. Site-directed mutagenesis were performed to generate plasmids harboring coding sequences of His6-SUMO-BsParB(WT)-KCK (m0067) and His6-SUMO-BsParB(R80A)-KCK (m0069) using oHK050F and oHK050R as primers. The plasmid harboring coding sequences of His6-SUMO-ECE-BsParB(WT) (m0064) were generated using oHK048F and oHK048R as primers and m0043 as a substrate. Contrary to other plasmids, the plasmid harboring coding sequences of His6-SUMO-ECE-BsParB(R80A) (m0070) was generated by following the vendor-supplied NEBuilder HiFi DNA Assembly Master Mix (NEB E2621S, Ipswich, MA) protocol. First, the His6-SUMO-BsParB(WT) plasmid (pTG011 = m0041) was linearized and the majority of SUMO-BsParB(WT) coding sequences were removed by PCR using oHK038F and oHK038R as primers. Then, gfhK009 and gfhK010 were used as gene fragments with both containing 23 bp overlaps. After NEBuilder HiFi DNA assembly, NEB 5-alpha competent *E. coli* cells (NEB C2987H, Ipswich, MA) were transformed with the reaction mixture. The sequences were confirmed using T7, oHK023, oHK024, oHK025, and oHK026 oligos. See Tabs 7 and 8 in Data S1 for the list of plasmids used in in vitro assays and the oligonucleotide sequences, respectively.

**Protein expression and purification**

Rosetta2(DE3)pLysS competent cells (EMD Millipore, Burlington, MA) transformed with a plasmid were cultured overnight at 37°C in the presence of 100 μg/mL ampicillin and 20 μg/mL chloramphenicol. 1 L of LB medium with 80 μg/mL ampicillin was inoculated with the overnight culture and grown at 37°C until the OD 600 reached 0.4–0.6. Protein expression was induced with 500 μM isopropyl-β-D-thiogalactoside (IPTG), and the culture was shaken at 30°C for an additional 4 h. The cells were harvested by centrifugation at 4°C. The cell pellets were resuspended in PBS buffer and spun at 5,000 g. They were resuspended in ParB lysis buffer (20 mM Tris, pH 8.0, 1 M NaCl, 50 mM imidazole, 5 mM 2-mercaptoethanol), supplemented with 0.1 mM phenylmethylsulfonyl fluoride (PMSF) and a protease inhibitor cocktail (Roche, Basel, Switzerland) (Total volume: 45 mL), and flash-frozen. BsParB proteins were purified based on a two-step tandem purification method as previously described23 but with some modifications. Briefly, after thawing the harvested cells, additional 0.9 mM PMSF (total 1.0 mM PMSF), 50 mg/mL lysozyme, 3 μL of universal nuclease (Thermo Fisher Scientific 88701, Waltham, MA), and 5 mM 2-mercaptoethanol were added, and it was left in ice for 30 min. Cells were lysed by sonication and centrifuged twice in an FA-6x50 rotor: first at 11,000 g for 30 min, then at 20,133 g for 30 min. The clarified supernatant was centrifuged at 4°C. The supernatant was dialyzed together overnight at 4°C against ParB dialysis/storage 1 buffer (20 mM Tris, pH 8.0, 350 mM NaCl, 10 mM imidazole, 5 mM 2-mercaptoethanol, 1 mM MgCl₂, 10% glycerol). After centrifuging the dialyzed proteins at maximum speed for 10 min, the supernatant was allowed to interact with the Ni-NTA resin for at least 1 h at 4°C. Then, the flowthrough was collected. 0.5 mL of the ParB dialysis/storage 1 buffer to the Ni-NTA resin column was added multiple times, and the eluents were collected. Running an SDS-polyacrylamide (SDS-PAGE) gel indicated that the flowthrough and the eluent fractions...
contained ParB protein, while the cleaved His6-SUMO and His6-Ulp1 remained in the resin. The flowthrough and the peak fractions were pooled and dialyzed against ParB dialysis/storage 2 buffer (20 mM Tris, pH 8.0, 350 mM NaCl, 10% glycerol), where 5 mM 2-mercaptoethanol was included in case of KCK-tagged protein purifications. The protein concentration was measured by a NanoDrop One spectrophotometer (Thermo Scientific, Waltham, MA) using 32.58 (kDa) and 7,450 (M⁻¹ cm⁻¹) as its molecular weight and extinction coefficient, respectively. The purified proteins (Figure S1A) were run on a 4–15% precast polyacrylamide gel (Bio-Rad, Hercules, CA) with Tris/Glycine/SDS running buffer (Bio-Rad, Hercules, CA). InstantBlue Coomassie protein stain (Abcam, Cambridge, United Kingdom) was used to stain for the polyacrylamide gel. The gel image was obtained using UVP Uv-solo touch gel documentation system (Analytik Jena, Jena, Germany) and provided in the Figure S1A without any image processing.

**DNA and quantum-dot preparations**

One end of bacteriophage lambda DNA (or parS DNA) was labeled with a biotin to tether the DNA onto the single-molecule microfluidic flow cell, and the other end was labeled with a digoxigenin to attach a quantum dot (Figure 1A) as previously described. Briefly, Lambda-BL1Biotin and Lambda-Dig2 oligos (Tab 8 in Data S1) were treated with T4 polynucleotide kinase (PNK) (NEB, Ipswich, MA) for phosphorylation at 37°C for 1 h. A 15-fold molar excess of the phosphorylated Lambda-BL1Biotin oligo was introduced for annealing to a 12-base 5'-single-stranded overhang on one end of lambda DNA (or parS DNA). The mixture of DNA and oligo was incubated at 65°C for 10 min and slowly cooled down, and then ligated by T4 ligase for 2 h at room temperature. The other end of the lambda DNA (or parS DNA) was tagged with a digoxigenin by supplementing a 60-fold molar excess of the phosphorylated Lambda-Dig2 oligo at 45°C. After 30-min incubation, the mixture was slowly back to room temperature followed by a 2-h ligation step at room temperature. Since the sequences of Lambda-BL1Biotin and Lambda-Dig2 oligos are complementary to each other, it is important to remove unreacted excess oligos. After running a 0.4% agarose gel overnight at 4°C, the desired DNA band was excised and put into a dialysis tube. Applying an electric field allowed DNAs to leave the excised agarose gel, but DNAs were confined to the dialysis tube volume. DNAs were collected, and ethanol precipitation was performed to recover doubly-tagged lambda DNAs (or parS DNAs) in EB buffer (10 mM Tris-Cl, pH 8.5).

As we previously did, anti-digoxigenin antibody-conjugated quantum dot 605 (Invitrogen, Waltham, MA) was prepared following Invitrogen’s Qdot 605 antibody conjugation kit (Q22001MP) manual. However, since this kit was discontinued, all the kit components were separately purchased including Qdot 605 ITK amino (PEG) quantum dots (Invitrogen Q21501MP) and superdex 200 (prep grade) (Cytiva 17104301). For the antibody, anti-digoxigenin fab fragments (Roche 1214667001, Basel, Switzerland) were used.

**Nonspecific fluorescence BsParB protein labeling**

BsParB(WT) and BsParB(R80A) proteins were incubated with sulfo-Cyanine3 NHS ester dye (Lumiprobe 11320, Hunt Valley, CA). Each labeled protein and Cyanine3 dye concentrations were measured three times using Nanodrop, and the averaged values were used as final concentrations. The protein labeling efficiencies were 21.8%, 23.4%, 19.7%, 30.1%, 32.0%, and 30.0% for BsParB(WT), KCK-BsParB(WT), BsParB(WT)-KCK, BsParB(R80A), KCK-BsParB(R80A), and BsParB(R80A)-KCK, respectively. These numbers correspond to about 0.4 and 0.6 Cyanine3 dyes per each BsParB wild-type and R80A mutant protein dimers, respectively.

**Fluorescent dye labeling on cysteine residue**

The KCK-BsParB(WT) protein had been stored in a buffer containing 5 mM 2-mercaptoethanol, which can interfere maleimide dye labeling. First, using Micro Bio-Spin P-30 gel columns (Bio-Rad 7326223, Hercules, CA), the buffer was exchanged into a new buffer containing 30 μM tris(2-carboxyethyl)phosphine (TCEP) (Thermo Fisher Scientific 77720, Waltham, MA) devoid of 2-mercaptoethanol (20 mM Tris-base, pH 8.0; 10% glycerol; 350 mM NaCl; 30 μM TCEP). After determining the protein concentration, we added 5-fold molar excess of Alexa Fluor C2 maleimide dye (Thermo Fisher Scientific A20347, Waltham, MA) and incubated it at 4°C overnight. The labeled protein was separated from unreacted dye via Micro Bio-Spin P-30 gel columns (Bio-Rad 7326223, Hercules, CA) using a buffer that contains 20 mM Tris-base, pH 8.0, 10% glycerol, 350 mM NaCl, and 5 mM 2-mercaptoethanol. The protein and the labeled dye concentrations were measured using 283,000 (cm⁻¹ M⁻¹), 651 nm, 0.00, and 0.03 for the Alexa 647 extinction coefficient (vendor supplied value for the Lot number 2633288), corresponding wavelength, the correction factor at 260 nm, and the correction factor at 280 nm, respectively. The Alexa 647 maleimide labeling efficiency was 74.7% implying that each dimer has about 1.5 labeled Alexa 647 dyes.

**Single-molecule assays with unlabeled proteins**

Surface-passivated coverglasses were prepared by aminopropyl silanization (Millipore Sigma A3648, St. Louis, MO) and PEGylation (PEG: polyethylene glycol) (Laysan Bio, Arab, AL) as previously described. A microfluidic flow cell was constructed from a quartz plate (Technical Glass Product, Painesville, OH) adhered to the PEGylated coverglass via double-sided tape (Grace Bio-Labs, Bend, OR) with rectangular cuts that make up the flow cell channels. Inlet and outlet tubing were inserted through holes on the quartz plate and made air-tight with epoxy. In-depth description of single-molecule flow-stretching assays was already provided in previous
Single-molecule assays with labeled proteins

After quantum dot (QD)-labeled DNAs are tethered, unbound QD-DNAs were washed away by flowing imaging buffer supplemented with 0.05x casein (Vector Laboratories, Newark, CA; stock concentration: 10x) and 0.2 mg/mL bovine serum albumin (BSA) (New England Biolabs, Ipswich, MA). For the experiments with Alexa Fluor 647 maleimide-labeled protein, after 2-min incubation, imaging buffer supplemented with 0.05x casein and BSA (Vector Laboratories, Newark, CA) were used. The QD was diluted to 50 nM in the imaging buffer (without casein and BSA) and applied to the flow cell at 50 g/min. To separately observe quantum dot 605 on DNA and Alexa 647-labeled proteins, OptoSplit II image splitter (Cairn Research, Faversham, United Kingdom) was placed between the microscope and the EMCCD. The images were recorded every 200 ms with 100-millisecond exposure time using the Micro-Manager software. Regions-of-interest (ROIs) of quantum dots as a function of time were determined by Gaussian-fitting-based custom-written MATLAB software codes.

Fluorescence microscopy

Fluorescence microscopy was performed using a Nikon Ti2 microscope (Nikon Instruments, Melville, NY) equipped with Plan Apo 100x/1.45NA phase contrast oil objective and an sCMOS camera. Images were cropped and adjusted using MetaMorph software. Final figure preparation was performed in Adobe Illustrator.

ChIP-seq

Chromatin immunoprecipitation (ChIP) was performed as described previously. Briefly, cells were crosslinked using 3% formaldehyde for 30 min at room temperature and then quenched using 125 mM glycine, washed using PBS, and lysed using lysozyme. Crosslinked chromatin was sheared to an average size of 250 bp by sonication using Qsonica Q800R2 water bath sonicator. The lysate was precleared using Protein A magnetic beads (GE Healthcare/Cytiva 28951378, Marlborough, MA) and then incubated with anti-ParB antibodies overnight to reverse the crosslinks. The DNA was further treated with RNaseA, Proteinase K, extracted with PCI, resuspended in 100 μL EB and used for library preparation with the NEBNext Ultra II kit (E7645S). The library was sequenced using Illumina Illuoseq500 (Illumina, San Diego, CA) at IU Center for Genomics and Bioinformatics. The sequencing reads were mapped to B. subtilis PY79 genome (NCBI Reference Sequence NC_022898.1) using CLC Genomics Workbench (Qiagen, Hilden, Germany). We note that the genome coordinate of this genome is shifted 168 genome (NC000964) used in our previous study. Sequencing reads were normalized by the total number of reads, plotted and analyzed using R. Next-generation sequencing samples used in this study can be found in Data S1.

Immunoblot analysis

Exponentially growing cells were collected and resuspended in lysis buffer (20 mM Tris pH 7.0, 1 mM EDTA, 10 mM MgCl₂, 1 mg/mL lysozyme, 10 μg/mL DNase I, 100 μg/mL RNase A, 1 mM PMSF and 1% protease inhibitor cocktail (Millipore Sigma, P8340, St. Louis, MO) to a final OD₆₀₀ of 10 for equivalent loading. The cell resuspensions were incubated at 37 °C for 10 min for lysozyme treatment, followed by the addition of an equal volume of 2x Laemmli Sample Buffer (Bio-Rad 1610737, Hercules, CA) containing 10% β-Mercaptoethanol. Samples were heated for 15 min at 65 °C prior to loading. Proteins were separated by precast 4–20% polyacrylamide gradient gels (Bio-Rad 4561096, Hercules, CA) and electroblotted onto mini PVDF membranes using Bio-Rad Transblot Turbo system and reagents (Bio-Rad 1704156, Hercules, CA). The membranes were blocked in 5% nonfat milk in phosphate-buffered saline (PBS) with 0.5% Tween 20, then probed with anti-ParB (1:5000) or anti-SigA (1:10,000) diluted into 3% BSA in 1x PBS-0.05% Tween 20. Primary antibodies were detected using Immun-Star horseradish peroxidase-conjugated goat anti-rabbit antibodies (Bio-Rad 1705046, Hercules, CA) and Western Lightning Plus ECL chemiluminescence reagents as described by the manufacturer (PerkinElmer NEL1034001, Waltham, MA). The signal was captured using ProteinSimple Fluorchem R system (Bio-Technne, Minneapolis, MN). The intensity of the bands was quantified using ProteinSimple AlphaView software.
Plasmid construction for in vivo experiments

The list of plasmids can be found in Tab 7 in Data S1.

pWX1092 [pelB::Psoj-spo0J(\parS)-mgfpmut3 tet] was constructed by an isothermal assembly reaction containing three fragments: 1) pWX516 digested with HindIII and BamHI, and gel purified; 2) spo0J (\parS) amplified from pWX563 using oWX2974 and oWX2975; 3) mgfpmut3 amplified from pWX563 using oWX2976 and oWX2977. The construct was sequenced using oWX507, oWX669, and oWX670.

pWX1093 [pelB::Psoj-KCK-spo0J(\parS)-mgfpmut3 tet] was constructed by an isothermal assembly reaction containing three fragments: 1) pWX516 digested with HindIII and BamHI, and gel purified; 2) KCK-spo0J (\parS) amplified from pWX563 using oWX2978 and oWX2975; 3) mgfpmut3 amplified from pWX563 using oWX2976 and oWX2977. The construct was sequenced using oWX507, oWX669, and oWX670.

pWX1103 [pelB::Psoj-mgfpmt3-spo0J-R80A(\parS)-KCK cat] was constructed by an isothermal assembly reaction containing two PCR products: 1) pWX611 amplified using oWX3001 and oWX418; 2) pWX611 amplified using oWX3002 and oWX2071. This procedure introduced the R80A mutation to pWX611, which is pelB::Psoj-mgfpmt3-spo0J(\parS)-KCK cat. The construct was sequenced using oWX507, oWX669, and oWX670.

pWX1104 [pelB::Psoj-spo0J-R80A(\parS)-mgfpmut3 tet] was constructed by an isothermal assembly reaction containing two PCR products: 1) pWX1092 amplified using oWX3001 and oWX418; 2) pWX1092 amplified using oWX3002 and oWX2071. This procedure introduced the R80A mutation to pWX1092. The construct was sequenced using oWX507, oWX669, and oWX670.

pWX1105 [pelB::Psoj-KCK-spo0J-R80A(\parS)-mgfpmut3 tet] was constructed by an isothermal assembly reaction containing two PCR products: 1) pWX1093 amplified using oWX3001 and oWX418; 2) pWX1093 amplified using oWX3002 and oWX2071. This procedure introduced the R80A mutation to pWX1093. The construct was sequenced using oWX507, oWX669, and oWX670.

pWX1106 [pelB::Psoj-soj-spo0J-R80A(\parS)-KCK cat] was constructed by an isothermal assembly reaction containing two PCR products: 1) pWX612 amplified using oWX3001 and oWX418; 2) pWX612 amplified using oWX3002 and oWX2071. This procedure introduced the R80A mutation to pWX612, which is pelB::Psoj-soj-spo0J(\parS)-KCK cat. The construct was sequenced using oWX507, oWX1086, and oML77.

pWX1107 [pelB::Psoj-KCK-spo0J(\parS) tet] was constructed by an isothermal assembly reaction containing two PCR products: 1) pWX1093 amplified using oWX3004 and oWX418; 2) pWX1093 amplified using oWX3003 and oWX2071. This procedure introduced a stop codon and removed mgfpmut3 from pWX1093. The construct was sequenced using oWX507 and oML85.

pWX1108 [pelB::Psoj-KCK-spo0J-R80A(\parS) tet] was constructed by an isothermal assembly reaction containing two PCR products: 1) pWX1107 amplified using oWX3001 and oWX418; 2) pWX1107 amplified using oWX3002 and oWX2071. This procedure introduced the R80A mutation to pWX1107. The construct was sequenced using oWX507 and oML85.

pWX1167 [pelB::Psoj-ECCE-spo0J(\parS) tet] was constructed by an isothermal assembly reaction containing two PCR products: 1) pWX1107 amplified using oWX3197 and oWX418; 2) pWX1107 amplified using oWX3198 and oWX2071. This procedure introduced the ECE tag and removed the KCK tag from pWX1107. The construct was sequenced using oWX507 and oML85.

pWX1168 [pelB::Psoj-ECCE-spo0J-R80A(\parS) tet] was constructed by an isothermal assembly reaction containing two PCR products: 1) pWX1108 amplified using oWX3197 and oWX418; 2) pWX1108 amplified using oWX3198 and oWX2071. This procedure introduced the ECE tag and removed the KCK tag from pWX1108. The construct was sequenced using oWX507 and oML85.

pWX1169 [pelB::Psoj-ECCE-spo0J(\parS)-mgfpmut3 tet] was constructed by an isothermal assembly reaction containing two PCR products: 1) pWX1103 amplified using oWX3197 and oWX418; 2) pWX1103 amplified using oWX3198 and oWX2071. This procedure introduced the ECE tag and removed the KCK tag from pWX1103. The construct was sequenced using oWX507, oWX669, and oWX670.

pWX1170 [pelB::Psoj-ECCE-spo0J-R80A(\parS)-mgfpmut3 tet] was constructed by an isothermal assembly reaction containing two PCR products: 1) pWX1105 amplified using oWX3197 and oWX418; 2) pWX1105 amplified using oWX3198 and oWX2071. This procedure introduced the ECE tag and removed the KCK tag from pWX1105. The construct was sequenced using oWX507, oWX669, and oWX670.

QUANTIFICATION AND STATISTICAL ANALYSIS

Not all measurement groups passed the normality test (See Tab 3 in Data S1). Therefore, in this study, we report the results of nonparametric Mann-Whitney test in Figures 1E and 1F. However, we obtained similar results from two-sided Welch’s t-test (Figures S5A and S5B) since the t-test results are still valid when the sample sizes are large (>25) and there are not extreme outliers. All the statistical analyses (Shapiro-Wilk normality test, Mann-Whitney test, and two-sided Welch’s t-test due to different variances and sample sizes) for DNA compaction rates were performed using Prism software (GraphPad, San Diego, CA). The exact sample sizes (n), mean, and standard error of the mean are provided in Tabs 1 and 2 in Data S1. The normality test results are available in Tab 3 in Data S1. Tabs 4 and 5 in Data S1 show the exact p values for comparing wild-type (and its KCK-tagged versions) and R80A mutant (and its KCK-tagged versions) compaction rates, respectively. The reproducibility of single-molecule experiments for each experimental condition was checked by performing the same experiments at least three times.
Supplemental information

A framework to validate fluorescently labeled DNA-binding proteins for single-molecule experiments

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Figure S1. KCK-tags lead to quantitative and qualitative compaction rate changes, Related to Figures 1, S2, S3, S5, and S7.

(A) InstantBlue Coomassie-stained SDS-PAGE gel of recombinant *B. subtilis* ParB proteins used in this study. The protein ladder (Gold Biotechnology, #P007-500) is on the left. The unnecessary superfluous gel lanes on both sides of this image were removed for clarity.

(B) *parS* DNA compaction rates by BsParB(WT), KCK-BsParB(WT), and BsParB(WT)-KCK proteins in the absence and presence of 1 mM CTP or 1 mM CTPγS. (n = 29–64 from 3–5 experiments). Error bars: SEM. The numbers indicate compaction rate fold changes. (C) *parS* DNA compaction rates by BsParB(R80A), KCK-BsParB(R80A), and BsParB(R80A)-KCK proteins in the absence and presence of 1 mM CTP or 1 mM CTPγS. (n = 35–47 from 3–4 experiments). Error bars: SEM. The numbers indicate compaction rate fold changes. (D) For direct comparisons, the compaction rates shown in (B), (C) and Figures 1C and 1D are consolidated. (n = 29–74 from 3–8 experiments). Error bars: SEM. (B-D) See Tab 1 in the Supplemental File S1 for detailed sample number (n) information.

(E-F) Since not all results pass the Shapiro-Wilk normality test, we employed the Mann-Whitney tests to compare DNA compaction rates in Figures 1E and 1F. However, Welch’s t-test results are still informative as long as there are not extreme outliers and there are enough (>25) data points [S1]. Indeed, the Welch’s t-test results provided here are very similar to the ones from the Mann-Whitney tests. (E) Top: The Welch’s t-test p value color scheme. Bottom: The Welch’s t-test comparisons for compaction rates by wild-type BsParB and its KCK-versions. (F) The Welch’s t-test comparisons for BsParB(R80A) and its KCK-versions. (E-F) Cyan, green and yellow boxes highlight qualitative protein property changes due to the KCK-tags for visual aids. See Tab 1 in the Supplemental File S1 for detailed sample number (n) information.

Figure S2. Wild-type BsParB proteins compact DNA towards the tether point, Related to Figures 1 and S1. Representative kymographs for (untagged) wild-type BsParB, KCK-BsParB, and BsParB-KCK proteins. One end of DNA is tethered to the microfluidic sample chamber surface, and the other is labeled with a quantum dot 605. In the beginning, the average quantum dot position is approximately the same as the DNA tether point due to the lack of flow. Turning on the flow stretches DNA. Accompanying proteins lead to the DNA compaction towards the tether point. [Protein] = 50 nM, [CTP] = 0, lambda DNA without any *parS* sites.
Figure S3. DNA compaction by KCK-BsParB(WT) in the presence of reducing agents, Related to Figures 1 and S1. (A) Lambda DNA compaction rates taken and adapted from Figure 1C for convenient comparison with (D). -39x and -2.7x denote 39-fold and 2.7-fold compaction rate decreases, respectively. (B) A representative kymograph that shows that inclusion of 1 mM β-mercaptoethanol leads to the fluorescence intensity decrease and nonspecific binding of quantum dot-DNA-protein to the flow cell surface. (C) A representative kymograph that exhibits similar technical challenges as (B) in the presence of 1 mM dithiothreitol (DTT). (D) Lambda DNA compaction rates by KCK-BsParB(WT) in the presence of 1 mM DTT both with and without CTP (n = 39 from 6 experiments for no CTP and n = 30 from 4 experiments for 1 mM CTP). Error bars: SEM; ****p < 0.0001. -2.8x denotes 2.8-fold compaction rate decrease.
Figure S4. KCK tags do not significantly alter the level of wild-type or R80A ParB, Related to Figure 2. (A) Western blot of GFP-tagged ParB variants. Although GFP-ParB levels are higher than ParB-GFP levels, the R80A mutation or KCK tag does not change the protein levels. SigA levels are shown to control for loading. (B) Western blot of ParB variants. The R80A mutation or KCK tag does not dramatically change the protein levels. Asterisk indicates the ParB band. SigA levels are shown to control for loading. These experiments were performed in two biological replicates and the result from one set of experiment was shown.

Figure S5. Integrated fluorescence intensities of BsParB(WT), KCK-BsParB(WT), and BsParB(WT)-KCK on lambda DNA, Related to Figures 1, 3, and S1. (A) Integrated fluorescence intensities of BsParB(WT), KCK-BsParB(WT), and BsParB(WT)-KCK on lambda DNA in the absence of CTP (n = 31~47 from 2~4 experiments). Error bars: SEM; *0.01 < p < 0.05, **0.001 < p < 0.01, and ****p < 0.0001. (B) DNA compaction rates taken and adapted from Figure 1C for easy comparison with (A).
**Figure S6.** The ECE-tag slows down DNA compaction by the wild-type BsParB protein, Related to Figure 4. Lambda and parS DNA compaction rates by BsParB(WT) (n = 43–74 from 3–5 experiments), and ECE-BsParB(WT) (n = 30–48 from 3 experiments) both in the presence and absence of CTP. Error bars: SEM; ****p < 0.0001. See Tab 1 in the Supplemental File S1 for detailed sample number (n) information.

**Figure S7.** BsParB(R80A) DNA compaction rates in different conditions, Related to Figures 1 and S1. DNA compaction rates by 50 nM BsParB(R80A) on lambda DNA and parS DNA in the presence and absence of magnesium ions ([MgCl₂] = 2.5 mM), CTP (1 mM), and CTPγS (1 mM) (n = 34–58 from 3–4 experiments). DNA Compaction rates in the presence of CTP and in the absence of magnesium ions are highlighted in red. The absence of magnesium and presence of CTP could explain why the previous study [S2] did not detect DNA compaction by BsParB(R80A). Error bars: SEM; ****p < 0.0001. See Tabs 1 and 2 in the Supplemental File S1 for detailed sample number (n) information.
Supplemental references
