Binding Properties of Various Cationic Porphyrins to DNA in the Molecular Crowding Condition Induced by Poly(ethylene glycol)

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ABSTRACT: The binding modes of various cationic porphyrins to DNA in an aqueous solution and under the molecular crowding condition induced by poly(ethylene glycol) (PEG) were compared by normal absorption, circular dichroism (CD), and linear dichroism (LD) spectroscopy techniques. Large negative CD and LD signals in the Soret absorption regions of the meta- and para-TMPyP [meso-tetakis (n-N-methylpyridiniumyl) porphyrin (meta, n = 3) and (para, n = 4)] were apparent in the aqueous solution, indicating an intercalative-binding mode, while a positive CD spectrum and a less intense negative LD spectrum for the ortho-TMPyP (n = 2)-complexed DNA suggested a major-groove-binding mode. These binding modes are retained under a molecular crowding condition, suggesting that the PEG cluster cannot access the TMPyPs that are intercalated between the DNA base pairs or that bind at the major groove. The spectral properties of the ortho-, meta-, and para-trans-BMPyP [trans-bis(N-methylpyridinium-yl)diphenyl porphyrin, n = 2,3,4]-bound DNA in an aqueous solution correspond to neither the intercalative-binding nor the groove-binding mode, which is in contrast with the TMPyP cases. The spectral properties under the molecular crowding condition are altered considerably for all of the three trans-BMPyPs compared to those in an aqueous solution, suggesting that the matted PEG cluster is in contact with the cationic trans-BMPyPs, causing a change in the polarity of the porphyrin environment. Consequently, trans-BMPyPs bind to the external side of the DNA.

INTRODUCTION

The interaction between native DNA and cationic porphyrins has been a fascinating research area due to its applications in photodynamic therapy and cancer detection. Various binding modes of cationic porphyrins to native and synthetic DNAs in aqueous solutions including intercalation, groove binding, and external binding have been reported. The number and positions of the charges of cationic porphyrins are important factors that affect the binding mode of porphyrins to synthetic and native DNAs due to the electrostatic interaction between the negatively charged phosphodiester backbone and the positively charged pyridinium moieties. Four positive charges are required for porphyrin intercalation between the GC base pairs of native DNA and synthetic poly[d(G-C)]

poly[d(A-T)] as the [porphyrin]/[DNA base] ratio increased. The rotational ability of the periphery pyridinium ring of porphyrin and, hence, its capacity to form a planar structure with the porphine ring in the intercalation pocket, which is specific for n = 3 and 4, are believed to be the origin of the comparable binding modes for these cationic porphyrins. In contrast, trans-bis(N-methylpyridinium-yl)diphenyl porphyrin (n = 2, 3, 4, referred to as o-, m-, and p-trans-BMPyPs, respectively, Scheme 1b) are extensively stacked along the DNA stem even at a very low [porphyrin]/[DNA base] ratio, suggesting that four positive charges are essential for the porphyrin intercalative-binding mode.

Poly(ethylene glycol) (PEG, depicted in Scheme 1a) is one of the most commonly used macromolecules for simulating cell-like environments. The impact of molecular crowding on...
specific biological processes, including DNA condensation and the formation of the DNA duplex and triplex, has been studied. The influence of the molecular weight of PEG on the thermal stability of a double-stranded DNA was also investigated. The thermal stability of a duplex DNA depended on the length of the nucleotide and the cosolute structure, as well as the size of the molecular crowding reagent, PEG.

Recently, the effect of the molecular crowding condition induced by PEG on the binding modes of small molecules, including \( p \)-TMPyP, 9-aminoacridine, ethidium, and 4',6-diamidino-2-phenylindole (DAPI), to DNA was reported. In the presence of PEG molecules, the intercalative-binding mode of \( p \)-TMPyP to a native DNA resembled that observed in an aqueous solution.

As mentioned above, the importance of the location and the number of charges of the periphery cationic ions of porphyrin to the binding mode of a cationic porphyrin with DNA has been reported. In this study, the effect of the molecular crowding condition induced by PEG on the binding modes of various cationic porphyrins (Scheme 1), which exhibited a variety of binding modes to native DNA, was investigated.

## RESULTS AND DISCUSSION

### Absorption Spectra

The effect of the molecular crowding condition on the binding mode of \( p \)-TMPyP to DNA has been investigated based on the optical spectroscopic properties in aqueous and 30% PEG solutions. The intercalative-binding mode of \( p \)-TMPyP to DNA is retained in the PEG solution, suggesting that the molecular crowding condition did not alter the binding property of \( p \)-TMPyP. Figure 1 depicts the absorption spectra of \( o \)-, \( m \)-, and \( p \)-TMPyP in aqueous and PEG solutions in the presence and absence of DNA. In the absence of DNA, the molecular crowding condition induced a slight change in the absorption spectrum in the Soret absorption region. The maximum absorbances at 415, 419, and 424 nm for \( o \)-, \( m \)-, and \( p \)-TMPyPs, respectively, in PEG solutions, as those in aqueous buffer solutions. The absorbance was retained for \( o \)- and \( p \)-TMPyPs, while it slightly increased for \( m \)-TMPyP.
These changes in the absorption spectra may be the result of the change in the polarity of the solution induced by PEG. Upon binding to DNA, large alterations were observed for all three porphyrins (Table 1). In the \textit{m-} and \textit{p-}TMPyP cases, significant hypochromism and a large red shift at the absorption maximum occurred, while these changes were comparably smaller in the \textit{o-}TMPyP case (Figure 1, insets). By combining these results and other optical spectroscopic studies, both \textit{m-} and \textit{p-}TMPyPs were suggested to intercalate between the DNA base pairs, while \textit{o-}TMPyP binds at the major groove of the DNA. The reason for the different binding modes for these porphyrins is that the rotation of the periphery pyridinium ring is forbidden in the \textit{o-}TMPyP case, which prevents \textit{o-}TMPyP from adopting a planar structure. The patterns of the change in the absorption spectra upon binding to DNA were similar for all of the three porphyrins under the molecular crowding condition (Figure 1). An investigation of the absorption spectrum (Table 1, 7.5 nm red shift and 41.3% hypochromism) and other optical properties showed that the intercalative-binding mode of \textit{p-}TMPyP was retained in the presence of PEG. A similar change in the absorption spectrum for \textit{m-}TMPyP upon binding to the DNA in the PEG solution (Table 1, 40.5% hypochromism and 11.8 nm red shift) and the circular dichroism (CD) and linear dichroism (LD) results (see below) indicated that \textit{m-}TMPyP also exhibited an intercalative-binding mode, which is the same in the aqueous solution and under the molecular crowding condition. The extent of the change in the absorption of \textit{o-}TMPyP upon complexation with DNA is similar in the aqueous solution and under the molecular crowding condition, which also suggests a retained binding mode.

The absorption spectra of \textit{o-}, \textit{m-}, and \textit{p-}trans-BMPyP complexed with the native DNA in the aqueous buffer solution and under the PEG condition are shown in Figure 2. The absorption maxima for \textit{o-}, \textit{m-}, and \textit{p-}trans-BMPyPs in the absence of DNA and in the aqueous solution appeared at 414, 416, and 418 nm, respectively. These maxima shifted toward longer wavelengths by 3–4 nm under the molecular crowding condition. The absorbance was retained for \textit{p-}trans-BMPyP, while it increased by 12 and 25% for \textit{m-} and \textit{o-}trans-BMPyP, respectively. These changes in the absorption spectra reflect the changes in the polarity of these solutions under PEG and aqueous conditions. Upon \textit{o-}trans-BMPyP interaction with

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**Table 1. Percentage Hypochromicity and Red Shift of the Soret Bands of \textit{o-}, \textit{m-}, and \textit{p-}trans-BMPyPs and \textit{o-}, \textit{m-}, and \textit{p-}TMPyPs in an Aqueous Buffer Solution and under PEG Conditions upon Binding to DNA**

| compounds | \( R \) | \begin{tabular}{c|c|c} \text{aqueous} & \text{PEG} \\ \text{hypochromism} & \text{red shift} & \text{hypochromism} & \text{red shift} \\ (%) & (nm) & (%) & (nm) \end{tabular} |
|-----------|---------|---------------------------------|---------------------------------|
| BMPyP     | \textit{ortho}- | 26.30 & 4.2 & 6.05 & 0.8 |
|           | \textit{meta}-  | 58.20 & 8.8 & 27.00 & 0.3 |
|           | \textit{para}-  | 54.64 & 3.6 & 28.74 & 1.1 |
| TMPyP     | \textit{ortho}- | 10.36 & 3.3 & 21.59 & 1.8 |
|           | \textit{meta}-  | 54.17 & 15.6 & 40.53 & 11.8 |
|           | \textit{para}-  | 48.38 & 13.0 & 41.33 & 7.5 |

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**Figure 2.** Absorption spectra of (A) \textit{o-}, (B) \textit{m-}, and (C) \textit{p-}trans-BMPyP complexed with DNA (red curves) in a PEG solution. The black curves denote DNA-free BMPyPs. Insets: Absorption spectra in the aqueous buffer solution of BMPyPs bound to DNA (blue curves) and those in the absence of DNA (black curves). [DNA] = 100 \( \mu \)M, [BMPyP] = 10 \( \mu \)M.
DNA (at a mixing ratio of 0.1), a 26% hypochromism and ∼4 nm red shift were observed in the aqueous solution. When m- and p-trans-BMPyP were bound to the DNA, the changes in the absorption spectra were a 58% hypochromism and a 9 nm red shift and a 54% hypochromism and a 4 nm red shift, respectively. Under the molecular crowding conditions, the absorbance decreased by 6, 27, and 29% for o-, m-, and p-trans-BMPyPs, respectively, while the maximum wavelengths were maintained. The alterations in the absorption spectra upon binding to the DNA in an aqueous solution and under the molecular crowding condition are summarized in Table 1. Summarily, m- and p-TMPyPs produced a large hypochromism and red shift in the absorption spectrum upon binding to the DNA both in the aqueous solution and under the molecular crowding condition, which can be attributed to the intercalative-binding mode (supported by polarized spectrosopies, see below). In the case of o-TMPyP, less hypochromism and red shift were shown than those for m- and p-TMPyPs, which means that o-TMPyP binds to the external side of the DNA, maybe at the major groove, in both environments. The molecular crowding condition did not alter the binding mode of any TMPyP. In contrast, the alteration of the absorption spectrum owing to the binding of trans-BMPyP to DNA in the aqueous solution and under the molecular crowding condition produced a slightly different pattern.

**CD Spectra.** A strong negative CD signal in the Soret absorption region has been assigned to the cationic porphyrin species intercalated between the DNA base pairs. Both m- and p-TMPyPs produced such negative CD signals at ∼436 and 446 nm in an aqueous solution (Figure 3), reflecting their intercalative-binding modes. The shapes and intensities of the CD spectra of m- and p-TMPyPs were not substantially altered even under the molecular crowding condition, suggesting that the binding modes of these porphyrins were not affected by the presence of PEG. The strong positive CD signal in the Soret absorption region, indicative of the o-TMPyP–DNA complex both in an aqueous solution (maximum at 425 nm) and under the molecular crowding condition (maximum at 427 nm), suggested that o-TMPyP binds at the groove or to the external side of the DNA. In addition to the absorption spectra, a CD spectrum indicated that the binding modes of o-, m-, and p-TMPyPs were retained even under the molecular crowding condition. Thus, it is conceivable that the PEG molecules do not directly encounter the cationic porphyrins.

The CD spectra of o-, m-, and p-trans-BMPyPs that complexed with the DNA in two different buffer systems are depicted in Figure 4. For the aqueous buffer environment, both o- and p-trans-BMPyPs produced clear bisignate CD spectra with positive maxima at 430 and 435 nm and negative minima at 415 and 420 nm in the Soret region upon forming complexes with DNA. The wavelength of the p-trans-BMPyP shifted toward longer wavelengths by ∼5 nm compared to the o-trans-BMPyP case. The shape of the CD spectra for o- and p-trans-BMPyPs coincide neither with the intercalative-binding type nor with the groove-binding type. Under the molecular crowding condition, the shape of the CD spectrum changed to display a positive CD signal with their maxima at ∼428 and ∼434 nm for o- and p-trans-BMPyPs, respectively. However, the intensities of the CD spectra are distinctively lower compared to those bound at the major groove (see the o-TMPyP case above). This observation suggested that the

![Figure 3](https://example.com/figure3.png)  
**Figure 3.** CD spectra of (A) o-, (B) m-, (C) p-TMPyPs complexed with DNA under the molecular crowding condition and those in an aqueous solution (inset). [DNA] = 100 μM, [BMPyP] = 10 μM.

![Figure 4](https://example.com/figure4.png)  
**Figure 4.** CD spectra of (A) o-, (B) m-, and (C) p-trans-BMPyP complexed with native DNA in a PEG solution and in an aqueous solution (inset) [DNA] = 100 μM, [BMPyP] = 10 μM.
presence of PEG in the solution alters the CD spectra of the o- and p-trans-BMPyP complexes; thus, PEG could encounter porphyrins. The m-trans-BMPyP–DNA complex produced two negative CD signals in the aqueous solution, which changed to negative CD under the molecular crowding condition. Furthermore, the CD spectrum of the m-trans-BMPyP–DNA complex was affected by the presence of PEG, as shown in the absorption spectrum. As with the solvent conditions, the number and positions of the positive charges of porphyrin are affect to the different binding modes to DNA.

**LD Spectra.** Generally, LD is a powerful tool for determining the binding geometry for DNA-bound drugs. In other words, it has been proved to be a powerful tool in measuring the angle between the electric transition moment of the DNA-bound drug and DNA helix axis. In the flow-orientation apparatus, a large negative LD signal appears for DNA with its shape symmetrical to the normal DNA absorption spectrum because the in-plane electric transition moments of the DNA bases align perpendicularly to the flow direction. The intercalating molecules, such as 9-aminoacridine, produce a negative LD signal in their absorption wavelength range because their in-plane electric transition moments are parallel to the DNA bases in the intercalation pocket. Contrarily, the minor-groove-binding molecules, including DAPI, exhibit positive LD signals in their absorption ranges due to the \( \sim 45^\circ \) angle between the electric transition moment of DAPI and the native DNA helix axis (or the DNA base plane). Figure 5 depicts the LD spectra of o-, m-, and p-TMPyPs complexed with the DNA. Similar LD spectra for these cationic porphyrins measured in an aqueous solution have been reported. As expected, all three complexes produced large negative LD signals in the DNA absorption region. In the m- and p-TMPyP cases (panels B and C), large negative LD signals with magnitudes higher than those in the DNA absorption region were apparent, while for o-TMPyP (panel A), the magnitude of the signal was lower than that in the DNA absorption region. From these LD results, it was concluded that m- and p-TMPyPs intercalate between the DNA base pairs. The DNA stem near the intercalated site tilts substantially. Conversely, an in-depth analysis showed that the two electric transition moments, i.e., in planes B\(_x\) and B\(_y\) in-plane electric transitions, of o-TMPyP tilt at the angles of 59–63 and 43–49°. From this result, o-TMPyP was suggested to bind at the major groove of DNA. Essentially, the appearance of the LD spectra in the aqueous solution is basically retained in the presence of PEG for all of the three porphyrins. This observation indicated that the binding geometries of all of the three porphyrins change slightly under the molecular crowding condition, probably because the clustered PEG polymer cannot be close enough to encounter the porphyrins.

The appearances of LD spectra for o-, m-, and p-trans-BMPyPs, complexed with DNA in the aqueous solution, are significantly different from those of TMPyPs (Figure 6). The negative LD signal centered at \( \sim 423 \text{ nm} \) was apparent for the o-trans-BMPyP–DNA complex. The magnitude is distinctively smaller than those observed for the TMPyP–DNA complexes (Figure 6, panel A), suggesting a large tilt of the molecular plane of porphyrin relative to the DNA helix axis. In contrast, a complicated LD spectrum in the Soret region appeared under the molecular crowding condition: two positive LD maxima at \( \sim 411 \text{ and } \sim 437 \text{ nm} \) were apparent, while for o-TMPyP (panel A), the magnitude of the signal was lower than that in the DNA absorption region. From these LD results, it was concluded that m- and p-TMPyPs intercalate between the DNA base pairs. The DNA stem near the intercalated site tilts substantially. Conversely, an in-depth analysis showed that the two electric transition moments, i.e., in planes B\(_x\) and B\(_y\) in-plane electric transitions, of o-TMPyP tilt at the angles of 59–63 and 43–49°. From this result, o-TMPyP was suggested to bind at the major groove of DNA. Essentially, the appearance of the LD spectra in the aqueous solution is basically retained in the presence of PEG for all of the three porphyrins. This observation indicated that the binding geometries of all of the three porphyrins change slightly under the molecular crowding condition, probably because the clustered PEG polymer cannot be close enough to encounter the porphyrins.

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![Figure 6. LD spectra of the o-, m-, and p-trans-BMPyP–DNA complexes (panels A, B, and C, respectively) in the aqueous solution (black curves) and under the molecular crowding condition (red curves). Measured LD spectra were normalized to −1 at 260 nm for easy comparison. [DNA] = 100 μM, [BMPyP] = 10 μM.](https://dx.doi.org/10.1021/acsomega.0c00471)
these small negative or positive LD signals in the Soret region can exclude the possibility of intercalative- or groove-binding modes for o-trans-BMPyP. A bisignate LD spectrum in the Soret region was observed in the m-trans-BMPyP–DNA complex case (Figure 6, panel B) with its positive and negative maxima at ~415 and 436 nm, respectively. The magnitude of this LD signal noticeably decreased when the environment was changed from an aqueous to a molecular crowding environment. In the p-trans-BMPyP–DNA complex case (Figure 6, panel C), a complicated small LD signal with positive peaks at ~416 and ~437 nm and a negative peak at ~452 nm was apparent in the aqueous solution, which changed to a large positive LD signal at 421 nm with a small negative peak at ~452 nm. The LD signals of neither m-trans-BMPyP nor p-trans-BMPyP matched with those observed from the intercalative-binding modes of the m- and p-TMPyPs–DNA complexes (Figure 5, panels B and C). Although a detailed analysis of the LD spectrum by calculating the reduced LD spectrum, which is defined by dividing the measured LD by the normal absorption spectrum and is related to the angle of the in-plane electric transition moments of porphyrin to the native DNA helix axis, is not carried out, it is conclusive that the binding geometries of all of the three BMPyPs were altered by the presence of PEG. This observation is in contrast with the cases of TMPyPs, which were either intercalated or bound at the major groove. Moreover, the matted PEG cluster may not have been close enough to affect the intercalated or groove-bound porphyrins. Consequently, BMPyPs are located outside the DNA, where encountering PEG is possible.

**Binding Modes of Cationic Porphyrin to DNA and the Effect of the Molecular Crowding Condition.** It has been well documented that m- and p-TMPyPs, which can form a planar structure because the periphery pyridinium ring can rotate freely, intercalate between the DNA base pairs.12,25 This type of binding mode produced a large red shift and hypochromism in the Soret region of the absorption spectrum, a negative CD signal, and a negative large LD signal. In the o-TMPyP case, the alteration in the absorption spectrum was less significant. A positive CD signal and a negative LD signal had significantly small magnitudes compared with those of the intercalated porphyrin. The appearance of a polarized spectrum is identical to that under the molecular crowding condition, although a slight difference was observed in the absorption spectrum. This observation indicated that the binding modes of all of the three TMPyPs are retained under the molecular crowding condition. In other words, the matted PEG cluster may not be close enough to affect the intercalated or groove-bound cationic porphyrins. Oppositely, the complicated bisignate CD spectra for all of the three trans-BMPyPs with very small intensities suggested that none of trans-BMPyP was intercalated or bound at the groove of the DNA. None of the LD signals for trans-BMPyPs (the trisignate small LD spectrum for p-trans-BMPyP, the bisignate spectrum for m-trans-BMPyP, and the small negative LD for o-trans-BMPyP) coincided with those of the intercalated or groove-bound porphyrins. Thus, in addition to the CD spectra, the LD spectra suggested that trans-BMPyPs bound to the external side or on the surface of the DNA. Upon the addition of PEG, the polarized spectral characteristics of trans-BMPyPs were altered substantially, supporting that trans-BMPyP could encounter PEG.

Finally, it is worth noting that the absorption and CD spectra of DNA were not altered in the molecular crowding condition (data not shown), indicating that the secondary structure of DNA retained in the presence of PEG, although the PEG molecules had been known to change the degree of hydration of DNA. In other words, the PEG at a given concentration did not alter the secondary structure of DNA. Therefore, a direct interaction between DNA and PEG cannot be evident by these optical spectroscopic methods. On the other hand, the magnitude of LD increased significantly by the presence of PEG. It may be elucidated by an increase in the solution viscosity by the presence of PEG. DNA orients more efficiently in the more viscous solution, resulting in an increased LD signal.

**CONCLUSIONS**

The binding modes of the intercalated m- and p-TMPyPs and the major-groove-bound o-TMPy in an aqueous solution were retained under the molecular crowding condition created by PEG. In contrast, the binding modes of o-, m- and p-trans-BMPyPs were altered by the presence of PEG, suggesting that these cationic porphyrins bind to the external side of the DNA. Considering the size of the PEG cluster, it is rational that PEG cannot infiltrate inside the DNA and affect the binding mode of porphyrin. The variation in binding modes of o-, m-, and p-trans-BMPyP may be attributed to the difference in the location of positive charges and the rotation ability of the periphery pyridinium ring.

**EXPERIMENTAL SECTION**

Calf thymus DNA and PEG 8000 were purchased from Sigma-Aldrich and Promega, respectively. Porphyrins, such as o-, m-, and p-trans-BMPyPs and o-, m-, and p-TMPyPs, were purchased from Frontier Scientific, Inc. (Utah). A 5 mM cacodylate buffer at pH 7.0 was used as the aqueous solution, while 35% (v/v) PEG 8000 was mixed with cacodylate buffer to achieve the molecular crowding condition. The 35% PEG, expressed as a percentage by volume, is equal to 0.5M in molar concentration units. The PEG concentration of 35% (v/v) was increased by PEG. In contrast, the binding modes of o-, m-, and p-trans-BMPyP were altered by the presence of PEG, suggesting that these cationic porphyrins bind to the external side of the DNA. Considering the size of the PEG cluster, it is rational that PEG cannot infiltrate inside the DNA and affect the binding mode of porphyrin. The variation in binding modes of o-, m-, and p-trans-BMPyP may be attributed to the difference in the location of positive charges and the rotation ability of the periphery pyridinium ring.

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Calf thymus DNA and PEG 8000 were purchased from Sigma-Aldrich and Promega, respectively. Porphyrins, such as o-, m-, and p-trans-BMPyPs and o-, m-, and p-TMPyPs, were purchased from Frontier Scientific, Inc. (Utah). A 5 mM cacodylate buffer at pH 7.0 was used as the aqueous solution, while 35% (v/v) PEG 8000 was mixed with cacodylate buffer to achieve the molecular crowding condition. The 35% PEG, expressed as a percentage by volume, is equal to 0.5M in molar concentration units. The PEG concentration of 35% (v/v) was decided to be “optimal” because the DNA started to be precipitated at higher PEG concentration. The concentrations of the porphyrins were measured spectrophotometrically in the aqueous solution using the extinction coefficients of $\varepsilon_{415\text{nm}} = 233 960$, $\varepsilon_{418\text{nm}} = 252 400$, and $\varepsilon_{419\text{nm}} = 240 000$ cm$^{-1}$M$^{-1}$ for o-, m-, and p-BMPyPs, respectively. Those for o-, m- and p-TMPyPs were $\varepsilon_{413\text{nm}} = 239 000$, $\varepsilon_{417\text{nm}} = 278 000$, and $\varepsilon_{421\text{nm}} = 226 000$ cm$^{-1}$M$^{-1}$, respectively. The extinction coefficient for the DNA was $\varepsilon_{260\text{nm}} = 6700$ cm$^{-1}$M$^{-1}$. The path length for all of the absorption and CD measurements was 0.5 cm, and the results were corrected for 1 cm. The CD spectrum was averaged over five measurements to enhance the signal-to-noise ratio. The absorption spectra were measured using a Shimadzu ultraviolet-visible (UV–vis) spectrometer. The circular and linear dichroism spectra were recorded on a J715 (Jasco, Tokyo, Japan) spectropolarimeter. An inner rotating flow cell was used for the LD measurement.

Although porphyrins are achiral, they induce a CD signal in the Soret absorption region due to the interaction between the electrical transition of porphyrin and those of the chirally arranged nucleobases.13 A large negative CD signal in the Soret region is indicative of the intercalated porphyrin, while a positive CD signal reflects the porphyrins bound to the external side or at the groove of the DNA. A negative LD signal appears in the DNA absorption region (~260 nm) from the flow LD setup adopted in this study. A large negative LD signal
in the Soret region is expected for the intercalated porphyrin because the in-plane electric transitions of porphyrin are parallel to the DNA bases.23

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**Author Contributions**

The manuscript was written through the contribution of all authors. All authors have given approval to the final version of the manuscript.

**Notes**

The authors declare no competing financial interest.

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**ABBREVIATIONS USED**

CD, circular dichroism; LD, linear dichroism; PEG, poly(ethylene glycol)

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