# Selective Recognition of Uracil and its Derivatives Using a DNA Repair Enzyme Structural Mimic 

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## 1. General Information

Chemicals were used as purchased without further purification. Flash chromatography was performed over silica gel (70-230 mesh) and monitored through thin layer chromatography (TLC) on silica gel plates. ${ }^{1} \mathrm{H}$ and ${ }^{13} \mathrm{C}$ NMR spectra were recorded using a 400 MHz instrument with $\mathrm{CDCl}_{3}, \mathrm{D}_{2} \mathrm{O}$, and $\mathrm{CD}_{3} \mathrm{OD}$ as solvents. Chemical shifts of protons are given in ppm relative to the signal of TMS as the internal standard; chemical shifts of carbon nuclei are reported in ppm relative to solvent signals used as internal standards. The structure of the complex formed between uracil and receptor $\mathbf{1}$ was calculated using Spartan'06. ${ }^{1}$

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$\mathrm{Pd}\left(\mathrm{PPh}_{3}\right)_{4}$ ( $191 \mathrm{mg}, 0.165 \mathrm{mmol}$ ) was added under a $\mathrm{N}_{2}$ stream to a mixture of 1,8-dibromonaphthalene ( $1.40 \mathrm{~g}, 4.90 \mathrm{mmol}$ ), pyrenylboronic acid ( $1.21 \mathrm{~g}, 4.90 \mathrm{mmol}$ ), and 1,2-dimethoxyethane ( 30 mL ) in a $100-\mathrm{mL}$ three-neck round-bottom flask. A degassed solution of $\mathrm{K}_{2} \mathrm{CO}_{3}(2.92 \mathrm{~g}, 21.5 \mathrm{mmol})$ in water ( 15 mL ) was added and the resulting mixture was heated under reflux for 13 h under $\mathrm{N}_{2}$. After cooling to room temperature, the aqueous phase was extracted with $\mathrm{CH}_{2} \mathrm{Cl}_{2}$, the combined organic phases were dried $\left(\mathrm{MgSO}_{4}\right)$ and filtered, the solvents were evaporated in vacuo, and the residue was recrystallized from EtOAc ( $5-10 \mathrm{~mL}$ ) to afford 4 as a yellow solid ( $1.15 \mathrm{~g}, 57 \%$ ). ${ }^{1} \mathrm{H}$ NMR ( $400 \mathrm{MHz}, \mathrm{CDCl}_{3}, \mathrm{ppm}$ ) $\delta 7.33(\mathrm{t}, J=7.6 \mathrm{~Hz}, 1 \mathrm{H}), 7.58(\mathrm{~m}, 3 \mathrm{H}), 7.72(\mathrm{~d}, J=7.2$ Hz), 7.89-8.22 (m, 10 H ).

## 3. Determination of dimerization constants for 1 by dilution experiment ${ }^{2}$

The dimerization constant for $\mathbf{1}$ was determined by diluting a sample from its maximum solubility $(9.00 \mathrm{mM})$ to the minimum concentration $(0.28 \mathrm{mM})$ required for detection of a signal by ${ }^{1} \mathrm{H}$ NMR spectroscopy at 298 K . The chemical shift at 6.064 ppm at high concentration was followed. The chemical shift of $\mathbf{1}$ increased gradually to 6.592 ppm , as the concentration of $\mathbf{1}$ decreased. The data were then fitted to a nonlinear regression curve on a PC using the following equation (1):

$$
\begin{equation*}
\delta=\delta_{\mathrm{m}}-\left[\left(\delta_{\mathrm{m}}-\delta_{\mathrm{d}}\right) / c\right]\left[c+0.25 / K_{\mathrm{d}}-\left(0.5 c / K_{\mathrm{d}}+0.0625 / K_{\mathrm{d}}\right)^{1 / 2}\right] \tag{1}
\end{equation*}
$$

where $\delta, \delta_{\mathrm{m}}, \delta_{\mathrm{d}}$, and $c$ are the observed chemical shift, the chemical shift of the monomer, the chemical shift of the dimer, and the total concentration of the receptor; $K_{\mathrm{d}}$ is the dimerization constant (Figure S1).


FIGURE S1. Measurement of the dimerization constant for $\mathbf{1}$ in $\mathrm{D}_{2} \mathrm{O}$ using NMR spectroscopy.

## 4. Determination of binding stoichiometry through Job plot analysis ${ }^{2}$

A Job plot was used to identify the binding stoichiometry of the complex formed between uracil and $\mathbf{1 a}$ at 298 K . To construct a Job plot, two stock solutions of $\mathbf{1}$ and uracil were prepared at the same concentrations $(10 \mathrm{mM})$ in $\mathrm{D}_{2} \mathrm{O}$. For ${ }^{1} \mathrm{H}$ NMR spectroscopic analysis, 11 solutions were prepared by mixing the two stock solutions at volume ratios of $0: 500,50: 450,100: 400$, 150:350, 200:300, 250:250, 300:200, 350:150, 400:100, $450: 50$, and $500: 0 \mu \mathrm{~L}$. The concentrations of the complex of 1 a with uracil were estimated using equation (2) and the chemical shift of the $\mathrm{C}(5) \mathrm{H}$ hydrogen atom of uracil (initially at 5.7107 ppm ). The plot of the concentrations of the complex against the molar fraction of uracil created a Job plot, which revealed 1:1 binding between uracil and receptor 1a (Figure S2).

$$
\begin{equation*}
\text { [complex }]=[\mathrm{U}]\left(\delta_{\mathrm{obs}}-\delta_{\mathrm{u}}\right) /\left(\delta_{\mathrm{c}}-\delta_{\mathrm{u}}\right) \tag{2}
\end{equation*}
$$

where [U], $\delta_{\mathrm{c}}, \delta_{\mathrm{obs}}$, and $\delta_{\mathrm{u}}$ are the concentration of uracil, the chemical shift of uracil in the complex, the observed chemical shift of uracil during binding, and the chemical shift of uracil in the absence of $\mathbf{1 a}$, respectively.


FIGURE S2. Job plot for the complex formed between uracil and 1a.

## 5. Plot of $\log K_{\mathrm{b}}$ with respect to values of $\mathrm{p} K_{\mathrm{a}}$ of $\mathrm{N}(1) \mathrm{H}$ units of uracil and its derivatives

Based on the data in Table S1, Figure S3 present a plot of $\log K_{\mathrm{b}}$ with respect to the values of $\mathrm{p} K_{\mathrm{a}}$ of the $\mathrm{N}(1) \mathrm{H}$ units of uracil, thymine, 5 -formyluracil, 5 -fluorouracil, and 5-nitrouracil.

TABLE S1. Values of $\mathrm{p} K_{\mathrm{a}}$ and $\log K_{\mathrm{b}}$ for Uracil and its Derivatives ${ }^{3}$

| compound | $\mathrm{p} K_{\mathrm{a}}$ of $\mathrm{N}(1) \mathrm{H}^{\mathrm{a}}$ | $\mathrm{p} K_{\mathrm{a}}$ of $\mathrm{N}(3) \mathrm{H}^{\mathrm{a}}$ | $\log K_{\mathrm{b}}$ |
| :--- | :---: | :---: | :---: |
| Thymine (Thy) | 11.23 | 10.04 | 1.78 |
| Uracil (Ura) | 10.47 | 9.34 | 2.04 |
| 5-Formyluracil (5FoU) | 6.94 | 7.58 | 2.29 |
| 5-Fluorouracil (5FU) | 9.05 | 7.26 | 2.50 |
| 5-Nitrouracil (5NiU) | 5.66 | 6.91 | 2.62 |

[^0]

FIGURE S3. Plot of $\log K_{\mathrm{b}}$ with respect to the values of $\mathrm{p} K_{\mathrm{a}}$ of the $\mathrm{N}(1) \mathrm{H}$ units of uracil derivatives. The straight line is a line of best fit.

## 6. Complex structure viewed from another angle



FIGURE S4. Calculated structure of the complex formed between receptor 1a and uracil, viewed from another angle. The dotted lines represent hydrogen bonds; the two chloride ions have been omitted for clarity.

## 7. References

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[^0]:    ${ }^{\text {a }}$ Calculated using the Poisson-Boltzmann continuum-solvation model.

