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# pH-Controlled recognition of amino acids by urea derivatives of $\beta$ -cyclodextrin†

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Water soluble amphiphilic urea-substituted  $\beta$ -cyclodextrins were synthesized and applied as amino acid receptors. A great affinity towards nonpolar amino acids was observed, ranging from 2300 M<sup>-1</sup> for alanine to 54 800 M<sup>-1</sup> for tryptophan in a highly competitive environment (pH 8 phosphate-buffered water solution). Significant selectivity was observed, since carboxylates without the amino group (or having hydroxyl instead) remained not bound. Endoenthalpic effects were recorded for amino acids during titrations, pointing to a different mode of complex formation as compared to native  $\beta$ -cyclodextrin. We found a dramatic change in binding strength within the physiological pH range: with pH change from 8 to 6, affinity towards amino acids dropped from 54 000 to 500 M<sup>-1</sup>, making the receptors potentially appropriate for biotechnological purposes.

## Introduction

The ubiquity of amino acids is one of the main factors propelling various research efforts to develop more sophisticated tools to identify, bind, and control them. They are present in all living organisms, playing key roles in many biochemical processes, *e.g.* signal transmission and cellular structure building.<sup>1</sup> Therefore, identifying objects that interact with amino acids strongly and selectively is an ongoing objective of supramolecular chemistry. Analytical quantitative detection of amino acids is usually based on chromatographical or electrochemical techniques; their main drawback is that analytes often need to be derivatized prior to analysis.<sup>2,3</sup> The supramolecular approach to amino acid identification and binding appears to offer a solution, based on strong and selective interactions between amino acids and electrically neutral molecular receptors.<sup>4–6</sup> One very demanding issue in this field is that of pH-controlled binding-release systems, allowing for specific and targeted control of processes that involve amino acids.<sup>7</sup> An analogous approach is investigated in the field of specialized drug delivery systems and signal transduction regulation.<sup>8,9</sup>

The most common strategy towards the formation of complexes of receptors with amino acids utilizes structures with cavities available for the inclusion of guest species. Usually, a type of hydrophobic effect is employed to situate the amino acid inside the cavity.<sup>10,11</sup> This allows for the usage of such receptors under aqueous conditions, but, on the other hand, limits the range of

guests to less polar ones. In this manner, cucurbiturils,<sup>12–14</sup> calixarenes,<sup>15</sup> pilarenes,<sup>16</sup> and cyclodextrins<sup>17–19</sup> are exploited for amino acid binding. Another, widely applied approach involves the utilization of hydrogen bond formation, whereby various nucleophilic acceptors are usually bound by receptors.<sup>20–22</sup> This strategy is limited by the competing environment, *e.g.* polar solvents.<sup>23–25</sup> Therefore, efficient binding of nonderivatized amino acids in aqueous solutions still remains a challenge.<sup>1</sup>

In our recent studies we have shown that combining these two modes of interaction results in substantially improved recognition of amino acids in water.<sup>26</sup> The introduction of an amphiphilic substituent containing urea moiety to  $\beta$ -cyclodextrin ( $\beta$ -CD) resulted in receptors **1a–c** (Fig. 1), which appeared to be 1000-fold more efficient than native (underivatized)  $\beta$ -CD. Binding constants of up to 52 400 M<sup>-1</sup> (for L-tryptophane) were obtained, and the affinity was correlated with both the acidity of the urea protons and the lipophilicity of the amino acid. Unexpectedly, exclusion of isobutyl moiety from the side-chain structure caused a dramatic decrease in binding constants.

Inspired by these regularities, we decided to investigate how changes in the amphiphilic side-chain or pH of the environment

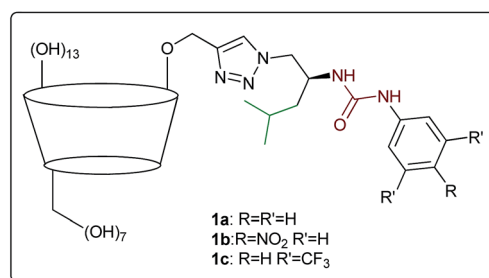


Fig. 1 Amphiphilic urea-derived  $\beta$ -CD receptors **1a–c**.

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would affect binding of various amino acids and carboxylates. We assumed that introduction of an additional aromatic ring (instead of isobutyl moiety) in the side-chain would enhance the interaction with nonpolar species, in particular with hydrophobic amino acids. We additionally assumed that receptors having such a structure would not undergo deprotonation, which would make them useful in a wide range of pH. In this report, we present such new  $\beta$ -CD derivatives with side-chains based on phenylalanine and leucine and describe their utilization in amino acid binding.

## Results and discussion

### Synthesis

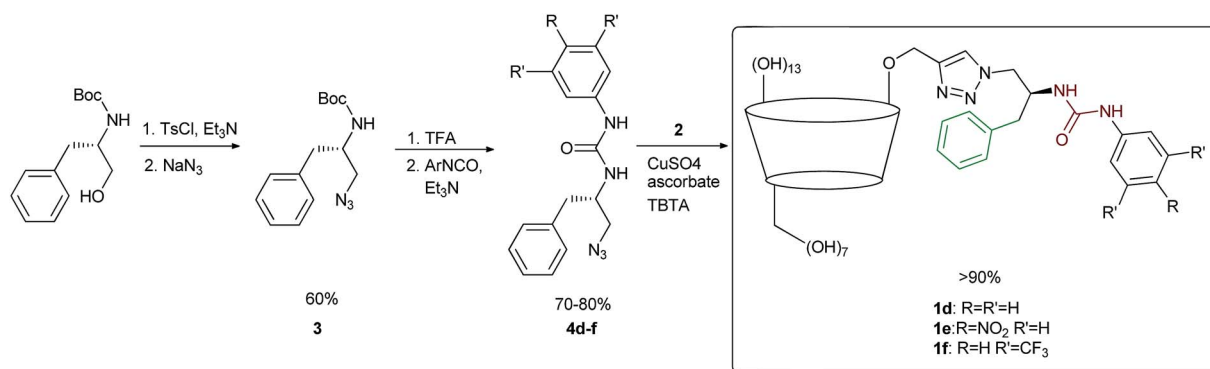
The structure of the target receptors was designed based on our previous findings concerning the behaviour of cyclodextrins and various platforms exploiting hydrogen bonding in carboxylate binding.<sup>27,28</sup> We showed that in the case of C-6 substituted  $\beta$ -CDs, intramolecular inclusion complex formation may occur, making the CD cavity much less available for the guest.<sup>29</sup> Therefore, we have developed a synthetic approach to efficient preparation of mono-2-functionalized  $\beta$ -CD, which can be then further modified *via* the azide-alkyne click chemistry methodology.<sup>30</sup> In such a manner we used mono-2-propargyl- $\beta$ -CD (**2**) to synthesize compounds **1d–f**, being phenyl analogues of the previously reported receptors **1a–c**. In this case N-Boc-L-phenylalaninol was tosylated and subsequently transformed into azide **3**. After Boc deprotection the amino group was functionalized with the corresponding commercially available aromatic isocyanate, yielding desired compound **4**. Next, azide-alkyne coupling with monopropargylated CD **2** was carried out (according to the known procedure), to yield receptors **1d–f** almost quantitatively (>90%). Consequently, we had in hand six receptors of type **1**, with varying side-chains originating from leucine and phenylalanine, having different acidity of the group. None of the compounds had any hydrogen atoms that would be deprotonated under pH < 10 (Scheme 1).

### Binding measurements

We were able to assess the role of the isobutyl/phenyl substituent in the complexation process, comparing it with previously

obtained reference compound having just the ethylene group between azide and urea functionalities.<sup>26</sup> We envisioned that the presence of the additional aromatic moiety should enhance the guest binding process without causing any additional self-inclusion complex formation (if the latter had been the case, leucine-derived compounds **1a–c** would have suffered from this as well). We decided to investigate the amino acid binding properties of receptors of type **1** at pH 8, being in the upper part of the physiological condition range. We used 50 mM phosphate buffer with ionic strength of about 140 mM (which corresponds well to the intracellular environment). We utilized isothermal titration calorimetry to gain fuller insight into the thermodynamics of the complexation process as well as to compare with previously reported data. In this case, titrations of L-amino acid into 2 mM solutions of receptors provided satisfactory sigmoidal curves allowing for the determination of enthalpies, binding constants, and interaction stoichiometries (Fig. 2). Similarly to our previous findings, receptors **1d–f** also exhibited tendencies to form higher-ordered superstructures, which was confirmed with dynamic light scattering (with aggregates of 164, 122, and 255 nm identified for respective receptors **1d–f**). However, during titration a 2 : 1 (host : guest) complexation model was usually identified, which confirmed the same mode of operation for receptors **1d–f** as compared to leucine-derived **1a–c**. Consequently, we applied the typical model of *n*-independent binding sites in the fitting procedure. First, we tested how these receptors complex nonpolar amino acids. The apparent binding constants are listed in Table 1.

We found that phenylalanine-derived receptors **1d** and **1f** bound alanine, phenylalanine, and tryptophan substantially more strongly than their analogues **1a** and **1c**. In the case of *p*-nitro-urea derivatives **1b** and **1e**, this tendency was reversed. Slightly lower binding constants for compound **1e** could be explained by  $\pi$ -stacking leading to the rearrangement of the binding site. As we have already shown, the presence and proper positions of two lipophilic substituents of the side-chain is essential for the binding, since an analogue with no substituent at the ethylene linker between urea and triazole groups showed no affinity towards amino acids at all. In the case of both series of receptors, an increase in the urea hydrogens' acidity resulted in higher  $K_a$ 's (Fig. 3). This is consistent with our assumption that the urea moiety provides hydrogen bonding for the carboxylate group of an amino acid.



Scheme 1 Synthesis of receptors **1d–f**.



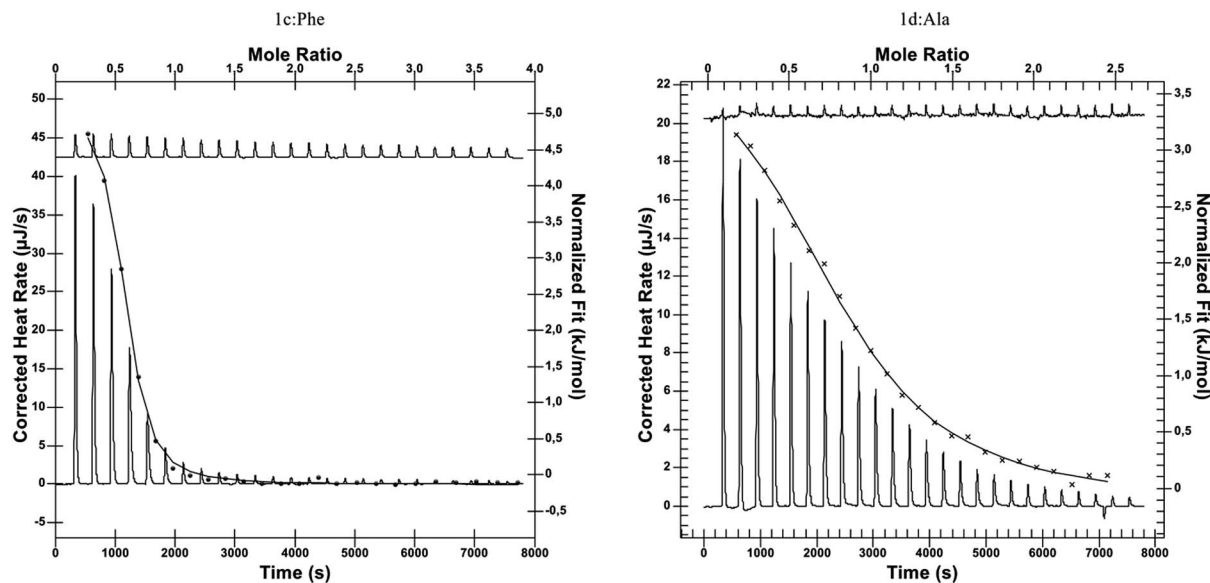


Fig. 2 Representative thermograms of ITC experiments: L-Phe titrated to **1c** (left) and L-Ala titrated to **1d** (right).

Table 1 Binding constants for L-amino acid and receptor **1a–f** complexes<sup>a</sup>

Receptor	$K_a$ ( $10^3$ M <sup>-1</sup> )		
	Ala	Phe	Trp
<b>1a<sup>b</sup></b>	2.3	7.0	9.8
<b>1b<sup>b</sup></b>	2.1	20.2	34.4
<b>1c<sup>b</sup></b>	5.0	22.4	52.4
<b>1d</b>	4.6	16.5	19.1
<b>1e</b>	2.1	5.3	23.4
<b>1f</b>	5.1	23.0	54.8

<sup>a</sup> Aa (250 μL, 10–16 mM) was titrated to **1** (949 μL, 2 mM), stirred at 300 rpm. <sup>b</sup> Data from ref. 26.

All the reactions proved to be endothermic, strongly entropy-driven, with enthalpies varying between 1.5 and 5.5 kJ mol<sup>-1</sup> (Table 2). This would confirm that the mode of interaction with amino acids is similar for all the receptors. We observed that for

corresponding pairs of leucine- and phenylalanine-derived receptors the enthalpies were lower, probably indicating better conformational preorganization of compounds **1d–f** for guest binding.

Next, we investigated the scope of guests that could interact with receptors of type **1**. We analysed the previously thoroughly examined model receptor **1c** in binding of tyrosine, phenylglycine, and serine as well as 2-phenylbutyric and mandelic acids (Table 3). Tyrosine exhibited a binding constant two times lower than phenylalanine. The conformationally more constrained phenylglycine appeared to be even less effectively bound by receptor **1c**. It could be inferred that, for tight interaction, both the carboxylic group and the pendant arm of the guest have to be in a proper position, which would make these two structural elements essential for complex formation. On the other hand, serine was bound with similar strength to phenylalanine, even though it is far more polar and does not contain aromatic moiety. Replacing the amino group with hydroxyl or aliphatic substituent led to dramatic decreases in affinity constants, which proved that the presence of the amino group in the guest structure is necessary for efficient binding. In fact,

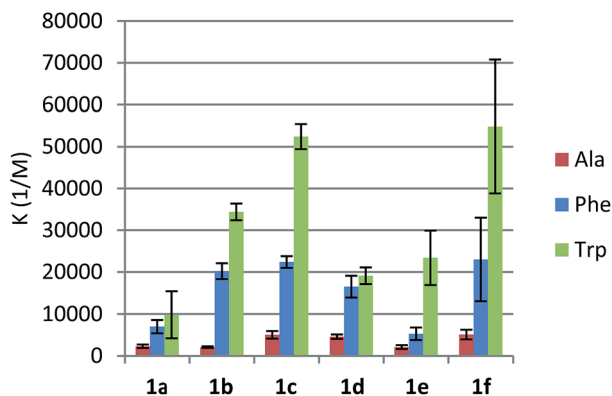


Fig. 3 Comparison of binding effectiveness of receptors **1a–f**.

Table 2 Enthalpies of L-amino acid and receptor **1a–f** complexes formation

Receptor	$\Delta H^a$ (kJ mol <sup>-1</sup> )		
	Ala	Phe	Trp
<b>1a<sup>b</sup></b>	2.99	4.18	4.02
<b>1b<sup>b</sup></b>	4.89	4.90	5.42
<b>1c<sup>b</sup></b>	3.72	5.51	4.46
<b>1d</b>	2.92	4.10	5.19
<b>1e</b>	4.23	3.10	4.18
<b>1f</b>	3.08	1.69	1.55

<sup>a</sup> Apparent enthalpy measured by ITC. <sup>b</sup> Data from ref. 26.





- 8 O. Swiech, P. Dutkiewicz, K. Wójciuk, K. Chmurski, M. Kruszewski and R. Bilewicz, *J. Phys. Chem. B*, 2013, **117**, 13444–13450.
- 9 O. Swiech, M. Majdecki, A. Debinski, A. Krzak, T. M. Stępkowski, G. Wójciuk, M. Kruszewski and R. Bilewicz, *Nanoscale*, 2016, **8**, 16733–16742.
- 10 M. V. Rekharisky and Y. Inoue, *J. Am. Chem. Soc.*, 2002, **124**, 2144–2154.
- 11 K. A. Connors, *Chem. Rev.*, 1997, **97**, 1325–1357.
- 12 J. Zhang, Y.-Y. Xi, Q. Li, Q. Tang, R. Wang, Y. Huang, Z. Tao, S.-F. Xue, L. F. Lindoy and G. Wei, *Chem.-Asian J.*, 2016, **11**, 2250–2254.
- 13 L. a Logsdon, C. L. Schardon, V. Ramalingam, S. K. Kwee and A. R. Urbach, *J. Am. Chem. Soc.*, 2011, **133**, 17087–17092.
- 14 P. Rajgariah and A. R. Urbach, *J. Inclusion Phenom. Macrocyclic Chem.*, 2008, **62**, 251–254.
- 15 L. Mutihac, J. H. Lee, J. S. Kim and J. Vicens, *Chem. Soc. Rev.*, 2011, **40**, 2777.
- 16 M. Bojtár, A. Paudics, D. Hessz, M. Kubinyi and I. Bitter, *RSC Adv.*, 2016, **6**, 86269–86275.
- 17 C. Liu, J. Lian, Q. Liu, C. Xu and B. Li, *Anal. Methods*, 2016, **8**, 5794–5800.
- 18 Q. Huang, L. Jiang, W. Liang, J. Gui, D. Xu, W. Wu, Y. Nakai, M. Nishijima, G. Fukuhara, T. Mori, Y. Inoue and C. Yang, *J. Org. Chem.*, 2016, **81**, 3430–3434.
- 19 J. Zhou, Y. Liu, Z. Zhang, S. Yang, J. Tang, W. Liu and W. Tang, *Nanoscale*, 2016, 5621–5626.
- 20 V. Amendola, L. Fabbriizzi and L. Mosca, *Chem. Soc. Rev.*, 2010, **39**, 3889–3915.
- 21 N. Busschaert, C. Caltagirone, W. Van Rossom and P. a. Gale, *Chem. Rev.*, 2015, **115**, 8038–8155.
- 22 K. Choi and A. D. Hamilton, *Coord. Chem. Rev.*, 2003, **240**, 101–110.
- 23 G. V. Oshovsky, D. N. Reinhoudt and W. Verboom, *Angew. Chem., Int. Ed.*, 2007, **46**, 2366–2393.
- 24 E. A. Kataev and C. Muller, *Tetrahedron*, 2014, **70**, 137–167.
- 25 G. Castronuovo, V. Elia, A. Pierro and F. Velleca, *Can. J. Chem.*, 1999, **77**, 1218–1224.
- 26 P. Stepniak, B. Lainer, K. Chmurski and J. Jurczak, *Carbohydr. Polym.*, 2017, **164**, 233–241.
- 27 J. Jurczak, P. Dydio, P. Stepniak and T. Zielinski, *RSC Adv.*, 2016, **6**, 41568–41571.
- 28 J. Jurczak, P. Dydio, P. Stepniak and T. Zielinski, *Sens. Actuators, B*, 2016, **237**, 1–14.
- 29 K. Chmurski, P. Stepniak and J. Jurczak, *Carbohydr. Polym.*, 2016, **138**, 8–15.
- 30 K. Chmurski, P. Stepniak and J. Jurczak, *Synthesis*, 2015, **47**, 1838–1843.

