

# (Thia)calixarenephosphonic Acids as Potent Inhibitors of the Nucleic Acid Chaperone Activity of the HIV-1 Nucleocapsid Protein with a New Binding Mode and Multitarget Antiviral Activity

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# 1 (Thia)calixarenephosphonic acids as potent inhibitors of the

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## 4 activity

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## 27 ABSTRACT

28 The nucleocapsid protein (NC) is a highly conserved protein that plays key roles in HIV-1 replication through its nucleic 29 acid chaperone properties mediated by its two zinc fingers and 30 31 basic residues. NC is a promising target for antiviral therapy, 32 particularly to control viral strains resistant to currently 33 available drugs. Since calixarenes with antiviral properties have been described, we explored the ability of calixarene 34 35 hydroxymethylphosphonic or sulfonic acids to inhibit NC 36 chaperone properties and exhibit antiviral activity. By using 37 fluorescence-based assays, we selected four calixarenes 38 inhibiting NC chaperone activity with sub-micromolar  $IC_{50}$ 39 values. These compounds were further shown by mass 40 spectrometry, isothermal titration calorimetry and 41 fluorescence anisotropy to bind NC with no zinc ejection, and 42 to compete with nucleic acids for the binding to NC. Molecular dynamic simulations further indicated that these 43

44 compounds interact via their phosphonate or sulfonate groups 45 with the basic surface of NC, but not with the hydrophobic plateau at the top of the folded fingers. Cellular studies 46 47 showed that the most soluble compound CIP201 inhibited the 48 infectivity of wild-type and drug-resistant HIV-1 strains at 49 low micromolar concentration, primarily targeting the early 50 steps of HIV-1 replication, and notably the entry step. Moreover, CIP201 was also found to inhibit the flipping and 51 52 polymerization activity of reverse transcriptase. Calixarenes 53 form thus a class of non-covalent NC inhibitors, endowed 54 with a new binding mode and multi-target antiviral activity.

55 Keywords: Nucleocapsid protein, HIV-1, Fluorescence,56 calixarenes, NC inhibitors

57

### 58 INTRODUCTION

During the last two decades, the number of drugs acting as 1 2 inhibitors of entry/fusion, reverse transcription, integration, 3 and protease cleavage developed to fight HIV disease has 4 gradually increased. Though being endowed with efficient 5 antiviral activity, all these compounds select for resistant strains, as a result of the ability of HIV-1 to rapidly mutate<sup>1</sup>. 6 7 Even in the classical treatment scheme, namely the Highly 8 Active Anti-Retroviral Therapy (HAART), which combines 9 anti-retroviral drugs of different classes, treatment failures 10 due to drug resistance are still observed.

11 Thus, new compounds targeting novel and highly conserved 12 viral targets such as the nucleocapsid protein (NC) could be 13 helpful to limit or prevent the emergence of drug resistance. 14 NC exhibits a chaperone activity which enables the structural 15 rearrangement of nucleic acids (NAs) into their most stable 16 conformation. This activity relies on the ability of NC to bind and dissociate rapidly from its NA targets, to destabilize 17 moderately stable NA secondary and tertiary structures and to 18 19 promote the annealing of complementary NA sequences<sup>2-5</sup>. 20 This NC activity is thought to be critical in the reverse 21 transcription process, where NC likely chaperones the 22 annealing of the primer tRNA to the primer binding site (PBS) 23 and the two strand transfers that are required for the synthesis 24 of the proviral DNA by reverse transcriptase<sup>6,7</sup>. NC is a small 25 basic protein that binds with high affinity  $(10^{13} - 10^{14} \text{ M}^{-1})^8$ 26 two zinc ions on two strictly conserved finger motifs (CCHC) 27 through their cysteine and histidine residues (Figure 1a).Upon 28 zinc binding, the NC protein adopts its functional folding leading to the formation at the top of the folded fingers of a 29 30 hydrophobic plateau that involves the amino acids Val13, Phe16, Thr24, Ala25, Trp37, Gln45 and Met46<sup>9-14</sup>. This 31 32 plateau is critical for interaction with target NAs, notably through a stacking of the Trp37 residue with the 33 34 nucleobases<sup>15–17</sup>. This key role of the plateau is further 35 illustrated by the fact that single mutation of any of its residues 36 results in non-infectious viral particles<sup>18</sup>.

Due to its key functions in HIV-1 replication and its high 37 conservation, NC appears as an ideal target for antiretroviral 38 39 therapy. Several strategies, including zinc ejectors, non-40 covalent NC binders and noncovalent NA binders of different 41 chemical classes (see Discussion section for more details) 42 have been developed, but were not fully successful, due to low specificity or to limited antiviral activity or therapeutic 43 index<sup>19-21</sup>. In order to develop new compounds directed 44 45 against NC, we have focused our interest on calixarenes, a large family of macrocyclic aromatic compounds bearing 46 47 phenolic groups, widely used in supramolecular chemistry<sup>22,23</sup>. Calixarenes are rigid vase-like macrocycles 48 49 with a well-established chemistry. These molecules can be obtained through accessible and relatively cheap organic 50 51 synthesis routes, which also allow the versatile functionalization of their macrocyclic core<sup>24-26</sup>. Calixarenes 52 are also receptors in supramolecular recognition studies <sup>27,28</sup> 53 54 that can bind and/or host small molecules through their cavity<sup>29,30</sup> making them suitable for drug delivery purposes.<sup>31-</sup> 55 <sup>33</sup>. Calixarenes have been investigated among others as 56 57 biologically-active molecules in a number of applications, and are recently emerging as candidate therapeutics against 58 multiple diseases<sup>34–36</sup>. However, their mechanism of action is 59 generally poorly elucidated, so that calixarenes are mostly 60 used as tool compounds in chemical biology studies. 61

We have also considered this family for two reasons. First, 62 calixarenes endowed with antiviral activity were first 63 64 described in the patent of Hwang et al.37, in which the para-65 sulfonatocalix[4]arene and its analogs were characterized as anti-HIV agents. Thereafter, synthetic strategies were 66 developed by inserting carboxylate substituents on the 67 calixarene backbone leading to antiviral molecules that have 68 been tested on humans<sup>38–41</sup>. Additional calixarene derivatives 69 with anti-HIV activities were further developed<sup>42-44</sup> and 70 71 recently reviewed.<sup>45</sup> Their mechanism of action revealed that they may act as inhibitors of HIV fusion, integration and viral 72 73 cleavage<sup>25,46–48</sup>. protease Second, calixarene hydroxymethylphosphonic acids<sup>49–51</sup>have been shown to form 74 host-guest complexes with free amino acids<sup>52,53</sup> that are 75 76 stabilized by electrostatic interactions between the positively 77 charged terminal -NH3<sup>+</sup> group of the amino acids and the 78 negatively charged phosphonic acid moiety of calixarenes. 79 Similarly, since the NC protein is highly basic with a large number of solvent-exposed positively charged lysine and arginine residues<sup>16,54,55</sup>, we hypothesized that this class of 80 81 calixarenes may inhibit NC and thus, HIV infection by 82 83 competing with nucleic acids for the binding to NC.





84

86 **Figure 1.** NC peptides (a), calixarene compounds (b to f), and 87 cTAR and dTAR oligonucleotides used in this study (g).

88 In this manuscript, we tested the ability of a series of 89 calixarene hydroxymethylphosphonic or sulfonic acids 90 (Figure 1b-f) to interact with NC and inhibit the binding of

this protein to its target nucleic acids, preventing the 1 2 promotion of the destabilization and annealing of the 3 complementary sequences. Molecular modelling and 4 mutational studies indicated that calixarenes exhibit a new 5 binding mode where their phosphonate or sulfonate groups 6 interact with the basic surface of NC. The antiviral activity 7 and cellular cytotoxicity of the most efficient compound were 8 tested using HIV pseudoviruses, as well as replication-9 competent wild-type (WT) and drug-resistant strains. This 10 compound was also tested in humanized mice infected with HIV-1. Finally, the mechanism of action of this calixarene 11 12 was investigated through biochemical and cell-based assays.

#### 13 RESULTS

# 14 Inhibition of NC chaperone properties:15 selection of the most active compounds

A series of calixarenes was synthetized and characterized as 16 17 described in supplementary information (Figures S1 and S2). 18 To test their ability to inhibit NC chaperone activity, we used 19 a fluorescence assay based on the NC-mediated 20 destabilization of the stem-loop structure of cTAR DNA 21 (Figure 1g), the complementary sequence of the 22 transactivation response element, involved in minus strand 23 DNA transfer during reverse transcription<sup>56</sup>. This assay as 24 well as all fluorescence-based assays in this study were 25 performed with the truncated NC(11-55) peptide (Figure 1a) that contains the zinc finger domain responsible of the specific 26 nucleic acid binding and destabilization activities<sup>10,57</sup>, but is 27 28 deleted of the basic N-terminal domain that is responsible of 29 the strong NA aggregation activity of NC and thus, of strong 30 light scattering<sup>58</sup>. The assay is based on the use of cTAR 31 labelled at its 5' and 3'ends by a Rh6G fluorophore and a 32 Dabcyl fluorescence quencher, respectively<sup>59</sup>. In the absence 33 of NC(11-55), the proximity of cTAR ends induces a strong 34 fluorescence quenching of Rh6G by the Dabcyl group (Figure 2, black curve). Addition of a 10-fold molar excess of NC(11-35 36 55) to cTAR induces the melting of the bottom of the cTAR 37 stem, leading to an increase in the distance between the two 38 fluorophores which restores the Rh6G fluorescence (Figure 2, 39 red curve). As a consequence, a positive hit will be detected 40 by its ability to inhibit partially or totally the NC(11-55)-41 induced increase of Rh6G fluorescence. 42 Calixarenes were first added to the NC(11-55)/cTAR complex 43 at a concentration of 10 µM, which corresponds to a molar

ratio of 10:1 in respect to NC(11-55). Interestingly, C933, 44 45 C934, CIP200 and CIP201 induced a 75 to 97% reversion of 46 the NC(11-55)-promoted increase in Rh6G emission, 47 suggesting that these four compounds can efficiently inhibit 48 the NC destabilization activity. In contrast, the five other 49 compounds induced only a marginal change in the same 50 conditions. After further increase of the calixarene concentration to 100 µM, a full reversion of the NC(11-55)-51 52 induced increase in Rh6G emission was observed with C933, 53 C934,CIP200, CIP201, C131 and C932, while a 53 and 78 % 54 reversion was observed for C145 and C931, respectively.





57 Figure 2. Inhibition of the NC(11-55)-induced cTAR 58 destabilization by the calixarenes. Emission spectra of Rh6G-5'-59 cTAR-3'-Dabcyl (0.1 µM) were recorded in the absence (black) 60 and in the presence of 1 µM NC(11-55) before (red) and after 61 addition of 10 µM (blue) or 100 µM (green) CIP201. Buffer: 25 62 mM Tris (pH = 7.5), 30 mM NaCl and 0.2 mM MgCl<sub>2</sub>. 63 Temperature: 20°C. Excitation wavelength was 520 nm. The 64 DMSO concentration was less than 2% v/v for all experiments. 65 The IC50 values for the inhibition of NC(11-55)-induced cTAR 66 destabilization by the tested calixarenes are shown in the table. 67 N.A. = Not Active

68

69 In contrast, no fluorescence change was induced by C935. 70 indicating that it is unable to inhibit the NC(11-55)-induced 71 destabilization of cTAR. Notably, this compound differs from 72 the other tested calixarenes by the fact that it possesses four 73 propyl chains at the lower rim and two bromine substituents 74 at the upper rim of the calixarene core. Assuming that the OH 75 groups may be solvent exposed when calixarenes are bound 76 to  $NC^{60}$ , the O-propyl chains become then unfavorably 77 solvent-exposed. Moreover, the two bromine substituents 78 may sterically hinder the inclusion of NC residues in the 79 calixarene central core cavity or form a steric obstacle for the 80 binding of C935 to the NC. Determination of the IC<sub>50</sub> values 81 revealed that the other tested calixarenes could be divided into 82 two classes (Figure 2, table). The first class comprising the 83 four most active compounds (C933, C934, CIP200 and 84 CIP201) is characterized by  $IC_{50}$  values in the range 3-5  $\mu$ M, 85 close to the concentration of the NC peptide used in the assay. 86 The second class (C131, C932, C145 and C931) is 87 characterized by  $IC_{50}$  values in the range 40-90  $\mu$ M and is thus 88 far less efficient. Based on the difference in activities of the 89 two classes, we focused our next efforts only on the 90 compounds of the first class.

91 In order to confirm the ability of the four selected compounds 92 to inhibit the NC chaperone properties, we checked their 93 effect on the NC(11-55)-promoted cTAR/dTAR annealing 94 reaction (Figure 3), which relies on both the nucleic acid destabilizing and aggregating activities of NC<sup>61,62</sup>. We used in 95 96 this test a cTAR sequence labelled with Alexa488 97 (fluorophore) and Dabcyl (quencher) at its 5' and 3' ends, 98 respectively. In the absence of NC, the fluorescence signal is 99 low (Figure 3a) due to the close proximity of both cTAR ends 100 and the strong fluorescence quenching of the Alexa488 101 emission by the Dabcyl group. Of note, Alexa 488 was 102 preferred to Rh6G, due to its lower tendency to bind to

1 calixarenes at the high concentrations used in this assay (data 2 not shown). After addition of NC(11-55) at 8 eq, we observed 3 an increase of the fluorescence signal as a result of the 4 destabilization of cTAR by NC(11-55) (Figure 3a)<sup>56</sup>. A further 5 increase in the fluorescence signal was observed when both 6 NC-coated sequences were mixed together in order to allow 7 the annealing reaction to proceed (Figure 3a and b). Real-time 8 annealing kinetics were monitored in pseudo-first order 9 conditions by following the increase of the Alexa488 10 fluorescence at 519 nm. The same plateau was reached in the absence and in the presence of calixarenes, indicating that the 11 same final product (extended duplex) was formed. However, 12 the reaction was slowed down in the presence of all four 13 14 selected calixarenes (Figure 3b), clearly indicating that they efficiently counteract the NC-chaperoned annealing reaction. 15 The kinetic traces were fitted using<sup>61,63</sup>:

16 17

18 
$$I(t) = I_F - (I_F - I_0)e^{-k_{obs}(t-t_0)}$$
(1)

19 where  $t_0$  is the dead time,  $k_{obs}$  is the observed kinetic rate 20 constant, and  $I_0$  and  $I_F$  are the fluorescence intensities before 21 dTAR addition and at completion of the reaction, respectively. 22 NC annealing activity was calculated as the ratio  $k_{obs}/k_{obs0}$ . 23 where  $k_{obs}$  and  $k_{obs0}$  are the kinetic rate constants in the 24 presence and in the absence of calixarenes, respectively.  $IC_{50}$ 25 values were obtained by fitting to equation (4) the variation of the percentages of inhibition (% inh = 100 - % of NC 26 27 annealing activity) as a function of the concentration of 28 calixarene (Figure 3c). The  $IC_{50}$  values were in the 29 submicromolar range, up to 10 times lower than those 30 obtained for the destabilizing activity (Figure 2, table). The 31 lowest value was observed for C933, which was about two to 32 three times more active than the other three compounds 33 (Figure 3, table).



35 Figure 3. Inhibition of NC(11-55)-promoted cTAR/dTAR 36 annealing reaction by selected calixarenes. (a) Fluorescence 37 spectra of 10 nM Alexa488-5'-cTAR-3'-Dabcyl in the absence 38 (black line) and in the presence of 80 nM of NC (11-55) (red line) 39 and after annealing with 100 nM of dTAR in the presence of 800 40 nM of NC(11-55) (blue line). Excitation was at 480 nm. Buffer: 41 25 mM Tris (pH = 7.5), 30 mM NaCl and 0.2 mM MgCl<sub>2</sub>. 42 Temperature: 20 °C. (b) Effect of CIP201 on the NC-promoted 43 cTAR/dTAR annealing reaction. Kinetic traces of the annealing

44 reaction in the absence of CIP201 (black) and in the presence of 45 0.5  $\mu$ M (red), 1  $\mu$ M (blue), 2  $\mu$ M (magenta) and 2.5  $\mu$ M (green) 46 of CIP201. The kinetic traces were normalized. Excitation was at 47 480 nm. Emission was recorded at 519 nm. (c) Inhibition of the 48 NC(11-55)-promoted cTAR/dTAR annealing reaction as a 49 function of the concentration of C933 (red), C934 (green), 50 CIP200 (blue), and CIP201 (magenta). The curves were fitted to 51 equation (4). The concentration of DMSO was less than 2% v/v. 52 Table: IC50 values for the inhibition of the NC(11-55)-promoted 53 cTAR/dTAR annealing reaction by the tested calixarenes

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55 Thus, the selected calixarenes inhibit efficiently both the 56 nucleic acid destabilization and aggregation components of 57 NC(11-55) chaperone activity.

#### 58 Binding of calixarenes to NC

59 To determine whether the inhibitory activity observed in 60 Figures 2 and 3 resulted from the direct binding of the 61 calixarenes to NC(11-55) and not from zinc ejection, we used 62 non-denaturing mass spectrometry for NC(11-55) in the 63 absence or presence of a 10-fold molar excess of C933 or 64 C934(Figure 4).



**Figure 4.** Binding of C933 and C934 to NC(11-55) monitored by non-denaturing mass spectrometry. Deconvoluted mass spectra in non-denaturing conditions of 20  $\mu$ M NC(11-55) in 50 mM AcONH<sub>4</sub> at pH 7.0 in the absence (A) or in the presence of 200  $\mu$ M of C933 (B) or C934 (C) in 1% DMSO. \* [M + CH<sub>3</sub>COO] adduct. Experimental mass of each observed complex is given at the right part of the spectrum.

As previously described<sup>56,64-66</sup>, NC(11-55) is detected in its 74 zinc-bound form with a measured mass of  $5264 \pm 1$  Da (Figure 75 76 4A). In the presence of C933 (Figure 4B), signals 77 corresponding to free NC(11-55) (with its  $2 Zn^{2+}$  ions) as well 78 as to 1:1 and 1:2 NC(11-55):C933 complexes are detected. No 79 peak corresponding to zinc-free NC(11-55) or zinc-free 80 NC(11-55):C933 species is detected, indicating that C933 81 binding occurs without zinc ejection. Similar results were 82 obtained with C934, for which 1:1 and 1:2 NC(11-55):C934 83 complexes were detected along with free NC(11-55) (Figure 84 4C). Again no zinc-free peptide species were detected, 85 demonstrating the absence of zinc ejection upon C934 binding to NC(11-55). Similar experiments were performed with 86 87 CIP200 or CIP201, but led to weak MS signals not suitable

- 1 for interpretation (data not shown), due either to lower
- 2 ionization efficiencies of CIP200 and CIP201 in electrospray
- 3 or neutralization of the charges of the resulting complexes.
- 4 Altogether non-denaturing MS analysis clearly indicates that
- 5 C933 or C934 binds to NC(11-55) but does not induce zinc
- 6 ejection.
- 7 The absence of zinc ejection with CIP200 and CIP201 was
- 8 checked by monitoring the time-dependence of their
- 9 inhibition of the NC(11-55)-induced cTAR destabilization. A
- 10 fast inhibition was observed with both compounds (Figure S3)
- 11 in sharp contrast with the slow time-dependent inhibition
- 12 observed with zinc ejectors (see WDO-217, Figure S3), as a
- 13 consequence of the time requested to chemically react with 14 the zinc fingers and eject  $zinc^{64}$ . This fast inhibition further
- 15 suggests that CIP200 and CIP201 do not eject zinc, but rather
- 16 compete with nucleic acids for binding to NC(11-55).
- 17 To further characterize the binding of the calixarenes to
- 18 NC(11-55), we next determined their binding parameters by
- 19 ITC (Figure S4). The titration curves were adequately fitted
- 20 to equation (5), giving  $K_d$  values ranging from 0.7 to 2  $\mu$ M
- 21 (Table 1), close to the  $IC_{50}$  values determined for the 22 inhibition of NC chaperone activity (Figures 2 and 3). We
- found that the reaction of NC(11-55) was accompanied by a
- 25 Tould that the feaction of NC(11-55) was accompanied by a
- 24 favorable enthalpy contribution, ranging from -2.8 to -5.7
- 25 kcal/mol that represents roughly half of the total binding
- 26 energy (Table 1). The positive  $\Delta S$  values found for all 27 compounds indicated favorable entropic contributions,
- 28 suggesting that the formation of the complexes is partly driven
- 29 by a release of water molecules and/or ions.
- 30

31 **Table 1.** Thermodynamic parameters for the binding of 32 calixarenes to NC peptides.

Cmpd	NC	Kd	ΔH	ΔS
		(µM)	(kcal.mol <sup>-1</sup> )	(cal.mol <sup>-1</sup> .K <sup>-</sup>
				1)
C933	11-55	$0.7\pm0.2$	$-3.8\pm0.5$	$15 \pm 2$
	1-55	$0.15\pm0.1$	$-4.4\pm0.3$	$16 \pm 1$
C934	11-55	$1.8\pm0.6$	$-2.8\pm0.3$	17 ± 2
	1-55	$0.12\pm0.1$	$-2.5\pm0.2$	$23 \pm 2$
CIP200	11-55	$2 \pm 1$	-5 ± 2	8 ± 3
	1-55	$0.7\pm0.1$	$-3.1\pm0.1$	$17.7\pm0.5$
CIP201	11-55	$1.1 \pm 0.5$	$-5.7\pm0.9$	8 ± 2
	1-55	$0.2\pm0.1$	$-7.3\pm0.4$	$5.5 \pm 0.3$
	(1-55)\$3	$1.7\pm0.2$	$-4.7\pm0.9$	$10 \pm 3$

33	Buffer: 25 mM Tris ( $pH = 7.5$ ), 30 mM NaCl and 0.2 mM
34	MgCl <sub>2</sub> , $T = 20^{\circ}$ C. The thermodynamic parameters are
35	reported as means ± standard error of the mean for at least
36	three independent measurements.

- -

To investigate the contribution of the strong basic N-terminal domain of the peptide on calixarene binding, we performed ITC titrations with the full length NC. We found that  $K_d$  values are 3 to 15 times lower (Table 1) than those determined with the NC(11-55) mutant, suggesting that the basic N-terminal domain of NC significantly contributes to calixarene binding. Moreover, the basic residues between the two zinc fingers

- play an important role too in the binding of CIP201 to NC, asindicated by the about one order of magnitude change in the
- 47  $K_{\rm d}$  value when these residues were replaced by Ser residues in
- 48 the NC(1-55)S3 mutant (Table 1).
- 49 To provide further information on the binding process, the 50 electrostatic and non-electrostatic binding contributions were 51 determined from the variation of  $K_d$  with the concentration of 52 Na<sup>+</sup> ions<sup>67</sup>. The number m' of ion pairs and the non-53 electrostatic binding constant  $K_d(1M)$  between NC(11-55) and 54 the calixarenes were derived from:
- 55

56 
$$\log K_d = \log K_d (1M) + \psi_{Na^+} m' \log[Na^+]$$
 (2)  
57

58 The value of the fraction of Na<sup>+</sup> ions thermodynamically bound per negatively charged moiety,  $\psi_{Na^+}$ , was assumed to be 0.71 as for single-stranded DNA<sup>67,68</sup>. The plots of log  $K_d$ 59 60 versus log [NaCl] were found to be linear in the 10-100 mM 61 62 salt concentration range (Figure 5). Interestingly, the 63 contribution of the non-electrostatic interactions deduced 64 from the  $K_d(1M)$  values was found to be dominant, 65 representing 80 % to 90 % of the binding energy at 30 mM 66 NaCl. Moreover, the number m' of ion pairs between NC(11-67 55) and the calixarenes was about 1 in all the complexes. Of 68 note, a similar distribution of electrostatic and non-69 electrostatic contributions was observed for the binding of 70 NC(12-53) to a small d(AACGCC) oligonucleotide <sup>13,69</sup>.



72 Figure 5. Dependence on Na<sup>+</sup> ion concentration of the 73 equilibrium dissociation constant  $K_d$  for the binding of 74 calixarenes C933, C934, CIP200 and CIP201 to NC(11-55), as 75 determined by ITC at 20°C. The graph depicts the dependence of 76  $\log K_d$  on  $\log [Na^+]$ . Lines are least-squares fits of equation (2) to 77 the experimental points. The table provides the equilibrium 78 dissociation constant at 1 M Na<sup>+</sup> ( $K_d$  (1M)) and the numbers of 79 ion pairs (m') between NC(11-55) and the calixarenes. Buffer: 25 80 mM Tris (pH = 7.5), 0.2 mM MgCl<sub>2</sub>.

81

- Finally, we performed fluorescence anisotropy titrations to
  determine whether the calixarenes can compete with NAs for
  the binding to NC(11-55). To this end, we titrated cTAR
- 85 labeled by tetramethylrhodamine, TMR-5'-cTAR, by NC(11-
- 86 55) in the absence and in the presence of calixarenes (Figure

1 6). As expected, NC(11-55) was found to markedly increase 2 the fluorescence anisotropy of TMR-5'-cTAR, as a result of 3 the formation of the NC(11-55)/cTAR complex. All four 4 selected calixarenes were observed to shift the titration curves 5 toward higher NC(11-55) concentrations as compared to the 6 curve in the absence of calixarenes (Figure 6, black curve). 7 Thus, all four calixarenes compete with cTAR for the binding 8 to NC(11-55), which explains their ability to inhibit the NA 9 chaperone properties of the peptide. It should be noted that the 10 C145 used as negative control has, as expected, a marginal impact on the binding of NC (11-55) with cTAR (Figure 6, 11 compare orange and black curves). Moreover, a control 12 experiment was performed to check both by ITC and 13 14 fluorescence titrations that calixarenes do not bind to cTAR 15 (Figure S5A and B). Thus, the calixarenes hinder the binding 16 of NC(11-55) to cTAR, only by their binding to the peptide.





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**Figure 6.** Binding of NC(11-55) to TMR-5'-cTAR in the presence of calixarenes. The interaction between NC(11-55) and 0.1  $\mu$ M TMR-5'-cTAR was monitored through the fluorescence anisotropy changes of TMR. Titrations were performed at 20°C either in the absence (black) or in the presence of 20  $\mu$ M C933 (red), 20  $\mu$ M C934 (blue), 2.5  $\mu$ M CIP200 (magenta) or 2.5  $\mu$ M CIP201 (green) or 20  $\mu$ M C145 (orange). Buffer: 25 mM Tris pH

26 7.5, 30 mM NaCl and 0.2 mM MgCl<sub>2</sub>. Excitation wavelength was27 550 nm.

# 28 Molecular dynamics simulations of29 NC/calixarene complexes

30 To further rationalize our experimental data, and to 31 characterize the binding mode of selected calixarenes to NC, 32 we performed recognition experiments in silico through 33 molecular dynamics (MD) simulations. This method was 34 selected because of the complexity of calixarenes and the 35 flexibility of NC, which render other approaches (such as 36 molecular docking) ineffective towards this study. Each 37 calixarene was placed at a non-binding distance from the NC 38 surface (>40 Å) in a box of explicit water molecules, and then 39 unrestrained MD trajectories were produced for 0.5 µs in the 40 NPT ensemble. Using this approach, the four selected 41 calixarenes were found to recognize and bind NC, by 42 interacting with the basic surface at the top of the zinc fingers. 43 Similar to the previously reported complexes of calixarenes with isolated amino acids<sup>70,71</sup> or proteins<sup>60</sup>, the recognition 44 45 between calixarenes and the NC in silico is mostly driven by 46 electrostatic forces between the calixarene phosphonate or 47 sulfonate groups and basic NC residues (Figure 7 and Figure 48 S6 in the supplementary data). In contrast, OH or O-propyl 49 groups at the lower rim are exposed to the solvent and do not 50 seem to contribute to the binding of the protein. Similarly, no 51 interaction was observed with the specific hydrophobic 52 pocket of NC or through inclusion of the side chain of the key 53 residue Trp37 into the calixarene core. The formation of 54 NC/calixarene complexes is rather fast in MD simulations, as 55 observed by monitoring the distance between the target 56 residue and the mass center of the carbons bearing the 57 phosphonate or sulfonate groups (supplementary data, Figure 58 S7). Moreover, the NC/calixarene complexes were found to 59 be stable with time, since by analogy with other NC inhibitors<sup>66</sup>, we did not observe any dissociation of the 60 complexes during MD simulation. 61





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- As highlighted by the salt-dependence data of Figure 5, the 73 74 Coulomb electrostatic contribution in the final complexes 75 may be rather weak, due to the strong dielectric constant of 76 the solvent that considerably lowers electrostatic forces. In 77 fact, the NC/calixarene complexes are stabilized by cation- $\pi$ 78 stacking<sup>72,73</sup> and a number of H-bonds established directly, or 79 bridged by water molecules (Figure 7). In particular, 80 phosphonate groups at the upper rim of calixarenes C933, 81 C934, and CIP201 bind preferentially the side chain of Arg32 82 by both H-bond interactions and cation- $\pi$  stacking. The Arg32 83 residue is well included in the calixarene core of C933 (Figure 84 7A), and partially included in the core of C934 (Figure 7B). 85 In CIP201, the Arg32 residue is located at the upper rim of the calixarene molecule because the inner core is occupied by a 86 87 Na<sup>+</sup> ion (Figure 7C), whereas CIP200 targets the side chain of 88 Lys47, which is well included in the calixarene core (Figure 89 7D). 90 C933 and C934 proved to bind the NC in a highly comparable 91 manner by interacting with Arg32, as well as with Lys26, 92 Arg29, Lys34, and Lys47. C933 further interacts with Asn17 93 (Figure 7A), whereas C934 interacts with Lys3 and Gln45 94 (Figure 7B), this latter being also involved in the binding of
- other NC inhibitors<sup>65,66,74</sup>. Besides Arg32, CIP201 establishes 95
- H-bonds with Arg7, Lys14, Lys33, Lys34, and Glu42 (Figure 96
- 97 7C). In the case of CIP200, in addition to Lys47, the
- 98 compound interacts with Ile1, Gln2, Lys3, Arg10, Lys11,
- 99 Lys38, and Gln45 (Figure 7D).
- 100 Finally, to provide a structural explanation to the noticeable
- 101 entropic effect observed by ITC (Table 1), the change of NC
- hydration associated to the binding of CIP200 was evaluated 102

along MD trajectories. The comparison of the solvation of NC 103 104 target residues in the free protein (Figure S8A) with that in the 105 complex (Figure S8B) clearly shows that CIP200 displaces a 106 large number of water molecules from solvent-exposed NC 107 residues such as for example Lys47, in full line with the 108 measured increase in entropy.

109 Overall, MD simulations suggest that the phosphonate and 110 sulfonate groups of calixarenes are responsible for NC 111 recognition through long-range electrostatic interactions and for the stabilization of the final NC/calixarene complexes, 112 113 mainly through H-bond and cation- $\pi$  interactions with NC 114 basic residues. As a result, these molecules may inhibit NC by 115 competing with NAs for the binding to the protein and 116 occluding the accessibility to its hydrophobic pocket from the 117 solvent area.

118 To validity of the MD simulations is substantiated by the ITC 119 data with the NC(1-55)S3 mutant where the three positively 120 charged basic residues (<sup>32</sup>RKK<sup>34</sup>) of the linker acting as a 121 binding site for CIP201 are replaced by non-charged Ser 122 residues. ITC titration of NC(1-55)S3 by CIP201 revealed an 123 about one order of magnitude decrease in affinity as compared 124 to NC, with a significant change in the balance between the 125 enthalpy and entropy contributions (Table 1). Indeed, we 126 observed a two-fold less favourable  $\Delta H$  value together with a two-fold increase in the  $\Delta S$  value. These changes in  $\Delta H$  and 127 128  $\Delta S$  values strongly suggest that the binding of CIP201 is less 129 specific with the NC mutant as compared to NC <sup>75</sup>. Thus, the binding data with NC(1-55)S3 are fully in line with the MD 130 simulations and confirm the key role played by the <sup>32</sup>RKK<sup>34</sup> 131 132 sequence in the binding of CIP201.

### 2 Antiviral activity of CIP201 against wild-type 3 and drug-resistant HIV-1 strains

Next, our objective was to determine the antiviral activity of 4 5 the water soluble calixarene CIP201 acting as NC inhibitor. 6 Indeed, we selected this compound, as it remains highly 7 soluble in water (up to 100 mM) while the others calixarenes 8 were low soluble in aqueous solutions in the absence of 9 DMSO (solubility limits of C933, C934 and CIP200 were 10 measured at 400  $\mu M,\,6.5$  mM and 150  $\mu M$  respectively). To determine the antiviral activity of CIP201, we used two 11 cellular assays. The first one being based on Hela cells 12 13 infection with non-replicative pseudo-particles (anti-14 pseudovirus assay in Table 2) monitors only the inhibition of the early steps of infection. The second one being based on 15 16 cell infection by a wild-type HIV virus (NL4-3) is sensitive to inhibition in either the early phase of HIV infection 17 (MonoCycle) or both the early and late phases of HIV 18 infection (BiCycle). In both the anti-pseudovirus and 19 20 MonoCycle assays, CIP201 was found to inhibit HIV 21 infection with IC50 values of 3.3 - 21 µM with comparable 22 values in both MonoCycle and BiCycle assay, indicating that 23 this compound inhibited mainly, if not only, the early phases 24 of HIV replication. These  $IC_{50}$  values were found to be close 25 to the IC50 values of the NC chaperone assays (Figures 2 and 26 3) and the  $K_d$  values (Table 1). These similar values 27 determined by different independent experiments strongly 28 suggest that the antiviral activity of CIP201 may be related to 29 its ability to target NC. The cytotoxicity of CIP201 was very 30 low ( $CC_{50} > 5$  mM), giving an excellent selectivity index for this compound. However, it cannot be excluded at this step 31 32 that the low toxicity might be related to a limited cell 33 permeability of the compound.

<b>Table 2.</b> Antiviral activity and cytotoxicity of CIP201	•
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Anti pseudovirus assay <sup>a</sup>		Antiviral assays		
		MonoCycle	BiCycle	
			assay	assay
IC <sub>50</sub> <sup>a</sup>	CC50 <sup>b</sup>	SIc	IC <sub>50</sub> <sup>d</sup>	IC50 <sup>d</sup>
(µM)	(µM)		(µM)	(µM)
$21\pm3$	>5000	>230	$3.3 \pm 2$	$1.7\pm0.2$

<sup>a</sup> Inhibition activity of CIP201 on the infection of Hela cells by viral pseudoparticles.  $IC_{50}$  corresponds to the concentration at which the infection is decreased by 50%.  ${}^{b}CC_{50}$ : concentration required to cause 50% of cell death. <sup>c</sup> Selectivity index  $SI = CC_{50}/IC_{50}$ . <sup>d</sup> Inhibitory activities tested on HIV-1 wild-type reference strain NL4-3.

41

42	The compound CIP201 was then tested on a series of mutant
43	strains resistant to reference protease inhibitors (PI, strain
44	11808), nucleoside reverse transcriptase inhibitors (NRTI,
45	strain 7406), non-nucleoside reverse transcriptase inhibitors
46	(NNRTI, strain 12231) and integrase inhibitors (INI, strain
47	11845) (Table 3). CIP201 showed an antiviral activity against
,	

48 these representative resistant HIV-1 viral strains in the low 49 micromolar range, similar to that against the wild-type virus 50 (strain 114 i.e. NL4-3, Table 3). These data indicate that the 51 resistance mutations to drugs currently employed in clinical 52 practice do not affect the susceptibility to CIP201, reinforcing 53 the conclusion that NC could be the main target of the 54 calixarenes. Due to its favourable  $IC_{50}$  values and low toxicity, 55 CIP201 appears as a good starting point for the development 56 of new anti-HIV agents.

57 **Table 3.** Antiviral activity of CIP201 against drug-resistant 58 strains.

<sup>a</sup> Strain	IC50 (µM)	<sup>b</sup> Fold Change
114	$1.7 \pm 0.2$	1.0
(NL4-3)	1.7±0.2	1.0
11845	$23 \pm 0.4$	13
(INI)	$2.3 \pm 0.4$	1.5
11808	$1.8 \pm 0.1$	1.1
( <b>PI</b> )	1.0 ± 0.1	1.1
12231	$1.0 \pm 0.5$	0.6
(NNRTI)	$1.0 \pm 0.3$	0.0
7406	$1.5 \pm 0.2$	0.0
(NRTI)	$1.5 \pm 0.5$	0.9

<sup>a</sup> Reference number of the drug resistant strains obtained
through the NIH AIDS Reagent Program
(ARP,www.aidsreagent.org). <sup>b</sup>Ratio of the resistant virus
IC50 to wild-type reference virus IC50.

#### 63 Mechanism of action of calixarenes

64 As CIP201 was found to be active in the early steps of HIV replication, we performed complementary investigation to 65 66 further characterize its mode of action. As a first step, we 67 investigated the effects of CIP201 on the production of viral 68 nucleic acid intermediates. The data in Figure 8 suggests that 69 inhibition of HIV replication occurred mainly during pre-70 integration events. In particular, the amount of total HIV-1 71 DNA (Figure 8A) produced after reverse transcription (approximately 16 h post infection) was significantly 72 73 decreased in presence of CIP201. This decrease was similar 74 to that measured in the presence of rilpivirine (RPV), 75 indicating an impairment of reverse transcription or earlier 76 events. In contrast, CIP201 did not affect the levels of 2-LTR circles (Figure 8B). This absence of effect is in contrast with 77 78 the approximately 3 times higher amount of 2-LTR circles 79 observed with the integrase inhibitor raltegravir (RAL) as 80 compared to "no drug" control culture. This suggests that 81 CIP201 does not impair viral DNA integration. In addition, 82 the levels of intracellular HIV-1 RNA were comparable to 83 those measured in presence of RPV, reinforcing the 84 hypothesis of an early inhibitory activity for CIP201 (Figure 85 8C).





**Figure 8.** Quantification of HIV-1 nucleic acid intermediates produced in the presence of CIP201 (100  $\mu$ M), or reference compounds darunavir (DRV), rilpivirine (RPV), raltegravir (RAL) (2  $\mu$ M each) or no drug. (A) Total HIV-1 DNA measured at 16 hours post infection. (B) HIV-1 2-LTR DNA circles and (C) Intracellular HIV-1 RNA measured at 30 hours post infection. Values are shown as means with standard deviation bars derived from two measurements. Pairwise comparisons between CIP201 and each reference drug were made by Student t test. \*: p<0.05; \*\*: p<0.005.

- 94 In a second step, since compound CIP201 was observed to
- 95 possibly impair reverse transcription, we tested whether this
- 96 compound could directly inhibit RT activity. Using a FRET-
- 97 based assay previously developed in the laboratory<sup>76</sup>, CIP201
- 98 (Figure S9a) was found to strongly alter RT flipping and
- 99 polymerisation activity, indicating it may directly target RT.
- 100 Its effect was similar to that of Nevirapine, a non-nucleoside
- 101 RT inhibitor (NNRTI) that binds non-competitively to RT
- allosteric sites<sup>77,78</sup>. By fitting the dependence of RT inhibition
- 103 as a function of the concentration of CIP201 with equation (4),
- as a function of the concentration of CH 201 with equation (4), 104 an  $IC_{50}$  value of 0.9 (± 0.1)  $\mu$ M was determined for CIP201

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105 (Figure S9b), as compared to 49 ( $\pm$  4) nM for Nevirapine in

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- the same assay<sup>76</sup>. Altogether our data suggest that CIP201
  may have multiple molecular targets in HIV-1. However, as
  CIP201 is also active on RT resistant strains, it is believed that
  RT is not a major target of CIP201 in cellular assays and/or
  that CIP201 inhibits RT via a novel binding mode that is
  different from that of the established inhibitors.
- 112 To further decipher the mode of action of CIP201, we used a
- 113 Multi-Dosing Time protocol to test its effect comparatively to
- 114 reference inhibitors of entry (maraviroc), RT (lamivudine and
- 115 didanosine) and integrase (raltegravir) (Table 4).

<b>Table 4</b> . IC50 values obtained in the Multi-Dosing Time protocol using the pseudotype virus	assay.
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			Compounds	$IC_{50}$	
CIP201 incubation	CIP20 1	Maraviroc	Lamivudine	Didanosine	Raltegravir
Pre-incubation with the cells before infection	Inactive	$4.5 \pm 0.8 \text{ nM}$	Inactive	Inactive	Inactive
Incubation for 2 h during HIV-1 infection.	$19\pm2\;\mu M$	$5 \pm 2 \ nM$	$1.3 \pm 1 \text{ nM}$	$99 \pm 6 \text{ nM}$	$2\pm3\ \mu M$
Standard protocol for 48 h	$20 \pm 3 \ \mu M$	$7 \pm 3 \text{ nM}$	$1.3\pm0.6~nM$	$6.4\pm0.9~nM$	$4 \pm 1 \text{ nM}$
incubation for 2 h after viral entry	Residual activity	$3\pm 1 \; \mu M$	$0.6 \pm 0.4 \text{ nM}$	$9 \pm 2 \text{ nM}$	1.2 ± 1 nM
Incubation for 48 h after viral entry	Residual activity	$2.5\pm2~\mu M$	$1.3 \pm 0.7 \text{ nM}$	$120 \pm 40 \text{ nM}$	$4 \pm 3 \text{ nM}$

117  $IC_{50}$  values are expressed as a mean  $\pm$  SD. Two independent experiments were performed in triplicate.

118 In the standard protocol, CIP201 was incubated with the cells for 2 h during spinoculation and then, again for 48 h.

- 119 120
  - 121 When CIP-201 was pre-incubated with the cells for 2 hours 122 and then washed out before HIV-1 incubation, no effect was 123 observed on virus infection, suggesting that CIP201 likely 124 does not bind with high affinity to the plasma membrane in 125 order to protect the cells against HIV-1 infection. In contrast, 126 CIP201 protected U373-CD4-CCR5 cells against virus 127 infection when incubated together with the pseudotyped 128 viruses for 2 h (IC<sub>50</sub> =  $19 \pm 2 \mu$ M) or in the standard protocol where CIP201 was added both during spinoculation (for 2 h) 129 130 and at 2 h post-infection (for 48 h) (IC<sub>50</sub> = 20  $\pm$  3  $\mu$ M). 131 Moreover, CIP201 showed only residual activity when 132 incubated with cells 2 h post-infection (Figure S10 and Table

133 4). Thus, CIP201 resembles to the entry inhibitor maraviroc, 134 but differs from RT inhibitors that remain fully active when 135 provided for 2 or 48 h at 2 h post-infection. Therefore, our 136 data suggest that CIP201 mainly targets the HIV-1 entry step 137 during the first two hours of infection. The low activity of 138 CIP201 when provided 2 h after infection, in spite of its high 139 activity on NCp7 and RT in molecular assays, suggests that 140 CIP201 might not enter efficiently into cells. The lack of 141 activity on HIV-1 infection after cell pre-treatment wth 142 CIP201 and subsequent wash, confirms that CIP201 does not 143 enter efficiently into cells, and may primarily act by binding 144 to viral particles. Finally, its residual activity when added 2 h after infection (Figure S10) may tentatively be attributed to 145

- 1 CIP201 molecules that have been shuttled into cells through
- 2 viral particles docked on the cell surface, in order to inhibit
- 3 HIV-1 replication possibly by acting on RT and NCp7.
- 4

### 5 CIP201 activity in HIV-infected humanized NSG 6 mice

7 Finally, CIP201 was tested in humanized NSG mice 79 and 8 compared with the triple regimen Triumeq (abacavir, 9 dolutegravir, lamivudine) on viral replication and CD4 10 depletion after 7 weeks of treatment. After 5 weeks of HIV infection, although the mice have drunk the same volume of 11 12 sucralose solution among the three groups, we did not find any 13 effect of CIP201 on plasma viral load (Figure S10A) and on the CD4/CD8 ratio (Figure S10B) after 6 weeks of treatment. 14 In contrast, the mice treated with Triumeq reached 15 undetectable viral load and restored CD4 cell count. The 16 17 concentrations of CIP201 was further measured in the plasma, 18 spleen, liver and kidneys but was found to be below the LOD (i.e.  $10 \,\mu\text{g/mL}$ ). These results indicate that the lack of efficacy 19 20 of CP201 in infected humanized mice was probably due to 21 poor absorption, distribution, metabolism, and excretion 22 (ADME) and/or pharmacokinetic properties. Thus, CIP201 23 needs to be optimized for further development in therapy.

24

#### 25 **DISCUSSION**

26 Following our strategy to develop antiretroviral drug 27 candidates targeting the HIV-1 NC protein<sup>19</sup>, we evaluated the NC inhibitory properties and antiretroviral activity of a 28 number of functionalized calixarenes by means of an 29 30 integrated multidisciplinary approach. Using fluorescencebased methods, calixarenes C933, C934, CIP200 and CIP201 31 32 proved to inhibit efficiently the NC(11-55)-induced 33 destabilization of cTAR and subsequent annealing with 34 dTAR. Different from the largest class of NC inhibitors available to date, no zinc ejection was observed for these 35 36 molecules, making them valuable candidates for antiviral 37 therapy. Moreover, NC inhibition in the low to submicromolar range places these calixarenes within the most 38 potent non-zinc-ejecting NC inhibitors reported to date<sup>80,81</sup>. 39

40 By using ITC, the calixarenes were found to bind to NC with affinity in the low to sub-micromolar range in agreement with 41 42 the NC inhibition data. Moreover, the binding was found to 43 rely on balanced entropy and enthalpy contributions. This was further corroborated by MD simulation for each molecule, 44 45 showing that the recognition between NC and calixarenes is 46 driven by long-range electrostatic forces, and that calixarenes 47 bind basic residues at NC surface by means of H-bond and 48 cation- $\pi$  interactions, in line with the strong observed enthalpy 49 energy changes. Moreover, according to the binding mode 50 observed in the most populated cluster of MD frames, a 51 number of water molecules are released from NC residues 52 upon binding of calixarenes, consistent with the favourable entropy changes deduced from ITC. This release of water may 53 compensate for the loss of overall NC flexibility induced by 54 55 calixarene binding. From the ionic strength dependence of the

114

#### 115 CONCLUSION

affinity of calixarenes for NC, we further showed that the 56 57 binding of calixarenes C933, C934, CIP200 and CIP201 to 58 NC(11-55) involved about 1 ion pair and that non-59 electrostatic interactions represented 80% to 89% of the 60 binding energy at 30 mM NaCl. This suggests that long-range electrostatic interactions are likely required for recognition 61 between the two interacting species, but as suggested by MD 62 simulations, the complex is mainly stabilized by H-bonds, 63 64 cation- $\pi$  interactions and water release. Calixarenes C933, 65 C934, and CIP201 that bear phosphonate groups at the upper rim show a similar interaction pattern. They recognize and 66 bind basic residues of the NC linker (and notably Arg32) by 67 H-bond and cation- $\pi$  interactions, and establish a number of 68 69 H-bond contacts with basic residues at the top of zinc-fingers, a region of NC that is crucial for its biological functions.<sup>82,83</sup> 70 71 The key role of the basic residues of the NC linker in binding 72 to CIP201 was clearly confirmed using a NC mutant where 73 these residues were replaced by Ser residues (NC(1-55)S3, Figure 1a). Different from the other active calixarenes. 74 75 CIP200 is functionalized with sulfonate groups at the upper 76 rim, and targets the Lys47 by means of cation- $\pi$  interactions 77 through inclusion of the residue's side chain in its aromatic 78 core. CIP200 also interacts with a cluster of residues within 79 the N-terminal domain of NC, suggesting that the binding site 80 of calixarenes on NC may be modulated by specific functionalization at the upper rim of the aromatic core. 81

82 Importantly, the binding mode predicted for calixarenes was 83 not observed before for any type of NC inhibitors. The main 84 hypothesis that emerged by coupling computational with 85 biophysical and biochemical data is that this new binding 86 mode efficiently prevents NC to bind to its nucleic acid 87 targets. Moreover, the water soluble compound CIP201 was 88 found to inhibit replication of wild-type and drug-resistant 89 HIV-1 strains in a cellular model at low micromolar 90 concentration, by targeting the early steps of HIV-1 91 replication. Time of addition assays further revealed that 92 CIP201 has low cell permeability, likely due to its high 93 amount of negative charges, and mainly targets the viral entry 94 step. In addition, the residual activity observed after the HIV-95 1 entry step suggested that CIP201 molecules could have 96 entered cells when bound to viral particles and exerted their 97 antiviral activity on RT and NCp7 molecules. Both modes of 98 action are fully consistent with the low levels of HIV-1 DNA 99 and intracellular HIV-1 RNA measured in cells infected by 100 HIV-1 in the presence of CIP201.

101 Finally, CIP201 showed low cytotoxicity that can be at least 102 partly ascribed to the low cell permeability of the compound. 103 The low toxicity of CIP201 was further confirmed on infected 104 humanized mice, which showed no evidence of acute toxicity 105 during the treatment. Therefore, CIP201 stands as a very 106 interesting lead, since its efficacy in inhibiting HIV-1 107 replication is highly comparable to other NC inhibitors (Mori 108 et al, Sancineto et al, Iraci et al). Unfortunately, CIP201 was 109 found to be inactive in this animal model. This lack of efficacy 110 in vivo was related to the low compound's concentration in 111 blood and different organs, suggesting a high clearance and 112 poor tissue distribution likely due to its highly polar nature<sup>99</sup>. 113

116 In this study, we identified the CIP201 calixarene as an 117 antiviral compound active against both HIV-1 reference virus 118 and resistant viral strains, mainly by inhibiting the HIV-1

entry step. CIP201 was also found to inhibit the nucleic acid 1 2 chaperone activity of the HIV-1 NC as well as the flipping 3 and polymerisation activity of RT in molecular assays. The 4 inhibition of NC was predicted to result from the interaction 5 of CIP201 via its phosphonate or sulfonate groups with the basic surface of NC, which blocks the binding of NC to its 6 7 nucleic acid targets. This binding mode differs from that of 8 most other noncovalent NC inhibitors that target the 9 hydrophobic platform at the surface of the NC zinc fingers 10 (Mori et al, 2015). Importantly, due to its low permeability 11 the antiviral activity of this multi-target compound is certainly underestimated. Thus, CIP201 appears as a very promising 12 candidate for the development of anti-HIV drug candidates 13 14 targeting the NC.

However, efforts are still needed to further increase its 15 16 efficacy and improve its ADME and pharmacokinetic properties. To this aim, hit-to-lead optimization of CIP201 17 could be driven by the necessity to tune the hydrophilic-18 hydrophobic balance in order to ensure a better 19 20 pharmacokinetics profile and to enhance in vivo activity. This could be accomplished by chemical modifications at the lower 21 22 (narrow) rim or the upper (wide) rim of the macrocycle. 23 Interestingly, thiacalixarenes offer almost unlimited 24 possibilities for chemical modifications, including the 25 derivatization of the hydroxyl groups at the lower rim, or the 26 four reactive para-positions of benzene rings at the upper rim 27 by the inclusion of different functional groups with specific 28 chemical or physicochemical features. In the specific case of 29 CIP201, the phosphonate groups could be replaced by 30 bioisosters or other negatively charged groups such as for 31 instance the carboxylic acid, sulfone, triazole, and tetrazole 32 rings. In addition, sulfur atoms can be oxidized to convert the thiacalixarenes into calixarene sulfoxides or calixarenes 33 sulfone with four or six valent sulfur atoms respectively. 34 Besides chemical modifications, conformational changes to 35 36 the macrocyclic core can be designed in order to achieve 37 optimal interaction with NC. Thanks to the accessible 38 chemistry of calixarenes, and the reliable computational 39 protocol developed in this work, a large number of thiacalixarene derivatives could be preliminarily screened and 40 41 prioritized in silico for their interaction with NC, although this will be the subject of future works. 42

#### 43 **EXPERIMENTAL SECTION**

#### 44 Materials

45 All solvents for spectroscopic measurements were from

- 46 Sigma-Aldrich (Darmstadt, Germany). Acetonitrile was 47 purchased from Sigma-Aldrich (Darmstadt, Germany) with
- 48 high degree of purity for the HPLC analysis.
- 49 The synthesis and the characterization of the calixarenes used
- 50 in this study are described in the supplementary information.
- 51 Calixarenes C145 and CIP201 were directly solubilized in
- 52 water while the other calixarenes were first dissolved in
- 53 DMSO. Unless mentioned otherwise, experiments were
- 54 carried out in Tris buffer (25 mM Tris-HCl pH 7.5, 30 mM
- 55 NaCl, and 0.2 mM MgCl<sub>2</sub>)<sup>59</sup>. The percentage of DMSO was

- 56 between 1.3 and 2 % v/v in the final reaction mixtures. Fresh
- 57 calixarene solutions were prepared before all experiments.

#### 58 **Proteins**

59 In order to reduce the NA-aggregating properties<sup>58,101,102</sup> of the full-length NC which causes substantial light-scattering, we 60 performed the majority of experiments with the NC(11-55) 61 peptide (Figure 1a). This truncated peptide possesses the zinc 62 63 finger domain and aggregates NAs only at high concentrations<sup>58,103</sup>. NC, NC(1-55)S3 and NC(11-55) peptides 64 65 were synthesized by solid-phase peptide synthesis on a 433A 66 synthesizer (ABI, Foster City, CA), as previously described<sup>56,104</sup>. Peptides were stored lyophilized. The zinc-67 bound form of the peptides was prepared by dissolving them 68 in water, adding a 2.5-fold molar excess of zinc sulphate, and 69 70 raising the pH to its final value by adding buffer. The pH was 71 increased to its final value only after addition of zinc to avoid 72 the oxidation of the zinc-free peptide. The peptide 73 concentration was determined by using an extinction coefficient of  $5.7 \times 10^3 \, M^{\text{-1}} \, \text{cm}^{\text{-1}} \text{at } 280 \, \text{nm}$  for NC and NC(11-74 75 55).

#### 76 Oligonucleotides

77 All unlabelled and labelled oligodeoxynucleotides (ODNs) were synthesised and purified by IBA GmbH Nucleic Acids 78 79 Product Supply (Göttingen, Germany). Their concentrations 80 were determined by UV absorbance at 260 nm. For the doubly 81 labelled cTAR, the 5' terminus was labelled with 6-82 carboxyrhodamine (Rh6G) or with Alexa Fluor 488 via an 83 amino linker with a six carbon spacer arm. The 3' terminus of 84 cTAR was labelled with 4-(4'-85 dimethylaminophenylazo)benzoic acid (Dabcyl) using a 86 special solid support with the dye already attached. The singly 87 labelled cTAR labelled was with 88 carboxytetramethylrhodamine (TMR) at its 5' terminus. The 89 ODNs were purified by reverse-phase high performance 90 liquid chromatography (HPLC) and polyacrylamide gel electrophoresis. Extinction coefficients at 260 nm of  $5.15 \times$ 91 92  $10^{5} M^{-1} cm^{-1}$ , 5.56×10<sup>5</sup>  $M^{-1} cm^{-1}$ , 5.775 ×10<sup>5</sup>  $M^{-1} cm^{-1}$ , and 5.73 93  $\times 10^5$  M<sup>-1</sup> cm<sup>-1</sup> were used to determine the concentration of 94 dTAR, TMR-5'-cTAR, Rh6G-5'-cTAR-3'-Dabcyl, and 95 Alexa488-5'-cTAR-3'-Dabcyl, respectively.

#### 96 Absorption and fluorescence spectroscopy

97 Absorption spectra were recorded with a Cary 400 or a Cary 98 4000 spectrophotometer (Agilent). Fluorescence spectra and 99 anisotropy measurements were recorded at 20°C with a 100 Fluorolog or a Fluoromax 3 spectrofluorometer (Horiba 101 Jobin-Yvon) equipped with a thermostated cell compartment. 102 Excitation wavelengths were 520 nm for Rh6G-5'-cTAR-3'-103 Dabcyl, 550 nm for TMR-5'-cTAR, and 480 nm for 104 Alexa488-5'-cTAR-3'-Dabcyl. The spectra were corrected 105 for dilution, buffer fluorescence and wavelength-dependent 106 response of the optics and detectors.

107 To screen calixarenes (Cal), we used an assay in which we 108 tested their ability to inhibit the NC-induced destabilization of 109 cTAR<sup>59</sup>. The percentage of inhibition (% inh) obtained for 110 each calixarene concentration was calculated with equation 111 (3):

$$\%inh = \frac{I_{(cTAR+NC)} - I_{(cTAR+NC+Cal)}}{I_{(cTAR+NC)} - I_{(cTAR)}} \times 100$$

(4)

2 where  $I_{(cTAR)}$ ,  $I_{(cTAR+ NC)}$ , and  $I_{(cTAR+ NC+ Cal)}$  correspond to the 3 fluorescence intensity of cTAR alone, cTAR in the presence 4 of the NC(11-55)peptide, and cTAR in the presence of both 5 NC(11-55) and calixarene, respectively. To determine the  $IC_{50}$ 6 values, we plotted the percentage of inhibition against the 7 calixarene concentration (*C*) and fitted it with a modified 8 version of the dose-response equation<sup>105</sup>:

9 % 
$$inh = A_1 + \frac{(A_2 - A_1)}{1 + 10^{(\log(IC_{50}) - \log(C)) \times p)}}$$

10

11 where,  $A_1$  and  $A_2$  represent the percentage of inhibition in the 12 absence and with saturating concentrations of calixarene, 13 respectively. *IC*<sub>50</sub> represents the half maximal inhibitory 14 concentration, and *p* denotes the Hill coefficient.

Annealing kinetics were measured in pseudo-first order 15 conditions by adding a 10-fold excess of unlabelled dTAR to 16 17 the doubly labelled complementary sequence Alexa488-5'-18 cTAR-3'-Dabcyl. Excitation and emission wavelengths were 19 set at 480 nm and 519 nm, respectively to monitor the Alexa 20 488 fluorescence. NC(11-55) was added at a 8:1 molar ratio 21 to each reactant separately, and then the reaction was initiated 22 by mixing the peptide-coated ODNs together. Calixarenes 23 (C933, C934, CIP200 and CIP201) were added at different 24 concentrations to monitor their ability to perturb the NC-25 promoted cTAR/dTAR annealing rate constants  $k_{obs}$ . All 26 fitting procedures were carried out with Origin 8.6 software 27 using nonlinear least-squares methods and the Levenberg-

28 Marquardt algorithm.

# 29 Mass spectrometry in non-denaturing 30 conditions

31 Electrospray ionization mass spectrometry (ESI-MS) analysis 32 was performed in the positive ion mode on an electrospray 33 time-of-flight mass spectrometer (LCT, Waters, Manchester, 34 UK) equipped with an automated nanoESI source 35 (TriversaNanomate, Advion, Ithaca, NY). Calibration of the 36 instrument was performed using a 2 µM horse heart 37 myoglobin solution prepared in a mixture of water: acetonitrile 38 (1:1) acidified with 1% of formic acid. MS data were acquired 39 and analysed using the MassLynx 4.1 software (Waters, 40 Manchester, UK). For mass spectrometry experiments in nondenaturing conditions, NC(11-55) was prepared in water with 41 42 2.2 molar equivalents of ZnSO<sub>4</sub> and the concentration was 43 measured using an extinction coefficient of 5700 M<sup>-1</sup> cm<sup>-1</sup> at 44 280 nm. Before use, the protein was buffered with 50 mM 45 ammonium acetate (AcONH<sub>4</sub>) at pH 7.0. NC(11-55) protein (20 µM) was incubated with 200 µM of calixarenes(10 fold 46 47 excess, 1% of DMSO v/v in the final volume) at 20 °C for 15 48 min, before recording the mass spectra. In order to balance the 49 weak ionization due to the presence of DMSO, the analyses 50 under non-denaturing conditions were carried out with an 51 accelerating voltage (Vc) of 100 V, and the pressure in the 52 first pumping stage (backing pressure) of the instrument was fixed to 6 mbar. 53

#### 54 Isothermal Titration Calorimetry (ITC)

55 The binding of NC, NC(1-55)S3 and NC(11-55) to 56 calixarenes was investigated by Isothermal Titration 57 Calorimetry (ITC), using a Nano ITC microcalorimeter (TA

Instruments) at 20°C, in Tris-HCl (25 mM, pH 7.5) containing 58 59 0.2 mM MgCl<sub>2</sub> and 10, 30, 50 or 100 mM NaCl. The titration 60 experiments were performed by incremental injections (each 61 200 or 300s) of 2.5 µL aliquots of calixarene solutions(100, 62 150 or 200 µM)in 300 µL of a 8 µM peptide solution 63 contained in the reaction cell. The heat flow ( $\mu$ cal $\times$  s<sup>-1</sup>) 64 resulting from the interaction between the two partners was 65 continuously recorded. The quantity of heat Q accompanying 66 each injection was integrated over time and corrected for the 67 heat of dilution measured in an independent experiment in which the calixarene solution was injected into the buffer 68 69 alone. Instrument control, data acquisition, and analysis were 70 done with the NanoAnalyze software provided by the 71 manufacturer. Assuming 1:1 binding stoichiometry, the molar 72 heat of binding  $\Delta H^0$  and the binding dissociation constant  $K_d$ 73 were obtained by fitting the differential heat  $dO/dX_{tot}^{106}$  as a 74 function of the total calixarene concentration ( $[Cal]_{tot}$ )to 75 equation (5):

76

77 
$$\frac{1}{V_0\left(\frac{dQ}{dX_{tot}}\right)} = \Delta H^0\left(\frac{1}{2} + \frac{1 - \frac{(1+r)}{2} - X_r/2}{(X_r^2 - 2X_r(1-r) + (1+r)^2)^{1/2}}\right)$$
78 (5)

79 with  $1/r = [Cal]_{tot}K_d$ ,  $Xr = X_{tot}/[Cal]_{tot}$  and  $X_{tot}$  is the peptide 80 concentration in the reaction cell of volume  $V_0$ .

#### 81 Molecular Dynamics (MD) simulations

82 The ionization state of calixarenes was investigated by 83 **OUACPAC** from OpenEye, version 1.7.0.2 84 (https://www.eyesopen.com/quacpac). Partial charges were 85 then assigned at the am1-bcc level by antechamber from Amber12<sup>107,108</sup>. The full length NC from the NMR structure of 86 its complex with a small molecule (PDB: 2M3Z)<sup>98</sup> was used 87 88 as starting point in MD simulations after removal of the bound 89 ligand. MD simulations were performed with Amber12. The 90 ff12SB force field was used together with custom force field 91 parameters for Zn-binding residues and coordinated Zn ions, 92 as described previously<sup>17</sup>. A time step of 2 fs was used. C-H 93 bonds were restrained by the SHAKE algorithm. For each 94 system studied in this work, one molecule of NC and one 95 molecule of calixarene were placed in a rectilinear box of 96 TIP3P water molecules at a random distance higher than 40 Å 97 from each other. Neutrality of the system was achieved by 98 adding the proper number of Na<sup>+</sup> counter-ions. Each solvated 99 system was then submitted to a two-step energy minimization. 100 In the first step, water molecules were minimized around the 101 frozen solute (NC + calixarene), while in the second step the 102 solvated solute was energy minimized until convergence 103 (rmsd = 0.05). Each system was then heated up to 300 K 104 during 55 ps in the NVT ensemble and then equilibrated in 105 density for 110 ps at constant pressure. After these steps, 106 unrestrained MD trajectories were produced for 0.5 µs in the 107 NPT ensemble. Four replicas of MD trajectories of 0.5 µs 108 each were run to enhance statistical significance. Analysis of 109 MD trajectories was performed with cpptraj<sup>109</sup>. Electrostatic surface potential was calculated by the APBS program<sup>110</sup>. 110

#### 111 Cell-based antiviral assay with replication-112 defective HIV pseudoparticles

This assay (described in supplementary information) is based 1

2 on the infection of Hela cells by replication-defective HIV particles pseudotyped with the Vesicular Stomatitis Virus

3 4

glycoprotein<sup>111</sup> that bypass entry and mimic the early steps of

5 the HIV virus infection cycle (post-entry to integration).

6 For each tested calixarene, the percentage of inhibition (%inh) 7 was calculated with :

8

9 
$$\%inh = \frac{(Controlluciferasevalue) - (Sampleluciferasevalue)}{(Controlluciferasevalue)} \times 100$$
10
11 (6)

12 Each concentration of compound was tested in sextuplicate. The reverse transcriptase inhibitor AZT (1 µM) was used as a 13 14 positive control. To determine the  $IC_{50}$  values, we plotted the 15 percentage of inhibition against the calixarene concentration 16 and fitted it with the dose-response equation (4).

17 In parallel to the infectivity test, the cytotoxicity of the molecules was quantified in a MTT assay (3-(4,5-18 dimethylthiazol-2-yl)-2,5-diphenyl tetrazolium bromide)<sup>112</sup>. 19 20 Another plate of HeLa cells was thus prepared and treated in 21 the same conditions as for the infectivity assay. 24 h after 22 infection, the medium was replaced by a mix containing 100 µL of DMEM and 10 µL of 12 mM MTT solution in PBS and 23 24 cells were incubated during 4 h. In order to dissolve the 25 insoluble purple formazan reduced by living cells, 85 µL of 26 the mix was replaced by 50 µL of DMSO and gently shaken 27 for 10 min. The absorbance was then measured at 540 nm in 28 a spectrophotometer (Safas, Monaco) and expressed in 29 percentage of cytotoxicity, using the DMEM + DMSO 30 solution as the control.

#### Cell-based antiviral assay with replication 31 competent HIV-1 strains 32

33 The antiviral activity of calixarene CIP201 was evaluated by 34 measuring its IC50 values against the HIV-1 wild-type 35 reference strain NL4-3 and a panel of viruses with resistance 36 mutations to approved HIV-1 drugs (supplementary data, 37 Table S1) in a TZM-bl cell line based phenotypic assay<sup>113</sup>. 38 TZM-bl cells are characterized by luciferase and β-39 galactosidase reporter genes integrated in the cell genome 40 under the control of an HIV-1 LTR promoter. The expression 41 of reporter genes is regulated by the viral Tat protein, which 42 is produced following transcription of the integrated provirus. 43 Since the NC viral protein is thought to be involved in both 44 early and late events of HIV-1 life cycle, we adopted a re-45 infection assay, named BiCycle Assay, consisting in a first 46 cycle of replication in the T-cell derived MT-2 cell line 47 followed by an additional round of replication in TZM-bl 48 cells. MT-2 cells were seeded at a concentration of 50,000 49 cells/well in a 96-well plate and infected with the viruses at 50 multiplicity of infection (M.O.I.) 0.1 in the presence of five-51 fold dilutions of the compounds. After 48-72 h, 50 µL of 52 supernatant from each well, containing the virus produced in 53 the first round of infection, were used to infect TZM-bl cells seeded in a 96-plate well at a concentration of 30,000 54 55 cells/well. Two days later, cells were lysed by adding 40 µL of Glo Lysis Buffer (Promega) in each well for 5 min, then 40 56 57 µL of Bright-Glo Luciferase Reagent (Promega) were added 58 to each well for relative luminescence units (RLU) counting 59 using a Glo-Max Multi Detection System (Promega). RLU

values from each well were used to calculate the  $IC_{50}$  value of 60 each compound using the GraphPad v6.0 software. The 61 62 inhibition of the early events of viral replication was evaluated 63 through a single cycle replication assay in TZM-bl cells, 64 named MonoCycle Assay. The method consists in the infection of TZM-bl cells at M.O.I. 0.1 in presence of serial 65 66 five-fold dilutions of the drugs, similarly to the first round of infection of BiCycle Assay. After 48 hours, RLUs were 67 68 counted and  $IC_{50}$  values were calculated using the GraphPad 69 software. The reference drug-resistant viruses were obtained 70 through the NIH AIDS Reagent Program (ARP, 71 www.aidsreagent.org) and have been already characterized by 72 the Phenosense Assay (Monogram Biosciences), considered 73 as the reference assay for phenotypic investigation of HIV 74 drug resistance due to its consistent application in clinical 75 trials. The infectious clones were firstly transfected in 293LX 76 cells and then expanded in MT-2 cells.

#### Impact of CIP201 in the production of viral 77 78 nucleic acid intermediates

79 The mechanism of action of calixarene CIP201 was evaluated 80 through the quantification of viral nucleic acid intermediates produced during HIV-1 replication in cell culture. MT-2 cells 81 82 were infected with NL4-3 wild-type strain at M.O.I 0.1 in 83 presence of 100 µM of CIP201, or the reference integrase 84 inhibitor raltegravir, the protease inhibitor darunaviror the 85 reverse transcriptase inhibitor rilpivirine, all at 2 µM. The amount of viral cDNA produced after reverse transcription 86 87 was quantified through a real time PCR targeting the LTR 88 region at 16 h post infection, while 2-LTR circles and 89 intracellular viral polyadenylated RNA transcripts were 90 quantified with a specific real time protocol at 30 h post 91 infection. Each of the three HIV-1 nucleic acids species was 92 measured in two separate experiments and the values obtained 93 with CIP201 were compared pairwise with the values 94 obtained with each of the reference drugs considered, by 95 Student t test.

#### SUPPLEMENTARY DATA 96

97 Calixarene synthesis and characterization, CIP200 and 98 CIP201 do not eject zinc from NC(11-55), Binding of 99 calixarenes to NC(11-55), Absence of interaction of CIP201 100 with cTAR Molecular dynamics, Impairment of reverse 101 transcription by CIP201, Effect of CIP201 on cell infection 102 with the pseudotyped viruses, Evaluation of CIP201 in NSG 103 humanized mice infected with HIV-1, Antiviral assay with replication-defective HIV pseudoparticles, Description of 104 105 HIV-1 resistant strains.

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#### 117 DEDICATION

- 1 Authors wish to dedicate this work to their friends and collaborators Prof. Maurizio Botta and Prof. Olga 2
- 3 Zaporozhets, who passed away prematurely in 2019.

## 4 CONFLICT OF INTERESTS

5 None declared

6

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Calixarene CIP201

## Binding model of CIP201 to the HIV-1 nucleocapsid protein NC



 $K_d \approx 1 \ \mu M \implies$  blocks NC binding to nucleic acids  $\implies$  antiviral activity ( $IC_{50} \approx 1 \ \mu M$ ) with low cytotoxicity ( $CC_{50} > 5 \ mM$ ) on HIV-1 reference and resistant viral strains.