The cage complex $[\text{Pd}_2\text{L}_4]^4+$ (3) binds $n$-octyl glycosides in DCM/DMSO (9 : 1) solution with $K_a \approx 51 \text{ M}^{-1}$ for $n$-Oct-$\beta$-D-Glc and $K_a \approx 29 \text{ M}^{-1}$ for $n$-Oct-$\alpha$-D-Gal.

Carbohydrates are Nature’s most abundant and versatile molecules. Several diseases have been linked to processes involving carbohydrates (e.g. diabetes, infection, and cancer metastasis). Many other regular processes are also mediated by carbohydrate molecules, including fertilization, neuronal development, hormonal activities, immune surveillance and inflammatory responses. Understanding and intervening in these processes are therefore exploited in medicinal therapies, which generally have relatively low aqueous solubility binding molecules. One example is the macrocycle $1$, which generally have relatively low affinities for their target monosaccharides ($K_a \sim 10^{-2} - 10^{-3} \text{ M}^{-1}$) and are often rather non-selective. An inspirational exception is the affinity of $E. \text{coli}$ galactose chemoreceptor protein for glucose ($K_a = 10^{3} - 10^{4} \text{ M}^{-1}$). The structure of the binding site of this complex is shown in Fig. 1a (2GBP) and reveals a high degree of interaction complementarity. Two aromatic residues (Trp and Phe) sandwich the flat glucose molecule with hydrophobic CH⋯π interactions and an array of polar residues complement the hydroxyl exterior of glucose by hydrogen bonding. This interaction complementarity has been mimicked by artificial carbohydrate binding molecules. One example is the macrocycle $1$ shown in Fig. 1b, which comprises pyrenyl surfaces for CH⋯π interactions and polar isophthalamide spacers for hydrogen bonding. One drawback of such covalent constructs, however, is that their synthetic routes culminate in one (or more) macrocyclization step(s) that rarely exceed ∼20%. This drawback can in principle be remedied if the cyclization is accomplished by use of dynamic bonds, such as coordination bonds between a ligand (L) and a transition metal (M). Interestingly, $[\text{M}_2\text{L}_4]^+$ complexes in which M is a square planar $\alpha$ metal (e.g. Pd or Pt) and L is a dipyrilid ligand have been known for more than 20 years and generally have a fairly small cavity. While such $[\text{M}_2\text{L}_4]^+$ complexes are typically filled with counter anions, complex 2 shown in Fig. 1c was recently reported to bind $\alpha$-sucrose using CH⋯π interactions.

We envisioned that the polar isophthalamide spacers employed in $1$ could be combined with the easy synthesis of $[\text{M}_2\text{L}_4]^+$ type complexes such as 2. Indeed, structures like 3 shown in Fig. 1d have been reported, although they were mainly studied in the solid state and are reportedly only sparingly soluble in solvents such as $N,N$-dimethylformamide (DMF) and dimethyl sulfoxide (DMSO). Herein, we report a version of cage $3$ (cage 3') that is soluble in apolar media and show that the cavity of $3'$ binds to $n$-octyl glycosides. This facile

---

**Fig. 1** Cage design for binding carbohydrates: (a) Galactose lectin (2GBP) with $\alpha$-glucose, (b) Covalent macrocycle $1$, (c) Coordination cage 2 with aromatic (hydrophobic) spacers, (d) Coordination cage 3 with polar spacers (also used in this work). $R$ = a group that can be used to control solubility.
solubilisation was realized by installation of an aliphatic dendritic side group (R'), as is shown in Scheme 1.

The synthesis of the solubilizing group started with triple alkylation of acetonitrile with 3,3-dimethyl-1-bromobutane (4), which was obtained by bromination of the commercial available alcohol. The resulting nitrile 5 was reduced to amine 6, which was used to displaced one pentafluorophenyl (PFP) on 1,3,5-benzenetricarboxylic acid tris-PFP ester to form intermediate 7. The resulting compound was treated with a six-fold excess of 3-aminopyridine (8) forming the desired ligand 9 in 75% isolated yield (see section S2 for full details).

The intended [Pd₉]⁺⁺ caging complex was readily prepared in DMSO-δ₆ as is detailed on pages 22–30 of the ESL† To study this cage and its binding properties in a less competitive matrix, we probed if complex synthesis was also possible in a CD₂Cl₂/DMSO-δ₆ (9 : 1) solvent mixture.

As is shown in Fig. 2a, the stepwise addition of [Pd(MeCN)₄][BF₄]₂ to ligand 9 in this mixture resulted in significant downfield shifts and signal broadening of the ¹H-NMR signals in the aromatic region of 9 (∼7–10 ppm). No more changes were observed after a 50% excess of Pd. Sonication of this sample resulted in a well-defined spectrum of a major species in which all protons originating from 9 can be identified and are consistent with cage structure [Pd₉]⁺⁺ (i.e. 3'). The large downfield shifts of protons such as a (8.35 → 9.09 ppm) and d (8.89 → 9.87 ppm) are highly indicative of pyridyl-Pd coordination.¹⁻³ The DOSY NMR of this sample is shown in the bottom of Fig. 2a, and reveals that the diffusion constant (D) of the major species is substantially smaller than that of ligand 9 alone (log(D) = −9.42 vs. −9.21 for 9). Applying the Stokes–Einstein equation ñ to the measured log(D) of −9.42 predicts a radius of about 13.9 Å. This radius is in line with an estimated mean radius of 17.5 Å of a model 3', assuming the complex has an overall oblate spheroid shape (see Fig. S65†). Moreover, as is depicted in Fig. 2b, the isotope distribution and highest intensity isotopic mass of the major species measured in the final solution is in agreement with a 2 : 4 Pd : 9 ratio expected for [Pd₉]⁺⁺ (m/z = 694.8864, highlighted in yellow).

The binding of cage 3' for n-oct-β-D-Glc (10) and n-oct-β-D-Gal (11) was investigated by ¹H-NMR titration experiments in CD₂Cl₂/DMSO-δ₆ (9 : 1). Selected spectra of such a titration with 10 are shown in the left-hand side of Fig. 3 (see Fig. S51 and S59† for complete spectra of titrations with 10 and 11). With increasing concentration of glucoside 10, all resonances of 3' in the aromatic region (∼7–11 ppm) broadened and shifted. The resonances for the inwards oriented H-atoms labelled d (9.9), e (10.7) and f (9.0) broaden to an extend that they could barely be detected at 115 mM concentration of 10.

Fig. 2 Formation and characterization of 3’. (a) Top: NMR data of formation of 3’ from ligand 9 by stepwise addition of [Pd₉][MeCN]₄][BF₄]₂; bottom: comparison of DOSY NMR of 3’ and 9. (b) CSI HRMS isotope distribution of 3’ (4 + species) with indicated highest isotopic mass (measured, top and simulated, bottom).

Fig. 3 (a) Titration with OctGlc. (b) Plot experimental vs. calculated data for 1 : 1 binding for proton a. (c) Plot experimental vs. calculated data for 1 : 1 binding for proton g.
In contrast, the signals of H-atoms a (9.1) and g (8.6) remain much sharper throughout the titration and these data can be fitted to a 1:1 model of $3' \subset 10$. As is shown in the right-hand side of Fig. 3, both fits are consistent with an association constant ($K_a$) of 5.11 ± 1.8 M$^{-1}$.

A similar titration with n-oct-$\beta$-Gal (11) gave comparable observations, leading to a $K_a$ of 29.1 ± 4.8 M$^{-1}$ (Fig. S59 and S61†). This lower binding affinity of $3'$ for 11 can be rationalized by the axial hydroxyl group in the galactoside, presumably leading to a worse fit of 11 inside $3'$.

To probe if, as these data suggest, a simple 1:1 $[3' \subset 10]^{\ddagger \ddagger}$ complex had formed, this sample was investigated further. The DOSY-NMR spectrum of the sample (see Fig. S56†) gave a similar diffusion constant as pure cage $3'$ (Fig. 2a), indicating that the cage is still intact. Moreover, as can be seen in Fig. 4a, a cold spray ionisation high resolution mass spectrometric analysis (CRS-HRMS) revealed a species with a mass and isotope distribution consistent with the anticipated 1:1 molar ratio of $[3' \subset 10]^{\ddagger \ddagger}$ ($m/z$ = 767.9344). Shown in Fig. 4b is the full $^1$H-NMR spectrum of the sample (top), together with several of the $^{19}$F signals of $[3' \subset 10]^{\ddagger \ddagger}$ (a) or the glucoside (b). As can be seen from Fig. 5c, glucoside 10 establishes a total of four hydrogen bonds in this model, but only involving two out of four polar spacers; p3 (e...O1 and e...O6) and p4 (e...O4 and e...O5). The model thus suggests that the cavity in $3'$ is somewhat too large to fully encapsulate a glucoside such as 10 by hydrogen bonding. This in turn might rationalize the moderate binding affinity of $3'$ for glucoside 10 ($K_a \approx 51$ M$^{-1}$). There are also several weaker interactions between the inwards pointing pyridyl hydrogens d, and some hydroxyl O-atoms to which likely further stabilize the complex (shortest is 2.46 Å with O4). Such interactions have been observed as the major binding interaction in similar M2L4 complexes that do not have the much more acidic amide NH protons present in $3'$.

In conclusion, a new building block (9) is reported that forms a self-assembled molecular cage ($3'$) in the presence of Pd$^{2+}$. The cage has the proper size and functional groups to bind n-oct-$\beta$-Glc (10) with a $K_a$ of 51 M$^{-1}$ or n-oct-$\beta$-Gal (11) with 29 M$^{-1}$. We consider these relatively low affinities as a promising first step in establishing the principle that M2L4-like cages with a $H$-bonding interior such as $3'$ can bind carbohydrates in very competitive media. As such, one can actually

![Fig. 5 Molecular model of $[3' \subset 10]^{\ddagger \ddagger}$ obtained by a combined conformational search (MMFF) and DFT geometry optimization of the core structure with (nBu97X-D/6-31G*) as seen from the ‘top’ (a) or the ‘side’ (b) of the complex (see note † in text). In (c) a zoom-in of the hydrogen bonding pattern is presented. The average of the eight shortest d-CH⋯–HC(10) distances is 2.59 Å, while this is 3.65 Å for the eight shortest e-NH⋯–HC(10) distances (only very weak nOe observe, see Fig. 4b).

Fig. 4 CSI HRMS isotope distribution of $[3' \subset 10]^{\ddagger \ddagger}$ with indicated monoisotopic mass (measured, top and simulated, bottom) (a) and 1D selective nOe of $[3' \subset 10]^{\ddagger \ddagger}$ with $t_{180} = 500$ ms (b). See Fig. S60† for full mass spectrum, Fig. S58† for more nOe spectra, and see Fig. S59† for a plot with linear fit of peak intensity vs. $t_m$ in the region 50–700 ms.
consider these affinities as significant in the CD$_2$Cl$_2$/DMSO-d$_6$ (9 : 1) solvent used. It is known that DMSO is one of the most competitive solvents for carbohydrate recognition$^5$ and the first reported covalently-assembled cage for carbohydrate binding in a competitive medium (a biphenyl analogue of 1) has an affinity ($K_a$) of merely 4.6 M$^{-1}$ for α-glucose in water.$^{20}$

The ease with which carbohydrate binders such as 3′ can be prepared bodes well for their further development. We thus anticipate that future studies will unveil structures with improved affinities and selectivity.

Conflicts of interest
There are no conflicts to declare.

Acknowledgements
This research was financially supported by the Netherlands Organisation for Scientific Research (NWO) with VIDI grant number 723.015.006.

Notes and references
† Complex formation in DMSO-d$_6$ also led to a major species, although many other smaller peaks were also clearly visible (Fig. S27). These peaks reversibly disappeared when the sample was heated to 80 °C (see Fig. S29† for a VT study), indicating that the additional peaks originate from conformational flexibility in X.
§ Stokes –Einstein equation:

$$D = \frac{kT}{6\pi\eta r}$$

wherein $D$ is the molar diffusion coefficient (assuming a spherical size of the molecule), $k$ is the Boltzmann constant, $T$ is the temperature in Kelvin, $\eta$ the viscosity of the liquid and $r$, the hydrodynamic radius of the molecule. See section S1 of ESI for further details.

An initial model of [3′C10]$^+$ was subjected to a conformational search with the Merck Molecular Force Field MMFF (including the dendrimers), leading to one major binding conformer. The binding pocket of this structure was optimized with DFT/B97X-D/6-31G* leading to the core structure depicted in Fig. 5 (i.e., as depicted in Fig. 2 with $R’ = \text{CH}_3$). All the atoms in this structure were frozen again and the geometry of the resulting [3′C10]$^+$ structure was allowed optimize with MMFF to yield the final model used (while keeping the DFT optimized core-structure frozen). Calculations were done with Spartan 2016.

An initial model of [3′C10]$^+$ was subjected to a conformational search with the Merck Molecular Force Field MMFF (including the dendrimers), leading to one major binding conformer. The binding pocket of this structure was optimized with DFT/B97X-D/6-31G* leading to the core structure depicted in Fig. 5 (i.e., as depicted in Fig. 2 with $R’ = \text{CH}_3$). All the atoms in this structure were frozen again and the geometry of the resulting [3′C10]$^+$ structure was allowed optimize with MMFF to yield the final model used (while keeping the DFT optimized core-structure frozen). Calculations were done with Spartan 2016.


