Electronic Supplementary Information

Complexation mechanism of cucurbit[6]uril with hexamethylene diammonium cations in saline solution

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Simulation Details

The simulation systems were consisted of two kinds of molecules, viz. the sodium ion and hexamethylene diammonium (HD^{2+}), binding to cucurbit[6]uril (CB[6]). The initial coordinate of CB[6] was taken from three−dimensional crystal structure.[1] Four systems have been constructed to study the following processes. CB[6] successively binds with two sodium ions, resulting in two complexes, viz. CB[6]:Na^+ and CB[6]:$(Na^+)_2$. Furthermore, CB[6] binding with HD^{2+} in the present and absent of one sodium ion were investigated, either. The four systems were immersed in a water box, 49.99 × 49.99 × 49.92 $Å^3$, respectively. The number of atoms and simulation time for each system has been gathered in Table S1.

All simulations were performed with the MD program NAMD2.9.[2] CHARMM General force field parameters[3,4] have been used to represent the alkyldiammonium moiety, CB[6] and Na^+. The TIP3P model[5] was used for water. The temperature and the pressure were maintained at 313 K and 1 atm, respectively, employing Langevin dynamics and the Langevin piston method.[6] Long−range electrostatic forces were taken into account by means of the particle−mesh Ewald (PME) approach,[7] van der Waals interactions were truncated smoothly by mean of a 12−Å spherical cutoff with a switching function applied beyond 10 Å. The equations of motion were integrated with a time step of 2.0 fs, employing the multiple time step r−RESPA algorithm. Covalent bonds involving hydrogen atoms were constrained to their equilibrium value by means of the SHAKE/RATTLE algorithms,[8,9] except for water, for which the SETTLE algorithm was applied.[9] Periodic boundary conditions were applied in three directions of Cartesian space. Analysis and visualization of MD trajectories were performed with VMD.[10]

TABLE S1. Detailed information about molecular simulations.

	CB[6] − Na^+	CB[6]:Na^+ − Na^+	CB[6] − HD^{2+}	CB[6]:Na^+ − HD^{2+}
Number of atoms	11669	11650	11689	11631
Pathway (Å)	$0.0 \le \eta \le 10.0$	$2.0 \le \eta \le 10.0$	$0.0 \le \eta \le 12.0$	$-2.0 \le \eta \le -7.0$, $5.0 \le \xi \le 12.0$; $-3.0 \le \eta \le -7.0$, $0.0 \le \xi \le 7.0$
Simulation time (ns)	40	56	128	288 192

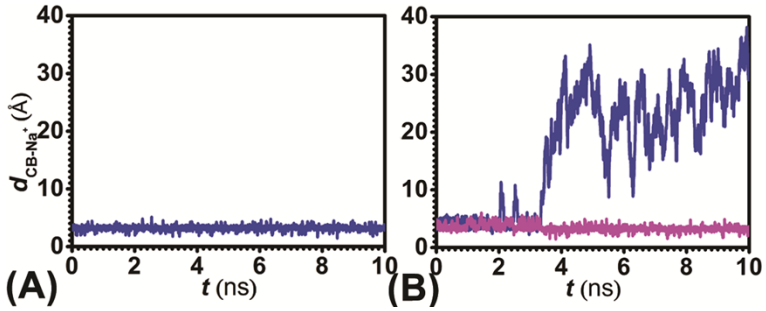

Figure S1. Variations of the distance between the barycenter of CB[6] and Na^+ obtained from additional 10−ns MD simulations for the CB[6]:Na^+ and CB[6]:$(Na^+)_2$ complexes in (A) Figure 1C and (B) Figure 1E.

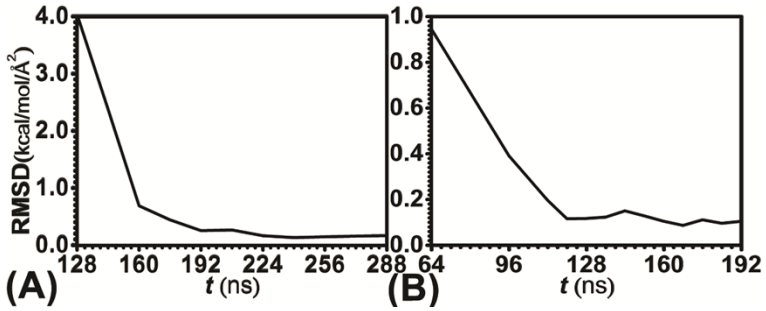

Figure S2. Time evolution of the root−mean−square deviation over the gradients of free−energy surfaces characterizing (A) the first and (B) the second stage of the binding process between CB[6]:Na^+ with HD^{2+}.

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