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Solvent Effects on the Motion of a Crown Ether/Amino Rotaxane

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Table S1. Detail of the molecular assemblies examined in this study.

Solvent	Number of atoms	Number of solvent molecules	Size of the simulation box (Å^3)	Simulation time (μs)
$CHCl_3$	11160	2194	65×50×76	2.7
water	25906	8572	66×49×75	2.8

The force-field parameters of the axle and the C[8] came from the widely used CHARMM general force field (CGenFF), which included bonded, non-bonded, atomic charges, and VDW parameters. The molecule topologies were generated from the online CGenFF program (https://cgenff.umaryland.edu).[1,2] The detailed parameters are shown in the following tables.

The axle

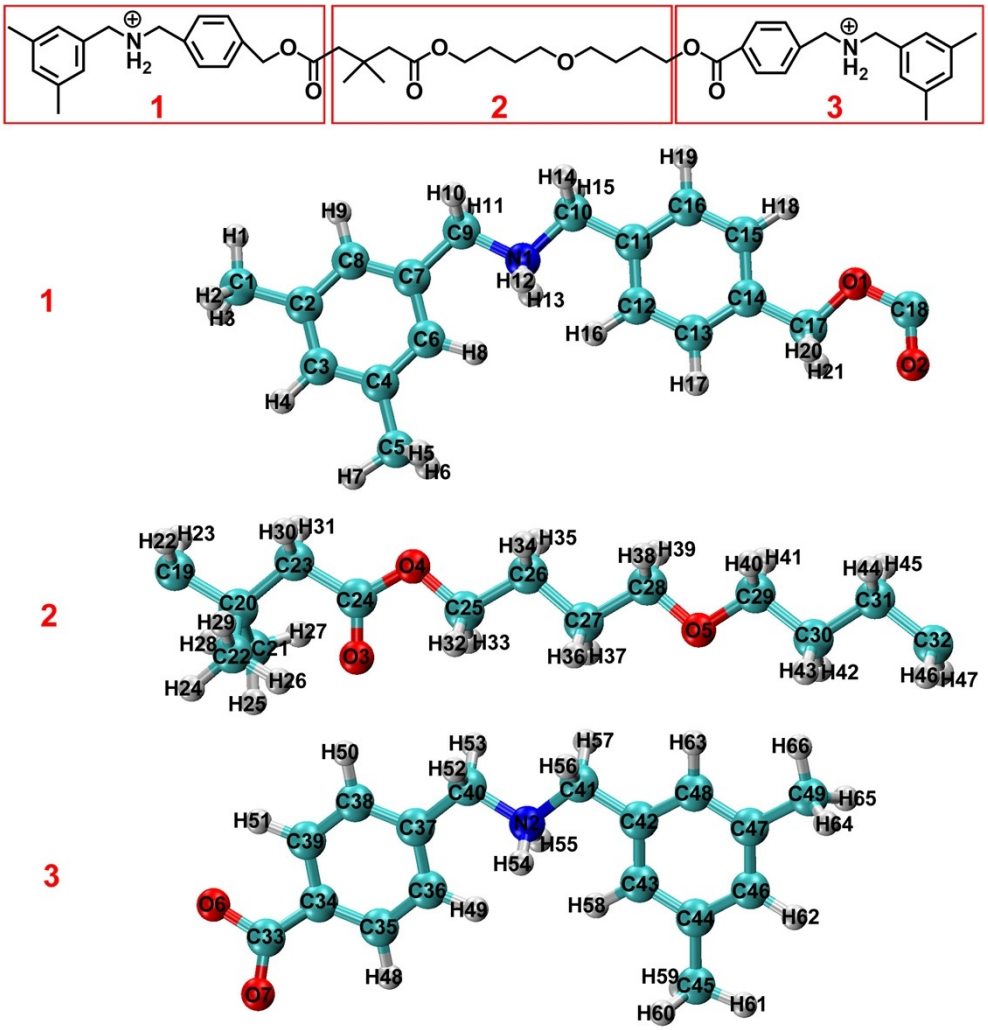

Table S2. The charge distributions of the axle.

ATOM	CHARGE	ATOM	CHARGE
C1	-0.269	H5	0.090
C2	0	H6	0.090
C3	-0.117	H7	0.090
C4	0	H8	0.115
C5	-0.269	H9	0.115
C6	-0.116	H10	0.090
C7	0.093	H11	0.090
C8	-0.116	H12	0.330
C9	0.127	H13	0.330
N1	-0.456	H14	0.090
C10	0.127	H15	0.090
C11	0.091	H16	0.115
O12	-0.108	H17	0.115
C13	-0.117	H18	0.115
C14	-0.006	H19	0.115
C15	-0.117	H20	0.090
C16	-0.108	H21	0.090
C17	0.064	H22	0.090
O1	-0.477	H23	0.090
C18	0.902	H24	0.090
O2	-0.632	H25	0.090
C19	-0.224	H26	0.090
C20	0.016	H27	0.090
C21	-0.275	H28	0.090
C22	-0.275	H29	0.090
C23	-0.224	H30	0.090
C24	0.902	H31	0.090
O3	-0.632	H32	0.090
O4	-0.489	H33	0.090
C25	0.081	H34	0.090
C26	-0.180	H35	0.090
C27	-0.182	H36	0.090
C28	0.010	H37	0.090
O5	-0.338	H38	0.090
C29	-0.010	H39	0.090
C30	-0.182	H40	0.090
C31	-0.180	H41	0.090
C32	0.059	H42	0.090

ATOM	CHARGE	ATOM	CHARGE
O6	-0.305	H43	0.090
O7	-0.493	H44	0.090
C33	0.471	H45	0.090
C34	0.083	H46	0.090
C35	-0.112	H47	0.090
C36	-0.115	H48	0.115
C37	0.091	H49	0.115
C38	-0.115	H50	0.115
C39	-0.112	H51	0.115
C40	0.127	H52	0.090
N2	-0.456	H53	0.090
C41	0.127	H54	0.330
C42	0.093	H55	0.330
C43	-0.116	H56	0.090
C44	0	H57	0.090
C45	-0.269	H58	0.115
C46	-0.117	H59	0.090
C47	0	H60	0.090
C48	-0.116	H61	0.090
C49	-0.269	H62	0.115
H1	0.090	H63	0.115
H2	0.090	H64	0.090
H3	0.090	H65	0.090
H4	0.115	H66	0.090

The C[8]

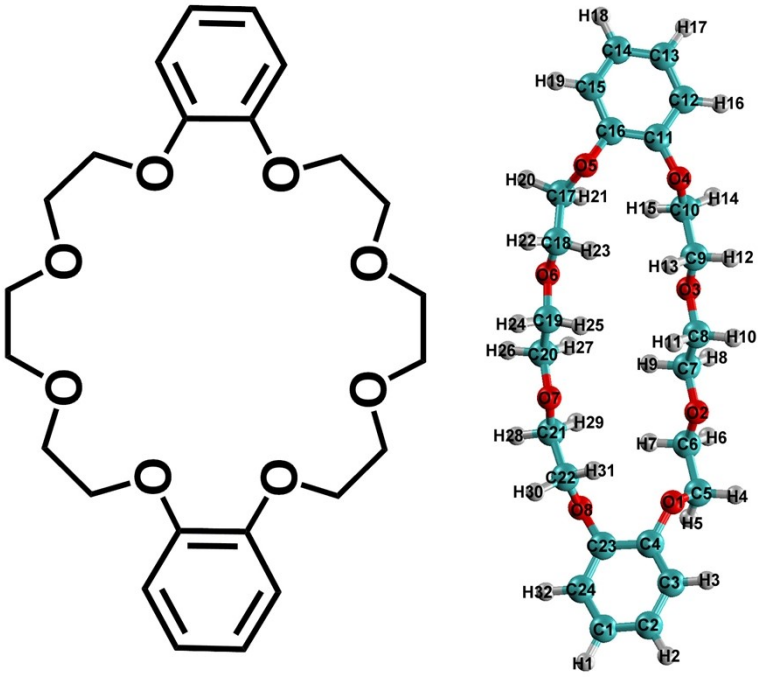

Table S3. The charge distributions of the C[8].

ATOM	CHARGE	ATOM	CHARGE
C1	-0.114	H1	0.115
C1	-0.114	H2	0.115
C2	-0.114	H3	0.115
C3	0.219	H4	0.090
C4	-0.390	H5	0.090
O1	-0.011	H6	0.090
C5	-0.011	H7	0.090
C6	-0.011	H8	0.090
C7	-0.338	H9	0.090
O2	-0.011	H10	0.090
C8	-0.338	H11	0.090
O3	-0.011	H12	0.090
C9	-0.011	H13	0.090
C10	-0.390	H14	0.090
O4	0.219	H15	0.090
C11	-0.014	H16	0.115
C12	-0.114	H17	0.115
C13	-0.114	H18	0.115
C14	-0.114	H19	0.115
C15	-0.114	H20	0.090

ATOM	CHARGE	ATOM	CHARGE
C16	0.219	H21	0.090
O5	-0.390	H22	0.090
C17	-0.011	H23	0.090
C18	-0.011	H24	0.090
O6	-0.338	H25	0.090
C19	-0.011	H26	0.090
C20	-0.011	H27	0.090
O7	-0.338	H28	0.090
C21	-0.011	H29	0.090
C22	-0.011	H30	0.090
O8	-0.390	H31	0.090
C23	0.219	H32	0.115
C24	-0.114		

Simulation details

1. Molecular Dynamics Simulations

NAMD[3] with the CHARMM 36 general force field (CGenFF)[2] were used for performing all the atomistic MDS. The rigid model of Dietz and Heinzinger (DH model),[4] which was merged into the CgenFF, was used to express $CHCl_3$. The TIP3P water model[5] were employed for representing water. The details of the charge distributions of the axle and the C[8] were demonstrated in Table S2 and S3. Covalent bonds involving hydrogen atoms were restrained to their equilibrium lengths by applying the SHAKE/RATTLE[6,7] and SETTLE algorithms.[8] The temperature was controlled at 198 K by using the Langevin dynamics[9] and the pressure was kept at 1 atm by adopting the Langevin piston method.[9] The r-RESPA multiple time step algorithm[10] was utilized to integrate the equations of motion with a time step of 4 and 2 fs for long- and short-range interactions, respectively. Long-range electrostatic forces were evaluated by use of the particle-mesh Ewald method,[11] and short-range van der Waals and electrostatic interactions were cut off by means of a smoothed 12.0 Å spherical bound. Visualization and analysis of the molecular dynamics trajectories were performed with the VMD program.[12]

2. Free-energy calculations

All the free-energy calculations were performed using the Colvars[13] module in NAMD. Well-tempered meta-eABF (WTM-eABF)[14,15] was employed to enhance sampling along the transition coordinate. The corrected *z*-averaged restraint (CZAR) estimator[16] was used to calculate the unbiased free energy landscapes and the MULE algorithm[17] was adopted to identify the lowest free-energy pathways. The variation of the free energy, $\Delta G(\xi, d)$, was determined by integrating the average force acting concomitantly on ξ and d. To avoid spurious folding of the axle, the backbone of the rotaxane was softly restrained to its extended conformation during the MDS. A soft harmonic potential was also used to prevent the chloride ions from approaching the rotaxane. Before implement the free-energy calculation, a 20 ns equilibrium MDS were performed for each solvated system. The total simulation time amounted to 2.7 and 2.8 μs for the rotaxane, respectively, in $CHCl_3$ and water.

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