

Supporting information

The Mechanism of Selective Binding Ability between Opiate Metabolites and Acyclic Cucurbit[4]uril: an MD/DFT Study

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1. Computational Details

MD simulations

Guests were located approximately 1.7 nm away from the host, using Packmol software.¹ Energy minimization was carried out, followed by 1 ns NVT (constant temperature/constant volume) simulations for thermal equilibration and 1 ns NPT (constant pressure/constant temperature) simulations for pressure equilibration. Subsequently, a periodic pulling simulation was carried out in GROMACS, which allowed the distance between the center of mass (COM) of the host and of the steroid ring of guests to be larger than half the box size, to form 1:1 host-guest complexes. The steroid ring of guests has pulled into the ACB[4] cavity with a harmonic force constant of 41840 kJ mol⁻¹ nm⁻² and a pulling rate of 0.001 nm ps⁻¹. To obtain the potential of mean force (PMF) profiles during the binding process, these windows were then used to perform umbrella sampling simulations.³ Each window was approximately run 30~50 ns.

After the simulation of each window converged, we constructed the PMFs with the weighted histogram analysis method (WHAM).⁴⁻⁵ Statistical uncertainties of the PMFs were estimated using the Bayesian bootstrap of complete histograms.⁵ The PMFs were defined to zero at ξ where host-guest interactions vanish. To reveal the essence of the formation of host-guest complexes in the binding process, the binding energy was analyzed through g_mmpbsa software package.⁶⁻⁷ The VMD software was used to visualize structures and molecular surfaces.⁸

2. Analytical Data

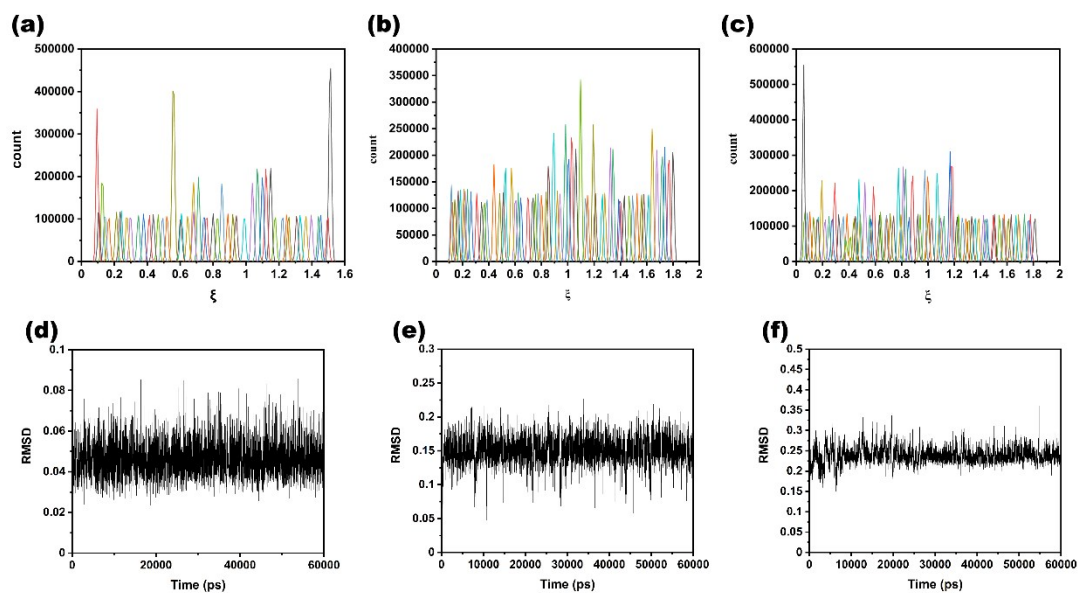


Fig. S1 Histogram of each configuration in the umbrella sampling window. (a), (d): NMOR@S1; (b), (e): MOR@S1; (c), (f): M3G@S1

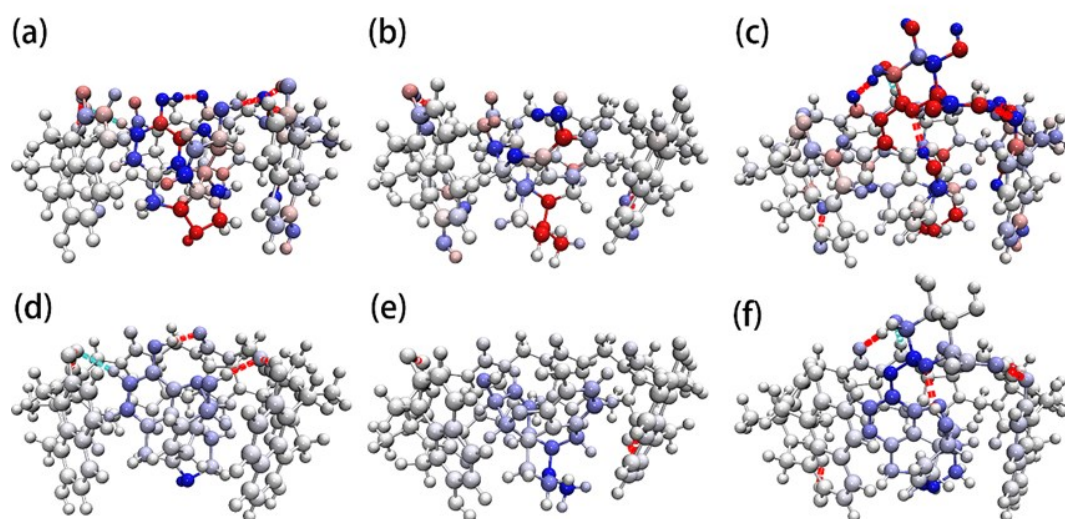


Fig. S2 Atomic coloring diagram of the complex for NMOR@S1, MOR@S1, M3G@S1. (a-c) are atomic contribution to total interaction energy; (d-f) are atomic contribution to dispersion interaction energy. Note: more blue the atoms color make a more negative contribution to interaction energy.

Table S1 QTAIM Parameters (in a.u.) Corresponding to the H---O BCP, the Electron Density at H---O BCP, ρ_{BCP} , its Laplacian, $-\nabla^2\rho_{BCP}$; the Kinetic Electron Energy Density, G_{BCP} ; the Potential Electron Energy Density, V_{BCP} ; the Total Electron Energy Density at BCP, H_{BCP} ; Electron localization function, ELF; Cor-Valece Bifurcation Index, CVBI.

		ρ_{BCP}	$-\nabla^2\rho_{BCP}$	G_{BCP}	V_{BCP}	H_{BCP}	ELF	CVBI
NMOR@S1	O ₄₃ ---H ₁₅₈	0.0195	0.0772	0.0168	-0.0139	0.0027	0.0563	0.0362
	O ₈ ---H ₁₅₇	0.0371	0.1297	0.0330	-0.0335	-0.0005	0.1146	-0.0170
	O ₅₉ ---H ₁₅₀	0.0105	0.0327	0.0072	-0.0062	0.0010	0.0386	0.0482
	O ₅₆ ---H ₁₅₂	0.0073	0.0225	0.0049	-0.0042	0.0007	0.0219	0.0614
	O ₂₆ ---H ₁₅₁	0.0029	0.0100	0.0022	-0.0017	0.0005	0.0056	0.0831
	O ₄ ---H ₁₆₀	0.0096	0.0310	0.0068	-0.0058	0.0010	0.0327	0.0762
	O ₄₀ ---H ₁₅₉	0.0081	0.0247	0.0055	-0.0048	0.0007	0.0287	0.0544
MOR@S1	O ₅₆ ---H ₁₅₁	0.0088	0.0301	0.0065	-0.0055	0.0010	0.0270	0.0596
	O ₂₆ ---H ₁₅₇	0.0045	0.0148	0.0032	-0.0026	0.0005	0.0122	0.0731
	O ₅ ---H ₁₅₇	0.0089	0.0310	0.0066	-0.0054	0.0012	0.0274	0.0564
	O ₁₂₁ ---H ₁₅₈	0.0036	0.0126	0.0026	-0.0021	0.0005	0.0083	0.0733
	O ₄₃ ---H ₁₅₈	0.0040	0.0137	0.0029	-0.0024	0.0005	0.0101	0.0716
	O ₄₃ ---H ₁₄₅	0.0059	0.0205	0.0046	-0.0040	0.0006	0.0240	0.0594
	O ₈ ---H ₁₄₅	0.0074	0.0241	0.0053	-0.0046	0.0007	0.0224	0.0607
	O ₈ ---H ₁₅₂	0.0052	0.0177	0.0038	-0.0032	0.0006	0.0139	0.0732
	O ₂₉ ---H ₁₅₂	0.0066	0.0197	0.0044	-0.0039	0.0005	0.0220	0.0653
	O ₁₂₀ ---H ₁₅₃	0.0065	0.0210	0.0046	-0.004	0.0006	0.0193	0.0627
	O ₁₂₀ ---H ₁₆₄	0.0046	0.0137	0.0030	-0.0025	0.0004	0.0151	0.0665
M3G@S1	H ₉₈ ---O ₁₅₆	0.0106	0.0373	0.0080	-0.0066	0.0013	0.0327	0.0538
	O ₁₂₁ ---H ₁₈₀	0.0308	0.1062	0.0258	-0.0251	0.0007	0.1017	-0.0027
	O ₄₃ ---H ₁₇₆	0.0017	0.0069	0.0013	-0.0009	0.0004	0.0028	0.0224
	O ₈ ---H ₁₇₅	0.0141	0.0487	0.0105	-0.0089	0.0016	0.0482	0.0488
	O ₈ ---H ₁₇₈	0.0079	0.0280	0.0060	-0.0050	0.0010	0.0219	0.0660
	H ₃₅ ---O ₁₅₉	0.0102	0.0338	0.0072	-0.0060	0.0012	0.0346	0.0862
	O ₂₉ ---H ₁₈₂	0.0292	0.1127	0.0263	-0.0244	0.0019	0.0835	0.0114
	O ₅₉ ---H ₁₆₃	0.0055	0.0174	0.0037	-0.0031	0.0006	0.0172	0.0770
	O ₅₆ ---H ₁₆₂	0.0078	0.0250	0.0054	-0.0045	0.0009	0.0264	0.0609
	O ₂₆ ---H ₁₆₅	0.0087	0.0281	0.0062	-0.0053	0.0009	0.0283	0.0558
	O ₅ ---H ₁₈₄	0.0065	0.0202	0.0045	-0.0039	0.0006	0.0210	0.0608
	O ₅ ---H ₁₇₂	0.0086	0.0281	0.0061	-0.0051	0.0009	0.0284	0.0554
	O ₄₀ ---H ₁₇₃	0.0075	0.0252	0.0051	-0.0046	0.0008	0.0220	0.0645
	O ₄₀ ---H ₁₇₁	0.0049	0.0177	0.0037	-0.0029	0.0008	0.0122	0.0710

Table S2 Average hydrogen bond number and average hydrogen bond lifetime (ps) after trajectory convergence.

	S1	NMOR	NMOR@S1	MOR	MOR@S1	M3G	M3G@S1
Host-Water	16.58(4.94)		15.26(8.09)		15.49(5.02)		15.18(5.58)
Guest-Water		6.26(4.79)	3.74(9.72)	4.89(4.37)	2.90(4.38)	12.41(4.62)	9.08(4.44)
Host-Guest			2.19(74.46)		1.49(22.28)		0.93(76.34)
Complex-Water			19.00(8.37)		18.40(4.91)		24.26(5.10)

3. References

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