Electronic Supplementary Information

A theoretical study on Sequence-dependent nanomolar binding of tripeptides

containing N-terminal Leucine by Cucurbit[7]uril

Ying Zhao¹, Fei Li², Fenfen Ma³, Junge Zhi¹, Guanglu Wu^{2,*}, Xiaoyan Zheng^{1,4,*}

¹ Key Laboratory of Cluster Science of Ministry of Education, Beijing Key Laboratory of Photoelectronic/Electrophotonic Conversion Materials, School of Chemistry and Chemical Engineering, Beijing Institute of Technology, Beijing, 100081, China.

² State Key Laboratory of Supramolecular Structure and Materials, College of Chemistry, Jilin University, Changchun, 130012, China

³ GuSu Laboratory of Materials, Suzhou 215123, Jiangsu, China.

⁴ Guangdong Provincial Key Laboratory of Luminescence from Molecular Aggregates (South China University of Technology), Guangzhou 510640, China

*E-mail: xiaoyanzheng@bit.edu.cn, guanglu@jlu.edu.cn

Contents

I. Supplementary method

Details of Independent Gradient Method (IGM) analysis

Isothermal Titration Calorimetry (ITC)

II. Supplementary Figures S1-S5

Figure S1 The chemical structural formulas of 17 tripeptides.

Figure S2 The equilibrium structures of CB[7]/tripeptide complexes.

Figure S3 The partial IGM isosurface analysis of CB[7]/LGX.

Figure S4 The entropy variations of the host and guest molecules.

Figure S5 The IGM isosurface analysis of CB[7]/IGX.

Figure S6-S8 Isothermal Titration Calorimetry Data for three systems.

III. Supplementary Tables S1-S4

Table S1 Thermodynamic parameters for comparing the binding of CB[7] to LGX with that to LXG.

Table S2 Thermodynamic parameters for comparing the binding of CB[7] to LGX with that to LGGX.

Table S3 Thermodynamic parameters for comparing the binding of CB[7] to LGX with that to IGX.

 Table S4 Thermodynamic parameters of CB[7] binding with tripeptide containing N-terminal aromatic AAs.

Table S5 Thermodynamic data of three systems on experiment compared with theoretical values.

I. Supplementary method

Details of Independent Gradient Method (IGM) analysis

The Independent Gradient Method (IGM)¹ method performed by Multiwfn 3.8 program² can estimate the noncovalent interactions between host CB[7] and guest molecules. $\delta g^{inter} = |\nabla \rho^{IGM, inter}| - |\nabla \rho|$ is the key descriptor in IGM, which depends on the magnitude of the norm of the electron density gradient calculated by IGM model $\nabla \rho^{IGM, inter}$ and the electron density gradient $\nabla \rho$. Besides, δg^{inter} represents the δg function in intermolecular regions which can depict the intermolecular interactions. The strong attractive/repulsive interaction and *v*dW interaction are shown in blue/red and green, severally. The volume cutoff is set as follows: $\delta g^{inter} = 0.01$, and other key settings are the program's default settings in all systems.

Reference

1. Lefebvre, C.; Rubez, G.; Khartabil, H.; Boisson, J.-C.; Contreras-García, J.; Hénon, E., Accurately extracting the signature of intermolecular interactions present in the NCI plot of the reduced density gradient versus electron density. *Physical Chemistry Chemical Physics* **2017**, *19* (27), 17928-17936.

Lu, T.; Chen, F., Multiwfn: A multifunctional wavefunction analyzer. *Journal of Computational Chemistry* 2012, *33* (5), 580-592.

Isothermal Titration Calorimetry (ITC)

ITC experiments were carried out with a MicroCal iTC200 at 298.15 K to study the binding force between CB[7] and three different tripeptides (LGG, LGH, and LGK) in aqueous solution. Concentration of CB[7] was calibrated by a titration with 1-adamantanamine of known concentration. Twenty-six injections were performed with 90-second spacing time. The titration traces were integrated by NITPIC, which produced thermograms for further fitting in SEDFHAT. Two individual titrations were carried out for each peptide and a global fitting over the two repeated experiments was performed using the single-site model. The final figures were generated using GUSSI.

II. Supplementary Figures S1-S5



LGG













LGD









LGN

LGE











LGY



LGF





Figure S1 The chemical structural formulas of 17 tripeptides.



CB[7]/LGG



CB[7]/LGR



CB[7]/LGH







CB[7]/LGK





CB[7]/LGA

CB[7]/LGS















CB[7]/LGC



CB[7]/LGE

CB[7]/LGQ



Figure S2 The equilibrated structures of CB[7]/tripeptide complexes after MD simulation. Color codes: cyan refers to C; white refers to H; red refers to O; blue refers to N.



Figure S3 IGM isosurface analysis of LGM, LGY and CB[7]/LGW.



Figure S4 The entropy variations of the host $(-T\Delta S_{Host})$ and guest $(-T\Delta S_{Guest})$ molecules.



Figure S5 IGM isosurface analysis of CB[7]/IGH, CB[7]/IGP, CB[7]/IGK and CB[7]/IGD.

Thermodynamic parameters for binding between tripeptides and CB[7]

From ITC experiments, a series of thermodynamic parameters, including Gibbs free energy changes (ΔG), binding constant (K_a), enthalpy changes (ΔH) and entropy changes ($T\Delta S$), are obtained for the binding of each tripeptide with CB[7], as shown below in Figure S6-S8.



Figure S6 Thermogram at 298.15 K for the titration of CB[7] (1.3 mM) into LGG (0.08 mM or 0.09 mM) aqueous solutions.



Figure S7. Thermogram at 298.15 K for the titration of CB[7] (1.3 mM) into LGH (0.08 mM or 0.09 mM) aqueous solutions.



Figure S8. Thermogram at 298.15 K for the titration of CB[7] (1.3 mM) into LGK (0.11 mM or 0.09 mM) aqueous solutions.

III. Supplementary Tables S1-S4

Table S1 Thermodynamic parameters of binding free energy (ΔG), enthalpy (ΔH), and entropy (- $T\Delta S$) in kcal/mol as well as the binding constant K_a in M⁻¹ for comparing the binding of CB[7] to LGX with that to LXG (X = R, H, P, K and D).

	ΔG	Ka	ΔH	$-T\Delta S$
CB[7]/LGR	-12.4	1.1×10 ⁹	-16.3	3.9
CB[7]/LRG	-9.5	8.3×10 ⁶	-9.8	0.3
CB[7]/LGH	-9.3	6.0×10^{6}	-9.3	0
CB[7]/LHG	-5.8	1.7×10^{4}	-9.8	4.0
CB[7]/LGP	-8.8	2.6×10 ⁶	-8.8	0
CB[7]/LPG	-2.6	78.4	-7.9	5.3
CB[7]/LGK	-8.5	1.6×10^{6}	-8.8	0.3
CB[7]/LKG	-7.3	2.1×10 ⁵	-9.8	2.5
CB[7]/LGD	-8.5	1.6×10 ⁶	-8.8	0.3
CB[7]/LDG	-4.4	1.6×10 ³	-10.0	5.6

Table S2 Thermodynamic parameters of binding free energy (ΔG), enthalpy (ΔH), and entropy (- $T\Delta S$) in kcal/mol as well as the binding constant K_a in M⁻¹ for comparing the binding of CB[7] to LGX with that to LGGX (X = R, H, P, K and D).

	ΔG	Ka	ΔH	$-T\Delta S$
CB[7]/LGR	-12.4	1.1×10 ⁹	-16.3	3.9
CB[7]/LGGR	-7.6	3.4×10 ⁵	-9.3	1.7
CB[7]/LGH	-9.3	6.0×10^{6}	-9.3	0
CB[7]/LGGH	-6.6	6.4×10 ⁴	-9.6	3.0
CB[7]/LGP	-8.8	2.6×10 ⁶	-8.8	0
CB[7]/LGGP	-5.2	6.1×10 ³	-9.6	4.4
CB[7]/LGK	-8.5	1.6×10 ⁶	-8.8	0.3
CB[7]/LGGK	-8.1	8.0×10 ⁵	-9.3	1.2
CB[7]/LGD	-8.5	1.6×10 ⁶	-8.8	0.3
CB[7]/LGGD	-6.9	1.1×10 ⁵	-10.0	3.1

Table S3 Thermodynamic parameters of binding free energy (ΔG), enthalpy (ΔH), and entropy (- $T\Delta S$) in kcal/mol as well as the binding constant K_a in M⁻¹ for comparing the binding of CB[7] to LGX with that to IGX (X = R, H, P, K and D).

	ΔG	Ka	ΔH	$-T\Delta S$
CB[7]/LGR	-12.4	1.1×10 ⁹	-16.3	3.9
CB[7]/IGR	-2.4	56.0	-8.4	6.0
CB[7]/LGH	-9.3	6.0×10 ⁶	-9.3	0
CB[7]/IGH	-4.4	1.6×10 ³	-7.6	3.2
CB[7]/LGP	-8.8	2.6×10 ⁶	-8.8	0
CB[7]/IGP	0.2	7.1×10 ⁻¹	-7.9	8.1
CB[7]/LGK	-8.5	1.6×10^{6}	-8.8	0.3
CB[7]/IGK	-2.2	40.1	-7.2	5.0
CB[7]/LGD	-8.5	1.6×10 ⁶	-8.8	0.3
CB[7]/IGD	0.6	3.7×10 ⁻¹	-7.9	8.5

, , ,		e "		
	ΔG	Ka	ΔH	$-T\Delta S$
CB[7]/FGG	-5.7	1.4×10^{4}	-12.4	6.7
CB[7]/FGE	-12.8	2.1×10 ⁹	-19.6	6.8
CB[7]/FGK	-11.9	4.7×10 ⁸	-18.2	6.3
CB[7]/FGR	-11.6	2.8×10 ⁸	-18.4	6.8
CB[7]/FGH	-10.2	4.7×10 ⁷	-17.2	7.0
CB[7]/FGS	-3.6	4.2×10 ²	-12.5	8.9
CB[7]/FGL	-2.9	1.3×10 ²	-11.7	8.8
CB[7]/FGD	-2.3	4.7×10	-12.6	10.3
CB[7]/FGQ	-1.8	2.1×10	-13.1	11.3
CB[7]/FGM	-1.3	8.9	-12.5	11.2
CB[7]/FGY	0.4	0.5	-13.5	13.9
CB[7]/WGG	-9.1	4.5×10 ⁶	-12.4	3.3
CB[7]/WGR	-15.1	9.5×10 ¹⁰	-18.2	3.1
CB[7]/WGK	-3.0	1.4×10 ²	-11.7	8.7
CB[7]/WGH	-6.5	5.4×10 ⁴	-12.0	5.5
CB[7]/YGG	-4.9	3.7×10 ³	-11.5	6.6
CB[7]/YGR	-14.9	7.0×10 ¹⁰	-17.0	2.1
CB[7]/YGK	-15.4	1.7×10 ¹¹	-16.7	1.3
CB[7]/YGH	-7.8	4.8×10 ⁵	-10.0	2.2

Table S4 Thermodynamic parameters of CB[7] binding with tripeptide containing N-terminal aromatic AAs, including ΔG , ΔH , $-T\Delta S$ in kcal/mol as well as the binding constant K_a in M⁻¹.

Table S5 Thermodynamic data of three systems on experiment compared with theoretical values, including ΔG ,

 ΔH , $-T\Delta S$ in kcal/mol as well as the binding constant K_a in M⁻¹.

	ΔG		Ka		ΔH	ΔΗ		$-T\Delta S$	
	Cal.	Exp.	Cal.	Exp.	Cal.	Exp.	Cal.	Exp.	
LGG	-8.1	-7.9	8.0×10 ⁵	6.4×10 ⁵	-9.1	-6.8	1.0	-1.1	
LGH	-9.3	-8.1	6.0×10 ⁶	9.1×10 ⁵	-9.3	-7.4	0	-0.7	
LGK	-8.5	-8.2	1.6×10 ⁶	9.5×10 ⁵	-8.8	-6.6	0.3	-1.6	