

## Supporting Information

The effects of Zn<sup>2+</sup> binding on the structural and dynamic properties of amyloid  $\beta$  peptide associated with Alzheimer's disease: Asp<sup>1</sup> or Glu<sup>11</sup>?

Liang Xu<sup>1,2,\*</sup>, Xiaojuan Wang<sup>3</sup>, Xicheng Wang<sup>4</sup>

<sup>1</sup>School of Chemistry, Dalian University of Technology, Dalian 116023, China.

<sup>2</sup>State Key Laboratory of Fine Chemicals, Dalian University of Technology, Dalian 116023, China.

<sup>3</sup>School of Chemical Machinery, Dalian University of Technology, Dalian 116023, China.

<sup>4</sup>Department of Engineering Mechanics, State Key Laboratory of Structural Analyses for Industrial Equipment, Dalian University of Technology, Dalian 116023, China.

Corresponding author E-mail: xuliang@dlut.edu.cn.

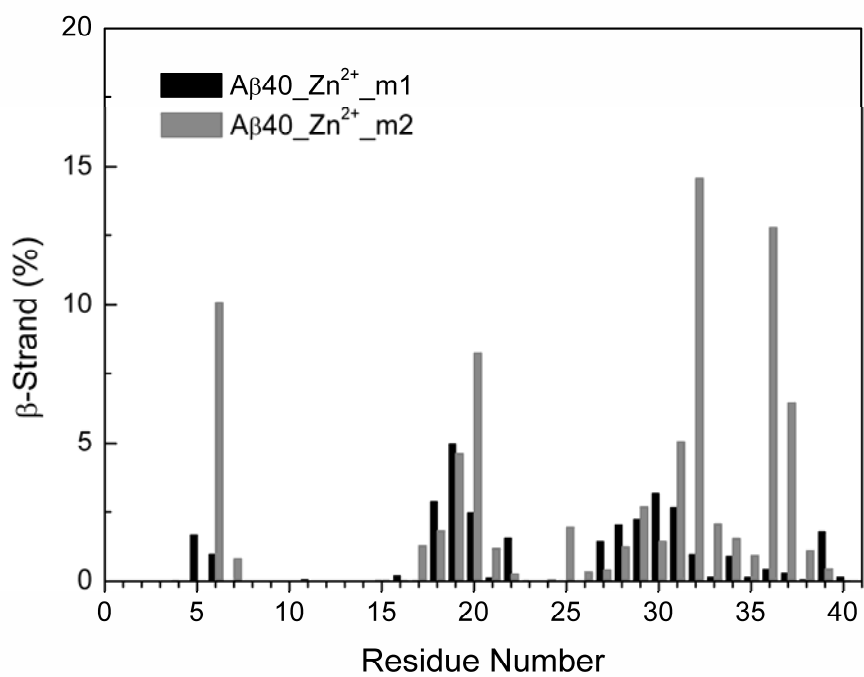


Fig. S1. The  $\beta$ -strand contents averaged over the last 100-ns REMD simulations of systems  $\text{Zn}^{2+}$ -A $\beta$ 40\_m1 and  $\text{Zn}^{2+}$ -A $\beta$ 40\_m2.

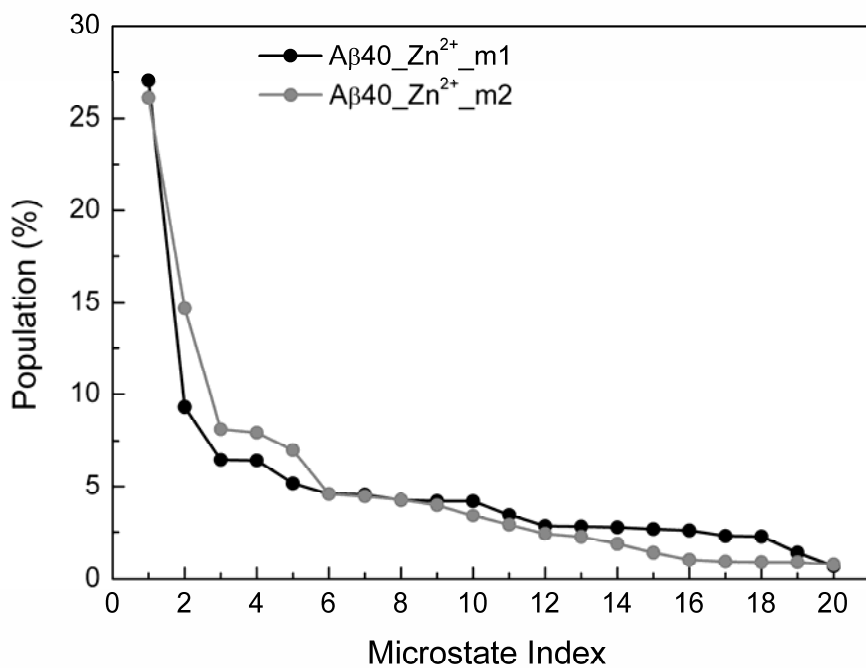


Fig. S2. The populations for the 20-node network graphs shown in Figures 6 and 7.

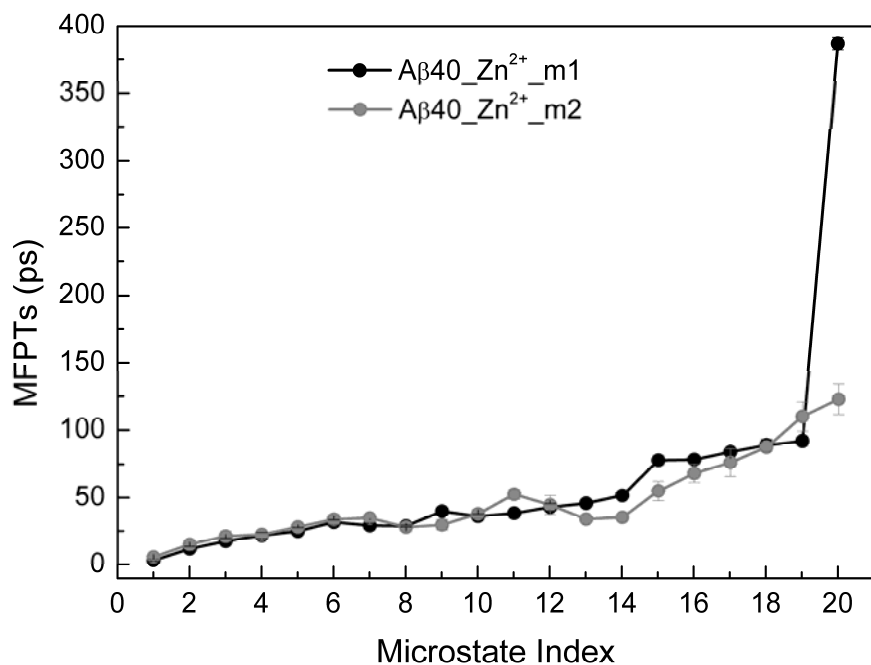


Fig. S3. The mean first passage times (MFPTs) calculated for each node in the MSM networks of two systems.

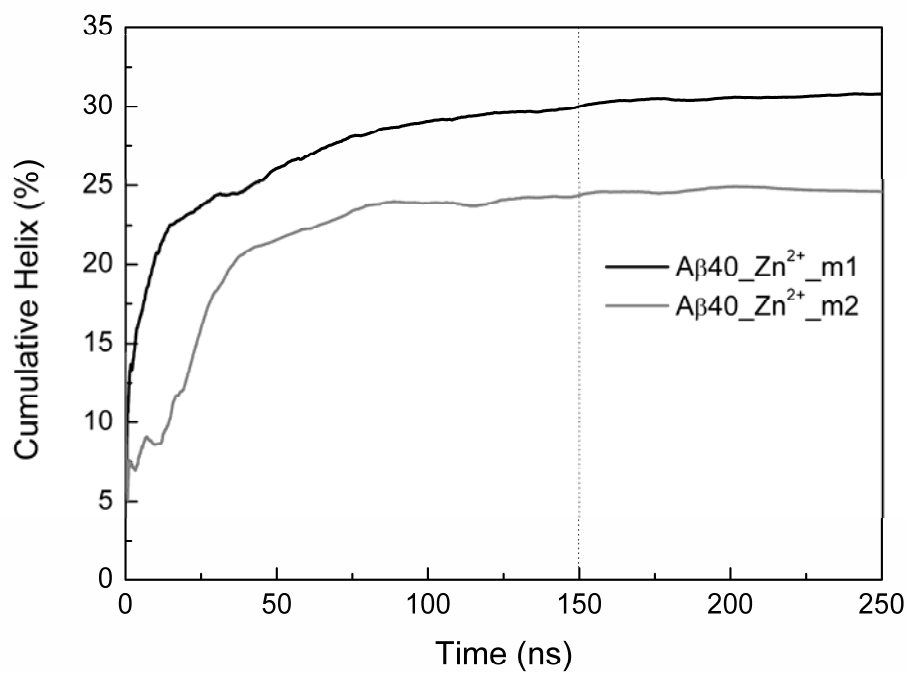


Fig. S4. The cumulative helix contents (including  $\alpha$ -helix,  $3_{10}$ -helix, and  $\pi$ -helix) over the 250-ns REMD simulations of systems Zn<sup>2+</sup>-Aβ40\_m1 and Zn<sup>2+</sup>-Aβ40\_m2.

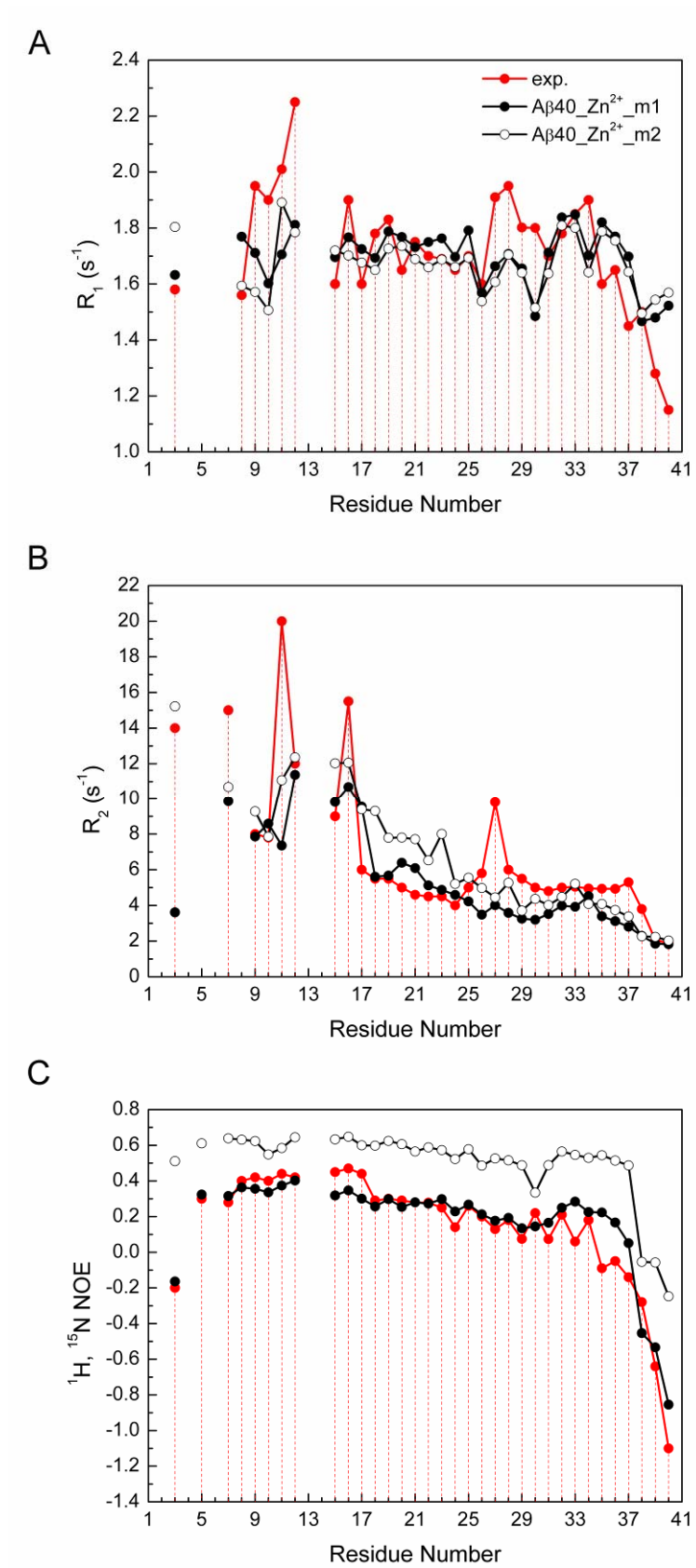
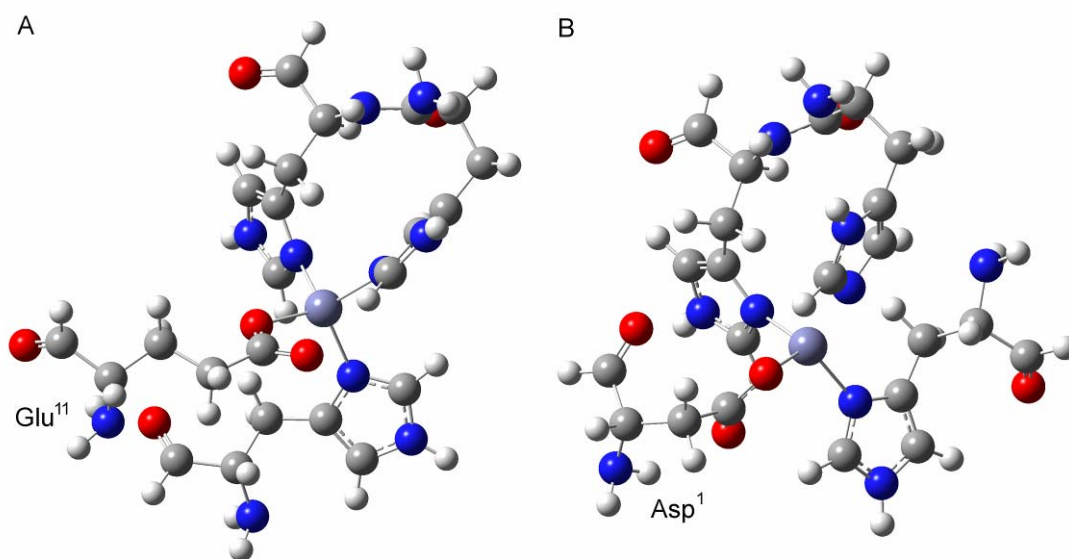


Fig. S5. Comparison of simulated and experimental  $^{15}N$  relaxation rates and NOE values for

Zn<sup>2+</sup>-Aβ40\_m1 and Zn<sup>2+</sup>-Aβ40\_m2.

Table S1. Energy components used for the calculation of the binding free energies of Zn<sup>2+</sup> to Aβ40.

Structure	S <sub>vibration</sub> (gas, 298.15 K, cal mol <sup>-1</sup> K <sup>-1</sup> )	G (gas, 298.15 K, Hartree)	S <sub>vibration</sub> (solvation, 298.15 K, cal mol <sup>-1</sup> K <sup>-1</sup> )	G (solvation, 298.15 K, Hartree)
model	181.456	-3673.794852	162.570	-3673.887363
structure A				
model	169.315	-3634.510648	154.931	-3634.596824
structure B				
His-His	72.984	-945.6216361	76.788	-945.6570515
Glu	30.235	-475.7210686	26.362	-475.8179694
Asp	20.702	-436.4393052	21.850	-436.5342886
His	28.889	-473.3797251	28.742	-473.3972433
Zn	38.384 (translational)	-1778.171976	38.384 (translational)	-1778.864814



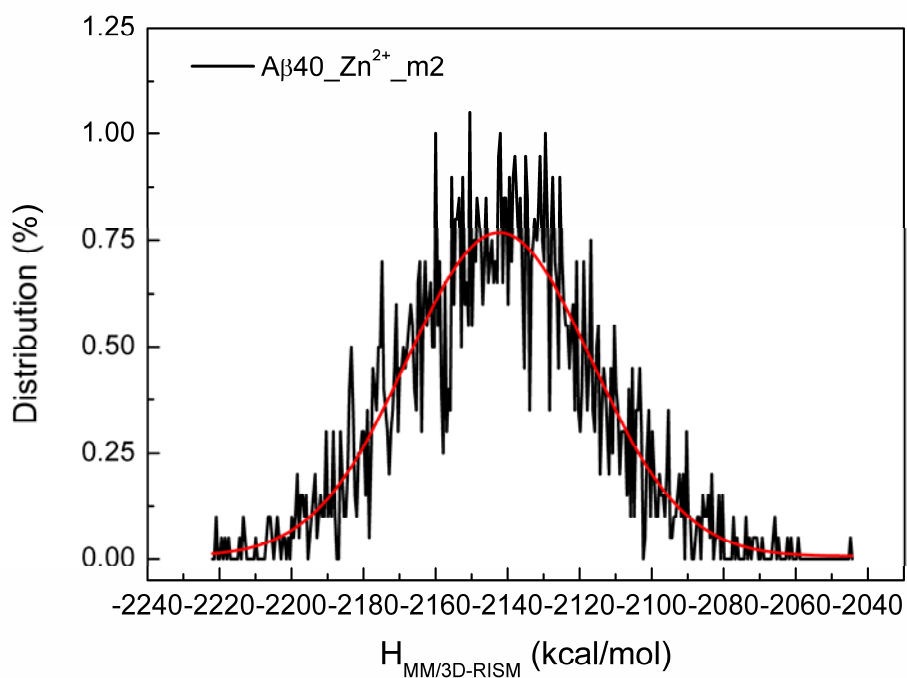
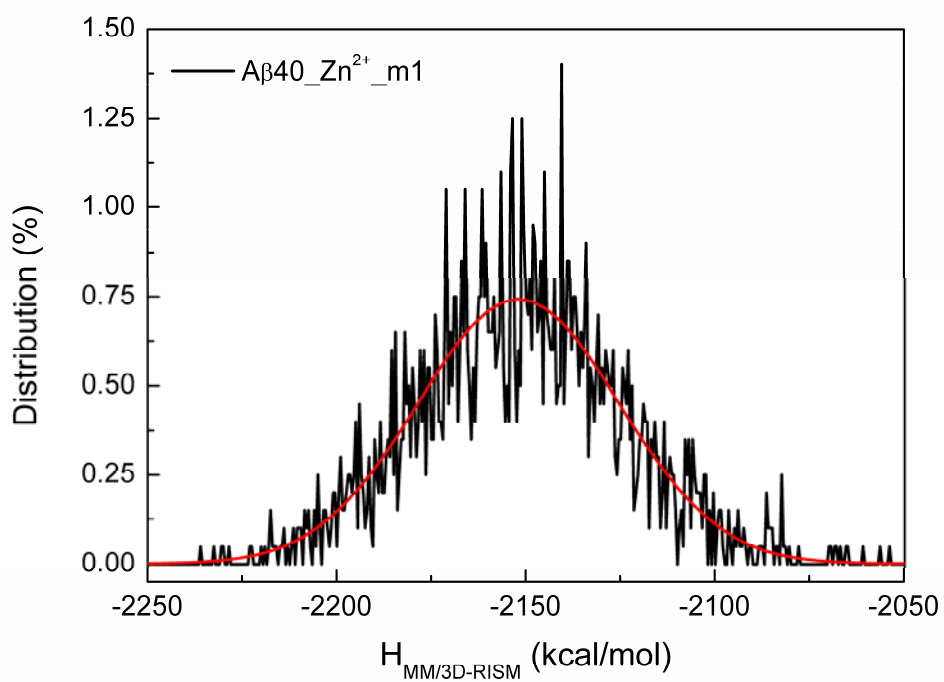


Fig. S6. The distribution of enthalpy of  $Zn^{2+}$ -bound  $A\beta_{40}$  peptides. Red curves denote the fit by Gaussian function.