

# **Exploration of the Misfolding Mechanism of Transthyretin Monomer: Insights from Hybrid-Resolution Simulations and Markov Model Model Analysis**

Shuangyan Zhou<sup>1</sup>, Jie Cheng<sup>1</sup>, Ting Yang<sup>1</sup>, Mingyue Ma<sup>1</sup>, Wenying Zhang<sup>1</sup>,

Shuai Yuan<sup>1, \*</sup>, Glenn V. Lo<sup>2</sup>, Yusheng Dou<sup>2</sup>

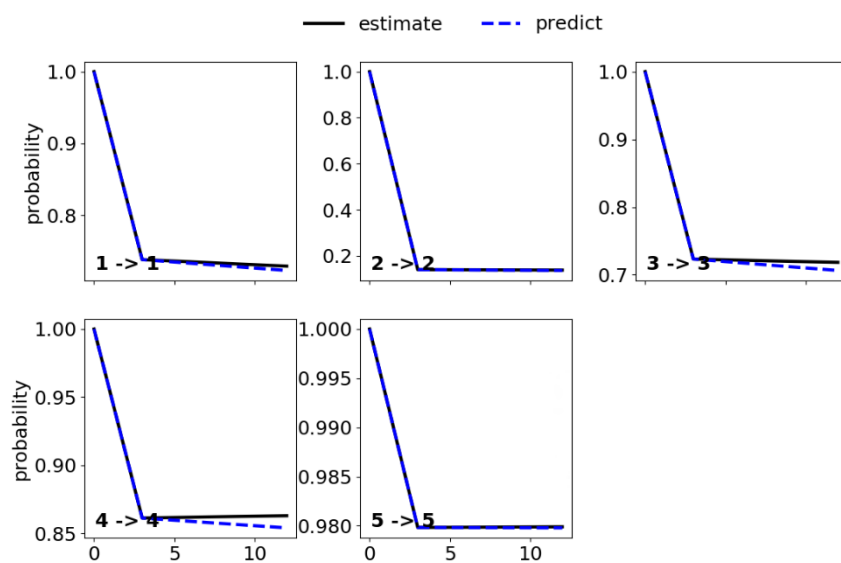
<sup>1</sup> Chongqing Key Laboratory on Big Data for Bio Intelligence, Chongqing University of Posts and Telecommunications, Chongqing 400065, China

<sup>2</sup> Department of Chemistry and Physical Sciences, Nicholls State University, P.O.

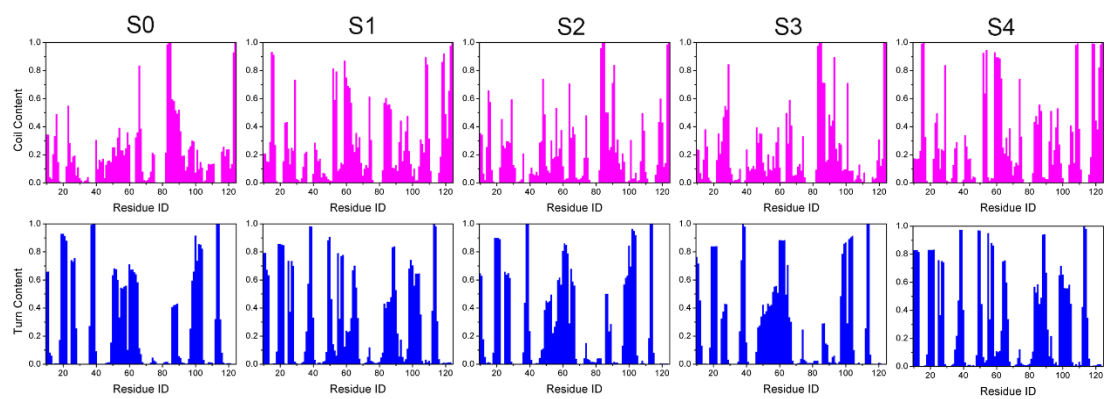
Box 2022, Thibodaux, Louisiana 70310, USA

\* Corresponding author

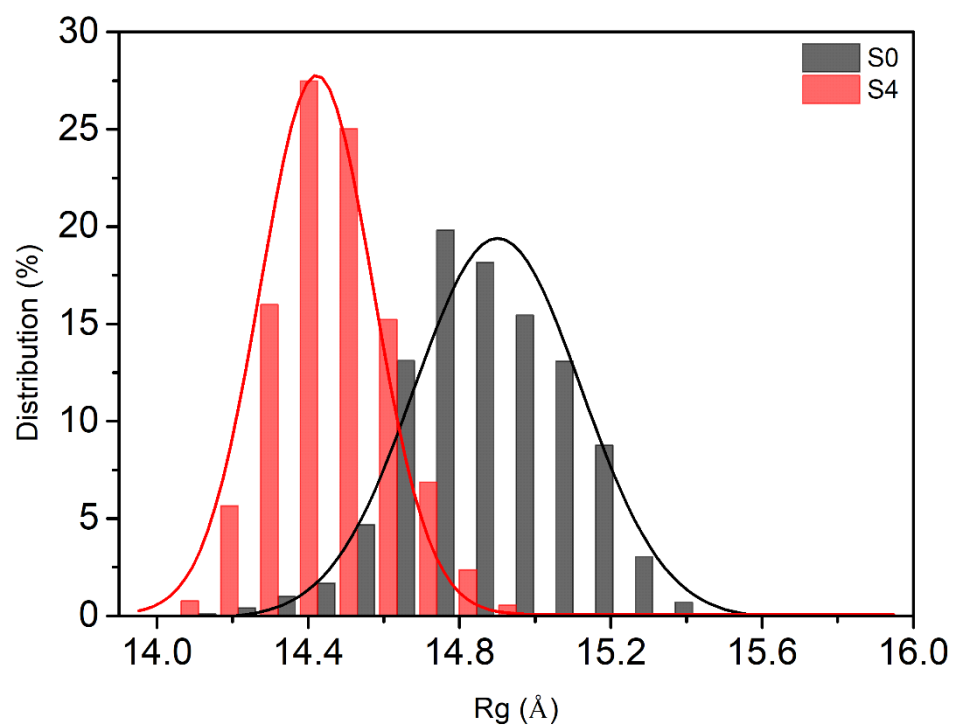
E-mail address: yuanshuai@cqupt.edu.cn



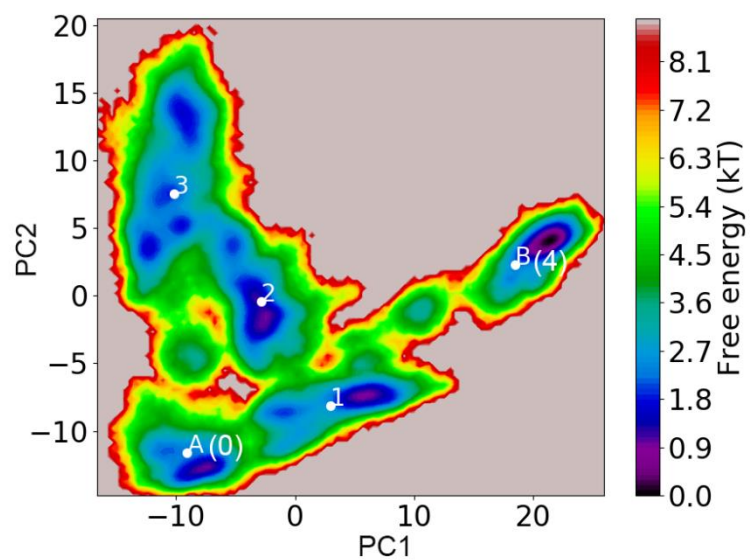
**Figure S1.** Chapman-Kolmogorov tests of the MSM constructed at lag time of 3 ns with 5 macrostates.



**Figure S2.** Probabilities of residues in TTR monomer adopting coil and turn structure for each macrostate.



**Figure S3.** Distribution of radius of gyration ( $R_g$ ) of macrostates S0 and S4.



**Figure S4.** Free energy space of TTR monomer with average location of corresponding macrostates labeled. A and B representing the initial and final states in the transition pathways, respectively.