## **Supporting Information**

## Non-destructive Inhibition of Metallofullerenol $Gd@C_{82}(OH)_{22}$ on WW domain: Implication on Signal Transduction Pathway

Seung-gu Kang<sup>1</sup>, Tien Huynh<sup>1</sup>, and Ruhong Zhou<sup>1,2</sup> \*

<sup>1</sup> Computational Biology Center, IBM Thomas J. Watson Research Center Yorktown Heights, NY 10598 (USA)

<sup>2</sup> Department of Chemistry, Columbia University, New York, NY 10027 (USA)

\* Corresponding author: <a href="mailto:ruhongz@us.ibm.com">ruhongz@us.ibm.com</a>

**Figure S1. a)** Root-mean square deviation (rmsd) and **b)** root-mean square fluctuation (rmsf) of the WW domain in the binary system with four  $Gd@C_{82}(OH)_{22}$  molecules. **c)** rmsd and **d)** rmsf of the WW domain when with both  $Gd@C_{82}(OH)_{22}$  and the PRM.

**Figure S2. a)** The residue types of WW domain. Colors represent residue type depending on polarity: blue for positively charged, red for negatively charged, green for polar, white for non-polar and yellow for key binding site residues. **b)** Electrostatic potential around the WW domain with blue for positive and red for negative fields calculated by APBS tool. T1 and T2 indicate the first and second turn of the WW domain, respectively. The two PRM binding grooves are indicated with arrows, to which  $Gd@C_{82}(OH)_{22}$  also binds. The first two Pro's of the PPxY motif are packed into the groove-1, and the Tyr of the PPxY is accommodated by the groove-2.

Figure S3. Binding free energy landscape between the full sequence of WW domain (46 residues) with  $Gd@C_{82}(OH)_{22}$  (a), and PRM (b). The total number of atoms in the ternary system is ~20,000. The solvated system was also run 5 times, with simulation length about 150ns each. All the other simulation details are the same as the truncated system with the functional unit (L13-P42) only. Similarly, **D** and **S** of two axes in the free energy diagrams indicate distance and contact area. The subscripts P, K, L and M represent protein, key residues, PRM ligand and  $Gd@C_{82}(OH)_{22}$ , respectively. The local energy minima are indicated with free energy numbers. With the full sequence of WW domain,  $Gd@C_{82}(OH)_{22}$  again wins the competition over the native ligand PRM in its binding with the WW domain, with  $\Delta\Delta G \approx -0.53$  kcal/mol, despite the more flexible terminal residues (which affect the shapes and details of the free energy landscapes somewhat). These findings are consistent with the results from the functional unit (L13-P42) only, indicating  $Gd@C_{82}(OH)_{22}$  can potentially inhibit the WW domain function.

.

Figure S1.

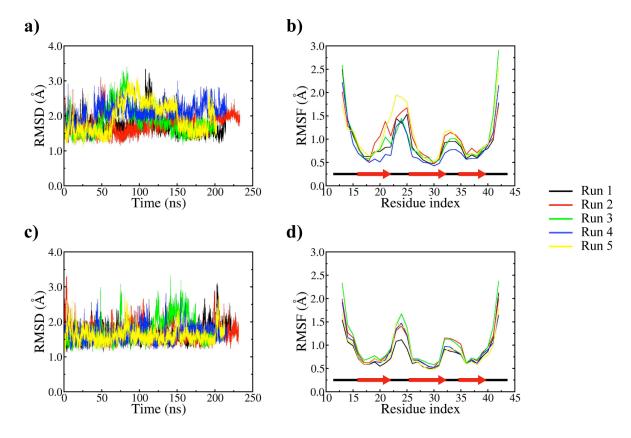


Figure S2.

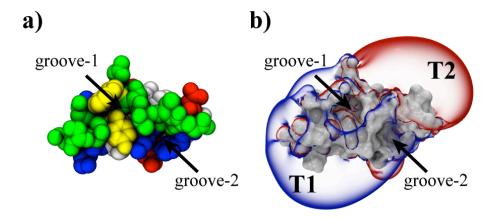
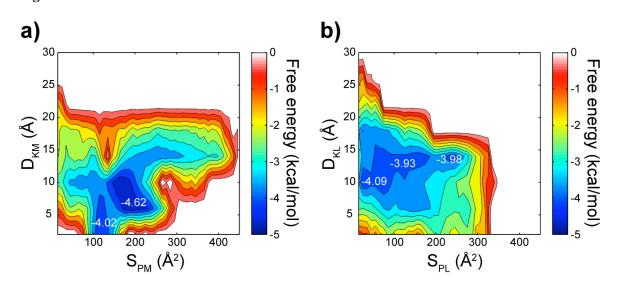


Figure S3.



## References

Baker, N. A., Sept, D., Joseph, S., Holst, M. J. & McCammon, J. A. Electrostatics of nanosystems: application to microtubules and the ribosome. *Proc Natl Acad Sci USA* **98**, 10037-10041, (2001).