

## **SUPPLEMENTARY MATERIAL**

### **Molecular Dynamics Simulation Strategies for Protein-Micelle Complexes**

Xi Cheng<sup>1</sup>, Jin-Kyoung Kim<sup>2</sup>, Yangmee Kim<sup>2</sup>, James U. Bowie<sup>3</sup>, and Wonpil Im<sup>1</sup>

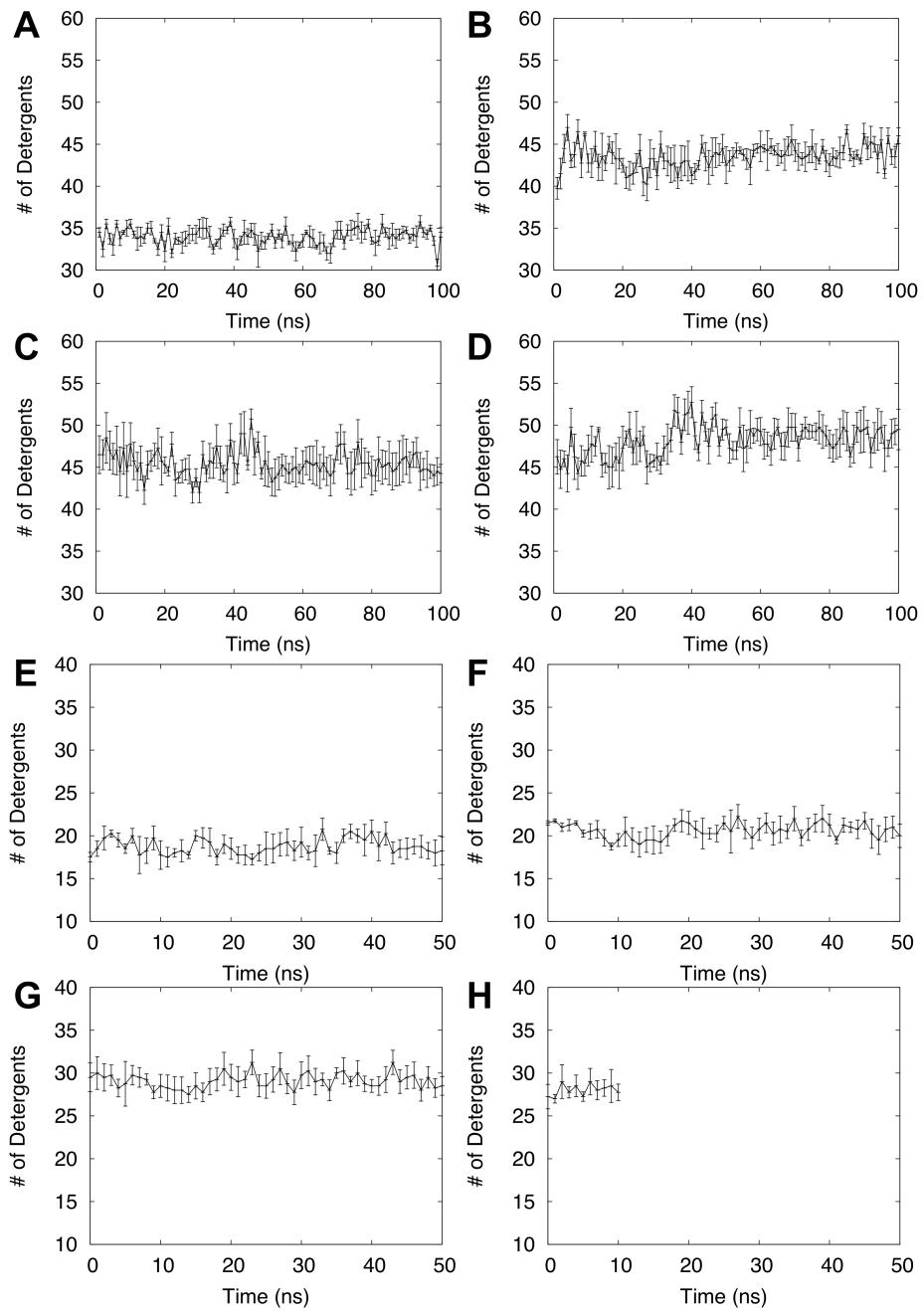
<sup>1</sup>Department of Molecular Biosciences and Center for Computational Biology,  
The University of Kansas, 2030 Becker Drive, Lawrence, KS 66047, USA

<sup>2</sup>Department of Bioscience and Biotechnology, Konkuk University, Seoul 143-701, Korea

<sup>3</sup>Department of Chemistry and Biochemistry, UCLA,  
611 Charles E. Young Dr. E, Los Angeles, CA 90095-1570, USA

Correspondence:

Wonpil Im  
Phone: (785) 864-1993  
Fax: (785) 864-5558  
E-mail: [wonpil@ku.edu](mailto:wonpil@ku.edu)



**Figure S1.** The average number of detergents in direct contact with (A-D) KvAP VSD and (E-D) papilioxin as a function of time in the micelle systems of (A) 40 DHPC, (B) 60 DHPC, (C) 80 DHPC, (D) 100 DHPC, (E) 60 DPC, (F) 100 DPC, (G) 200 DPC, and (H) 300 DPC. The number of detergents and the error bars are the average and the standard errors over five replicated simulations.