

# Modeling protein-micelle systems in implicit water

Rodney E. Versace and Themis Lazaridis\*

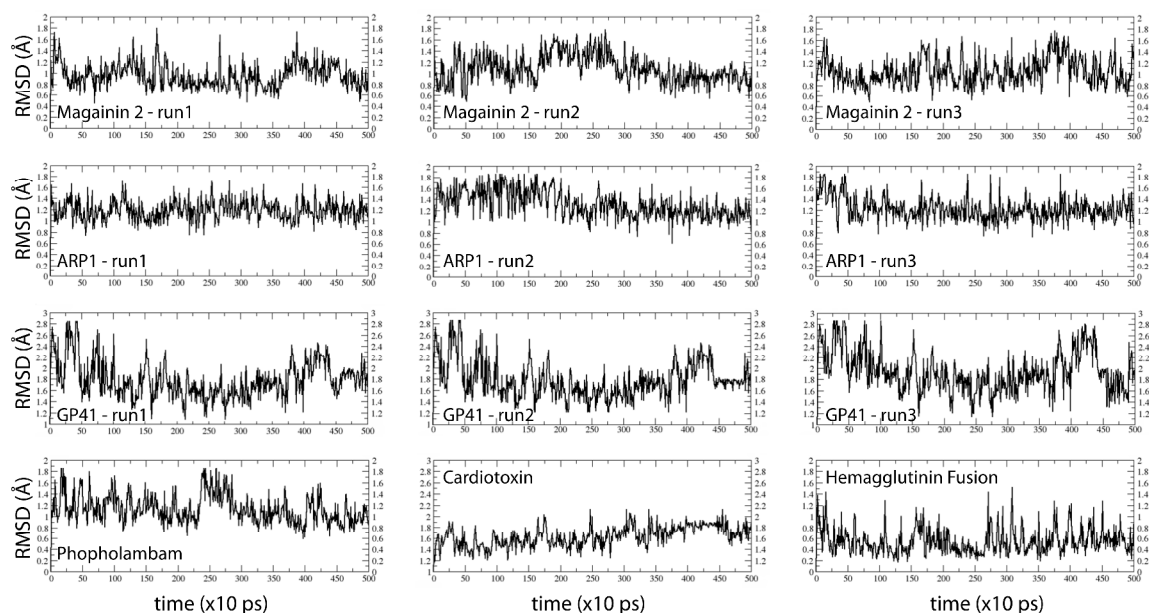
Department of Chemistry, The City College of New York,

160 Convent Avenue, New York, New York 10031

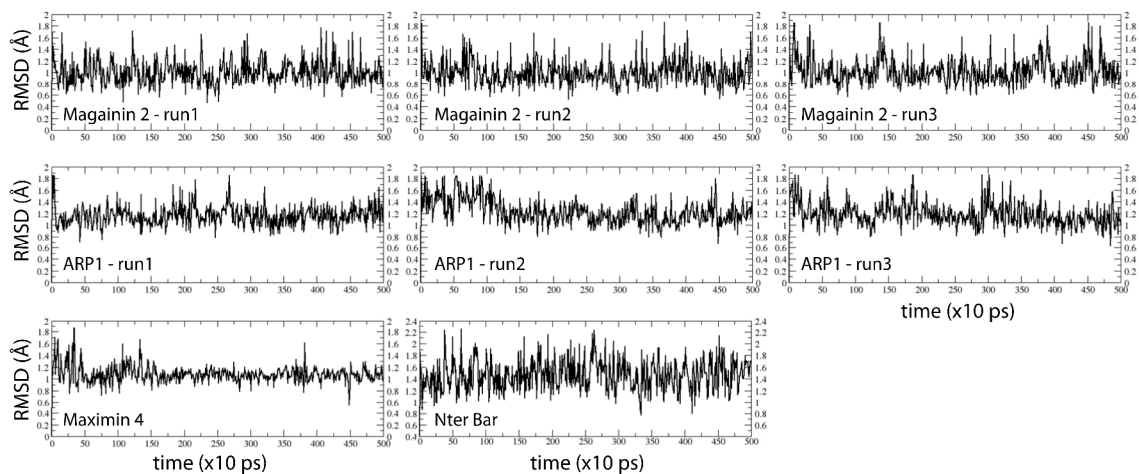
## SUPPORTING INFORMATION

**Table S1.** Average RMSD values from three independent 5-ns simulations

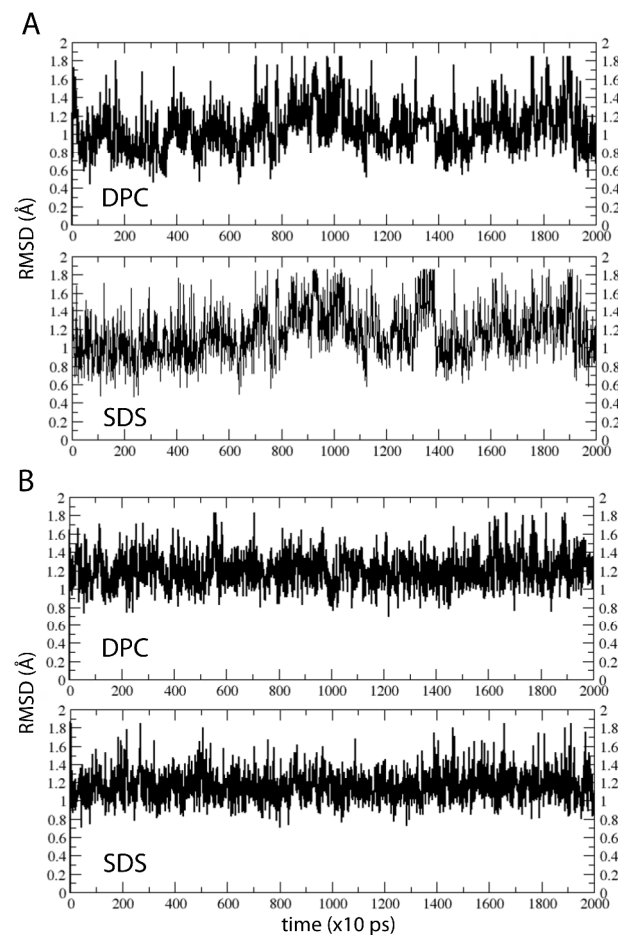
Micelle System	Protein Name	RMSD (Å) run 1	RMSD (Å) run 2	RMSD (Å) run 3
DPC	Magainin 2	1.2 ± 0.3	1.1 ± 0.3	1.1 ± 0.3
	ARP1	1.2 ± 0.2	1.3 ± 0.3	1.2 ± 0.2
	GP41	1.6 ± 0.4	1.7 ± 0.4	1.0 ± 0.4
SDS	Magainin 2	1.0 ± 0.2	1.0 ± 0.2	1.0 ± 0.2
	ARP1	1.2 ± 0.2	1.2 ± 0.3	1.2 ± 0.3



**Figure S1.** Time evolution of the RMSD value of the protein against its NMR structure for 5 ns in DPC micelles.



**Figure S2.** Time evolution of the RMSD value of the protein against its NMR structure for 5 ns in SDS micelles.



**Figure S3.** Time evolution of the RMSD value of the protein A) Magainin 2 and B) ARP1 against their respective NMR structure for 20 ns in DPC and SDS micelles.