Abstract Submitted
for the MAR08 Meeting of
The American Physical Society

Diffusion of Transmembrane Proteins: Beyond the Saffman-Delbrück Model TATIANA KOURIABOVA, MARK HENLE, ALEXANDER J. LEVINE, University of California, Los Angeles — The hydrodynamic model of Saffmann and Delbrück [*PNAS* **72** 3111 (1975)] predicts that the diffusion constant D of proteins embedded in a fluid membrane exhibits a weak logarithmic dependence on the radius a of the protein. However, recent experiments by Gambin *et al.* [*PNAS* **103** 2098 (2006)] have observed a much stronger $1/a$ dependence for proteins embedded in model membranes. Local interactions between a transmembrane protein and the lipids that surround it can cause the lipids to deform by, for example, stretching or compressing their tails, or by tilting their long axis with respect to the membrane's surface. In this talk, we show that these deformations lead to additional sources of energy dissipation which cause the protein diffusion constant $D \sim 1/a$, as observed by Gambin *et al.* Our model incorporates the lipid stretch and tilt degrees of freedom into a traditional hydrodynamic model by introducing additional scalar and vector fields, respectively.

Tatiana Kouriabova
University of California, Los Angeles

Date submitted: 18 Dec 2007 Electronic form version 1.4