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Lattice-Boltzmann-based simulations of membrane protein dynamics TYLER SHARBY, RYAN PHELPS, MICHAEL ANTONELLI, Department of Biology and Marine Biology, Roger Williams University, JENNIFER KREFT PEARCE, Department of Physics, Roger Williams University — The cell membrane is a complex structure composed of a phospholipid bilayer and embedded proteins. Recent work has shown that regions of different mobility exist in the membrane due to a variety of factors and that protein motion can be significantly subdiffusive due to the presence of stationary obstacles. We present work that shows that the combination of stationary obstacles and regions of different mobility can lead to aggregation of proteins in certain regions of the cell membrane. The concentration of stationary proteins is below the percolation threshold. The mechanism of this process is hydrodynamically-mediated interactions of diffusing proteins with themselves, as in hydrodynamic memory, and with obstacles.

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