

Abstract Submitted
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Formation and organization of protein domains in the immunological synapse ANDREAS CARLSON, Harvard University, School of Engineering and Applied Sciences and the Wyss Institute, L. MAHADEVAN, Harvard University, School of Engineering and Applied Sciences and Department of Physics — The cellular basis for the adaptive immune response during antigen recognition relies on a specialized protein interface known as the immunological synapse. Here, we propose a minimal mathematical model for the dynamics of the IS that encompass membrane mechanics, hydrodynamics and protein kinetics. Simple scaling laws describe the dynamics of protein clusters as a function of membrane stiffness, rigidity of the adhesive proteins, and fluid flow in the synaptic cleft. Numerical simulations complement the scaling laws by quantifying the nucleation, growth and stabilization of proteins domains on the size of the cell. Direct comparison with experiment suggests that passive dynamics suffices to describe the short-time formation and organization of protein clusters, while the stabilization and long time dynamics of the synapse is likely determined by active cytoskeleton processes triggered by receptor binding. Our study reveals that the fluid flow generated by the interplay between membrane deformation and protein binding kinetics can assist immune cells in regulating protein sorting.

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