

Modeling receptor-ligand binding kinetics in immunological synapse formation.

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Abstract

The formation of an immunological synapse between two immune cells is a central process in immunity allowing the exchange of information that is of direct relevance for the cells' activation states. The macromolecules at the cell-cell interface form a characteristic spatial pattern whose functional impact is largely unknown today. We perform computer simulations of the immunological synapse formation using an agent-based model approach that monitors the motion and interaction of individual molecules and takes the binding kinetics of receptors and ligands explicitly into account. The emerging molecular patterns are in agreement with those observed in geometrically repatterned immunological synapses. Furthermore, our model predicts that the diversity of molecular patterns, including dynamic and multifocal structures, is directly related to the receptor-ligand binding affinity.

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