

# Molecular Modelling of the Complex hIFN $\gamma$ -hIFN $\gamma$ R-Heparin-Derived Oligosaccharides

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Human interferon gamma (hIFN- $\gamma$ ) is an important antiviral and immunomodulating signaling molecule, which is also related to several autoimmune diseases. The cytokine expresses its activity through a specific extracellular receptor, the Interferon gamma receptor (hIFN $\gamma$ R). Understanding the process of hIFN- $\gamma$  – hIFN $\gamma$ R complex formation is crucial for finding a mechanism for suppressing IFN- $\gamma$  biological activity.

We performed multiple molecular dynamics simulations to study the formation of the complex between interferon gamma and its receptors. It was found that the highly positively charged flexible C-terminal tails of the cytokine interact with negatively charged domains in the receptor molecules. This interaction prevents the proper orientation of the hIFN- $\gamma$  molecule relative to the receptors, so that the binding sites remain separated in space. It became evident that another participant is necessary for the cytokine-receptor binding to occur.

It is known that interferon gamma binds to heparin-derived oligosaccharides. These are linear highly negatively charged carbohydrates, occurring as an integral component of the basement membrane of all mammalian cells. In order to simulate the interaction between hIFN- $\gamma$ , hIFN $\gamma$ R and heparin-derived oligosaccharides with various degree of polymerisation, we first developed force field parameters for the monosaccharide N-sulfated glucosamine. The CHARMM compatible parameters were developed using the Force Field Toolkit of the molecular visualization and manipulation program VMD.

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