

Nanodynamics of MHC/Peptide complexes and its dependence on MHC polymorphism

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The causative role of the human major histocompatibility gene HLA-B27 in spondyloarthropathies, a common group of chronic inflammatory rheumatic diseases, is not understood, but the HLA-B27 molecule itself appears as the strongest predisposing factor for pathogenesis. The B*2709 subtype exhibits limited association to ankylosing spondylitis (AS) and differs only at one position in the peptide binding groove from the common, AS-associated subtype B*2705. It is proposed to investigate the peptide dynamics and conformational changes in a comparative study with these two differentially disease-associated HLA-B27 subtypes, complexed with two self-peptides and a sequence-related foreign peptide of viral origin. Advantage will be taken of different new developments in molecular dynamics simulations and peptide synthesis, and these techniques will be combined with real-time fluorescence depolarization measurements to address the main questions: (1) Is there a correlation between peptide dynamics and HLA-B27 polymorphism? (2) Can differential peptide dynamics be linked to the biological response in terms of T cell activity? Photocontrol of differential peptide dynamics by means of photoswitchable peptide analogs will provide additional insight into the peptide dynamics of HLA/peptide complexes and its dependence on HLA polymorphism.

Projektbeteiligte

Prof. Dr. Ulrike Alexiev

Freie Universität Berlin
Institut für Experimentalphysik
Berlin

Dr. Rainer Böckmann

Universität des Saarlandes
Zentrum für Bioinformatik Saar
Theoretical & Computational Membrane Biology
Gebäude C7.1
Saarbrücken

Prof. Dr. Karola Rück-Braun

Technische Universität Berlin
Institut für Chemie
Berlin

Prof. Dr. Andreas Ziegler

Charité - Universitätsmedizin Berlin
Institut für Immunogenetik
Berlin

Prof. Dr. Rosa Sorrentino

Università degli Studi di Roma
"La Sapienza"
Dipartimento di Biologia Cellulare
e dello Sviluppo
Rom
Italien