NOBEL SYMPOSIA SERIES

# Learning the shape of the immune and protein universe


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**Wednesday, 2 November | 16:00-17:00**
**Room 114 in the Physics building, Wits University**

### BIOGRAPHY

Armita Nourmohammad is an Assistant professor of Physics at the University of Washington, Seattle. Dr Nourmohammad works at the interface of statistical physics and biology and develops theoretical and data driven approaches to study evolutionary processes across scales. Dr Nourmohammad obtained her PhD in 2012 from the University of Cologne, and then joined Princeton University as a James S. McDonnell postdoctoral fellow, where she started working on immunological problems from a biophysical and an evolutionary perspective. In 2017 Dr Nourmohammad joined the Max Planck Society as Max Planck Research Group Leader and the University of Washington as an Assistant Professor of Physics. Dr Nourmohammad is a recipient of an NSF CAREER award, NIH MIRA award, and the APS-DBIO Early Career Award.


### ABSTRACT

The adaptive immune system consists of tens of billions of B- and T- cells with unique surface receptors that can recognize and mount specific responses against the multitude of pathogens. Pathogens in return can escape the immune challenge, forming a co-evolutionary arms race. Immune recognition relies on molecular interactions between immune receptors and pathogens, which in turn is determined by the complementarity of their 3D structures and amino acid compositions, i.e., their shapes. However, the relationships between immune receptor sequence, protein structure, and specificity are very difficult to quantify in practice. In this talk I will discuss how the growing amount of immune repertoire sequence data together with protein structures can shed light on the organization of the adaptive immune system. I will introduce physically motivated machine-learning approaches to learn representations of protein micro-environments in general, and of immune receptors, in particular. The learned models reflect the relevant biophysical properties that determine a protein's stability, and function, and could be used to predict immune recognition and to design novel immunogens e.g. for vaccine design.


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