

Seminar

Prediction of vaccine efficacy through cross-omics integration

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When & where

Friday 12 October 2018
9:00 – 10:00 hrs
Meeting room CK-3,
route 470

Host

Mihai Netea,
Dept. of Internal Medicine

Registration

Not required

Abstract

The efficacy of vaccines at an individual level is highly variable. It is therefore important to capture the impact of genetic and biological molecules on the immune response to vaccines to better understand variability in efficacy of vaccines. In my talk, I will describe novel strategies to study these factors by simultaneously modeling information from genome, transcriptome, proteome, metabolome, microbiome and environmental profiles.

Key Publications

- Integration of multi-omics datasets and deep phenotyping enables prediction of cytokine production in response to pathogens. *Nat. Immunol.* 776-786, 2018
- A Functional Genomics Approach to Understand Variation in Cytokine Production in Humans. *Cell* 1099–1110.e14, 2016
- Inter-individual variability and genetic influences on cytokine responses to bacteria and fungi. *Nat. Med.* 952–960, 2016.