

## Overview of the Infect-ERA Second Joint Transnational call – 2014

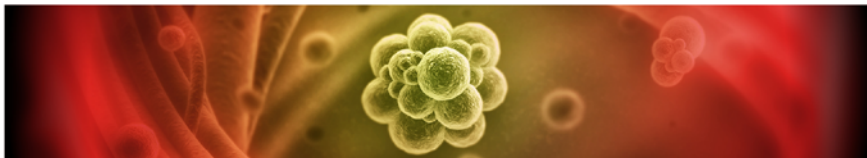
Pursuant to Infect-ERA's objective of understanding the basic biological aspects of human infection caused by bacteria, fungi, viruses and protozoa, the second Joint Transnational Call (JTC 2014) addressed the following topics:

1. Assessment of the role of commensal flora in homeostasis and microbial pathogenicity and elucidation of how commensal organisms or probiotics can be used to prevent or treat infections.
2. Development and application of new techniques to investigate the initial steps of the infection process.

The call was launched on January 2014 and resulted in the submission of **118** eligible pre- proposals. The peer review panel invited **34** candidates to submit a full proposal. **8** projects were recommended for funding.

Part of the funding was earmarked for consortia of young scientists

(all scientists 2-9 years after PhD or equivalent)




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Collaborate with Infect-ERA, an European Initiative supporting Research on Human Infectious Diseases

Infect-ERA is an ERA-NET funded under the Seventh Research Framework Programme (2013–2016). To date, it is a consortium of 14 partners from 11 countries.  
More information at: <http://www.infect-era.eu/>

Collaborate with Infect-ERA will allow you to:

- Register your company on our database to reach >300 researchers working in the field of human infectious diseases
- Build up research consortia and apply to yearly calls for proposals
- Advertise training and job opportunities
- Attend Infect-ERA networking events



For information on European funding programs and national funding programs related to research mobility and international cooperation, please have a look: <http://www.infect-era.eu/cross-boarder-fundings>



Andreas Pichlmair

partner countries:



Denmark



France



Austria



Germany

## ERASE: Evaluating viral RNA/DNA-bound proteins Across SpeciEs

**Project coordinator:** Andreas Pichlmair, Max-Planck Institute of Biochemistry, Germany  
apichl@biochem.mpg.de

**Project partners:** Jacques Colinge, Institut de Recherche en Cancérologie de Montpellier - INSERM U896, France

Jürgen Hausmann, Bavarian Nordic GmbH, Germany

Jean-Luc Imler, CNRS-UPR9022, Institut de Biologie Moléculaire et Cellulaire, France

Soren Paludan, Aarhus University, Denmark

Giulio Superti-Furga, Center for Molecular Medicine, Austrian Academy of Sciences, Austria

### Project description:

Antiviral immunity has evolved over the ages into a successful but highly complex and multi-faceted defense system. Many of the ancient antiviral mechanisms were conserved during the evolutionary process. The aim of ERASE is to identify proteins binding to viral nucleic acids by mass spectrometry in different species and to use these data to identify evolutionarily conserved antiviral proteins. Candidate proteins will be evaluated for antiviral activities in diverse organisms and will be tested for potential antiviral activity using a poxvirus immunization system. We anticipate that our unbiased approach will not only shed new light on the evolution of the innate immune system but also facilitate identification of potential candidates for antiviral targeting.

