KEYFACTS

START	DURATION	FUNDING	TEAM
January 2025	5 years	€ 7.3 Mio	7 Partners

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www.combine-marv.eu

PARTNERS

- Karolinska Institutet
- University of Oslo
- VIB science meets life
- Marburg University
- HZI Helmholtz Centre for Infection Research
- Institute of Biochemistry
- EURICE European Research and Project Office GmbH

Funded by the European Union

COMBINE

Towards Improved Pandemic Preparedness

Advancing Our Understanding of Virus Cell Entry
Using Marburg virus as a Model

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ABOUT

With viral disease emergence expected to accelerate **preparing for future pandemics** is paramount! Robust pandemic preparedness does not only mean saving lives during outbreaks but also protecting economies, supporting societal stability, and strengthening the resilience of global systems.

Any viral infection begins with the attachment of the virus to host cells and subsequent activation of cellular receptors. Therefore, it is essential to identify the cellular factors and mechanisms involved to **understand how viruses infiltrate host cells and ultimately combat emerging infectious diseases.** This is why COMBINE explores how viruses enter cells using Marburg virus (MARV) as a model and develops a versatile experimental pipeline that serves as a blueprint for rapid international efforts in creating vaccines and treatments for emerging viral threats.

IMPACT

COMBINE will

- strengthen the European and global virology community with new tools and knowledge to research and combat Marburg virus (MARV) and other emerging viruses;
- reduce the health threat of emerging viral diseases in Europe though specific treatment and vaccination;
- reduce premature mortality and health care burden of MARV infection though specific treatment and vaccination;
- contribute to patients and citizens being more knowledgeable of Marburg virus;

hence increase pandemic preparedness.

THE COMBINE APPROACH

The COMBINE project employs a three-step approach to investigate the virus-host cell interaction and cellular uptake of Marburg virus (MARV). The approach uses a unified inverted attachment platform that halts and synchronizes infection at the cell binding stage, is compatible with BSL4 conditions, and integrates multi-Omics technologies.

IDENTIFICATION

In the first step, advanced technologies are integrated with a synchronized infection assay to identify key virus and cell components—such as attachment factors and functional receptors—that define the signature of virus-cell activation.

CHARACTERISATION

The next step is to characterise how key viral and cell proteins help MARV enter by using multi-omics, imaging, and interaction studies to track changes in various tissues and build a detailed model of the infection process.

INHIBITION

The final step is to inhibit MARV entry by targeting key virus-cell interactions using large-scale screening to identify compounds that block viral attachment or activation.

The COMBINE approach will not only reveal new insights on MARV cell entry but will be further developed into a blueprint experimental pipeline for the streamlined identification and antiviral targeting of proteins involved in the virus attachment process – that may be applied to other viruses.