

# 1 YEAR OF COMBINE

## Laying the Foundations for Understanding Viral Entry

One year into its implementation, the EU-funded research project COMBINE has successfully laid strong scientific and collaborative foundations to advance our understanding of how viruses enter host cells. Using the Marburg virus (MARV) as a model, COMBINE focuses on the earliest and most critical step of viral infection: virus-cell attachment and entry. By identifying the host factors and molecular mechanisms involved at this stage, the project aims to develop new pipelines for antiviral strategies and pandemic preparedness.

### What is COMBINE about?

With viral disease emergence expected to accelerate in the coming decades, preparing for future pandemics is paramount. Beyond protecting lives during outbreaks, robust pandemic preparedness safeguards economies, sustains societal functioning, and strengthens the resilience of global systems. Since every viral infection begins with the interaction between viral surface proteins and host cell receptors, understanding this process is essential for combating emerging infectious diseases.

Against this backdrop, COMBINE seeks not only to deepen scientific insight into MARV entry mechanisms and potential therapeutic targets, but also to develop an innovative and transferable experimental pipeline. This pipeline is conceived as a versatile blueprint that can be rapidly adapted to other emerging viruses, facilitating cross-country collaboration and accelerating the development of novel drugs and vaccines.



## Building the Project Framework

### Management and Communication

The first year of COMBINE was marked by important organisational milestones that ensure efficient coordination across the consortium and support high-quality scientific progress. Clear and robust management structures were established alongside a dedicated communication strategy to support internal coordination and external outreach.

In January 2025 the project officially launched with a [Kick-off Meeting in Braunschweig, Germany](#), bringing together partners from across Europe to align on scientific objectives, workflows, and timelines.

Over the course of the year, COMBINE has established a presence on LinkedIn and Bluesky, regularly informing followers about the progress of the project and providing informative insights into the field of virology.

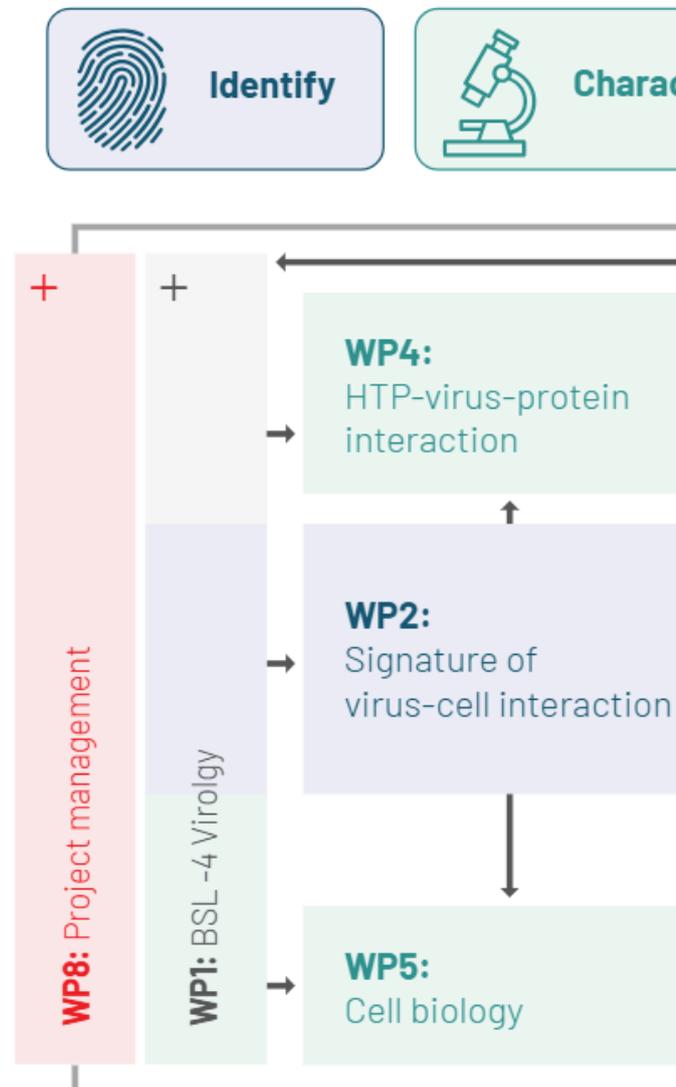
### Scientific Advisory Board

In addition, a Scientific Advisory Board was set up to provide independent guidance and strategic input. The board is composed of internationally recognised experts.

Together, these structures form a solid backbone for the successful research endeavour of COMBINE over its full duration.

### Engaging with the Scientific Community

From the beginning, COMBINE has actively engaged with the wider scientific community. Project partners presented the project's aims and early progress in [science talks](#) and at international events such as the [Defender International Symposium](#). These activities helped position COMBINE within the broader landscape of virology and pandemic preparedness research, while fostering valuable exchange with other initiatives, experts in the field, and interested lay audiences.



## Advancing the Science: First-Year Achievements

Despite being in its early phase, COMBINE has already achieved substantial scientific progress across its work packages. Since one of our main goals is to establish experimental pipelines that enable rapid interrogation of newly emerging viral pathogens, the consortium developed new model systems and analytical assays and implemented them in a coordinated manner across multiple sites in Europe. During the first year, we established an advanced MARV infection model that enables direct observation of early virus–cell interactions, providing a critical foundation for studying virus–host processes in relevant cellular contexts. In parallel, COMBINE researchers developed and validated sensitive assays to investigate and inhibit interactions between the viral glycoprotein and host cell factors, including the successful implementation of a robotic, high-throughput screening platform. This represents a key step towards systematically identifying potential antiviral targets at the virus entry stage.

In addition, the project laid important groundwork for proteomics-based analyses, enabling the large-scale investigation of host cell proteins involved in MARV entry. These efforts ensure that COMBINE is well prepared to generate and integrate complex datasets in the coming project phases.

## Looking Ahead: The 2026 Roadmap

Building on the strong foundations laid in its first year, COMBINE will significantly expand its scientific activities and outputs over the coming year. Upcoming work will focus on generating comprehensive host surfaceome and whole-cell proteome datasets, providing an in-depth view of the cellular landscape encountered by MARV during entry. These data will be complemented by the reprocessing and integration of proteomics datasets, aimed at maximising data quality and uncovering new biological insights.

At the same time, COMBINE will advance the development of high-throughput platforms to map MARV–host protein interactions and further elucidate the molecular mechanisms of MARV entry. The project will also establish MARV–infected primary cell systems as shared resources for analysing cell-type-specific signatures of infection. A particular highlight of the upcoming phase will be the use of synthetic cell-like systems to reconstitute and visualise MARV binding events, enabling direct observation of virus–host interactions using advanced imaging approaches.



## A Strong Start for a High-Impact Project

After its first year, COMBINE is on track to achieve its ambitious objectives. By combining expertise in virology, proteomics, synthetic biology, and systems biology, the project is paving the way for new antiviral strategies and a transferable technology pipeline that can be rapidly applied to future emerging viruses.



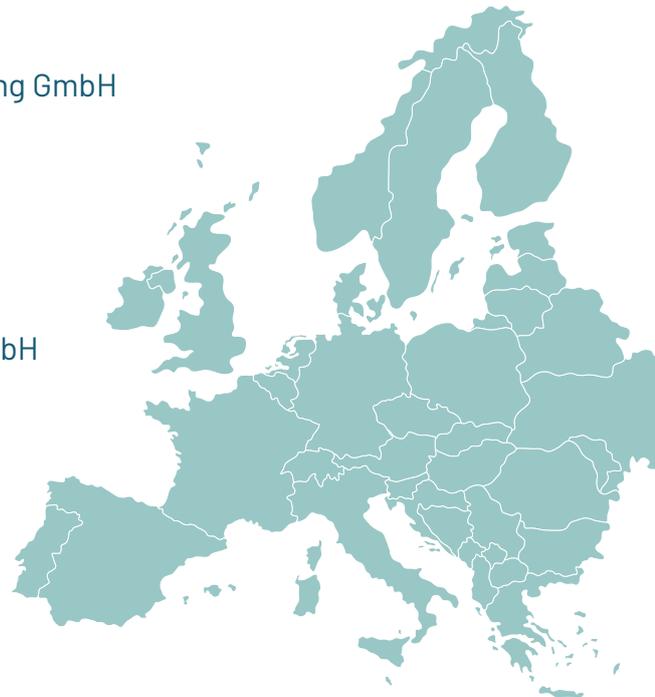
“Over the past year, we have built a strong and highly collaborative network across European laboratories, united by the joint goal of developing new tools and establishing robust experimental pipelines for the rapid investigation of emerging viral pathogens. In the second year, we will begin to deploy these newly established platforms to address key questions in the biology of MARV infection. I am proud of what we have achieved in the first year and excited about the discoveries and progress the next 12 months will bring.”

**Christian Sieben, COMBINE coordinator**

As COMBINE moves into its next project year, the consortium looks forward to delivering new scientific insights, strengthening international collaboration, and contributing to global pandemic preparedness.

## The COMBINE consortium

<b>HZI</b>	Helmholtz-Zentrum für Infektionsforschung GmbH
<b>UMR</b>	Philipps Universität Marburg
<b>UiO</b>	Universitetet i Oslo
<b>KI</b>	Karolinska Institutet
<b>IBRA</b>	Institutul de Biochimie
<b>VIB</b>	Vlaams Instituut voor Biotechnologie
<b>EURICE</b>	European Research and Project Office GmbH



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