





Peer Community In Microbiology

A growing community to navigate the deluge of sequencing data and provide a RdRp-based framework for data-oriented RNA virus biology

Sebastien Massart based on peer reviews by **Mart Krupovic**  and **Ishi Keenum** 

Alexander G. Lucaci, Hisham M. Shaikh, Li Chuin Chong, Rachid Tahzima, Marco Forgia, Karima Ben Mansour, Shoichi Sakaguchi, So Nakagawa, Xin Hou, Tatiana Demina, Philmar Raj Jayaraj Mallika, Anne Kupczok, Spyros Lytras, Humberto Debat, Justine Charon, Michael Louie Urzo, Milica Raco, Rachel Seongeun Kim, Ricardo Rivero, Dimitris Karapliafis, Leyla Sirkinti, Laura Luebbert, Luca Nishimura, Rayan Chikhi, Lander De Coninck, Florian Charriat, Emma Soufir, Vladimir Gajdov, Thomas Krannich, Gytis Dudas, Cédric Lood, Josue Rodríguez-Ramos, Anja Pecman, Uri Neri, Almut Werner, Mia Le, Bolaji Osundahunsi, Nils Peter Petersen, François Maclot, Serafin Gutierrez, Sofia Paraskevopoulou, Luke Hillary, Ingrida Olendraite (2026) Consensus statement from the second RdRp Summit: towards a unified framework for RNA virus biology. Zenodo, ver. 4, peer-reviewed and recommended by Peer Community in Microbiology. <https://doi.org/10.5281/zenodo.20029832>

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The sequence databases are growing exponentially thanks to the continuous evolution of high throughput sequencing technologies. These “petabase” datasets can now be analysed at large-scale through a plethora of algorithms for virus identification, protein structure prediction, evolutionary inference... These advances are rapidly expanding the known RNA virosphere, revealing unexpected levels of diversity. Nevertheless, a rapidly growing domain is often lacking standards and frameworks to ensure quality, validity and inter-operability of the generated information.

In this context, the article from Lucaci *et al.* (2026) represents a key milestone, supported by 43 virologists, as it captures this field at a decisive transition point: RNA virus discovery and characterization is moving from opportunistic sequence detection toward a more systematic, interoperable and quantitatively grounded discipline. By centering the discussion on RNA-dependent RNA polymerase, the principal conserved marker of RNA viruses, the authors provide a coherent framework for connecting viral discovery, taxonomy, structural biology, evolutionary inference, and data standardization.

The article originates from the second RdRp summit, aiming to gather and structure the community of virologists in this field and translates its conclusions into concrete community priorities and a call for joining the initiative. The priorities include standardized benchmarking of RNA virus discovery tools, improved approaches for virus–host relationship inference, structure-guided phylogeny, better recovery of segmented genomes, and sustained knowledge exchange through community initiatives such as the RNA Virus Journal Club.

This community-driven orientation gives the article value beyond a conventional review: it proposes shared directions for improving reproducibility, comparability, and biological interpretation across RNA virus research. So, in our “data-rich” scientific environment, this consensus statement should help to structure future research axes, tool development, and collaborative initiatives in RNA virus biology.

References:

Alexander G. Lucaci, Hisham M. Shaikh, Li Chuin Chong, Rachid Tahzima, Marco Forgia, Karima Ben Mansour, Shoichi Sakaguchi, So Nakagawa, Xin Hou, Tatiana Demina, Philmar Raj Jayaraj Mallika, Anne Kupczok, Spyros Lytras, Humberto Debat, Justine Charon, Michael Louie Urzo, Milica Raco, Rachel Seongeun Kim, Ricardo Rivero, Dimitris Karapliafis, Leyla Sirkinti, Laura Luebbert, Luca Nishimura, Rayan Chikhi, Lander De Coninck, Florian Charriat, Emma Soufir, Vladimir Gajdov, Thomas Krannich, Gytis Dudas, Cédric Lood, Josue Rodríguez-Ramos, Anja Pecman, Uri Neri, Almut Werner, Mia Le, Bolaji Osundahunsi, Nils Peter Petersen, François Maclot, Serafin Gutierrez, Sofia Paraskevopoulou, Luke Hillary, Ingrida Olendraite (2026) Consensus statement from the second RdRp Summit: towards a unified framework for RNA virus biology. Zenodo, ver.4 peer-reviewed and recommended by PCI Microbiology <https://doi.org/10.5281/zenodo.20029832>

Reviews

Evaluation round #1

DOI or URL of the preprint: <https://doi.org/10.5281/zenodo.17663618>

Version of the preprint: 3

Authors' reply, 04 May 2026

We are thankful for these comments as they have raised the overall quality of our manuscript.

[Download author's reply](#)

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Decision by [Sebastien Massart](#), posted 20 March 2026, validated 20 March 2026

The manuscript provides a comprehensive overview of recent progress, ongoing challenges, and community-driven initiatives in RdRp research. It is timely and relevant, particularly given the rapid expansion of RNA virus discovery.

In addition to the comments made by both reviewers, please find in attachment a list of suggestions and comments that might contribute to rise the clarity, usefulness or impact of the manuscript for the entire community of virologists.

Looking forward receiving the revised version of the manuscript [Download recommender's annotations](#)

Reviewed by [Mart Krupovic](#) , 08 January 2026

In this manuscript, Lucaci and colleagues present a consensus statement from the second RdRp Summit. The authors provide an overview of the RNA virology field, highlighting some of the recent advances and challenges, and outline several community projects and future initiatives, which are expected to further advance the field. The manuscript is clearly written and I found it informative and enjoyable to read. In my opinion, this article will be useful for both experienced RNA virologists and those just starting on this path. For this type of articles, there is not much what one can suggest for improvement. However, below are a couple of minor points, which I would like the authors to consider.

Page 5, top: "replicate via a rolling circle mechanism (RCA)" – remove the abbreviation (not used anywhere else in the text). Instead, consider adding a reference to the paper where RCR of ambiviruses was demonstrated (PMID: 37147358).

Page 9: check for redundancy –

"As the field of RNA biology continues to expand at an unprecedented pace and is spurred on by advances in short- and long-read sequencing technologies, structural prediction, artificial intelligence, and metagenomics - it has become increasingly important to align efforts around shared methodologies, standards, and infrastructures."

vs

"As the field of RNA biology expands at an unprecedented pace, spurred on by significant advances in short-read and long-read sequencing technologies, structural prediction, AI, and metagenomics, it becomes increasingly important to align efforts around shared methods, standards, and infrastructures."

Reviewed by [Ishi Keenum](#) , 19 March 2026

The authors present a strong report out of the recent meeting and outline advances in RNA virus biology. While the group is undertaking solid efforts towards standardization, it would be helpful to have more concrete information about the activities being implemented. How well attended are journal clubs? The designation of challenges is helpful to understand where key researchers in the field see gaps. How was consensus reached? Is this all summit attendees listed as authors?

Overall, the manuscript seems to lack purpose, can the authors work to cement and prioritize future initiatives in an order. Are there explicit standards or benchmarks the group can agree on for some of the proposed future initiatives?

Specific notes:

AI should be defined as an acronym if it is going to be used.

Figure 3 is very blurry.

Title and abstract

Does the title clearly reflect the content of the article? [Yes]

Does the abstract present the main findings of the study? [Yes] (Appropriate for a consensus paper; summarizes themes, not "findings" in an empirical sense)

Introduction

Are the research questions/hypotheses/predictions clearly presented? [No] (Not structured as hypotheses; goals are broad and descriptive)

Does the introduction build on relevant research in the field? [Yes]

Materials and methods

Are the methods and analyses sufficiently detailed to allow replication by other researchers? [No] (No formal methods; this is a consensus/opinion piece)

If applicable, are sample sizes clearly justified? [I don't know / Not applicable] (No empirical sampling)

Are the methods and statistical analyses appropriate and well described? [No] (No statistical framework; descriptions are high-level)

Results

In the case of negative results, is there a statistical power analysis? [I don't know / Not applicable]

Are the results described and interpreted correctly? [Yes] (Within scope of a narrative/consensus summary)

Discussion

Have the authors appropriately emphasized strengths and limitations? [No] (Strengths emphasized; limitations of approaches/tools/community efforts are underdeveloped)

Are the conclusions adequately supported without overstating implications? [Yes] (Generally reasonable, though somewhat aspirational)