MVI-2 | Mapping miRNA–miRNA Regulatory Circuits: Implications for Immune Regulation and Viral Pathogenesis

Host unit	Main supervisor	Co-supervisor
Institute of Microbiology and Virology (MVI) **Explore the host institute** Host–Pathogen Interactions group	Prof. Bhupesh Kumar Prusty **View research profile** **Visit the research group**	Dr Zaiga Nora-Krūkle **View research profile**

APPLICANT FREEDOM The topic defines a research area, not a pre-written project. Applicants may propose a distinct, original approach provided that it remains scientifically aligned with the theme and demonstrably feasible in the host environment.

Research context and rationale

Recent evidence has revealed a previously unrecognized layer of post-transcriptional regulation in which miRNAs can influence the biogenesis, stability, or activity of other miRNAs, thereby affecting broader cellular regulatory networks. This thematic area focuses on the systematic identification and characterization of miRNA-miRNA regulatory interactions using computational, molecular, and systems biology approaches. Particular emphasis may be placed on understanding how these interactions shape immune responses, host-pathogen interactions, and viral pathogenesis, while providing new opportunities for biomarker discovery and therapeutic development.
The thematic opportunity builds on the host group's previous research on viral miRNAs and the regulation of host miRNA biogenesis and stability, providing a basis for further mechanistic investigation of miRNA cross-regulation.

Indicative scientific scope

Projects may combine computational prediction, sequencing and targeted mechanistic validation to investigate miRNA cross-regulation. Applicants should define a focused biological context and avoid proposing an unbounded map of all possible miRNA interactions.

Examples of research questions

- Which miRNA-miRNA interactions are reproducible and biologically consequential in a defined immune or viral context?

- What molecular mechanisms govern the formation, stability or processing of the proposed regulatory circuits?
- How do viral factors or infection-related cellular states alter these circuits?
- Can network-level findings be validated experimentally and linked to measurable immune phenotypes?

Possible approaches

- In silico prediction and network analysis followed by prioritised experimental validation.
- Small-RNA or transcriptomic sequencing, where justified by power and cost.
- Reporter assays, perturbation experiments, qPCR and molecular interaction studies.
- Cellular models of immune regulation or viral pathogenesis within the host's approved scope.
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METHODS NOTE The approaches above are indicative. Applicants should select and justify methods appropriate to their own questions rather than attempt to include every method listed.

Relevant host expertise and resources

Expertise: miRNA biology, viral pathogenesis, immune regulation, molecular biology, transcriptomics and host-pathogen interactions.

- Single-cell and sequencing-related infrastructure, including 10x Genomics and TapeStation platforms.
- Real-time PCR, nucleofection, fluorescence microscopy and automated capillary Western blotting.
- Bioinformatics/HPC capability for sequence and network analysis.

ACCESS CONDITION Access to the specialised resources listed above is subject to the conditions described in the separate MVI Host Profile and to project-specific arrangements.

Interdisciplinary and intersectoral opportunities

- Molecular virology, RNA biology, immunology, computational biology and systems-level analysis.
- Potential applied AI or advanced computational collaboration only where it is necessary for the approved research design.

Potential collaboration and secondment pathways

Topic-specific collaboration opportunities include RNA biochemistry expertise provided by Dr. Archana B. Prusty and Prof. Utz Fischer at Julius-Maximilians-Universität Würzburg. Dr. Prusty is a proposed external mentor for this research area. Any project-specific involvement or placement is subject to agreement; scientific collaboration does not in itself imply formal KEY-RSU Associated Partner status.

- Aarhus University, proteomics/metabolomics, bioenergetics, sequencing, patient models and research training.
- University of Skövde, precision medicine and translational medicine.
- Royal College of Surgeons Ireland, single-cell multi-omics.
- Spanish National Research Council, single-cell and multi-omic analysis, flow cytometry and immune-signature interpretation.
- National Institute of Research and Innovation, SPF rodent handling, in-vivo study design.
- SIA APPLY, applied AI, computer vision, predictive modelling and production-oriented digital-health development.

SECONDMENT STATUS Participation in a mandatory secondment of 6–12 weeks forms part of KEY-RSU. The final host, duration, objectives and outputs will be agreed for the selected fellow and aligned with the approved KEY-RSU rules and Career Development Plan. The researcher remains employed by RSU throughout the secondment. Additional host organisations may be considered, subject to confirmation of their suitability, compliance with KEY-RSU requirements and any necessary approvals.

Research training and career development

The research environment offers opportunities to develop an interdisciplinary profile across infection biology, RNA biology, molecular and cellular methods, and computational analysis, according to the selected project. Training and mentoring may include project planning, research data management, Open Science, scientific writing and communication. Opportunities to contribute to guest lectures, practical laboratory sessions and the mentoring of bachelor's and master's students will be tailored to the researcher's expertise and institutional arrangements. Individual priorities and activities will be agreed through the Career Development Plan.

Applicant background

Relevant background: Applicants should hold a doctoral degree and demonstrate a strong research background in molecular biology, RNA biology, virology, immunology, bioinformatics, or another relevant discipline. Candidates should demonstrate the ability to develop and lead independent research, formulate innovative scientific questions, and integrate computational and experimental approaches to address complex biological problems where relevant to the proposed project, including through complementary collaboration. Assessment will consider the quality, originality, and relevance of the applicant's research contributions, as well as evidence of collaboration, mentoring, supervision, knowledge sharing, and engagement with the wider research community. Experience in supporting doctoral, master's, or undergraduate researchers, as well as the ability to contribute to a stimulating research and training environment, will be considered an asset. Expertise in specific methodologies will be evaluated in the context of the proposed research and the applicant's overall competencies and potential.

No additional position-specific eligibility requirement should be inferred from this profile unless it is explicitly included in the approved Full Call Text.

Competences that may strengthen the proposal

The following experience may strengthen a proposal but is not an automatic eligibility requirement:

- RNA or miRNA biology;
- molecular virology, immunology or host–pathogen interactions;
- small-RNA, transcriptomic or other sequencing-based research;
- bioinformatics, network analysis or computational prediction;
- reporter assays, molecular perturbation or interaction studies;
- experimental validation of computationally generated hypotheses.

Applicants may be stronger in either experimental or computational research. Where relevant, the proposal should explain how complementary expertise and validation capacity will be secured.

Feasibility boundaries

- Proposals should focus on well-defined biological questions and include a realistic strategy for experimental validation.
- Access to viral models, sequencing resources, specialised datasets, and computational infrastructure is subject to project needs, approvals, availability, and allocated resources.
- The study design should incorporate appropriate measures to ensure robustness, reproducibility, and control of false-positive findings.
- Computational predictions should be prioritised and supported by biologically meaningful validation in relevant model systems.
- Dependence on proprietary datasets, unconfirmed collaborations, or extensive additional resources should be clearly justified and accompanied by feasible alternative approaches.
- Projects should maintain a balanced scope that can be realistically achieved within the fellowship period and available resources.

Ethics, data and responsible research

- Biosafety requirements depend on the chosen viral or cellular model.
- Sequence data must be managed under FAIR principles while respecting any sensitivity or reuse restrictions.
- Computational predictions must be transparently documented and not presented as validated mechanisms without experimental evidence.

Expected contribution

The research is expected to clarify an emerging layer of post-transcriptional regulation and establish credible links between miRNA cross-regulation, immune responses and viral pathogenesis.