DC4: Advanced protocols for Native RNA sequencing by ONT

Host institution: Istituto Italiano di Tecnologia, Center for Genomic Sciences, Milan, Italy

Supervisor: Dr. Francesco Nicassio

Co-Supervisors: Prof. Winston Timp, Johns Hopkins University (Academic); Dr. Federico Forneris, Instituto Universitatrio di Studi Superiori di Pavia (Academic); Dr. Logan Mulroney, National Human Genome Research Institute (Academic); Dr. Thomas Frischmuth, baseclick GmbH (Industrial)

Project description: DC4 will develop advanced protocols for Oxford Nanopore native RNA sequencing that overcome current barriers to clinical adoption. The project pursues three integrated objectives: i) optimise sample and library preparation for clinical specimens; ii) design and implement a targeted enrichment workflow for native RNA that preserves single-molecule signals, including RNA modifications; iii) deliver a proof-of-principle diagnostic RNA panel based on ONT direct RNA sequencing. This work sits in WP2 (Direct RNA sequencing) with validation links to WP4 (Identification and Delivery of Therapeutic Nucleic Acids).

The experimental plan is staged across beneficiaries and associated partners. At IIT, the candidate will optimise native RNA protocols on MinION/PromethION platforms, establish appropriate IVT controls, and receive training in RNA modification analysis and quantification. Building on this foundation, targeted approaches will be developed in collaboration with baseclick, leveraging click-chemistry to enable selective library preparation, and developing advanced enrichment and depletion strategies with Prof. Winston Timp's group at Johns Hopkins University. Final optimisation and validation on clinical-grade samples will be carried out with Flomics Biotech. This collaborative and intersectoral pathway ensures both technological maturation and clinically oriented testing, directly supporting the project's objectives and expected outcomes.

Expected outcomes include robust, transferable protocols for native RNA sequencing, a targeted sequencing workflow suitable for low-abundance transcripts, and a proof-of-principle diagnostic panel, with potential for IP-protected DRS production.

Host laboratory: The PhD fellow will be based in Milan, at the Center for Genomic Science of the Istituto Italiano di Tecnologia (IIT), in the laboratory of Dr. Francesco Nicassio. The group investigates how non-coding RNAs and RNA modifications regulate gene expression and contribute to cancer development, with a strong focus on long-read sequencing and integrative multi-omics approaches. The laboratory has established recognised expertise and a pioneering role in native RNA sequencing with Oxford Nanopore technologies, combining experimental innovation and computational analysis. Its work spans from benchmarking approaches for RNA modification detection and the development of exprimental and analytical tools for applications in cancer and virology.

Ongoing projects provide a strong foundation for the DC4 project, including a large dataset for long-read transcriptomics in human cancer, the IIT RNA Flagship dedicated to epitranscriptomic technologies, and the international FANTOM6 initiative on non-coding RNAs and chromatin regulation. These efforts place the laboratory at the intersection of technology development and translational applications.

Secondments: This project is carried out in strong collaboration with the following groups, and visits to their laboratories are expected during the project. A willingness to travel and spend time abroad is therefore essential:

- Dr. Thomas Frischmuth, baseclick GmbH, Germany
- Prof. Winston Timp, Johns Hopkins University, USA
- Dr. Marc Weber, Flomics Biotech SL, Spain

Eligibility conditions:

- Master's degree in Biology, Biotechnology, or related disciplines.
- Applicants must be doctoral candidates, i.e. not already in possession of a doctoral degree.
- Mobility rule: researchers must not have resided or carried out their main activity in the country of the recruiting beneficiary for more than 12 months in the 36 months immediately before their recruitment date.

Required Skills:

- Prior research experience in molecular or cellular biology, biotechnology, or related disciplines, ideally including RNA biology or genomics.
- Familiarity with sequencing technologies, bioinformatics analysis, or protocol development will be considered an advantage.
- Proficiency in the English language is required, as well as good communication skills, both oral and written. Successful candidates will need to provide an English test (e.g. IELTS, TOEFL, Cambridge English). You may be exempt if you are a national of a majority native-English speaking country, or have qualifications / degree that has been taught and assessed in English. The supervisor can also confirm during the interview that a candidate has the required level of English.

Enquiries

For general information about the INT2ACT Doctoral Network visit the project website (www.int2act.eu) or send an email to int2act@gmail.com. For additional information on this project please contact Dr. Francesco Nicassio (francesco.nicassio@iit.it).

How to apply

To learn more about the application process, visit the INT2ACT recruitment web page (https://int2act.eu/open-positions/).

Required documents:

1. Statement of interest (limit of 2,500 characters) explaining why you wish to be considered for the fellowship and which qualities and experience you will bring to the role.
2. Curriculum vitae et studiorum.
3. A certificate of University examinations taken (with marks).
4. A final degree certificate translated in English. If, at the time of application, candidates should not be yet in possession of a degree certificate, they can submit it at the time of the examination.

All documents must be merged into a single PDF file, in the order listed above.
A limited number of applicants will be invited for an interview and will be required to provide contact information of up to two contact person for reference letters.

Application deadline

The closing date for applications is **January 31 2026.**