



Post-Doc NCN SONATA: Visualising and Investigating Eukaryotic Genomic and Centromere Organisation

Keywords: repeatome, centromere, satellite DNA, transposable elements, comparative genomics, bioinformatics, machine learning, genome architecture

Department of Bioinformatics at the Institute of Biochemistry and Biophysics of the Polish Academy of Sciences, Warsaw, led by Prof. Piotr Zielenkiewicz, is seeking a highly motivated, creative, and independent Postdoctoral Researcher to join our team under the supervision of Dr Piotr Włodzimierz. The position is funded by the National Science Centre (NCN) under the SONATA project no. 2025/59/D/NZ2/03120, titled: “Visualising and Investigating Eukaryotic Genomic and Centromere Organisation”.

Research topic

Long-read sequencing has driven an explosion in the number and quality of eukaryotic genome assemblies, including, for the first time, complete centromeric sequence. Yet many assemblies remain structurally unexplored, in part because no widely accessible tool exists for integrated genome architecture and centromere annotation despite centromeres being of crucial interest in fields from medical genetics to plant breeding and speciation research.

This project builds on the prior work: the tandem-repeat annotation software TRASH, the prototype Centromere Annotation Pipeline (CAP), and the ongoing project which surveyed centromere architecture across more than 300 eukaryotic genomes - giving the group an unusually rich, curated starting resource: over 23 million annotated satellite repeats across 263 families, transposon and gene annotation for every genome, and a time-calibrated phylogeny with centromere architecture mapped onto it.

Building on this foundation, the SONATA project aims to (i) develop a machine learning assisted method for predicting centromere location and architecture from sequence data alone, (ii) turn this into an accessible, modular annotation and visualisation tool combining gene, transposon and tandem repeat annotation with the CAP centromere-prediction module, and (iii) apply the tool at scale to further expand the genomic architecture atlas as a public resource for the community.

Job description

The postdoctoral researcher's core activity will be to lead a **research project in repeatome and genome architecture evolution**, within the scope of the SONATA programme described above. Possible research directions include:

- The evolutionary interplay between satellite DNA and transposable elements in centromeres.
- Comparative or machine-learning approaches to identify novel centromere-associated sequence or epigenetic signatures.
- Centromere architecture in currently under-sampled eukaryotic lineages (e.g. microbial eukaryotes, fungi, protists).
- Mechanisms of satellite higher-order repeat formation, repeat homogenisation, or centrophilic transposon adaptation.

Requirements

- A PhD in bioinformatics, computational biology, genomics, or a related field. Holders of a PhD in computer sciences, mathematics or physics may apply with a record of experience in a biology-related field. To be eligible, applicants must have obtained their doctoral degree in the year of employment on the project or within the 12 years preceding 1 January of that year (this period may be extended by documented career breaks – please contact us if applicable).
- A demonstrated ability to design and drive a research project independently.

- Understanding of statistical methods used in biological data science.
- Proficiency in a scripting or programming language (e.g. Python or R) and comfort working in a Linux/HPC environment.
- Ability to survey the literature, analyse data critically, and draw conclusions.
- Good scientific communication skills in English.

The following would be considered an advantage:

- A background in genome-scale bioinformatics analysis: comparative genomics, sequence/repeat annotation, or phylogenetics.
- Prior experience with centromere biology, satellite DNA, or transposable element analysis (e.g. RepeatMasker, TRASH, EDTA, TESorter or similar tools).
- Experience analysing long-read sequencing (PacBio HiFi, Oxford Nanopore) or Hi-C data.
- Experience applying machine learning methods to genomic data.
- A track record of scientific publications in genomics, evolutionary biology, or a related area.

Candidates will be selected through an open competition, in accordance with the principles set out in the [European Charter for Researchers and the Code of Conduct for the Recruitment of Researchers](#)

Terms and conditions of employment

Employment on the project under a full-time employment contract for **3 years** (36 months). Remuneration in accordance with the NCN SONATA regulations: up to **210,000 PLN total employer cost (gross gross, i.e. including the employer's share of social security contributions) per year**.

Planned start date: **November/December 2026**, or depending on the candidate's availability.

Deadline for submitting applications: 28 October 2026. *The recruitment period may be extended; any extension will be announced on the recruitment platform and this listing.*

We offer

- A positive, collaborative working environment with 100% focus on research (no teaching obligations).
- 26 days of annual leave for fixed-term contracts.
- 21 days of possible home office work annually.
- Participation in international courses, workshops, and conferences and collaborating with the group's international partners (e.g. University of Cambridge, Max Planck Institute for Plant Breeding Research, University of Sussex).
- Support from the IBB Welcome Center for relocation, and possible short-term stay in the Institute's hotel, on site employee-only parking.
- Voluntary participation in Multisport programme and additional health insurance packages.
- Additional annual remuneration and motivational allowance (depending on research achievements affiliated with IBB PAS, at the Institute's Director discretion).

Evaluation of candidates

Stage I – application review. The Recruitment Committee, composed of the Project Leader and designated independent IBB PAN researchers, will assess submitted applications and select candidates whose qualifications and experience best match the project's requirements. We reserve the right to contact only candidates shortlisted for the second stage.

Stage II – interview. Shortlisted candidates will be invited to an interview, during which they will be asked to briefly present their main research project, followed by discussion. The meeting will also be an opportunity to learn more about the project and its working conditions.

Required documents

- Copy of the PhD diploma (and its nostrification, if the doctoral degree is not recognised by the NAWA Qualifier).
- CV including scientific achievements and a brief list of methods/techniques known to or used by the candidate.
- List of publications.
- A letter of intent (max. 1 page, 12 pt) explaining why you are interested in this project.
- Contact details for, or a reference letter from, a previous employer or PhD supervisor.
- Signed “Information clause on the processing of personal data for IBB PAS recruitment” available at the web site [<https://ibb.edu.pl/en/career/career/>]
- Signed and filled out “Application form for IBB PAS recruitment” available at the web site [<https://ibb.edu.pl/en/career/career/>]

How to apply

Applications should be sent in English via the recruitment platform:

<https://system.erecruiter.pl/FormTemplates/RecruitmentForm.aspx?WebID=b065659edd334f1b84d40ad65dd8b471>

In case of any difficulties, please contact: recruitment@ibb.waw.pl