Fourth Call for Proposals for Transnational Access Projects at EASI-Genomics

European Advanced infraStructure for Innovative Genomics

Timeline:
Call open: 01.03.2022 8:00 CET
Proposal submission deadline: 10.04.2022 23:55 CET
Notification of applicants: by 01.07.2022
Start of projects: latest 4 months after notification

EASI-Genomics is a European Genomics Infrastructure Horizon 2020 project. This novel infrastructure supports researchers in **next-generation sequencing** and **other high-end genomics applications** and **genomic data analysis**. The infrastructure is accessible worldwide to researchers from both Academia and the Industry. EASI-Genomics invites external users to apply for access by opening several calls for proposals. Academic research groups and scientific institutions are highly encouraged to submit projects collaborating with SMEs.

EASI-Genomics will provide support to more than 150 projects for a total budget of 6 Mio € throughout the EU project. So far, a total of 105 projects have been awarded for a budget of over 5 Mio € in three access calls and an extraordinary call in response to the COVID-19 crisis. In this **fourth and final access call**, EASI-Genomics aims to support user projects for a total budget of up to 0.75 Mio €. The European Commission rules on Transnational Access apply, meaning that applicants will not be granted access to a facility located in their home country.

EASI-Genomics will support integrative projects covering expertise not available at the applicants' home institution sites, including high-throughput and cutting-edge sequencing and complex bioinformatics analysis. EASI-Genomics will cover the consumables and personnel required to perform the external user projects at the project partner facilities.

Interested users can submit proposals to the 4th TNA Call online via the [EASI-Genomics website (https://www.easi-genomics.eu/access/calls)](https://www.easi-genomics.eu/access/calls) **until April 10, 2022 (23:55 CET)**. Applicants will be asked to describe the objectives of their research and the desired experimental and computational methods required to achieve these objectives. **Valid ethical and legal documents relative to the research proposal need to be submitted directly online at the time of submission by the applicant.** EASI-Genomics can provide guidance for such documentation. Eligible proposals will be evaluated for scientific quality, feasibility, and impact. Proposals will be handled confidentially. EASI-Genomics strongly recommends external users contact the facilities offering the services of interest to discuss the feasibility of the intended project prior to submitting the proposal.

Details on the submission process, eligibility and evaluation criteria, and project implementation can be found at www.easi-genomics.eu

Topics of the Fourth Call for Proposals:

1) Long-read Sequencing with Oxford Nanopore Technology (ONT) or PacBio

We seek for the following applications: long-read genome sequencing, *de novo* assembly and annotation, structural variant detection, metagenomics, full-length mRNA and cDNA sequencing. The projects should focus on human disease or on ecologically and/or economically relevant species. Procedures available at EASI-Genomics laboratories for these projects are ONT DNA, cDNA and direct RNA sequencing, Iso-Seq (PacBio), and state-of-the-art data analysis support. Applicants need to provide a detailed description of the objectives of their project and explain **wet-lab and/or computational** procedures required for the execution of the project. Applicants need to describe available sample material and limitations in detail.

2) FFPE RNA and Exome Sequencing

Formalin-fixed paraffin embedded (FFPE) samples are the most abundant source of archived clinical specimens, but pose distinct challenges for nucleic acid isolation and analysis. Our specialized facilities offer RNA and exome sequencing from FFPE samples to enable projects based on archived material. Applicants need to provide a detailed description of the objectives of their project, provide information about the available sample materials such as fixation conditions and storage times, and explain **wet-lab and/or computational procedures** required for the execution of the project.

3) Single-cell Genomics

EASI-Genomics will support projects that require advanced single-cell multi-omics analysis. Techniques such as single-cell-3´- or 5’-tag RNA sequencing, feature-barcoding, full-length transcript sequencing, B- and T-cell receptor profiling, ATAC-Seq, or combinations thereof are available. Applicants need to provide a detailed description of the objectives of their project and explain **wet-lab and/or computational** procedures required for the execution of the project. Applicants need to describe sample material in detail, such as availability, viability, biosafety containment level, storage conditions.

4) Spatial Transcriptomics/*in situ* Sequencing

Recent advances in RNA sequencing technology enable the profiling of cellular gene expression heterogeneity at spatial resolution. EASI Genomics offers *in situ* sequencing for the investigation of spatial tissue organization. Applicants need to provide a detailed description of the objectives of their project and explain **wet-lab and/or computational** procedures required for the execution of the project. Applicants need to describe available sample material in detail.

5) Identification of Epigenetic Signatures

EASI Genomics offers technologies for profiling of epigenetic signatures such as DNA methylation, chromatin accessibility, or chromatin 3D-structure. Projects should focus on specific tissue/cell types to decipher epigenetic signatures with mechanistic relevance for human disease or ecologically and/or economically relevant species. Studies analyzing surrogate epigenetic markers (e.g. blood-derived) are advised against. Applicants need to provide a detailed description of the objectives of their project and **explain wet-lab and/or computational** procedures required for the execution of the project. Applicants need to describe available sample material in detail.

6) **Shallow Genome**

EASI-Genomics offers to sequence human genomes at a low coverage aiming at accurate genome-wide genetic variation detection, for example for GWAS or population studies, or copy number variation detection, for example in cancer tissue. Applicants need to provide a detailed description of the objectives of their project, available sample materials, and explain **wet-lab and/or computational** procedures required for the execution of the project.

7) **Liquid Biopsy/Biomarker Discovery in Complex Diseases Using cfDNA**

EASI-Genomics offers whole-genome sequencing and whole genome bisulfite sequencing analysis on cell-free DNA on disease monitoring approaches as well as control samples. Applicants need to provide a detailed description of the objectives of their project and explain **wet-lab and/or computational** procedures required for the execution of the project. Applicants need to describe available sample material in detail.

8) Sequencing of Urine Microbiome and of Urothelial Cell DNA

EASI-Genomics solicits project proposals in 16S microbiome analysis from urine of healthy and diseased, as well as sequencing of urothelial cell DNA, such as from urinary tract or bladder cancer patients. Applicants need to provide a detailed description of the objectives of their project and explain **wet-lab and/or computational** procedures required for the execution of the project. Applicants need to describe available sample material in detail.

9) Integrative Data Analysis

EASI-Genomics provides data analysis for already existing data sets. In this case, applicants should describe available data including sequencing technology used to generate it and the objective of the analysis.

10) Joint projects with EPIC-XS

In this call, EASI-Genomics will also consider projects using genomics and proteomic approaches. Applicants should submit the full proposal, including the work requested from EASI-Genomics and that from EPIC-XS. The genomics part will be assessed by the EASI-Genomics review, and shortlisted proposals will be shared with EPIC-XS for their evaluation.

For general inquiries and guidance on ethical documentation please contact the call managers at easi-genomics@mdc-berlin.de.
For consultation please contact the following experts:

Topic	Services	Facilities	Contact
Long-read Sequencing	Nanopore Seq	CEA-CNRGH	collab-easigenomics@cng.fr

	Nanopore Seq	CNAG	projectmanager@cnag.crg.eu
	PacBio	KU Leuven	info@genomicscore.be
FFPE RNA and Exome Seq	FFPE Exome Seq	CEA-CNRGH	collab-easigenomics@cng.fr
	FFPE Exome Seq	CNAG	projectmanager@cnag.crg.eu
	FFPE RNA Seq		
	FFPE Exome Seq	DKFZ - Genomics & Proteomics Core Facility	Contact form
	FFPE RNA Seq	SciLifelab (KTH)	support@ngisweden.se
Single-cell genomics	SC RNA Seq	BIH-Charité	omics@charite.de
	SC ATAC Seq		
	SC multiome Seq		
	SC TCR Seq		
	SC RNA + V(D)J Seq		
	SC RNA Seq	CNAG	projectmanager@cnag.crg.eu
	SC ATAC Seq		
	SC multiome Seq		
	SC TCR Seq		
	SC RNA + V(D)J Seq		
Spatial transcriptomics/*in situ* sequencing	In situ Seq	BIH-Charité	omics@charite.de
	In situ Seq - image analysis/integrative data analysis		
Identification of Epigenetic Signatures	WG ox-BS Seq	CNAG	projectmanager@cnag.crg.eu seq@medsci.uu.se
	HiC Seq (seq & integrative data analysis)		
	HiC Seq (incl. library generation)	CEA-CNRGH	collab-easigenomics@cng.fr
	Low input WG BS Seq	DKFZ - Genomics & Proteomics Core Facility	Contact form
	HiC Seq (seq & integrative data analysis)		
	HiC Seq (incl. library generation)	SciLifeLab (KTH)	support@ngisweden.se
	ATAC Seq		
Shallow Genome	sWGS	CEA-CNRGH	collab-easigenomics@cng.fr
Liquid Biopsy	cfDNA Seq	CEA-CNRGH	collab-easigenomics@cng.fr
Sequencing of Urine	16S Seq	CAU Kiel	ccga@ikmb.uni-kiel.de
	Targeted NGS (DNA)		
Integrative Data Analysis (across all topics)	Integrative data analysis	CNAG	projectmanager@cnag.crg.eu
		DKFZ - Omics IT and Data Management Core Facility	odcf-service@dkfz.de
		BIH-Charité	omics@charite.de