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

European Advanced infraStructure for Innovative Genomics

Timeline:

Call open: 15.01.2021 8:00 CET
Proposal submission deadlines: 01.03.2021 23:59 CET
Notification to applicants: by 01.07.2021
Start of projects: latest 6 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 academic researchers, research groups and scientific institutions. Furthermore, projects from industry, including SMEs will be supported. Throughout four calls for access, EASI-Genomics will support more than 150 projects for a total budget of 6 million € until the end of 2022. The first two access calls and an extraordinary call in response to the COVID-19 crisis awarded a total of 72 projects for a total budget of appr. 4 million €. The rules of the European Commission only allow Transnational Access; applicants will not be granted access to a facility that is in their home country.

EASI-Genomics will support integrative projects covering expertise that is not available at the applicants' home institution sites including high-throughput and cutting-edge sequencing, complex bioinformatic analysis and possibly DNA extraction (e.g. ancient DNA). **Of note, EASI-Genomics also 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. EASI-Genomics will cover the costs of consumables and personnel required to perform the external user projects at the project partner facilities.

EASI-Genomics invites external users to apply for access by opening several calls for proposals. Interested users can submit proposals to the 3rd Call online via the **EASI-Genomics website (https://www.easi-genomics.eu/access/calls) until 1st of March, 2021, 23:59 CET**. EASI-Genomics can provide guidance for such documentation. As pilots to Horizon Europe we encourage project applications with a focus on the mission areas (e.g. cancer, soil health and food). 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 will have to be submitted directly online at the time of submission by the applicant.** Eligible proposals will be evaluated for scientific quality, feasibility, and impact. Proposals will be handled confidentially. EASI-Genomics recommends external users to contact the facilities offering the services of interest in order to discuss the feasibility of the submitted project prior to the submission of the proposal.

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

Topics of the third call for proposals:

i) **Sequencing of ancient DNA**.
EASI-Genomics offers to sequence ancient DNA at its state-of-the-art equipped facilities with special expertise in DNA isolation and sample preparation from challenging specimens. 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.

ii) **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.

iii) **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 spatial transcriptomics and *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.

iv) **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/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.

v) **Long-read sequencing with Oxford Nanopore Technology.**
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/economically relevant species. Procedures available at EASI-Genomics laboratories for these projects are Oxford Nanopore long-read DNA and RNA sequencing 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 in detail.

vi) **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.

Cross-topic applications are supported.

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**
Sequencing of ancient DNA	Ultra low ancient DNA Seq	DNA Lab and Core Facility IG (Tartu U)	cls83@ut.ee
Single-cell genomics	SC RNA Seq	SNP&SEQ Platform at NGI/SciLifeLab (UU)	seq@medsci.uu.se
	SC RNA + V(D)J Seq		
	SC DNA Seq		
	SC RNA Seq	BIH-Charité	info@bihealth.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		
	SC RNA Seq	Scientific Genomics Platforms (MDC)	thomas.conrad@mdc-berlin.de
	SC ATAC Seq		
	SC multiome Seq		
	SC RNA + V(D)J Seq		
Spatial transcriptomics/*in situ* sequencing	In situ Seq (barcodes)	SciLifeLab (SU)	support@ngisweden.se
	In situ Seq (RCA)		
	In situ Seq (image analysis/integrative data analysis)		
	In situ Seq (RCA)	BIH-Charité	info@bihealth.de
	In situ Seq (image analysis/integrative data analysis)		
	Spatial RNA Seq	ScilLifelab (KTH)	support@ngisweden.se

	Spatial RNA Seq	Scientific Genomics Platforms (MDC)	thomas.conrad@mdc-berlin.de
Identification of epigenetic signatures	HiC Seq (incl. library generation)	CEA-CNRGH	collab-easigenomics@cng.fr
	WG ox-BS Seq		
	WG ox-BS Seq	CNAG	projectmanager@cnag.crg.eu seq@medsci.uu.se
	HiC Seq (seq & integrative data analysis)		
	Low input WG BS Seq	SNP&SEQ Platform at NGI/SciLifeLab (UU)	seq@medsci.uu.se
	Low input WG BS Seq	DKFZ - Genomics & Proteomics Core Facility	Contact form
	HiC Seq (incl. library generation)	SciLifeLab (KTH)	support@ngisweden.se
	ATAC Seq		
Long-read sequencing with Oxford Nanopore Technology	Nanopore Seq	CEA-CNRGH	collab-easigenomics@cng.fr
	Nanopore Seq	SciLifeLab (KTH)	support@ngisweden.se
	Nanopore Seq	CNAG	projectmanager@cnag.crg.eu
FFPE RNA and Exome Seq	FFPE Exome Seq	CEA-CNRGH	collab-easigenomics@cng.fr
	FFPE RNA Seq		
	FFPE Exome Seq	CNAG	projectmanager@cnag.crg.eu
	FFPE RNA Seq		
	FFPE Exome Seq	DKFZ - Genomics & Proteomics Core Facility	Contact form
	FFPE Exome Seq	SNP&SEQ Platform at NGI/SciLifeLab (UU)	seq@medsci.uu.se
	FFPE RNA Seq	ScilLifelab (KTH)	support@ngisweden.se
Cross-topic: advanced data analysis	Integrative data analysis	CNAG	projectmanager@cnag.crg.eu
		CEA-CNRGH	collab-easigenomics@cng.fr
		Scientific Genomics Platforms (MDC)	thomas.conrad@mdc-berlin.de
		SNP&SEQ Platform at NGI/SciLifeLab (UU)	seq@medsci.uu.se
		SciLifeLab (KTH)	support@ngisweden.se
		DKFZ - Omics IT and Data Management Core Facility	odcf-service@dkfz.de
		DNA Lab and Core Facility IG (Tartu U)	cls83@ut.ee
		BIH-Charité	info@bihealth.de
		SciLifeLab (SU)	support@ngisweden.se