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

European Advanced infraStructure for Innovative Genomics

Timeline:

Call open: 15.10.2019 8:00 CET

Proposal submission deadlines: 01.12.2019 20:00 CET

Notification to applicants: by 01.04.2020

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 open to academic researchers, research groups and scientific institutions. Projects from industry, including SMEs can be supported. Throughout four calls for access, EASI-Genomics will provide support to more than 150 projects for a total budget of 6 million € over the next four years. The first call for access awarded 32 projects for a total budget of 1.5 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 can also provide support for 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. Costs of external user projects for consumables, computation and for personnel required at the facilities will be covered by EASI-Genomics.

EASI-Genomics invites external users to apply for access by opening several calls for proposals. Interested users can submit proposals to the 2nd Call online via the **EASI-Genomics website (https://www.easi-genomics.eu/access/calls) until December 01, 2019, 20:00 CET**. Applicants are asked to describe the objectives of their research and the desired experimental and computational methods required to achieve these objectives. The objective of the EASI-Genomics Infrastructure is to support projects from study design, through sequence to data analysis. Projects requesting sequencing support that could be provided by a commercial sequencing service provider will be viewed less favorably. 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

Topics of the second call for proposal:

i) **Sequencing of ancient DNA**.
EASI-Genomics offers to sequence ancient DNA at its state-of-the-art equipped facilities. 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 in single-cell analysis, *i.e.* single-cell DNA- and RNA-sequencing. Techniques such as single-cell-3´tag RNA sequencing, single-cell full-length transcript sequencing, single-cell -ATAC-sequencing, single-cell -DNA methylation sequencing and single-cell RNA sequencing 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.**
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 in human disease.**
Studies analysing surrogate epigenetic markers (*e.g.* blood-derived) are advised against. Applicants should instead focus on specific tissue/cell types to decipher epigenetic signatures with mechanistic relevance to disease. 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) **Full-length transcript sequencing using long-read sequencing (PacBio)**.
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) **Long-read sequencing with Oxford Nanopore Technology.**
Researchers with projects requiring long-read genome sequencing for *de novo* assembly and annotation, structural variant detection, metagenomics, full-length mRNA sequencing, and cDNA can apply. Procedures available at EASI-Genomics laboratories for these projects are Oxford Nanopore long-read DNA and RNA sequencing in the wet lab 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.

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 DNA Seq	Genomics Core Leuven (KU Leuven)	info@genomicscore.be
	SC DNA/RNA Seq		
	SC RNA Seq		
	SC RNA Seq	SNP&SEQ Platform at NGI/SciLifeLab (UU)	seq@medsci.uu.se
	SC RNA + V(D)J Seq		
	SC RNA Seq	BIH-Charité	info@bihealth.de
	SC RNA Seq	CNAG	projectmanager@cnag.crg.eu
	SC RNA Seq	Scientific Genomics Platforms (MDC)	sasha.sauer@mdc-berlin.de
Spatial transcriptomics/*in situ* sequencing.	In situ Seq (barcodes)	SciLifeLab (SU)	support@ngisweden.se
	In situ Seq (RCA)	SciLifeLab (SU)	support@ngisweden.se
	Spatial RNA Seq	ScilLifelab (KTH)	support@ngisweden.se
Identification of epigenetic signatures in human disease	HiC Seq	CEA-CNRGH	collab-easigenomics@cng.fr
	WG ox-BS Seq		
	RRBS		
	WG ox-BS Seq	CNAG	projectmanager@cnag.crg.eu
	HiC Seq		
	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	online contact form
	ATAC Seq	BIH-Charité	info@bihealth.de
Full-length transcript sequencing using long-read sequencing	PacBio Seq	Genomics Core Leuven (KU Leuven)	info@genomicscore.be
Long-read sequencing with Oxford Nanopore Technology.	Chromium Based Seq (scaffolding)	CEA-CNRGH	collab-easigenomics@cng.fr
	Nanopore Seq		
	Chromium Based Seq (scaffolding)	CNAG	projectmanager@cnag.crg.eu
	Nanopore Seq		
	Chromium Based Seq (scaffolding)	SciLifeLab (KTH)	support@ngisweden.se
	Chromium Based Seq (scaffolding)	SNP&SEQ Platform at NGI/SciLifeLab (UU)	seq@medsci.uu.se
	Chromium Based Seq (scaffolding)	Genomics Core Leuven (KU Leuven)	info@genomicscore.be
Cross-topic: advanced data analysis	Integrative data analysis	SciLifeLab (SU)	support@ngisweden.se
		CNAG	projectmanager@cnag.crg.eu
		CEA-CNRGH	collab-easigenomics@cng.fr
		Scientific Genomics Platforms (MDC)	sasha.sauer@mdc-berlin.de
		Genomics Core Leuven (KU Leuven)	info@genomicscore.be
		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