

## **1<sup>st</sup> Call for Proposals for Transnational Access Projects at EASI-Genomics** *European Advanced infraStructure for Innovative Genomics*

### **Timeline:**

**Call open:** 25.03.2019 8:00 CET

**Proposal submission deadlines:** 25.04.2019 20:00 CET

**Notification to applicants:** by 12.07.2019

**Start of projects:** latest 6 months after notification

**EASI-Genomics** is a European Genomics Infrastructure Horizon 2020 project, which started on 1<sup>st</sup> February 2019. This novel infrastructure supports researchers from European member and associated states in **next generation sequencing** and **other high-end genomics applications**, and **genomic data analysis**. The infrastructure is accessible to academic researchers, research groups and scientific institutions. Furthermore, projects from industry, including SMEs can be supported. EASI-Genomics will support more than 150 projects for a total budget of 6 million € over the next 4 years. The rules of the European Commission only allow Transnational Access; applicants cannot request access to a facility that is in their home country.

The support offered by Transnational Access comprises wet-lab and/or large-scale genomics data analysis. Of note, EASI-Genomics can also provide 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 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 1<sup>st</sup> Call online via the [EASI-Genomics website](https://www.easi-genomics.eu/access/calls) (<https://www.easi-genomics.eu/access/calls>) until **April 25, 2019, 20:00 CET**. 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 proposal.

**Details on submission process, eligibility and evaluation criteria, and project implementation can be found at [www.easi-genomics.eu](http://www.easi-genomics.eu)**

### **Topics of the 1<sup>st</sup> 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) Microbiome analyses of population-based and disease cohorts.** The EASI-Genomics Infrastructure solicits project proposals in microbiome analysis. Proposals should focus on the human microbiome in relation to human disease. Applicants need to explain the scientific value and quality control of the sample cohort(s). Wet-lab and/or computational procedures required for support should be specified.

- iii) **Single-cell genomics.** EASI-Genomics will support projects in single-cell analysis. Techniques such as sc-3' tag RNA sequencing, sc-full length transcript sequencing, sc-ATAC-sequencing, sc-DNA methylation sequencing and *in situ* RNA sequencing are available. Applicants need to describe the objective of the research proposed, what samples are available and within what timeframe. Procedures required for wet lab and/or for data analysis support need to be clearly outlined.
- iv) **Identification of epigenetic signatures in human disease.** EASI-Genomics will support studies relating epigenetic features to disease. Studies with samples derived from blood or analysing surrogate epigenetic markers are excluded. Studies should focus on specific tissues/cell types to decipher epigenetic signatures with mechanistic relevance to disease. Applicants must specify available samples. Procedures required for wet lab and/or for data analysis support should be detailed.
- v) **DNA and chromatin alterations.** Projects should focus on mechanistically studying DNA and chromatin architecture alterations relevant to disease. For example, this can include analysis of the effect of structural variation or other functional analyses. Applicants need to describe the relevance of available sample materials for disease-relevant and mechanistic analyses. Applicants should specify wet-lab and/or computational procedures required for support.
- vi) ***De novo* sequence assembly and annotation projects of species of ecological and economic relevance.** The EASI-Genomics Infrastructure will support integrated projects in *de novo* assembly and annotation of ecologically and/economically relevant species. Applicants need to describe available samples including their economical and/or ecological relevance. Procedures available at EASI-Genomics laboratories for these projects are Illumina short-read DNA and RNA sequencing and Oxford Nanopore long-read DNA and RNA sequencing in the wet lab and state-of-the-art data analysis support for *de novo* genome assembly and annotation.

Topic	Services	Facilities	Contact
<b>Sequencing of ancient DNA</b>	Ultra low ancient DNA Seq	DNA Lab and Core Facility IG (Tartu U)	<a href="mailto:merilin.raud@ut.ee">merilin.raud@ut.ee</a>
<b>Microbiome analyses of population-based and disease cohorts</b>	16S Seq	CCGA (CAU)	<a href="mailto:ccga@ikmb.uni-kiel.de">ccga@ikmb.uni-kiel.de</a>
	Metagenome Seq		
<b>Single-cell genomics</b>	SC DNA Seq	Genomics Core Leuven (KU Leuven)	<a href="mailto:info@genomicscore.be">info@genomicscore.be</a>
	SC DNA/RNA		
	Seq SC RNA Seq		
	SC RNA Seq	SNP&SEQ Platform at NGI/SciLifeLab (UU)	<a href="mailto:seq@medsci.uu.se">seq@medsci.uu.se</a>
	SC RNA + V(D)J Seq		
	SC RNA Seq	BIH-Charité	<a href="mailto:info@bihealth.de">info@bihealth.de</a>
	SC RNA Seq	CNAG	<a href="mailto:projectmanager@cnag.crg.eu">projectmanager@cnag.crg.eu</a>
	SC RNA Seq	Scientific Genomics Platforms (MDC)	<a href="mailto:sasha.sauer@mdc-berlin.de">sasha.sauer@mdc-berlin.de</a>
	SC TCR Seq	CCGA (CAU)	<a href="mailto:ccga@ikmb.uni-kiel.de">ccga@ikmb.uni-kiel.de</a>
<b>Identification of epigenetic signatures in human disease</b>	HiC Seq and RRBS	CEA-CNRGH	<a href="mailto:collaboration@cng.fr">collaboration@cng.fr</a>
	WG ox-BS Seq		
	WG ox-BS Seq	CNAG	<a href="mailto:projectmanager@cnag.crg.eu">projectmanager@cnag.crg.eu</a>
	Low input WG BS Seq	SNP&SEQ Platform at NGI/SciLifeLab (UU)	<a href="mailto:seq@medsci.uu.se">seq@medsci.uu.se</a>
	Low input WG BS Seq	DKFZ - Genomics & Proteomics Core Facility	<a href="#">online contact form</a>
	ATAC Seq	BIH-Charité	<a href="mailto:info@bihealth.de">info@bihealth.de</a>
<b>DNA and chromatin alterations</b>	HiC Seq and RRBS	CEA-CNRGH	<a href="mailto:collaboration@cng.fr">collaboration@cng.fr</a>
	ATAC Seq	BIH-Charité	<a href="mailto:info@bihealth.de">info@bihealth.de</a>
<b>De novo sequence assembly and annotation projects of species of ecological and economic relevance</b>	Chromium Based Seq (scaffolding)	CNAG	<a href="mailto:projectmanager@cnag.crg.eu">projectmanager@cnag.crg.eu</a>
	Nanopore Seq		
	Chromium Based Seq (scaffolding)	SciLifeLab (KTH)	<a href="mailto:support@ngisweden.se">support@ngisweden.se</a>
	MP Seq		
	Chromium Based Seq (scaffolding)	SNP&SEQ Platform at NGI/SciLifeLab (UU)	<a href="mailto:seq@medsci.uu.se">seq@medsci.uu.se</a>
<b>Cross-topic: advanced data analysis</b>	Integrative data analysis	CNAG	<a href="mailto:projectmanager@cnag.crg.eu">projectmanager@cnag.crg.eu</a>
		CEA-CNRGH	<a href="mailto:collaboration@cng.fr">collaboration@cng.fr</a>
		CCGA (CAU)	<a href="mailto:ccga@ikmb.uni-kiel.de">ccga@ikmb.uni-kiel.de</a>
		Scientific Genomics Platforms (MDC)	<a href="mailto:sasha.sauer@mdc-berlin.de">sasha.sauer@mdc-berlin.de</a>
		Genomics Core Leuven (KU Leuven)	<a href="mailto:info@genomicscore.be">info@genomicscore.be</a>
		SNP&SEQ Platform at NGI/SciLifeLab (UU)	<a href="mailto:seq@medsci.uu.se">seq@medsci.uu.se</a>
		SciLifeLab (KTH)	<a href="mailto:support@ngisweden.se">support@ngisweden.se</a>
		DKFZ - Omics IT and Data Management Core Facility	<a href="mailto:odcf-service@dkfz.de">odcf-service@dkfz.de</a>
		DNA Lab and Core Facility IG (Tartu U)	<a href="mailto:merilin.raud@ut.ee">merilin.raud@ut.ee</a>
		BIH-Charité	<a href="mailto:info@bihealth.de">info@bihealth.de</a>