Extraordinary Call for Proposals for Access Projects related to the COVID-19 crisis

EASI-Genomics

European Advanced infraStructure for Innovative Genomics

Timeline:
Call open: 18.05.2020 14:00 CEST
Proposal submission deadlines: 30.06.2020 20:00 CEST
Notification to applicants: at the latest by 15.07.2020
Start of projects: before 31.08.2020
Proposals will be evaluated continuously starting from 31.05.2020 and initiated upon acceptance.

EASI-Genomics is a European Genomics Infrastructure Horizon 2020 project, which started on 1st February 2019. This novel infrastructure supports researchers 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, as well as industry, including SMEs. EASI-Genomics will support more than 150 projects for a total budget of 6 million € over the next 4 years.

The support offered comprises wet-lab and/or large-scale genomics data analysis. EASI-Genomics encourages wide-reaching and innovative integrative projects that draw on the high level of expertise of EASI-Genomics facilities and foster scientific collaboration opportunities between the facilities and the applicant's team. Costs of external user projects for consumables and personnel required at the facilities will be covered by EASI-Genomics.

In light of the current Covid-19 crisis, EASI-Genomics is taking the measure to issue an extraordinary call. EASI-Genomics invites external users to apply for access with proposals related to the COVID-19 epidemic for a total budget of 0.5 million €. The Transnational Access rule that applied to EASI-Genomics' previous calls will exceptionally be waived. However, EASI-Genomics will endeavor to achieve balanced access to services across all EU countries for each EASI-Genomics facility in the overall selection process.

This Extraordinary EASI-Genomics call will focus on **whole-genome (short- and/or long-read), whole exome and RNA sequencing of human patients from low-risk populations with severe forms of SARS-Cov-2 infection that have experienced adverse reactions or fatal outcomes**. Hence samples from **individuals below 50 years of age, with no underlying evident co-morbidities prior to the infection such as diabetes, hypertension, and overweight** will be considered in this call (e.g. fasting blood sugar level < 100 mg/dL (5.6 mmol/L), blood pressure < 120/80mmHg, Body Mass Index between 18.5 and 30). Clinical description according to GeCo - COVID-19 phenotype definition should be available for the patients to be included.
We propose to provide support for analysis of DNA and RNA samples extracted from patient blood and propose to carry out an individual and joint analysis with successful applicants to identify potential host factors and mechanisms contributing to adverse outcomes in this low-risk population of COVID-19 patients. Studies that have a longitudinal (e.g. repeat RNA sampling over the course of the disease) or familial aspects are welcome. If possible, each proposal should include at least 10 patients.

This project has received funding from the European Union's Horizon 2020 research and innovation programme under grant agreement No 824110.

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. Applicants should agree to share data with the scientific community and deposit data in the EGA.

Interested users can submit proposals to this extraordinary Call for COVID-19 related projects online via the **EASI-Genomics website** (https://www.easi-genomics.eu/access/calls) until **June 30th, 2020, 20:00 CEST**. Eligible proposals will be evaluated for scientific quality, feasibility, and impact. Proposals will be handled confidentially.

Of note:

- EASI-Genomics facilities only have the capacity to handle biosafety containment level 1 material.
- 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. EASI-Genomics can provide guidance for such documentation.
- EASI-Genomics will recommend procedures for DNA and RNA isolation.
- EASI-Genomics aims to capture clinical information in accordance with GeCo - COVID-19 phenotype definition (extended).
- EASI-Genomics will integrate variant calls into an instance of the RD-Connect Genome-Phenome Analysis Platform and provide an interface to include phenotype and clinical information.

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

Topics of the Extraordinary Call for projects related to the COVID-19 crisis:

i. **DNA Sequencing of host whole-genome or whole-exome of human low-risk patients with severe forms of SARS-Cov-2 infection that have experienced adverse reactions or fatal outcomes.** EASI-Genomics offers to sequence host whole-genome DNA isolated from blood samples at its state-of-the-art equipped facilities using short-read and long-read technology. Applicants need to provide a detailed description of the available sample materials and explain in detail how they obtained the samples.
    - **Whole-genome sequencing (WGS)**
        - **Short-read Illumina Sequencing**
        - **Long-read Oxford Nanopore Sequencing** (from High Molecular Weight DNA)
    - **Whole-exome sequencing (WES)**
        - **Short-read Illumina Sequencing**

ii. **Sequencing of host RNA of human low-risk patients with severe forms of SARS-Cov-2 infection that have experienced adverse reactions or fatal outcomes.** EASI-Genomics offers to sequence host RNA at its state-of-the-art equipped facilities. Applicants need to provide a detailed description of the available sample materials and explain in detail how they obtained the samples.
    - **RNA-Sequencing**
        - **Short-read Illumina Sequencing**

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iii. **Integrative data analysis of host and virus sequences from human low-risk patients with severe forms of SARS-Cov-2 infection that have experienced adverse reactions or fatal outcomes.**

iv. **EASI-Genomics will also consider projects requesting other advanced analyses, such as single cell analysis, for a limited number of patients.**

Topic	Services	Facilities	Contact
DNA Sequencing of host whole-genome or whole-exome of human low-risk patients with severe forms of SARS-Cov-2 infection	Illumina short-read high-throughput sequencing	CNAG CEA-CNRGH SNP&SEQ Platform at NGI/SciLifeLab (UU) BIH-Charité	projectmanager@cnag.crg.eu collab-easigenomics@cng.fr seq@medsci.uu.se info@bihealth.de
	Oxford Nanopore Technology long-read sequencing		
	Whole genome or whole exome		
Sequencing of host RNA of low-risk human patients with severe forms of COVID-19	RNA sequencing		
Advanced data analysis	Integrative data analysis	CNAG CEA-CNRGH CCGA (CAU) Scientific Genomics Platforms (MDC) Genomics Core Leuven (KU Leuven) SNP&SEQ Platform at NGI/SciLifeLab (UU) SciLifeLab (KTH) DKFZ - Omics IT and Data Management Core Facility DNA Lab and Core Facility IG (Tartu U) BIH-Charité	projectmanager@cnag.crg.eu collab-easigenomics@cng.fr ccga@ikmb.uni-kiel.de sasha.sauer@mdc-berlin.de info@genomicscore.be seq@medsci.uu.se support@ngisweden.se odcf-service@dkfz.de cls83@ut.ee info@bihealth.de
Other advanced analyses	Single Cell		
	Others		

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