

**HUMAN TECHNOPOLE
NATIONAL FACILITY FOR DATA HANDLING AND
ANALYSIS
CALL FOR ACCESS
24-DHA-PILOT
Amendment II**

The present amendment is aimed at *i.* revising the eligibility and admissibility process described in paragraph 4 and the evaluation of application process described in paragraph 6 of the Call for Access and *ii.* updating the service list, with the addition of the service SID: NF-60-002 – CryoEM Analysis.

1. The sentence “*Applications must be written in English and must be complete (i.e., consist of all the requested elements and information). Incomplete applications will be considered not eligible and will be rejected at the administrative review stage*” is revised as follows:

Applications must be written in English and must be complete (i.e., consist of all the requested elements and information) and respect all administrative and technical requirements (e.g., proposal or CV format, declarations, technical requirements of the services, sample requirements). Incomplete applications or applications that do not meet the requirements will be considered not admissible and will be rejected at the administrative review stage.

The sentence “*The NF User Access Office first performs an administrative review of the application to ensure that all the requested components have been provided, and that all eligibility criteria have been met*” is revised as follows:

The NF User Access Office first performs an administrative review of the application to ensure that all the requested components have been provided, and that all eligibility criteria have been met. Incomplete applications or applications that do not meet the requirements will be considered not admissible and will be rejected at the administrative review stage.

2. Addition of new service

(IU1) Bioimage Analysis

SID: NF-60-002 – CryoEM Analysis

Services description: The services we provide include, but are not necessarily limited to, the following use-cases:

- **Single-particle analysis (SPA):** Development of image processing pipelines for the reconstruction of single particle 3D density maps, starting from cryoEM raw datasets or pre-processed micrographs/particles. Map validation.
- **Atomic Model Building:** *De novo* model building from reconstructed 3D density maps, fitting of existing atomic structures and refining of atomic models. Model validation.
- **Analysis of Flexibility and Heterogeneity:** Development of image processing pipelines for local reconstruction and refinement of flexible regions and evaluation of the conformational heterogeneity landscape of the macromolecules.
- **Tomography reconstruction:** Development of image processing pipelines for the reconstruction and analysis of tomograms, starting from tilt-series containing fiducial markers or fiducial less. Segmentation of the tomograms and sub tomogram averaging (STA).

- **Custom pipeline development:** Construction of a pipeline combining two or more individual steps.

While these are examples of the services we can provide, we anticipate that most projects will require some combination of tools and services and so we will work with successful Applicants to craft pipelines that fulfil their analysis needs, as well as provide training and support in their future use. Our ethos is to work openly and transparently with our Users in the spirit of scientific collaboration. During the application phase, it will be necessary only to describe the data and the desired form of the analysis result; the precise details of the analysis will be discussed with the Applicants upon selection of the project.

Technical requirements: Applicants must ensure that the dataset is available at sufficient quantity and quality (for example resolution, contrast and signal-to-noise ratio) before the closing date of the application period. This will be assessed on example data submitted during the application phase. Applicants are responsible for uploading their image data to Human Technopole file servers at the initiation of the project, and for downloading the final results at the conclusion of the project.

Information to be provided in the application:

- General Project Information (ie sample description, experimental goals)
- Microscopy and Detector Details (ie model, voltage, magnification, pixel size etc)
- Data collection information (Total number of movies and exposure time per frame)
- Sample preparation (description of sample preparation procedures)
- Information about the target protein (ie symmetry, shape, size, existing atomic models, protein sequence)
- Preprocessing details (describe any image processing that has been done during or after collection, if any)
- Processing preferences (Software preferences, ie Relion, Cryospark, etc, resolution target)
- Data information (data size, formats, available metadata)
- Additional details –not mandatory -- (known artifacts ie drift, contamination, orientation bias)
- For the feasibility assessment, uploading a set of at least 10 movies/micrographs as part of the application process is required. It is important that these images accurately reflect the diversity of the data in the dataset (i.e., not the best set of possible images). Please ensure to include any applicable metadata. If CTF estimation is available, please include this as part of the application. To reduce the burden of Access for our Users, we will use, wherever possible, open-source software tools during the NF projects.

Delivery of results: Upon successful completion of the selected project, results will be delivered in a format of the Users choosing and depending on the project needs (typically .mrc or .pdb, but other formats or intermediate files may be delivered depending on User preferences). In addition, we will provide whatever software, code, and support is required for the User to reproduce the analysis at their home institute.

Access modality available: Access to NF services, Access with training