

**HUMAN TECHNOPOLE
NATIONAL FACILITY FOR STRUCTURAL BIOLOGY
CALL FOR ACCESS
24-SB-PILOT**

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1. INTRODUCTION

The Access of Researchers affiliated with Universities, *Istituti di Ricovero e Cura a Carattere Scientifico* (IRCCS), and Public Research Entities to Fondazione Human Technopole (HT) National Facilities (NFs) is regulated by the NF Access rules available on the NFs dedicated webpage ([link](#)).

Services offered by NFs are available through regular open calls for Access that are published yearly on the HT website ([link](#)) and are free of charge for the project (or aspects of the project) approved for Access.

The open call for Access is aimed at supporting Access to the technologies offered by the NFs and it is not meant to provide direct funding to the User. The costs for the activities to be performed at the NFs will be fully covered, including shipment of relevant material from and to the User's laboratory as well as travel and accommodation for the User while accessing the NF. Project-related costs (personnel, consumables, and other costs) at the User laboratory are not funded.

The User Access workflow comprises different steps, spanning from the initial submission of the application to evaluation and Access approval, Access to the performance of the service(s) and Access conclusion. A detailed description of the workflow is available on the NFs dedicated webpage ([link](#)).

1.1 Access modalities

Three different Access modalities can be requested. Their availability will vary, based on the service specifics of each NF:

- **“Simple” Access to NF or individual instruments thereof:** this modality is intended for Users involved in projects requiring technologies that are available at the NF for direct Access by User. This Access modality requires prior expertise with the technology of interest. After an initial introductory training aimed at defining the level of expertise of the User, the use of the instrument with limited supervision by NF staff is authorised. For defined NFs/ instruments/ services this Access modality may be restricted or not available.
- **Access to NF services:** This procedure entails the provision of services performed by NF staff on behalf of the User. NF services may include both standard services as well as, when foreseen by the technology development specifics of each NF, bespoke services conceived and discussed with the User. To allow the NF staff to best align the experimental activity to the research objective, the User may be invited, if needed, to assist the NF staff while performing the project or aspects of it.
- **Access to NF services including training:** This procedure entails training by NF staff to provide Users, in addition to or alternatively to the services described in the previous modality, with training courses and/or programs, aimed at transferring the expertise necessary for the independent use of the specific technology. In this case, technical and/or experimental activities are conducted with the active participation of the User. This type of Access is also aimed at researchers who want to acquire expertise for subsequent independent use of a specific technology in other laboratories.

2. TERMS AND DEFINITIONS

2.1 Access

“Access” refers to the authorized use of the NF and of the services offered. Such Access can be granted for sample preparation, set-up, execution and dismantling of experiments, education and training, expert support and analytical services, among others. Access to the NFs includes all infrastructural, logistical, technical and scientific support (including training) that is necessary to perform the aspects of the project approved for Access.

2.2 Researcher

“Researcher” is a professional engaged in the conception or creation of scientific knowledge. They conduct research and improve or develop concepts, theories, models, techniques, instrumentation, software or operational methods.

2.3 Principal Investigator

“Principal Investigator” (PI) is the Researcher affiliated with an eligible Institution with the role of independent Group Leader, who is responsible for coordinating the research activities conducted within the framework of the submitted project.

The PI shall hold a primary appointment as Group Leader at an eligible Institution, with the following requisites:

- Coordinate an independent research team.
- Have a supervisory role towards junior and/ or senior Researchers.
- Their Group has an autonomous budget sufficient to cover their current research expenses.
- Be the recipient of independent research funding as PI or co-PI.

Junior PI: Up to 6 years from their first appointment in an independent Group Leader position.

The period specified above may be extended beyond 6 years in the event of adequately documented career breaks, occurring before the submission of the application and resulting from:

- i.* Maternity leave: The time limit is increased by 18 months for each child born after their first appointment in an independent group leader position; if the Applicant is able to document a longer total maternity leave, the period of eligibility will be extended by a period equal to the documented leave, taken before the submission of the application. Maternity status must be documented by submitting the birth certificate of the child or children;
- ii.* Paternity leave: The time limit is increased by the actual amount of paternity leave taken before the application submission deadline for each child born after their first appointment in an independent group leader position. Paternity status must be documented by submitting the birth certificate of the child or children;
- iii.* Long-term illness of more than 90 days, or national service: The time limit is increased, for each eligible event occurring after their first appointment in an independent group leader position, by the actual amount of leave from which the Applicant has benefited prior to the application submission deadline.

Established PI: More than 6 years from their first appointment in an independent group leader position.

2.4 Applicant

“Applicant” is the Principal Investigator who applies to a NF open call for Access and who is responsible for the submitted project. They can be of any nationality and must be affiliated with an eligible Italian Institution, as detailed in [section 4](#).

2.5 User

A “User” is intended as a Researcher affiliated with an eligible Institution who accesses the NFs to perform the approved activities or to support the National Facility staff while performing the approved service.

If requested by the Applicant, the User of the NF can also be a separate member of their research team.

3. APPLICATION TYPE

Applicants shall select the type of application they want to submit, choosing between two options:

- a. **Standard** application for projects that are technically mature.
- b. **Proof-of-concept** application for:
 - i.* Projects with high scientific potential but with insufficient technical maturity or preliminary data.
 - ii.* Projects aimed at setting up the experimental conditions required for a standard project, including methods or technology development projects.
 - iii.* Time-limited Access projects (e.g., to acquire data to complete a manuscript, or preliminary data needed for a grant application, or single microscopy session).

4. ELIGIBILITY AND ADMISSIBILITY

PIs, as defined in [section 2.3](#) of this call, affiliated with an eligible Institution are eligible to apply. The Applicant’s role as a PI shall be confirmed by their Institution in a mandatory letter of Institutional endorsement.

Applications from Researchers who are not independent should be submitted by their group leader. Applicants are strongly encouraged to support NF Access by young Researchers (R1 and R2 profiles of the European Framework for Research Careers, [link](#)) who are part of their group. In this case, the Applicant shall indicate in the application form that the NF User is a member of their group, specifying User’s career stage.

Below are the links to the relevant lists of eligible Institutions:

Universities: This category includes Institutions recognized by the Ministry of University and Research ([link](#)). In detail:

- i. State funded public universities, listed under the following [link](#).
- ii. Specialized superior graduate schools or Institutions, listed under the following [link](#).
- iii. Legally recognized non-public universities, listed under the following [link](#).
- iv. On-line universities, listed under the following [link](#).

Istituti di Ricerca e Cura a Carattere Scientifico (IRCCS): this category includes Institutions recognized by the Ministry of Health and listed at the following [link](#).

Public research entities: this category includes Institutions recognized by the Ministry of University and Research and listed at the following [link](#).

Eligible Institutions are strongly encouraged to limit the number of applications to the very best 2/ NF, with at least 50% coming from Junior PIs.

Applicants shall declare that they have not received funding to perform the submitted project (limited to the aspects included for Access to the NF) in their own laboratory, home Institution or elsewhere. Applicants shall confirm the economic and scientific feasibility for the aspects of the project to be performed outside the NFs.

Applicants cannot request Access for the same service if an approved Access is ongoing. Before submitting a new application for the same service, Applicant shall consult with the NF staff and confirm that the ongoing Access will be completed before the end of the next evaluation round. A clear motivation for the request must be provided.

During the same application window, a PI can submit only one application to the NFs (i.e., participate to only one call for Access). If more than one application is submitted, all will be rejected during administrative review. Applicants who have an application under evaluation are not allowed to submit another application before receiving notification of the results.

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.

The application form consists of six components:

1. Applicant's general information.
2. Justification for requesting Access to the NF.
3. Abstract.
4. Project proposal, including:
 - a. *Significance.*
 - b. *Innovation.*
 - c. *Approach, including aims, preliminary data in support of the proposed experiments, experimental design and anticipated results.*
 - d. *Environment, including facilities and resources available to support the aspects of the project to be performed elsewhere (i.e., outside the NF).*

5. Applicant's CV in NIH biosketch format.
6. Letter of Institutional Endorsement, addressing the following points:
 - a. *Confirmation of the Applicant's role at their Institution, and their eligibility under the category of PI (see section 2.3).*
 - b. *Confirmation that relevant authorisations, declarations and accreditation from the competent authority(ies) have been obtained in order to process samples and data through the NFs.*
 - c. *Justification of the request for Access – including a statement on why the project cannot be performed at the Applicant's Institution.*
 - d. *Confirmation that the Applicant has not received funding for performing the submitted project, for the aspects to be performed at the NFs, in their own laboratory, home Institution, or elsewhere.*
 - e. *Confirmation of the project's economic and scientific feasibility for the aspects to be performed at the host Institution.*
 - f. *Acceptance of NF Access terms and conditions.*

The facsimile available as [Annex II](#) of this call shall be used as template.

7. Technical information, including:
 - a. *Requested service(s), as described in [Annex I](#) of this call.*
 - b. *Sample technical information.*
 - c. *Requested preliminary data for technical feasibility analysis (if applicable).*
 - d. *Whether the entire sample set is already available (otherwise indicate the date of availability of the entire sample set).*
 - e. *Resources and expertise to receive and process the products – data (e.g. Cryo-EM micrographs) or reagents (e.g. human iPSCs) – generated by the NF.*
 - f. *Research data management plan and bioinformatics support for data analysis, specifying:*
 - i. *How the bioinformatics analysis of the data generated by the NF will be performed (if such analysis is not provided by the NF for Data Handling and Analysis).*
 - ii. *How the data generated by the NF will be handled during and after the end of the project.*
 - iii. *Whether and how the data will be shared/ made Open Access.*
 - iv. *How data will be curated and preserved, including after the end of the project.*

Information provided in sections 1 and 6 are used for the eligibility and admissibility check.

Information provided in section 7 is used for assessing the technical feasibility of the aspects of the project to be performed at the NF.

The entire application is evaluated by the Standing Independent Evaluation Committee (SIEC) for assessing scientific merit.

5. APPLICATION SUBMISSION METHODS, CALL DEADLINE AND EVALUATION PERIODS

Applications shall be submitted exclusively through the web-based procedure managed by CINECA and accessible at the [link](#), according to the terms and methods there indicated.

Applications are accepted throughout the year and assessed in three evaluation rounds per year. The time between one evaluation round and the next one is considered an application window.

- Evaluation round 1: applications submitted between the 1st of January and the 30th of April will enter the first evaluation round (May/ June).
- Evaluation round 2: applications submitted between the 1st of May and the 31st of August will enter the second evaluation round (September/ October).
- Evaluation round 3: applications submitted between the 1st of September and the 31st of December will enter the third evaluation round (January/ February).

This first call for Access (Call ID: 2024-SB-Pilot) will be **open from the 10th of June 2024 (1 pm) to the 31st of December 2024 (1 pm)** and will involve 2 rounds of evaluation (September 2024 and January 2025).

A comprehensive list of services, available equipment and the technical requirements for Access as well as terms and conditions are available on the dedicated NFs webpage ([link](#)).

The complete list of offered services and technical requirements are available in the [Annex I](#) of this call.

6. EVALUATION OF APPLICATION

The evaluation procedure is conducted by the SIEC that is supported by a Panel of independent external Reviewers (Review Panel) selected by the SIEC on the basis of their scientific expertise.

Each Review Panel is composed of 2 SIEC members, who will act as Chairs, plus 10 appointed external Reviewers, with the relevant expertise.

Below is a scheme describing evaluation steps and timeline.



There are four application categories that are evaluated and ranked separately:

- Junior PI – Standard application

- Established PI – Standard application
- Junior PI – Proof of Concept application
- Established PI – Proof of Concept application

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.

The application is then sent to the Review Panel for assessing scientific merit and technical feasibility.

If the number of applications exceeds by a factor of 4 the estimated capacity of the NF, a triage will be applied within each application category by the relevant Review Panel.

Triage criteria will include:

- a. Justification for requesting Access to the NF.
- b. Field-Weighted Citation Impact (FWCI).
- c. Track record in securing research funding.

The application will remain confidential throughout the entire evaluation process. Reviewers will be asked to declare that they do not have any conflict of interest and they will be bound by a Confidentiality Agreement.

The application will be individually evaluated by three Reviewers who are part of the relevant Review Panel.

Proposals will be evaluated and ranked based on their average score, within each category.

An on-line meeting of the Review Panel may be requested by the Chairs if deemed necessary (for example to discuss proposals with highly discrepant scores).

At least 50% of the available Access will be allocated to applications from the two Junior PI categories.

6.1 Evaluation criteria

The scientific merit of the project is assessed based on the following criteria:

- **Significance:** Overall scientific merit of the proposed research. If all the experiments proposed are successful, how will the resulting knowledge advance the field?
- **Innovation:** Degree of innovation (conceptual and/ or technological), and ambition of the proposed study compared to the state-of-the-art in the relevant field.
- **Approach:** Appropriateness of proposed methodology, preliminary data in support of proposed experiments, and project feasibility.
- **Environment:** Facilities and resources available to support the aspects of the project to be performed elsewhere (i.e., outside the NF).
- **Justification for requesting Access to the NF:** Explanation on why the service cannot be performed at the host Institution, at a cost which is deemed affordable for the applicant.
- **Applicant:** PI's scientific background and expertise.

6.2 Scoring system

A numeric score between 1 (exceptional) and 9 (poor) is provided for each of the six evaluation criteria. Moreover, an overall project score including a short descriptive comment is provided as feedback to the Applicant.

- **HIGH:**
 - **Score 1 (Outstanding)** – The proposal successfully addresses all relevant aspects of the criterion. There are no weaknesses.
 - **Score 2-3 (Excellent - Very Good)** – The proposal addresses the criterion exceptionally well, aside from a small number of minor weaknesses.
- **MEDIUM:**
 - **Score 4-6 (Very good - Good)** – The proposal addresses the criterion well, but a number of weaknesses are present.
- **LOW:**
 - **Score 7-8 (Fair - Poor)** – The proposal broadly addresses the criterion, but there are significant weaknesses.
 - **Score 9 (Poor)** – The criterion is inadequately addressed, or there are serious inherent weaknesses.

6.3 Technical feasibility analysis

During the evaluation, the relevant experts from SIEC will receive a report from NF staff who will perform a comprehensive analysis of the proposed project's technical feasibility. Technical feasibility also includes an evaluation of the fulfilment of the technical requirements in terms of capacity to receive and process the research data generated by the NF, as described in the research data management plan. This latter evaluation is performed in consultation with the NF for Data Handling and Analysis.

Based on the technical maturity of the project, the application can be assessed as Feasible/ Not Feasible/ Pilot study required (switch from Standard to "Proof-of-Concept application track).

6.4 Evaluation results and Access approval

NF staff provides the SIEC with information on the resources needed (cost and time) to perform the highest ranked projects. The most positively evaluated applications that fulfil all technical requirements are approved for Access by SIEC, based on the capacity of the NF. NF staff schedules Access. A selected number of applications may be placed on a waiting list (in case of cancellations).

Evaluation results – Access approved, Access waitlisted, Access not approved – are communicated to the Applicant through the Access portal.

Applicants whose applications are placed on the waiting list will receive additional information advising whether the project can be Access approved or should be resubmitted within the subsequent application window.

7. AFTER ACCESS HAS BEEN APPROVED

After Access approval, a kick-off meeting is organized by the NF User Access Office and the Applicant is invited to meet NF staff to discuss the experimental design of the project and to finalize the project plan.

Once the project plan has been agreed, the NF User Access Office coordinates the signature of the required formal Agreements (e.g., Access Agreement, Collaboration Agreement, other) and the project can start.

8. AFTER ACCESS HAS BEEN COMPLETED

At the end of the activities carried out at the NF, and not later than 3 months thereafter if not differently agreed with the NF User Access Office, the User must submit a short report on the results obtained and the impact of the service on their research. Moreover, a final report to be published on the NFs website and describing the impact of the Access to the NF on the research project for which the service has been requested shall be provided upon publication of the relevant results. Users who will not be able to demonstrate the consistency and relevance of the activities carried out at the NF with the research project for which Access was requested will be considered not eligible to participate in the subsequent calls for Access.

Moreover, the User will be asked to fill in a brief, mandatory survey regarding their experience, providing feedback and suggestions for further service improvement.

The User must communicate to the NF User Access Office (via email to national.facilities@fht.org) any publication acknowledging the NF.

Research data obtained during Access shall be made available to the scientific community following the FAIR principles. User must inform the NF User Access Office (via email to national.facilities@fht.org) when and how the data are made public.

9. CONTACTS

Requests for information and/or clarifications concerning the application procedure may be sent to the dedicated e-mail address national.facilities@fht.org, indicating the call ID in the subject line.

10. REFERENCES

NF Access workflow_Convenzione ([link](#))

NF Access rules_Convenzione ([link](#))

NF Access Agreement_Convenzione ([link](#))

11. CHANGES TO THE CALL

Any changes or additions to this notice will be communicated through publication on the NFs website ([link](#)).

**ANNEX I: NATIONAL FACILITY FOR STRUCTURAL BIOLOGY:
SERVICES LIST**

**HUMAN TECHNOPOLE
NATIONAL FACILITY FOR STRUCTURAL BIOLOGY
CALL FOR ACCESS
24-SB-PILOT
SERVICE LIST**

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1. INTRODUCTION

The NF for Structural Biology stands as a one-of-a-kind scientific and technological hub for integrative structural biology. NF for Structural Biology consists of six units working together to (i) provide and support conventional practices, and (ii) promote and establish innovative workflows in the field of integrative structural biology. The Cryo-Electron Microscopy Unit (IU1) aims at identifying, visualizing, and characterizing biological players of interest, both isolated and within their cellular compartments. The Biomass Production Unit (IU2) provides Access to different cell lines for protein expression and performs scale-up of bioprocesses for large-scale productions. The Biophysics Unit (IU3) is a technological platform for biophysical characterization of macromolecules and their interactions. The Structural Proteomics Unit (IU4) relies on crosslinking mass spectrometry (XL-MS) to provide topological and structural restraints on protein-protein interactions in samples ranging from purified protein complexes to cellular fractions. The Dynamic Single-molecule Unit (IU5) provides tool to visualise biological processes in real-time with single-molecule sensitivity thanks to cutting-edge instruments that combine optical tweezers with fluorescence and label-free detection modules. Finally, the Technology Development Unit (IU6), which is expected to become operational in 2026-2028, will serve the purpose of fostering technological innovation in the field of integrative structural biology.

The strategic mission of the NF for Structural Biology is to expand and share its current expertise and technology with the entire Italian research community. The great majority of the instrumentation present in the NF is not available elsewhere in Italy, making it an attractive venue for all domestic researchers, from commercial and academic entities alike. In particular, the Cryo-EM Unit (IU1) will grant Access to high-end microscopes capable of determining structures of macromolecules to high resolution and providing detailed information on their cellular context. Notably, the Cryo-EM Unit is, as of now, the best if not the only laboratory in the country equipped to perform cryo-CLEM and cryo-ET as part of the workflow. The resources offered by the Biomass Production Unit (IU2), such as bioreactors and fermenters, are complemented with expertise in scaling up bioprocesses for large-scale protein production across several cell types, ranging from bacteria to mammalian cells. The Italian research community will also benefit from Access to a library of different cell lines and the necessary knowhow for their maintenance in culture. Furthermore, within the Biophysics Unit (IU3), investigators will in turn be able to combine different techniques to thoroughly and efficiently characterize their sample from a biophysical and biochemical perspective, resulting in an optimized if not ideal specimen for subsequent structural biology experiments. Finally, the Structural Proteomics Unit (IU4) will provide topological information at the single amino acid level, so as to be able to identify and characterize proximal and direct interactors *in vitro* and *in situ*. To the best of our knowledge, IU4 is unique in Europe offering XL-MS technology as a service. Similarly, the instrumentation within the Dynamic Single Molecule Unit (IU5) is, within the Italian landscape, the only one which will be Accessible to external Users.

2. SERVICE LIST

(IU1) Cryo-Electron Microscopy Unit

SID: SB-IU1-A – Negative Stain EM Screening

Services description: We offer sample preparation by negative stain EM followed by TEM imaging at 120 kV. A maximum of 1 specimen and 8 grids can be prepared and processed per unit of service. Imaging will be provided for a maximum of 8 continuous hours per unit of service. An optional “polishing” size-exclusion chromatography (SEC) step can be performed on thawed material by the Biophysics Unit, as and if specified in the request for this service. 400 mesh copper grids with amorphous carbon film layer will be used as support. Glow discharging will be performed by a Pelco EasyGlow device. Staining will be performed with a 2% (w/v) uranyl acetate aqueous solution. Imaging in TEM mode at 120 kV will be performed on a Thermo Scientific Talos L120C equipped with CETA 16M camera. Imaging conditions requested by the User, if provided, must be compatible with NF practices. This service will only be performed by NF staff.

Technical requirements: Biological specimens must have a total molecular weight greater than 150 kDa; glycerol, sucrose, phosphate (i.e., PBS) or detergents must not be present in the sample; concentration of purified biological sample must be higher than 0.01 mg/ml and the sample volume must be greater than 50 µl; the User should provide 10 ml of final sample buffer to allow preparation of dilutions; the sample is required to have demonstrated purity (i.e., SDS-PAGE) and homogeneity (e.g., elution profile from SEC).

Information to be provided in the technical requirements page of the application:

- Sample name
- Uniprot ID(s)
- MW (kDa), total in case of complex
- Buffer Composition
- Sample Concentration (mg/ml)
- Final Volume of purified sample (µl)
- SDS PAGE
- SEC chromatogram
- Any EM data already in literature

Access modality available: Access to NF services.

SID: SB-IU1-B – Cryo-EM Screening

Services description: This service provides sample preparation by plunge-freezing, grid clipping for autoloader system and cryo-TEM imaging at 200 kV. A maximum of 1 specimen and 8 grids can be prepared and processed per unit of service. An optional “polishing” SEC step can be performed on thawed material by the Biophysics Unit, as and if specified in the request for this service. Glow discharging will be performed by either a Pelco EasyGlow, a Quorum GloQube, or Solarus II plasma cleaner device. Plunge-freezing will be performed on a Thermo Scientific Vitrobot Mk IV or a Leica EM GP2. Applicants may provide TEM grid

supports of preference, otherwise NF staff will use holey TEM grid supports available. Imaging will be provided for a maximum of 8 continuous hours per unit of service. Cryo-TEM imaging will be performed only in EF-TEM mode at 200 kV on a Thermo Scientific Glacios equipped with a Falcon 4i direct electron detector and Selectris X energy filter. Imaging conditions requested by the User, if provided, must be compatible with NF practices. In case of grids showing optimal particle distribution and ice quality, this service can be extended for overnight data collection, if compatible with NF staff working hours. The User can also provide already-made cryo-TEM grids either unmounted or mounted on a Thermo Scientific cartridge. In case of an unmounted grid, clipping of the specimen in Thermo Scientific cartridges will be performed by NF staff. In case of User-provided already-clipped grids, these will be inspected by NF staff prior to acceptance. This service will only be performed by NF staff.

Technical requirements: Biological specimens must have a total molecular weight greater than 150 kDa; glycerol, sucrose, or detergents must not be present in the sample; concentration of purified biological sample must be equal or higher than 0.35 mg/ml and the sample volume must be greater than 50 μ l; the User should provide 10 ml of final sample buffer to allow preparation of dilutions; the sample is required to have demonstrated purity (i.e., SDS-PAGE) and homogeneity (e.g., elution profile from SEC). For a specimen to be imaged by cryo-ET, the area of interest must have a maximum thickness of 200 nm; Grids will be inspected by NF staff prior to acceptance: damaged or bent grids will not be loaded on the microscope.

Information to be provided in the technical requirements page of the application (not needed if requesting this service together with service SB-IU1-A):

- Sample name
- Sample type [Protein/ Cell/ Other]
- Uniprot ID(s)
- MW (kDa), total in case of complex
- Buffer Composition
- Concentration (mg/ml)
- Volume of purified sample (μ l)
- SDS PAGE
- SEC Chromatogram
- Any EM data already in literature

Access modality available: Access to NF services.

SID: SB-IU1-C – High-resolution Cryo-TEM Imaging

Services description: This service provides high-resolution cryo-TEM data collection of vitrified specimens. According to instrument availability and experimental needs, data collection will be carried out either on 200kV or 300kV microscope systems. A maximum of 1 specimen can be imaged per unit of service. To ensure efficient usage of high-end microscope time, a maximum of 4 grids can be loaded per unit of service. The User can provide cryo-TEM grids either unmounted or mounted on a Thermo Scientific cartridge. In case of an unmounted grid, clipping of the specimen in Thermo Scientific cartridges will be performed by NF staff. In

case of User-provided already-clipped grids, these will be inspected by NF staff prior to acceptance. Imaging at 200 kV will be performed on a Thermo Scientific Glacios while imaging at 300 kV will be performed on a Thermo Scientific Titan Krios G4, both equipped with a Falcon 4i direct electron detector and a Selectris X energy filter. Imaging conditions (i.e., dose, pixel size, magnification, etc.), if requested by the User, must be compatible with the NF best practices. Microscope Access is granted for a maximum of 24 continuous hours per unit of service, including all steps from clipping to loading and TEM alignments and according to NF staff availability. For single-particle acquisition, User might opt for beam-image shift assisted data collection (~ 450 – 600 movies/hour) or stage movement for each hole (~ 100 – 250 movies/hour). This service will only be performed by NF staff.

Technical requirements: Preliminary data must be provided, including representative micrographs and, if available, any 2D and 3D class averages or reconstructions, respectively; Not for screening purposes; Only for biological specimens with a total molecular weight greater than 150 kDa; glycerol, sucrose or detergents must not be included in the sample buffer unless specifically required for vitrification and/ or particle distribution purposes; For specimens to be imaged by cryo-ET, the area of interest must have a maximum thickness of 200 nm; Grids will be inspected by NF staff prior to acceptance: damaged or bent grids will not be loaded on the microscope.

Information to be provided in the technical requirements page of the application (not needed if requesting this service together with service SB-IU1-B):

- Experiment Type [Single-Particle Analysis/ Cryo-Electron Tomography]
- Sample name
- Sample type [Protein/ Cell/ Other]
- Uniprot ID(s)
- MW (kDa), total in case of a complex
- Buffer Composition
- Concentration (mg/ml)
- Representative cryo-EM micrographs to support particles distribution and grid quality
- 2D and 3D preliminary data, if available
- Any EM data already in literature

Access modality available: Access to NF services.

[SID: SB-IU1-D – Volume Electron Microscopy](#)

Services description: This service is designed to cover imaging on large volumes and includes sample preparation by either high-pressure freezing or chemical fixation, freeze substitution, resin embedding, section preparation by ultramicrotomy and S/TEM imaging at 300kV. The User can provide specimen already fixed, stained, embedded as well as already sectioned and made ready for EM acquisition. A maximum of 1 specimen can be processed per unit of service, and 4 samples maximum (i.e., replicates) can be prepared per specimen. High-pressure freezing will be performed on a Leica EM ICE. Freeze substitution will be performed on a Leica AFS2, and a User might specify a substitution protocol of preference,

which will be utilized if compatible with NF practices. Similarly, for chemical fixation, the User is allowed to specify their protocol of preference, which will be adopted if compatible with NF practices. For resin-embedding, the User could provide a resin of preference, or alternatively, the currently available resin be used. Sections of resin-embedded sample will be prepared on Leica UC7. A maximum of 1 resin-embedded sample can be processed for unit of service, to be sectioned in ribbons, and to be applied to a maximum of 4 TEM support grids. User might specify thickness of final sections, and these recommendations will be followed if compatible with the NF practices. User might provide TEM grid support of preference, otherwise the currently available grid support will be used. Imaging will be performed on a Thermo Scientific Spectra 300 kV either in TEM, equipped with CETA 2 camera, or STEM mode in BF/DF/HAADF. Imaging conditions, if requested by the User, must be compatible with NF practices. Microscope Access is granted for a maximum of 5 days per unit of service, including all steps from sample loading to alignments and collection, and according to NF staff availability. All steps of this service will only be performed by NF staff. To maximise efficient use and Access to high-end TEM instruments, priority will be given to applicants specifically requesting parts of this service (e.g. only sectioning, or only S/TEM imaging of already prepared sections).

Technical requirements: Only for biological specimen with total thickness smaller than 150 μm ; Only BSL-1 or BSL-2; User must provide 50 ml of final sample buffer to allow preparation of dilutions and for sample handling; for EM imaging, final sections must have maximum thickness of 250 nm for TEM and 500 nm for STEM.

Information to be provided in the technical requirements page of the application:

- Sample Description
- Sample preparation details (if already fixed, embedded, sectioned)
- Light Microscopy data if available

Access modality available: Access to NF services.

SID: SB-IU1-E – Cryo-FM Imaging

Services description: This service provides cryo-Fluorescence Microscopy imaging including sample preparation by plunge-freezing and grids clipping. A maximum of 1 specimen can be processed per unit of service, maximum 4 samples (i.e. replicates) can be prepared per specimen. Glow discharging will be performed by either a Pelco EasyGlow, a Quorum GloQube, or Solarus II plasma cleaner device. Plunge-freezing will be performed on a Thermo Scientific Vitrobot Mk IV or a Leica EM GP2. Applicants may provide TEM grid supports of preference, otherwise the NF staff will use the available TEM grid supports. Widefield imaging will be performed on a Leica Thunder cryo-CLEM system. Confocal imaging will be performed on a Leica Stellaris 5 cryo-CLEM system equipped with white light laser. Both microscopes are equipped with a 50x / 0.9 NA lens. This service is provided for a maximum of 8 continuous hours per unit of service, including plunging, clipping, and imaging. In case of User-provided already-clipped grids (in Thermo Scientific cartridges), these will be inspected by NF staff prior to acceptance. This service will only be performed by NF staff.

Technical requirements: Only for biological specimens with thickness smaller than 15 μm ; Only for cells in suspension, and in case of adherent cells, User must provide already plunge-

frozen grids; Only BSL-1 or BSL-2; User must provide 50 ml of final sample buffer to allow preparation of dilutions and for sample handling.

Information to be provided in the technical requirements page of the application:

- Sample Description
- Sample Buffer
- Light Microscopy data if available

Access modality available: Access to NF services.

(IU2) Biomass Production Unit

SID: SB-IU2-A – Protein Expression In Insect Cells

Services description: The service aims to cover the entire process of Baculovirus protein expression, starting from a Bacmid. Initially, commercial Sf9 cells are transfected with the Bacmid, supplied by the applicant, which contains the gene of interest and a fluorescence marker. The initial stage results in a low-titre Baculovirus suspension (P1 generation), followed by a second amplification (P2 generation) to produce a high-titre suspension. The P2 Baculovirus suspension could be directly used for protein expression or another round of Baculovirus amplification is performed before infecting commercial High Five insect cells (at 0.5×10^6 cells/ml). The virus amount used depends on the construct and might need optimization in initial small-scale infections. Protein expression is monitored indirectly by checking for the fluorescence marker (carried by the Bacmid) and cell viability. Finally, cells are harvested via centrifugation, and the pellet or supernatant is made available.

Technical requirements: 1. Sterile, endotoxin-free Bacmid, free from phenol and sodium chloride containing the gene/s of interest. Please note that 20 μ l of purified bacmid per P1 generation requested (indicative DNA concentration of 5 μ g/ μ l) is typically sufficient for 5 to 8 litres of protein expression; 2. Bacmid should have a fluorescence reporter gene (e.g. GFP, YFP) to monitor its expression; 3. Preliminary test or feasibility information supporting the production of recombinant Baculovirus and protein expression of interest.

Information to be provided in the technical requirements page of the application:

- Required volume of the desired protein expression (consider that commercial High Five insect cells are infected at 0.5×10^6 cells/ml)
- Preliminary tests or feasibility information from literature supporting the Baculovirus production of the protein of interest

Access modality available: Access to NF services.

SID: SB-IU2-B – Protein Expression In Mammalian Cells In Suspension

Services description: The service offers dedicated pipelines for small- and large-scale cell cultivation and protein expressions:

- Small scale: utilizing commercial Expi293F cells, transient transfection is conducted with a plasmid containing the gene/s of interest (potentially with a fluorescent marker), provided by the applicant. Cell cultivation and transfection take place in Erlenmeyer

flasks within dedicated shaker incubators; typically, 500 ml of cell culture per 2-liter flask is utilized up to a total cultivation volume of approximately 10 litres. Transfection of an Expi293F cell culture is performed at approximately 2 to 3×10^6 cells/ml, following a modified protocol with polyethylenimine (PEI). While no expression test will be performed, the efficiency of transfection can be readily assessed if the plasmid includes a fluorescent marker. Transfected cells are subsequently harvested by centrifugation, and either the frozen pellet or the refrigerated supernatant will be provided.

- Large scale: bioreactor cultivation and protein expression are performed either with commercial cell lines (e.g., Expi293F cells) transiently transfected with applicant-provided plasmids, or with any mammalian cell line adapted to suspension cultivation supplied by the applicant. Preliminary tests are normally performed using a 0.5 litres scale bioreactor to define and optimize bioreactor cultivation conditions. Subsequently, a 10 litres scale bioreactor enables large-scale cell cultivation and protein expression, employing both transient transfection protocols and stable cell line expressions. Moreover, the implementation of perfusion, utilizing an acoustic retention device, may be explored to increase the biomass production and, consequently, protein expression. Similar to small-scale operations, no expression test will be performed. Instead, monitoring of transfection efficiency for transient expression can be undertaken if the plasmid carries a fluorescent marker or fluorescently tagged protein of interest.

Technical requirements:

For transient protein expression:

1. Sterile, endotoxin-free plasmid DNA, free from phenol and sodium chloride containing the gene/s of interest.
2. Plasmid DNA should have the following specifications: Amount of 1.1 mg for each litre of cell expression culture (consider an approx. cell concentration of 2 to 3×10^6 cells/ml at the transfection); The DNA concentration should be greater than $1 \mu\text{g}/\mu\text{l}$ with a ratio Abs_{260 nm}/Abs_{280 nm} between 1.7 and 2.1.
3. The plasmid should contain a fluorescence reporter gene (e.g. GFP, YFP) if monitoring of transfection efficiency is required.
4. Preliminary test or feasibility information supporting the successful transfection using a mammalian cell line (including adherent cells) and proof of actual protein expression should be provided.

For stable cell line expression:

1. Cell line (BSL-1 or BSL-2), mycoplasma free, adapted for suspension cultures
2. Culture conditions should be provided.
3. Successful trials of suspension cultures conducted in flasks with volumes exceeding 100 mL, validated by confirmed protein expression.

Information to be provided in the technical requirements page of the application:

- Required volume of the desired protein expression experiment
- Preliminary tests or feasibility information from literature supporting the expression in mammalian cells of the protein of interest (for both transient and stable cell line expression)

- For request involving bioreactors, any pre-existing protocol that should be followed
- Localization of protein of interest (intracellular, membrane-embedded, or extracellular)

Access modality available: Access to NF services.

SID: SB-IU2-C – Protein Expression In Yeast and Bacteria Cells

Services description: The service offers dedicated pipelines for small- and large-scale cell cultures and expressions:

- Small scale: 15 litres fermenter useful for initial trial test before moving to larger scale fermenter or small expression using both bacteria and yeast cells. Typical culturing strategies are available such as batch and fed batch (up to 2 feeds). Max working volume of 10 litres.
- Large scale: 150 litres fermenter dedicated to large cultivation and protein production. Typical cultivation strategies are available, including batch and fed batch (up to 2 feeds). Max working volume of 100 litres.

In both cases, cells will be collected and separated from the supernatant using dedicated superspeed centrifuges or a High-Speed Tubular Centrifuge. Upon request, the cells can be lysed using a continuous flow cell disruptor or by a high-capacity cryogenic grinder.

Technical requirements: 1. Bacterial or yeast strains (BSL-1 or BSL-2); 2. growth/cultivation conditions available; 3. expression protocols available.

Information to be provided in the technical requirements page of the application:

- Required volume of the production
- Growth conditions
- Preliminary tests or feasibility information from literature supporting the production requested
- Any pre-existing protocol that should be followed
- Localization of the product of interest (intracellular or extracellular)

Access modality available: Access to NF services.

(IU3) Biophysics Unit

SID: SB-IU3-A – Characterisation of Macromolecular Samples

Services description: Structural biology and biochemical assays often require sample optimization to achieve stability and homogeneity, while understanding the oligomerisation state and precise composition of macromolecular complexes is crucial for unravelling their architecture. To address these needs, the Biophysics Unit offers a service leveraging various instruments to determine the molecular weights of species in solution and their thermal stability parameters. Techniques utilized include mass photometry, SEC-MALS, dynamic light scattering, and nanoDSF.

Technical requirements: Technical requirements vary based on the number of techniques employed, ranging from as little as 20 µl to several hundred µl of sample, at roughly 10-50 µM

concentration. More concentrated and abundant samples facilitate comprehensive characterisation through repeated experiments, typically necessary for in depth analysis. Initially, SEC elution profiles of the sample and the corresponding SDS-PAGE gel must be provided.

Information to be provided in the technical requirements page of the application:

- Uniprot ID(s)
- MW (kDa) total in case of complex
- Ligands
- Buffer Composition
- Concentration (μM)
- SDS PAGE
- SEC chromatogram
- Volume of purified sample (μL)

Access modality available: Simple Access, Access to NF services, Access with Training.

SID: SB-IU3-B – Measurement of Affinity Constants

Services description: The Biophysics Unit is equipped with instruments designed to determine the strength and biophysical properties of macromolecular or protein-ligand interactions, including association and dissociation constants, as well as stoichiometry of binding. Available techniques include isothermal titration calorimetry, microscale thermophoresis, and bio-layer interferometry (which can also be utilized for quantifying known components in complex mixtures).

Technical requirements: Technical requirements will depend on the chosen technique, but to ensure complete binding saturation in the assay at least one of the two components should be at a concentration approximately 10-20 times greater than the dissociation constant (K_d). Selection of the technique, and consequently sample requirements, will be influenced by factors such as strength of association, availability of the sample, its homogeneity, and overall biophysical properties of the system under investigation.

Information to be provided in the application:

- Uniprot ID(s)
- MW (kDa) of interacting species
- Rough estimate of K_d
- Buffer Composition
- Available concentrations of samples (μM)
- SDS PAGE (if available)
- SEC chromatogram
- Volume of purified sample (μL)

Access modality available: Simple Access, Access to NF services, Access with Training.

(IU4) Structural Proteomics Unit

SID: SB-IU4-A – Crosslinking MS Acquisition of Purified Protein Complex without Crosslinking Reaction Optimisation

Services description: The Structural Proteomics unit will perform crosslinking MS on a purified protein complex to identify protein-protein interactions and map residue distances. This service does not include preliminary crosslinking reaction optimisation, which should be performed by the User at their own institution (in consultation with NF staff). This service will only be performed by NF staff.

Technical requirements: The User must provide at least 80 µg of a purified protein complex (recombinant or and/ or isolated to high purity from endogenous sources), with amounts estimated by Bradford, BCA or by absorbance if the A260/A280 ratio is not suggestive of nucleic acid contamination. The sample must be in a buffer free of primary amines (e.g., Tris should be avoided). For complexes of less than 4 proteins and a mass of under 200 kDa, 40 µg are sufficient. Ideally, the sample should be prepared upon consultation with our NF and shipped as a protein precipitate, gel bands or frozen, as indicated by NF staff on a per project basis.

Information to be provided in the application:

- Uniprot ID(s)
- Buffer composition
- Amount available for single experiment (in µg)
- Can the experiment be repeated, if needed?
- SDS PAGE (if available)

Access modality available: Simple Access, Access with Training.

SID: SB-IU4-B – Crosslinking MS Acquisition of Purified Protein Complex with Crosslinking Reaction Optimisation

Services description: The Structural Proteomics unit will perform crosslinking MS on a purified protein complex to identify protein-protein interactions and residue distances. This service includes preliminary crosslinking reaction optimisation and proteomics acquisitions. These can be performed by our NF staff provided the protein sample, or by a visiting User with our assistance.

Technical requirements: The User must be able to produce at least 2 preps of 80 µg of a purified protein complex (recombinant or and/ or reconstituted from endogenous sources), with amounts estimated by Bradford, BCA or by absorbance if A260/A280 ratio are suggestive of no nucleic acid contamination. The sample must be in a buffer free of primary amines (e.g., Tris should be avoided). For complexes of less than 4 proteins and a mass of under 200 kDa, 2 preps of 40 µg are sufficient. Ideally, if stability is not a concern, the sample should be prepared fresh and shipped on ice, or on dry ice if the sample can withstand freeze/ thawing. In case of freezing, please notify us of the glycerol (or other cryoprotectant) concentration (if present) and provide us with buffer to exchange this out.

Information to be provided in the technical requirements page of the application:

- Uniprot ID(s)
- Buffer Composition
- Amount available for experiment (in µg)
- Can the experiment be repeated, if needed?
- SDS PAGE (if available)

Access modalities available: Simple Access, Access to NF services, Access with Training.

[SID: SB-IU4-C – Crosslinking MS Acquisition of Immuno-precipitate From Tagged Overexpressed Bait](#)

Services description: The Structural Proteomics unit will perform crosslinking MS to characterize the interactome of a particular target protein *in situ*. Crosslinking reactions can be performed on cells, in lysate or after competitive or otherwise non-denaturing (native) elution. As this experiment requires a careful and at times tricky design, preliminary results will be shared with the User and guidance provided to set or optimize the experimental conditions. This service will be performed by NF staff if the crosslinking reaction occurs at the home institution with guidance from us, or by a visiting User under our direct supervision if the entire workflow is requested.

Technical requirements: The User must have a working immunoprecipitation of their target protein with a visible band on a western blot and a known yield in the eluate (excluding antibody amount). Overexpressed protein with affinity enrichment followed by elution by tag cleavage or competition is recommended. For example, a protein overexpressed with FLAG tag, eluted with FLAG peptide. The peptide is then removed by dialysis and protein concentration is estimated by BCA or Bradford. The goal is to have a setup that can achieve over 100 µg of the eluted protein excluding the antibody or the competition peptide.

Information to be provided in the technical requirements page of the application:

- Cell type utilized and species
- Uniprot ID of bait
- Yield of IP and number of cells/amount of biomass utilized for the experiment
- Western blot (if available)
- SDS PAGE stained with Coomassie (if available)

Access modality available: Simple Access, Access to NF services, Access with Training

[SID: SB-IU4-D – Crosslinking MS Acquisition of Immuno-precipitate From Endogenous Material Or of Cellular Fraction](#)

Services description: The Structural Proteomics unit will perform crosslinking MS to characterize the topology of the protein-protein interactome of a particular target protein or enriched cellular fraction *in situ*. Examples include: interactome of pulldowns with an endogenously tagged protein of interest; interactome of vesicles/ cellular compartments;

interactome of bacterial cells or virus/ host interactions after pulldown of specific virulence factors. Crosslinking reactions can be performed on cells, on lysates or after competitive or otherwise non-denaturing (native) elution. As these experiments require careful design, the User will be granted Access to preliminary acquisitions to characterise the sample and set the correct reaction conditions, or guidance to perform the optimization at their home institution. This service will be performed by NF staff in collaboration with a visiting User.

Technical requirements: The User must have a working immunoprecipitation or enrichment of their target protein with a visible band on a western blot and on an SDS-page Coomassie-stained gel, or a biochemical or other type of enrichment of a cellular fraction of interest. The User must also perform their experiments in a system that can be scaled up in terms of biomass: as an example, hundreds of millions of cells are commonly needed to enrich for the protein and peptides of interest when these experiments are performed in HEK293T cells. The amount of material required will depend on the natural abundance of the protein or fraction of interest. The Biomass unit may be used to produce the required amounts. The goal is to have a setup that can yield over 150 µg of the fraction of interest.

Information to be provided in the technical requirements page of the application:

- Cell used and species
- Uniprot ID of bait if IP was performed
- Yield of IP in µg and number of cells/amount of biomass used to obtain it. Alternatively, typical amount of cellular fraction material available in micrograms of protein.
- Western blot (if available)
- SDS PAGE stained with Coomassie (if available)
- Availability of the User to visit the NF in person

Access modality available: Simple Access, Access with Training.

[SID: SB-IU4-E – Integrative Modelling with Crosslinking MS and Cryo-EM Data](#)

Services description: The Structural Proteomics unit will perform integrative structural modelling combining medium/ low resolution (from 7 to 30 Å) cryo-EM densities and crosslinking MS data acquired at our NF. In case of very large systems, negative stain data may also be used. This does not refer to model building in cryo-EM densities, but to calculations of localization of subunits or of areas not observed in EM maps. This task can be performed on data from services SB-IU4-A or SB-IU4-B only. Example software: DisVis, integrative modelling platform (IMP), AlphaLink/ AlphaLink2. This service will be performed by NF staff, but training will be available if requested, provided basic bioinformatics skills of the User (bash terminal, python).

Technical requirements: The User must already have the density map and have or be planning to obtain a crosslinking MS dataset for their protein complex in this evaluation round. The data must be on a recombinant or purified system. For data acquired at our NF, only services SB-IU4-A or SB-IU4-B can be integrated with this service.

Information to be provided in the technical requirements page of the application:

- Uniprot ID(s)

- Resolution of available EM data
- Type of available EM data (single particle cryo, cryo-ET, negative stain)
- List any other EM data in the literature
- List any crosslinking MS data if available or in literature, if possible specifying number of self and heteromeric crosslinks

Access modality available: Access to NF service, Access with Training.

(IU5) Dynamic Single-Molecule Unit

SID: SB-IU5-A – Experimental Design and Pilot Experiment

Services description: This service allows exploring the potential of single molecule techniques. It is dedicated to Users with no prior experience with dynamic single molecule (DSM) approaches who would like to obtain ‘proof of concept’ data necessary to plan future experiments. The unit is equipped with two state-of-the-art instruments: (1) c-trap and (2) c-trap edge. The c-trap relies on confocal scanning, and it is predominantly used for imaging in solution. C-trap edge has an option to switch between wide field fluorescence and TIRF. In addition, c-trap edge allows for label free imaging based on IRM, which makes this instrument ideal for imaging close to the surface. The Unit can assist in a very broad spectrum of experimental approaches. These are a few examples of experiments ‘in solution’:

(A) KYMOGRAPHS: (i) characterizing protein binding to DNA (possibly RNA); (ii) observation of protein diffusion/ direct motion on DNA; (iii) characterizing protein-protein interactions upon binding to DNA; (iv) identifying best DNA substrates (ssDNA vs. dsDNA, specific sequence of DNA structure) for protein binding

(B) FORCE SPECTROSCOPY: (i) detecting changes to DNA structure upon protein binding e.g. melting, looping, compaction; (ii) unfolding experiment of RNA hairpin or other secondary structures; (iii) detecting protein enzymatic activity (e.g. transcription)

Examples of ‘surface assays’:

(A) Motility assay which involves motor proteins

(C) Manipulation and characterization of mechanical properties of cell/ larger sub-cellular structures/ assemblies (e.g. microtubules)

‘Experimental design and Pilot Experiment’ will only be performed by the NF staff, ideally accompanied by the User. The User can spend up to 5 days in the NF, testing various samples. This stage aims to provide an initial experimental assessment – the User will identify the most suitable assay and instrumental configuration. Both instruments can be used. The outcome of this service are proof-of-concept data and a roadmap/ timeline for future projects developed together with the NF staff.

Technical requirements: Typically, about 500 μ l of 10 nM fluorescently-labelled protein is required to perform a single experiment. Ideally, small aliquots (5-10 μ l) of concentrated protein should be provided. Fluorescent dyes excited with 488 nm (“blue”), 561 nm (“green”), 638 nm (“red”) can be used. If the protein is tagged (strep tag or His tag) the unit can provide fluorescent probes that bind specifically to these motifs. The unit provides standard coated polystyrene beads and biotinylated DNA that can be used for the experiments.

Information to be provided in the technical requirements page of the application:

- Type of single molecule experiment: select among DNA binding protein/ transcription / replication/ motility assay/ unfolding/ other
- How is the protein labelled, please write 'not labelled' for pure force measurements
- Previous experience with single molecule techniques: select among no previous experience/ experiments performed at homebuilt instrument in my lab/ experiments performed at homebuilt instrument in collaboration/ experiments performed at commercial instrument in collaboration/ other
- Measurable parameter to be extracted from the data
- Reference publication if the assay has been already developed
- Representative data if available

Access modality available: Simple Access, Access to NF services.

SID: SB-IU5-B – Assay Development

Services description: This service is dedicated to projects aiming to explore and develop complex biochemical assays or assays that had never been performed before. Examples: activity assays (e.g., transcription), motility surface assays, cell manipulation assays. This service will only be performed by NF staff, ideally accompanied by the User. As part of this service, the NF staff will check sample quality, troubleshoot, and define optimal conditions for data acquisition. If possible, an automation protocol for the experiment can be developed to streamline future data collection. The User can spend up to 10 days in the NF, testing various samples. The work can be split into two visits. The outcome of this service is an established protocol that can be used for 'data acquisition' service.

Technical requirements: The User should have a clear understanding of the methodology and provide the anticipated assay design in the proposal. The User should specify in the application which probes are already available. The unit provides standard coated polystyrene beads and biotinylated DNA that can be used for the experiments. Typically, about 500 µl of 10 nM fluorescently-labelled protein is required to perform an experiment. Ideally, small aliquots (5-10 µl) of concentrated protein should be provided. Dyes excited with 488 nm ("blue"), 561 nm ("green"), 638 nm ("red") can be used. All other assay-specific components must be provided by the User.

Information to be provided in the technical requirements page of the application:

- Type of single molecule experiment: select among DNA binding protein/ transcription/ replication/ motility assay/ unfolding/ other
- How is the protein labelled, please write 'not labelled' for pure force measurements
- Previous experience with single molecule techniques: select among no previous experience / experiments performed at homebuilt instrument in my lab/ experiments performed at homebuilt instrument in collaboration/ experiments performed at commercial instrument in collaboration/ other
- Measurable parameter to be extracted from the data
- Reference publication if the assay has been already developed

- Representative data if available

Access modality available: Simple Access, Access to NF services, Access with Training.

SID: SB-IU5-C – Data Acquisition

Services description: This service is dedicated to projects where specific single molecule assays have been already established or, alternatively, should be combined with ‘assay development’ service as a simple ‘package’. Examples of experiments currently performed routinely by the unit: (i) detecting changes to DNA structure upon protein binding e.g., melting, looping, compaction; (ii) characterizing protein behaviour upon binding to DNA (diffusion, direct motion, interactions with other proteins). This service can be performed by the NF staff or by a trained User. The training can be provided by the unit as part of this service. Full training typically requires 3-5 days. The User can spend up to 10 days at the NF. The work can be split into two visits. Original data will be handed to the User as .h5 files. The unit will assist the User in Accessing the files using Pylake. In case of kymographs, NF staff can provide a short training on existing tools such as Lakeview.

Technical requirements: The User should have a clear understanding of the methodology and provide a detailed description of the assay. In the application, the User should specify the level of experience and provide preliminary data that will be reproduced during the project. Standard reagents can be provided.

Information to be provided in the technical requirements page of the application:

- Type of single molecule experiment: select among DNA binding protein/ transcription / replication/ motility assay/ unfolding/ other
- How is the protein labelled, please write 'not labelled' for pure force measurements
- Previous experience with single molecule techniques: select among no previous experience / experiments performed at homebuilt instrument in my lab/ experiments performed at homebuilt instrument in collaboration/ experiments performed at commercial instrument in collaboration/ other
- Measurable parameters to be extracted from the data
- Reference publication if the assay has been already developed
- Representative data if available

Access modality available: Simple Access, Access to NF services, Access with Training.

ANNEX II: LETTER OF INSTITUTIONAL ENDORSEMENT TEMPLATE

(Print on paper bearing the official letterhead of the host Institution)

Endorsement letter of the host Institution

To whom it may concern:

I, the undersigned, (*name of legal representative or special attorney*), born in (*city*) on(*date*), as legal representative (*or special attorney, by means of special power of attorney identified by*) and on behalf of(*name of the host Institution*), legal residence in (*referred to the host Institution*)(*city*), address, regarding the project (*title*)....., presented by(*Applicants's first name and surname*), as Principal Investigator on the call for Access to Human Technopole National Facilities.....(*ID of the call*),

Declare

- That the host Institution is among those eligible to participate in the call for Access as it belongs to the following eligible category: (select among University, IRCSS, Public Research Entities);
- That the Applicant, Dr (*Applicant's first name and surname*) is an independent group leader (Principal Investigator) affiliated with a primary appointment at the host Institution and that they meet the eligibility criteria as indicated in the call;
- That the Applicant has not received funding for performing elsewhere, the aspects of the project for which they are seeking here support from or Access to Human Technopole National Facilities;
- That the services requested here cannot be performed by the Applicant at the host Institution, at a cost which is deemed affordable for them.
- That relevant authorisations, declarations and accreditation from the competent authority(ies) have been obtained in order to process samples and data through Human Technopole;
- That, if applicable, biological specimens have been obtained with the corresponding approval of the Bioethics Committee and appropriately signed 'informed consent', both for their collection and their use, including conservation, manipulation, derivation and processing to be carried out by Human Technopole National Facilities;
- That, if samples were obtained from subjects who signed an 'informed consent', said informed consent allows that sequencing data and results are included in secure controlled Access databases and accessed/ used by authorized third parties;

and is committed

- To accept the terms and conditions to Access Human Technopole National Facilities as described in the National Facilities Access rules ([link](#));
- To sign the Access Agreement should the project be approved ([link](#))

For the host Institution (Applicant legal entity/beneficiary):

Date

Name and Title ;

Email and Signature of legal representative or delegated person

..... ;