CALL FOR PROPOSALS 2016

LARGE-SCALE GENOMICS PROJECTS

FRANCE GENOMIQUE

Institut de Génomique CEA/DSV, CP 5706, 91057 Evry Cedex

APPLICATION FORM

*Please tick the appropriate box:*

[ ]  My project is relevant to «Environmental and agronomical genomics» to be handled at Genoscope

[ ]  My project is relevant to «health and human genetics» to be handled at CNG

1. **Project title**

**2 Project Acronym (20 characters)**

**3 Principal investigator: Name - Address - Telephone - Fax – e-mail**

(If several laboratories are involved, please provide the name of the co-ordinator)

**4 Summary of the project (500 characters), do not justify, just describe**

1. **Size of the Project: provide a tentative estimate of the sequencing volume and of the bioinformatics analyses requested**

**DEADLINE FOR SUBMISSION OF PROJECTS: September 20th, 2016**

**After completion of the submission form:**

**a) Submit the form online to** <http://www.ibisa.net/france-genomique/>

**b) Please keep one copy for your own files**

**Contact:** contact@france-genomique.org

**6 Situate the project within its scientific context, describe the scientific community working in the field of this project. Maximum 5 pages.**

**7 Aim of the project, biological rationale for the utility of the sequence data**

Use this section to emphasize the scientific merits of your project. Your description should highlight the scientific questions to be addressed or answered, the importance of the research, the ability of the proposed research to advance our understanding of biology (relation to other genome sequences, relevance for the interpretation of other biological data, importance for understanding human health and disease, understanding of evolutionary processes in general, importance for understanding of basic biological processes, importance for other applications...). **Maximum 10 pages.**

**8 Starting material. Important: please indicate the number of samples to be sequenced. Describe the quality control procedure for your biological material. In case of species other than human, indicate their genome sizes. [[1]](#footnote-1)(1)**

 (i) Include the technical information:DNA/RNA source**,** abundance of DNA,DNA purity level**,** axeny, specific information on genome size (bibliographic references or techniques for estimation of size)**,** G+C content, information on ploidy,polymorphism level (details and methods of estimation), repeat structure with details about how these are known**,** etc.

 (ii) Include the genomic resources already in place to aid this project:reference genome, physical maps**,** genetic maps**,** transcriptomes**,** etc.

 (iii) In the case of metagenomes, are preliminary analyses available (analysis of 16S/18S rDNA, FISH, etc.)?

 (iv) In case several independent organisms are to be sequenced, include a brief description of each of them in table format.

**Maximum 3 pages.**

**9 Technical description of the sequencing phase of the project. Important: please indicate the volume of sequence requested per sample.**

You can suggest the technology to be used, but the final decision on technology choice will be made by CNG or Genoscope. In the case of *de novo* sequencing, indicate the need for finishing**[[2]](#footnote-2)(2)**.

**Maximum 3 pages.**

**10 How long after the notification will your biological material be available for sequencing?**

**11 Description of the Bioinformatics analyses: indicate what is requested from Genoscope or CNG, and what will be done by the proponent. France Génomique large-scale projects include access to bioinformatics capacities at the Genomics Institute (human resources and computing infrastructure), including sequence mapping, assembly and annotation. Therefore, bioinformatics description by the proponent should be centered on biological analyses posterior to these steps.[[3]](#footnote-3)(3)**

**Maximum 5 pages.**

**12 Please indicate if co-financing is available / envisaged for the project**

**13 Please add any other aspect that you believe to be of specific relevance for the evaluation of your project:**

**14 Information about the laboratory (please use a different page for each participating laboratory)**

**14.1** Role and contributions to the project of the laboratory

**14.2** Name and complete details of the laboratory (affiliation(s), address, telephone, fax, e-mail)

**14.3** Research interests of the laboratory

**14.4** Bioinformatics skills (access to calculation, programs installed, human resources available to the project or to be hired by the proponent in case of acceptance)

**14.5** Brief summary of previous results of the group which are directly related to the project (500 characters)

**14.6** Please append a selection (5 max) of your publications of the last three years with particular attention to those that are relevant to the present project

**15 Experts for the evaluation of the project**

**15.1** Please indicate a list of international experts that you wish to propose for the evaluation of your project. The proposed experts should have no links with your institution or with your project. The France Génomique Scientific Committee may decide at its own discretion to appeal to the suggested experts or not

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| --- | --- | --- | --- | --- | --- |
| **Surname****Given Name** | **Laboratory or Company** | **Email** | **Phone number** | **Country** | **Field of expertise**  |
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**15.2** Please indicate experts that you wish to exclude from the expertise of your project

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| --- | --- | --- | --- |
| **Surname****Given Name** | **Laboratory or Company** | **Country** | **Motive (e.g. potential conflict of interest, confidentiality, etc.)**  |
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1. (1) *Please document the description of the starting material as requested, or justify lack of information. Any missing information or insufficient description may result in rejection of your proposal.* [↑](#footnote-ref-1)
2. (2) *Because of the high pace of evolution of New Sequencing Technologies, we will not generally propose manual finishing of the genomes sequenced in the frame of this Call for Proposals. The shotgun strategy will be optimized (using adequate read lengths, fragment sizes, coverage, and technology mixes) in order to obtain high-quality draft sequences that are of sufficient quality to support most types of biological analyses. Directed approaches will only be proposed in exceptional, strongly supported cases.* [↑](#footnote-ref-2)
3. (3) *Please note that the capability of the proponent(s) to analyse and exploit the genomic data is considered of particular importance by the Scientific Committee for the evaluation of the projects. Insufficient description of the bioanalysis strategy may result in the rejection of the proposal.* [↑](#footnote-ref-3)