

## Important information for next generation sequencing (NGS) experiments

Interfaculty Bioinformatics Unit (IBU) and NGS Platform (NGSP), University of Bern  
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We are happy to support your NGS experiments. To ensure that everything runs as smoothly as possible, it is important that you keep in mind the following points:

### 1) Initiation of project

- a. **Contact us to discuss the design of your experiment.** We have a lot of experience with different applications and can advise you on the design of your experiment e.g. the most suitable sequencing technologies, level of replication, sequencing depth etc. We will also discuss our contribution to your experiment, which can take the form of a service or a collaboration. Ideally, this meeting should involve someone from IBU and NGSP.

Contact details:

IBU: [http://www.bioinformatics.unibe.ch/about\\_us/team/index\\_eng.html](http://www.bioinformatics.unibe.ch/about_us/team/index_eng.html)

NGSP: [http://www.ngs.unibe.ch/about\\_us/team/](http://www.ngs.unibe.ch/about_us/team/)

- b. It is your responsibility to **make sure all legal and ethical requirements are met** to perform the experiment and all planned analyses.
- c. You must inform the NGS Platform on any **hazards associated with your samples** (e.g. infectious material, pathogens).
- d. **Inform the bioinformaticians when your samples are sent for sequencing** so that they know to expect your data within the next weeks.

### 2) During the project

- a. **Inform the bioinformatician when the data are ready.** If the data were produced by the NGS platform in Bern, we will directly access the data. If the data were produced by an external provider, you will need to provide them on a hard drive or via campus cloud. We will not download data from external providers.
- b. Don't hesitate to contact us if you have questions about our work or need additional analyses or visualisations.

### 3) Data

- a. Let us know if you would like us to **submit your data to a public archive**, e.g. the European Nucleotide Archive. This is required by many journals before publication. Keep in mind that data submission takes time. If you need accession numbers for your paper, we need to submit the data **at least 2 weeks before the submission of the paper**.

At most data repositories, it is possible to keep the data private until a specified release date, which we will choose after consultation with you. It will be **your responsibility to keep track of the release date** and ask us to extend it if necessary, for example if publication of your paper is delayed. For human data, it is your responsibility to select a public repository and form of data **release appropriate for the informed consent** obtained from the patients.

- b. **Download the raw data** if you want to keep a backup copy yourself (which is highly recommended). Note that the links to your raw sequence files provided by the NGS platform Bern will remain **active for 6 months only**. If we need to re-upload data after this time period, **you will be charged a fee**.
- c. We will often share results via campus cloud. It is your responsibility to download all provided files **within 30 days** and store them locally. If we need to re-upload data after this time period, **you will be charged a fee**.

#### 4) Publication

- a. We can provide descriptions of our work for the material and methods section of your paper. Please obtain descriptions of the **laboratory procedures directly from NGSP within 1 month** after receiving the data.
- b. If the data were produced by the NGS platform, please mention this in the **acknowledgements** of your paper, for example: "Sequencing data were generated by the NGS Platform of the University of Bern".
- c. When we are coauthors on your paper, we would ask to **have at least 2 weeks to comment on the manuscript** before it is submitted. Regarding coauthorship, we adhere to the recommendations outline by the Proteomics Core Facility here <http://www.pmscf.dkf.unibe.ch/index.php?link=guidelines>. Specifically, coauthorship is warranted when members of the bioinformatics unit or the NGS platform make significant intellectual contributions to a manuscript.
- d. **We retain the right to use the data in anonymized form to present technical aspects** of our work in scientific publications (posters, talks and papers).