# How to submit samples or libraries?

→ complete our submission form (3 web pages) - *https://ige3.lims.unige.ch/app/*

**All samples / libraries inside a submission must follow the same protocol.**

If you have different types of submissions (e.g., RNA for RNA-seq and DNA for ChIP-seq), submit separate requests for each.

## 1 – « Contact informations » page

→ **Enter the PI (Principal Investigator) and user information.**

Note:

- Do not use special characters - including accented letters (e.g., é, ï).
- The .fastq files will be sent to the user.

## 2 – « Service » page

→ **Specify the sequencing request (read length / depth) w/wo the analysis.**

With:

*Run type* → select the desired read length for your submission.

*Total reads needed (multiple of 200 mio reads +/- 20%)*

→ this number applies to the entire submission

→ to calculate the correct value:

- multiply the number of samples by the reads required per sample.
- choose the closest multiple of 200 million reads.

*Bioinformatics analysis* → check the box if you want a bioinformatics analysis.

*Type of request* → indicate whether you are submitting **samples** (RNA, DNA, cells) or **pre-prepared libraries**.

## 3 – « Samples » page

→ **Provide the characteristics common to all samples.**

With:

*Library preparation type* → select the appropriate protocol to apply to your samples.

## or « Libraries » page

→ **Provide the characteristics common to all libraries.**

With:

*Library preparation kit chemistry* → select the library prep kit chemistry used to construct the libraries.

→ **Fill out the sample / library inventory table (direct entry or .csv file import – download the template).**

With:

*Tube label* → ensure that the tube label matches what is physically written on the tube (numbers are preferred).

*Sample name* → the sample names you provide will be used to create the .fastq filename and can differ from tube label if needed. Do not use special characters and spaces (underscores are acceptable substitutes).

Note regarding the **index information**:

- Download the list of indexes included in our database (button “Indexes in the database”)
- If your index is listed, only fill the *1st index name (i7)* column (and the *2nd index name (i5)* column if applicable).
- Else, provide the sequence in the *1st index sequence* column (and the *2nd index sequence* column if applicable). Be careful on the sequence orientation!

## Then confirm your request:

→ **Once the submission form is completed (the "SEND" button), you will receive an email which you must reply to in order to confirm your submission.** If you do not receive an email, check your spam or contact us.

**Available options for the Single Cell Sequencing:**

| | Submission form | | | | | | |
|---|---|---|---|---|---|---|---|
| | « Service » page | | | « Samples » page | | « Libraries » page | |
| *You want to perform:* | *Run type* | *Total reads needed (multiple of 200 mio reads +/- 20%)* | | *Sample type* | *Library preparation type* | *Library preparation kit chemistry* | *1st / 2nd index name* |
| ***Chromium / Universal 3' Gene Expression*** | | | | | | | |
| *a single-cell whole transcriptome profiling on fresh or frozen samples, w/wo on-chip multiplexing.* | Paired End Read - 28 + 90 cycles | *for GEX library*<br>*for CSP library* | 20'000 read pairs/cell<br>5'000 read pairs/cell | *specify if:*<br>single cells<br>single nuclei | single-cell RNA-seq (10x genomics) | **Chromium GEM-X 3' - v4**<br>*with multiplexing:* **Chromium GEM-X 3' 4-plex (OCM) - v4**<br>*previous kits: Chromium Next GEM 3' - v3.1* | *for GEX library* SI-TT-**<br>*for CSP library* SI-NT-** |
| ***Chromium / Flex Gene Expression*** | | | | | | | |
| *a single-cell sequencing on fixed - even FFPE - samples (human, mouse).* | Paired End Read - 28 + 90 cycles | | 10'000 read pairs/cell | fixed single cells | single-cell RNA-seq Flex (10x genomics) | **Chromium GEM-X Flex**<br>**Chromium GEM-X Flex – v2 (Apex)**<br>*previous kits: Chromium Next GEM Flex* | SI-TS-** |
| ***Chromium / Universal 5' Gene Expression*** | | | | | | | |
| *a single-cell gene expression and immunoprofiling on fresh or frozen samples (human, mouse), w/wo on-chip multiplexing.* | Paired End Read - 28 + 90 cycles | *for GEX library*<br>*for V(D)J library*<br>*for CSP library*<br>*for CRISPR library* | 20'000 read pairs/cell<br>5'000 read pairs/cell<br>5'000 read pairs/cell<br>5'000 read pairs/cell | *specify if:*<br>single cells<br>single nuclei | single-cell RNA-seq & immunoprofiling (10x genomics) | **Chromium GEM-X 5' - v3**<br>*with multiplexing:* **Chromium GEM-X 5' 4-plex (OCM) - v3**<br>*previous kits: Chromium Next GEM 5' - v2* | *for GEX library* SI-TT-**<br>*for V(D)J library* SI-TT-**<br>*for CSP library* SI-TN-**<br>*for CRISPR library* SI-TT-** |
| ***Chromium / Epi Multiome ATAC + Gene Expression*** | | | | | | | |
| *a single-cell gene expression and epigenomic profile from the same nucleus.* | *=> Proceed of two submissions! Add "_GEX" and "_ATAC" suffixes to the GEX and ATAC sample names respectively.* | | | | | | |
| *submission 1:* | Paired End Read - 28 + 90 cycles | *for GEX library* | 20'000 read pairs/nucleus | single nuclei | single-cell Multiome GEX (10x genomics) | **Chromium GEM-X Epi Multiome - GEX**<br>*previous kits: Chromium Next GEM Multiome - GEX* | *for GEX library* SI-TT-** |
| *submission 2:* | Paired End Read - 50 + 50 cycles | *for ATAC library* | 25'000 read pairs/nucleus | single nuclei | single-cell Multiome ATAC (10x genomics) | **Chromium GEM-X Epi Multiome - ATAC**<br>*previous kits: Chromium Next GEM Multiome - ATAC* | *for ATAC library* SI-NA-** |
| ***Chromium / Epi ATAC*** | | | | | | | |
| *a single-cell epigenomic profile.* | Paired End Read - 50 + 50 cycles | | 25'000 read pairs/nucleus | single nuclei | single-cell ATAC (10x genomics) | **Chromium Next GEM ATAC - v2** | SI-NA-** |

*GEX = Gene Expression*
*CSP = Cell Surface Protein*
*OCM = On-Chip Multiplexing*

**Available options for the Spatial Gene Expression:**

| | Submission form | | | | | |
|---|---|---|---|---|---|---|
| | « Service » page | | « Samples » page | | « Libraries » page | |
| *You want to perform:* | *Run type* | *Total reads needed (multiple of 200 mio reads +/- 20%)* | *Sample type* | *Library preparation type* | *Library preparation kit chemistry* | *1st / 2nd index name* |
| ***Visium / HD 3' Spatial Gene Expression*** | | | | | | |
| *a single-cell whole transcriptome spatial profiling, on fresh or frozen samples.* | Paired End Read - 43 + 75 cycles (Visium 3') | 550'000'000 reads pairs | single cells | Spatial Transcriptomics - Visium HD 3' | **Spatial Transcriptomics - Visium HD 3'** | SI-TT-** |
| ***Visium / HD Spatial Gene Expression*** | | | | | | |
| *a single-cell whole transcriptome spatial profiling, on fresh, frozen or fixed - even FFPE - samples (human, mouse).* | Paired End Read - 43 + 50 cycles (Visium) | *for fully-covered 6.5 mm Capture Area:*<br>*for FFPE sample* 275'000'000 reads pairs<br>*for fixed sample* 500'000'000 reads pairs<br>*for fresh/frozen sample* 700'000'000 reads pairs<br>*for fully-covered 11 mm Capture Area:*<br>*for FFPE sample* 825'000'000 reads pairs<br>*for fixed sample* 1'500'000'000 reads pairs<br>*for fresh/frozen sample* 2'100'000'000 reads pairs | *specify if:*<br>single cells<br>fixed single cells | Spatial Transcriptomics - Visium HD | **Spatial Transcriptomics - Visium HD - v2**<br>*previous kits: Spatial Transcriptomics - Visium HD* | SI-TS-** |