

# CELLENION

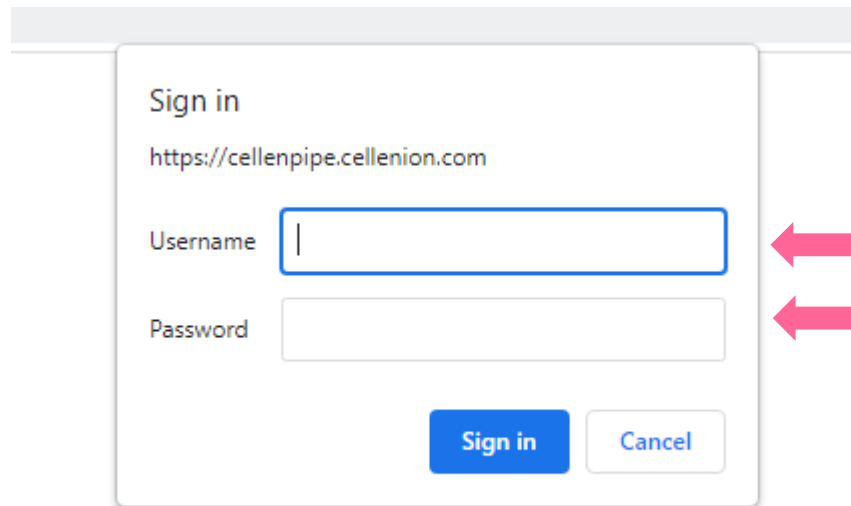
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cellenPIPE  
For cellenCHIP 384 3'RNA-seq kit  
HOW TO

# 1. Log in cellenPIPE



A screenshot of a web browser showing a login form for cellenPIPE. The form is titled "Sign in" and shows the URL "https://cellenpipe.cellenion.com". It contains two input fields: "Username" and "Password". Below the fields are two buttons: "Sign in" (blue) and "Cancel" (light blue). The "Username" field is highlighted with a blue border and a pink arrow points to it from the instruction box on the right.

**cellenpipe.cellenion.com**

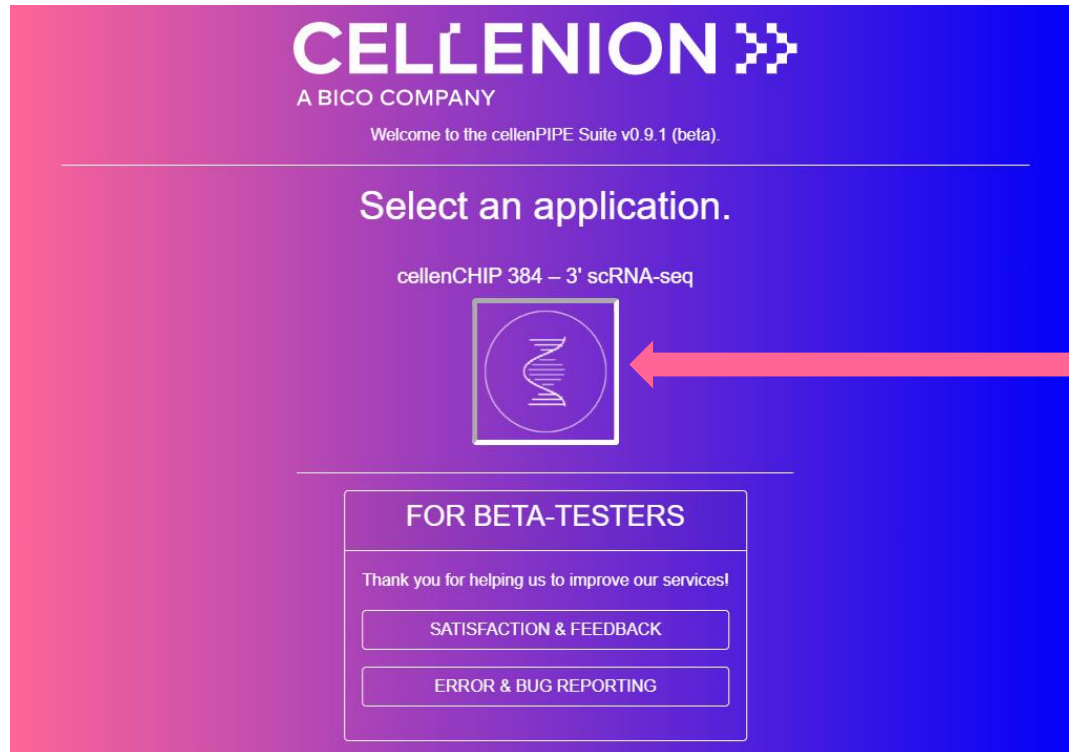
Log in cellenPIPE with the  
cellenCHIP-specific credentials

*Note: to log out, you have to close the browser*





## 2. Select the cellenPIPE application



From the home page, select  
cellenPIPE for 3' single cell  
RNA-sequencing application



### 3. Fill out the form and Click on the Launch button

The screenshot displays the 'cellenPIPE Web App v0.5.1 (beta)' interface. On the left, a sidebar shows 'Remaining uses: 1' and 'Executed runs: 2'. Below this, 'Your runs' section lists two runs: 'scRNA-seq-run1' (Status: 100%) and 'scRNA-seq-run2' (Status: 44.63%). The main area is titled 'CREATION OF A NEW RUN' and includes a 'Required: Agreement with the Terms of Services and Privacy Policy' checkbox, which is checked. The form consists of several steps: STEP 1: Run Name (scRNAseq-run3), STEP 2: Species / Reference Genome (Human: Homo sapiens / hg38), STEP 3: Infosample (test.xlsx), STEP 4: Read 1 - BC & UMI (spheror1\_5M.fastq.gz), STEP 5: Read 2 - cDNA (spheror2\_5M.fastq.gz), STEP 6: Read Length (nt 100), and STEP 7: Storage of the uploaded files (4 weeks of storage (default)). An optional email address (test@cellenion.com) is also provided. A 'Launch the cellenPIPE!' button is at the bottom right.

#### Fill out the form:

- Step 0: Agree to the Terms of Services
- Step 1: Choose a run name
- Step 2: Select the species & reference genome
- Step 3: Upload the infosample file
- Step 4: Upload the read 1 fastq.gz file
- Step 5: Upload the read 2 fastq.gz file
- Step 6: Select a read length
- Step 7: Select the mode of storage for the uploaded files
- Step 8: Indicate an email address to be notified when cellenPIPE execution ends

#### Click on the launch button!

*Note: Refer to the info icons ⓘ for more explanation*



## 4. Confirm the cellenPIPE run

Run Summary

Please check the following parameters:

STEP	ENTRY	STATUS
Run Name	scRNAseq-run5	✓
Species / Reference Genome	Human: Homo sapiens / hg38	✓
Infosample	samples_TJ-6_Spheroid_20.tsv	✓
BC & UMI	spheroR1_5M.fastq.gz	✓
Sequencing	spheroR2_5M.fastq.gz	✓
Read Length	cDNA: 50 nt	✓
Storage of uploaded files	4 weeks of storage	✓
Email	r.laffont@cellenion.com	✓

Number of sequenced cells: 20  
Estimated number of reads: 3.9 million  
Estimated duration of the cellenPIPE run: 0h 14min

Remaining uses: 1 >> 0

Do you still want to launch this cellenPIPE run?

Let's go! ➡

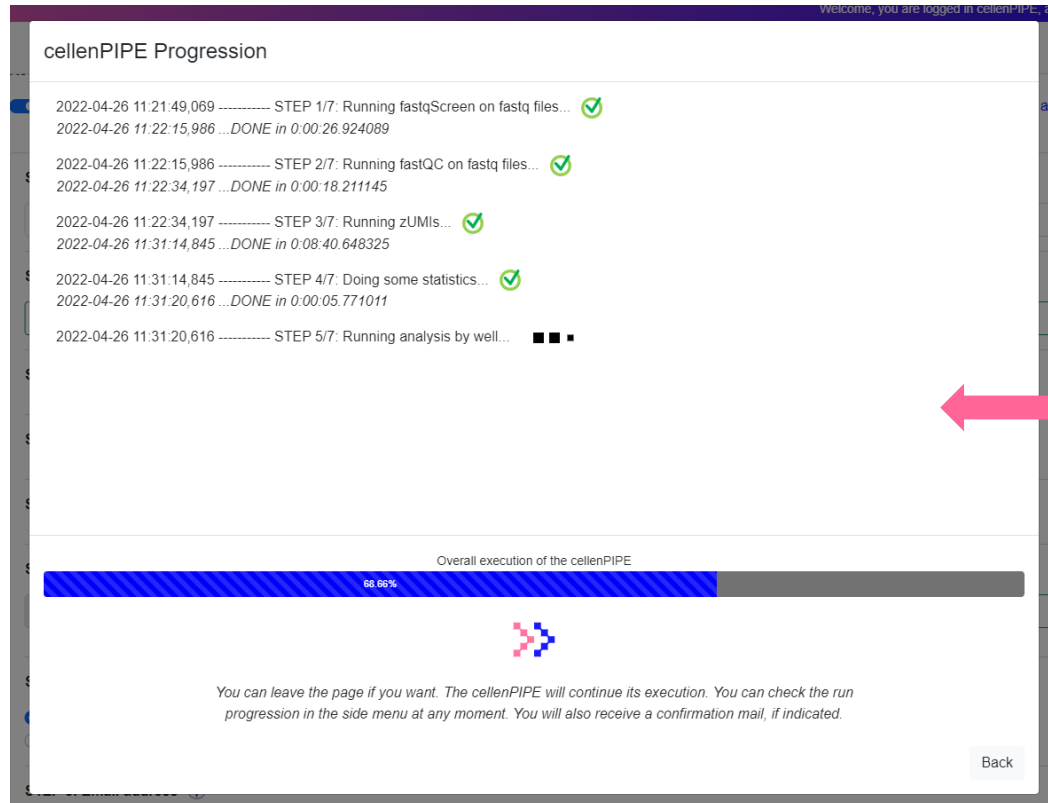
Back

- Check the parameters
- Confirm the run

*Note: Check carefully! The run will consume 1 use and last several hours.*



## 5. Wait until cellenPIPE execution has ended



- Wait until the completion of the run
- You can quit the application
- You will receive an email when the run is complete





## 5bis. Wait until cellenPIPE execution has ended

The screenshot displays the cellenPIPE web interface. On the left sidebar, under 'Your runs', there are two entries: 'scRNA-seq-run1' with a status of 100% and 'scRNAseq-run2' with a status of 44.63%. A pink arrow points from the 'scRNAseq-run2' entry to a text box on the right. The main area is titled 'CREATION OF A NEW' and shows the steps for creating a new run: STEP 1: Run Name (scRNAseq-run3), STEP 2: Species / Reference Genom (Human: Homo sapiens / hg38), STEP 3: Infosample (csv, tsv, xlsx), and STEP 4: Read 1 - BC & UMI (fastq.gz).

BACK

Remaining uses: 1  
Executed runs: 2

Your runs

Current runs Deleted runs

scRNA-seq-run1  
Status: 100%  
QC report Download

scRNAseq-run2  
Status: 44.63%  
QC report Download

CREATION OF A NEW

Required: Agreement with the Terms of  
By using the cellenPIPE application.

STEP 1: Run Name  
scRNAseq-run3

STEP 2: Species / Reference Genom  
Human: Homo sapiens / hg38

STEP 3: Infosample (csv, tsv, xlsx)

STEP 4: Read 1 - BC & UMI (fastq.gz)

- You can check at any moment the progression of the run via the sidebar





## 6. Reception of email when cellenPIPE has ended

Your cellenPIPE analysis is complete! scRNAseq-run5 - 2022-04-26



[Traduire le message en : Français](#) | [Ne jamais traduire à partir de : Anglais](#)

### Congratulations! Your cellenPIPE analysis is now complete!

Hello dear [redacted]

The cellenPIPE analysis for the run 'scRNAseq-run5' has been successfully completed. You can now download the results.

To download the results, including the cellenPIPE report, please log back into the web interface.

You will find the corresponding run in the sidebar. Click on the button "Download".

In order to extract the results from the zip folder, please use the following password:

**bzvPwNo1xlyWaloZ6xlc**

Remaining uses: 0

Run Summary:

- Creation date: 2022-04-26 11:21:39
- Run Name: scRNAseq-run5
- Species / Reference Genome: Human: Homo sapiens / hg38
- Infosample
- Read 1: [redacted]
- Read 2: [redacted]
- Read Length: cDNA: 50 nt
- Storage of uploaded files: 4 weeks of storage
- Number of sequenced cells: 20
- Number of reads: 5.0 million
- Duration of the cellenPIPE analysis: 0h 19min 40s

Thank you for using the cellenCHIP and cellenPIPE services!

We would be grateful if you could take some minutes to fill out the satisfaction & feedbacks form (see home page, beta-testers panel). We always aim to improve our services as much as possible and would love to read your comments!

If you experience any trouble or want to share more of your feedbacks, please contact the support team at [ticket@cellenion.com](mailto:ticket@cellenion.com)

See you soon,



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Warning: this email was sent automatically. Do not reply to this address.



- You will receive an email when the run is complete
- It contains a password to extract the results from a zip folder
- It displays also a summary of the run

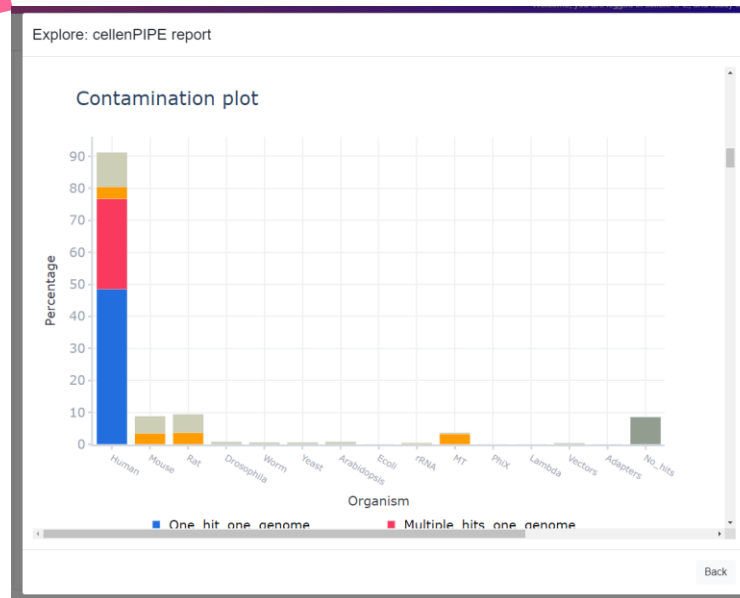


## 7. Explore the cellenPIPE report

 scRNAseq-run3 

Status: 100%

 Report  Download

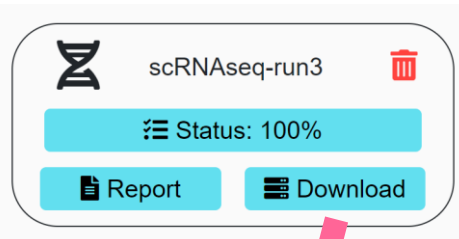


- From the sidebar, manage the cellenPIPE runs
- Explore the cellenPIPE report on your desktop, laptop or tablet computer!

*Note: go to the end of the cellenPIPE report to find links for Seurat reports.*



## 8. Download the results



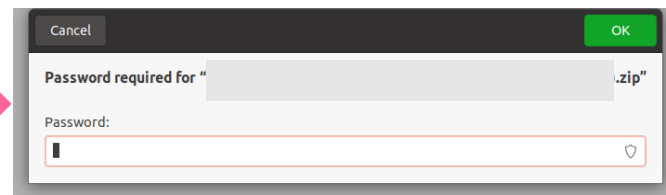
### Results: Download

You are downloading the results as a zip folder! It will be locked by the password you received in the email confirming the completion of the run.  
In this zip, you will find:

- the cellenPIPE report;
- results regarding quality check: contamination, FastQC, FastQScreen, genebody coverage, reads per cell...
- results regarding gene expression: count matrixes, common genes, clustering and Seurat analysis...
- zUMIs statistics

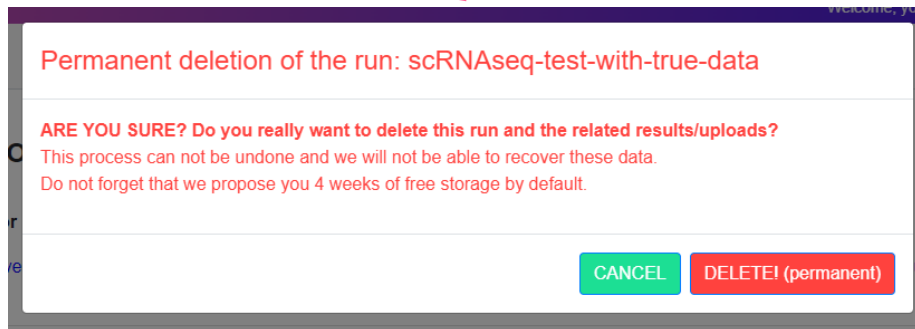
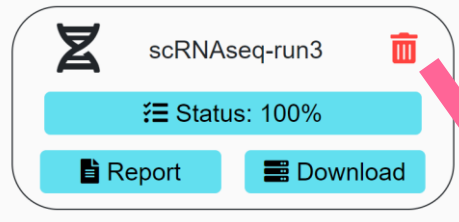
Back

- Download the zip folder
- Extract the results with the password provided in the email





## 9. Manage the storage of the cellenPIPE results

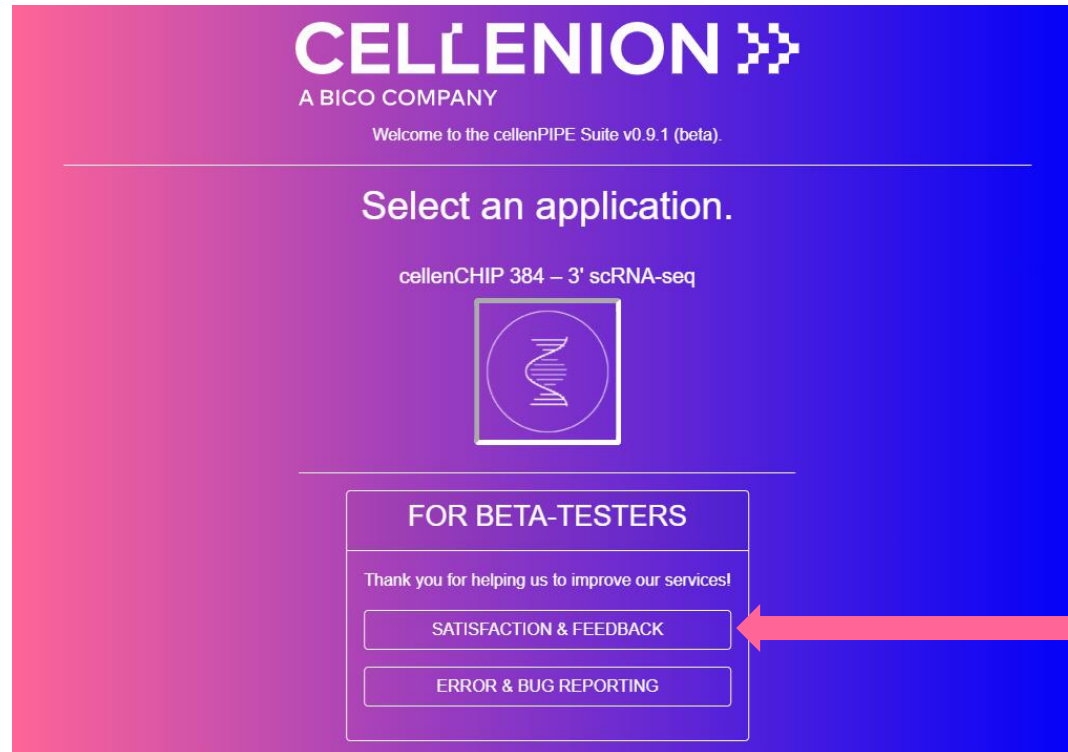


- Permanently delete the results at any moment

*Note: the storage of the results will expired after 4 weeks by default*



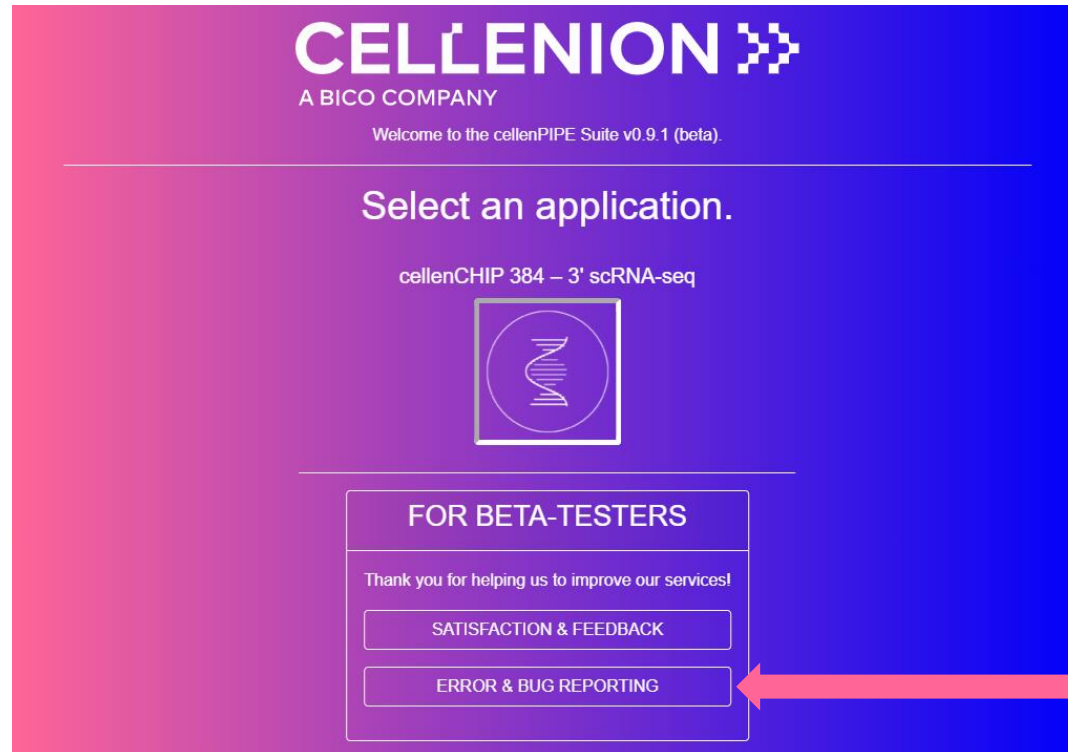
# 10. Let us know your satisfaction & feedback



From the home page:  
Share your satisfaction & feedback!  
5-10 min required



# 11. Report any encountered bug



From the home page:  
You can also share any bug or error  
that disturbed your cellenPIPE  
experience





JOIN THE  
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REVOLUTION 