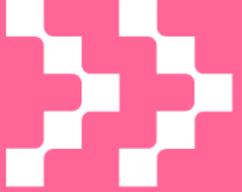


**CELLENION** 

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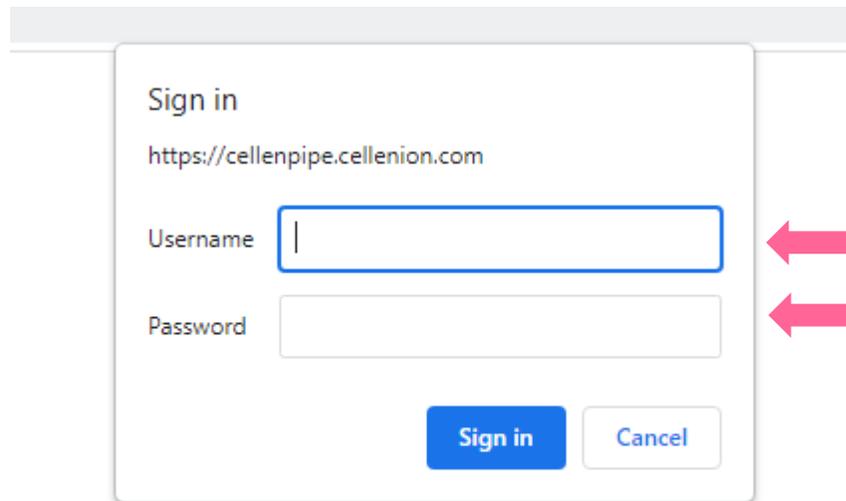
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cellenPIPE

For cellenCHIP 384 3'RNA-seq kit

HOW TO

# 1. Log in cellenPIPE



Sign in  
https://cellenpipe.cellenion.com

Username

Password

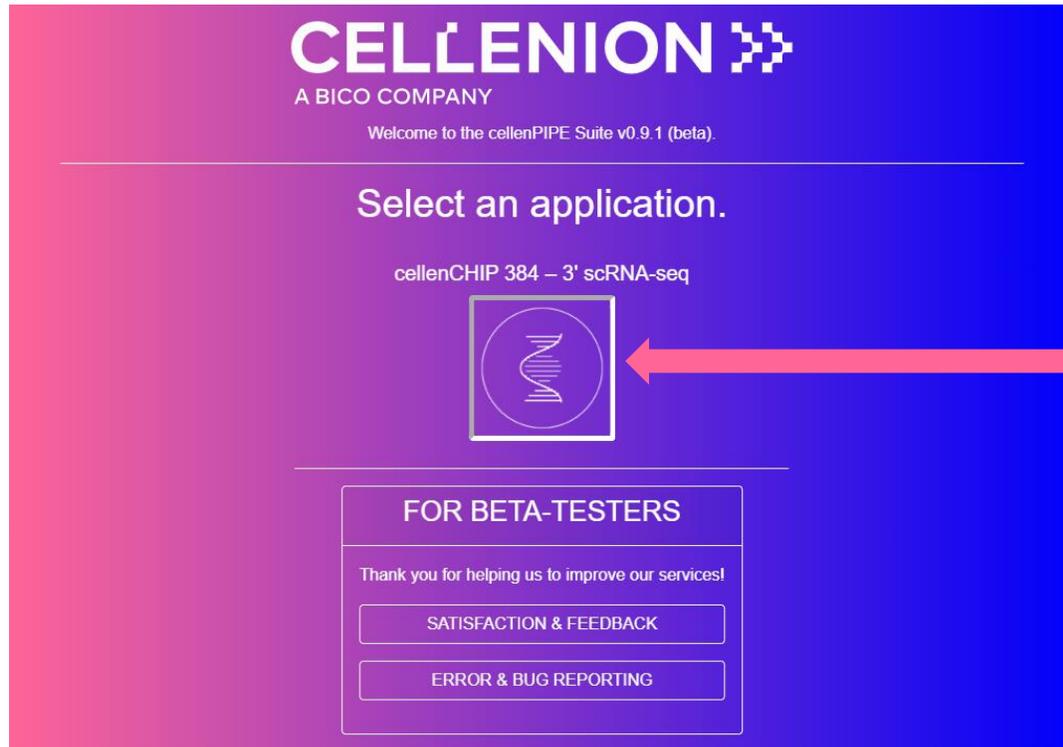
**cellenpipe.cellenion.com**

Log in cellenPIPE with the  
cellenCHIP-specific credentials

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



## 2. Select the cellenPIPE application



**CELLENION** >>>  
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Welcome to the cellenPIPE Suite v0.9.1 (beta).

---

Select an application.

cellenCHIP 384 – 3' scRNA-seq



FOR BETA-TESTERS

Thank you for helping us to improve our services!

SATISFACTION & FEEDBACK

ERROR & BUG REPORTING

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 shows the 'CREATION OF A NEW RUN' page in the cellenPIPE web application. The page is titled 'cellenCHIP 384 - 3'scRNA-seq' and includes a 'Dear cellenPIPEAdmin, welcome to the cellenPIPE Web App v0.5.1 (beta)' message. On the left, there is a sidebar with 'Remaining uses: 1' and 'Executed runs: 2'. Below this, there are two run cards: 'scRNA-seq-run1' (Status: 100%) and 'scRNA-seq-run2' (Status: 44.63%). The main form area is divided into several steps:

- STEP 1: Run Name**: A text input field containing 'scRNAseq-run3' with a green checkmark.
- STEP 2: Species / Reference Genome**: A dropdown menu showing 'Human: Homo sapiens / hg38'.
- STEP 3: Infosample (c1v; t1v; x1sv)**: A dashed box containing 'Uploaded: test.xlsx'.
- STEP 4: Read 1 - BC & UMI (fastq.gz)**: A dashed box containing 'Uploaded: spheroR1\_5M.fastq.gz'.
- STEP 5: Read 2 - cDNA (fastq.gz)**: A dashed box containing 'Uploaded: spheroR2\_5M.fastq.gz'.
- STEP 6: Read Length**: A dropdown menu showing 'nt 100' with a green checkmark.
- STEP 7: Storage of the uploaded files**: Radio buttons for '4 weeks of storage (default)' (selected) and 'No storage: IMMEDIATE deletion after the cellenPIPE completion'.
- Optional: Email address**: A text input field containing 'test@cellenion.com'.

At the bottom of the form is a blue button labeled 'Launch the cellenPIPE!' with a right-pointing arrow icon.

## 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! >>>

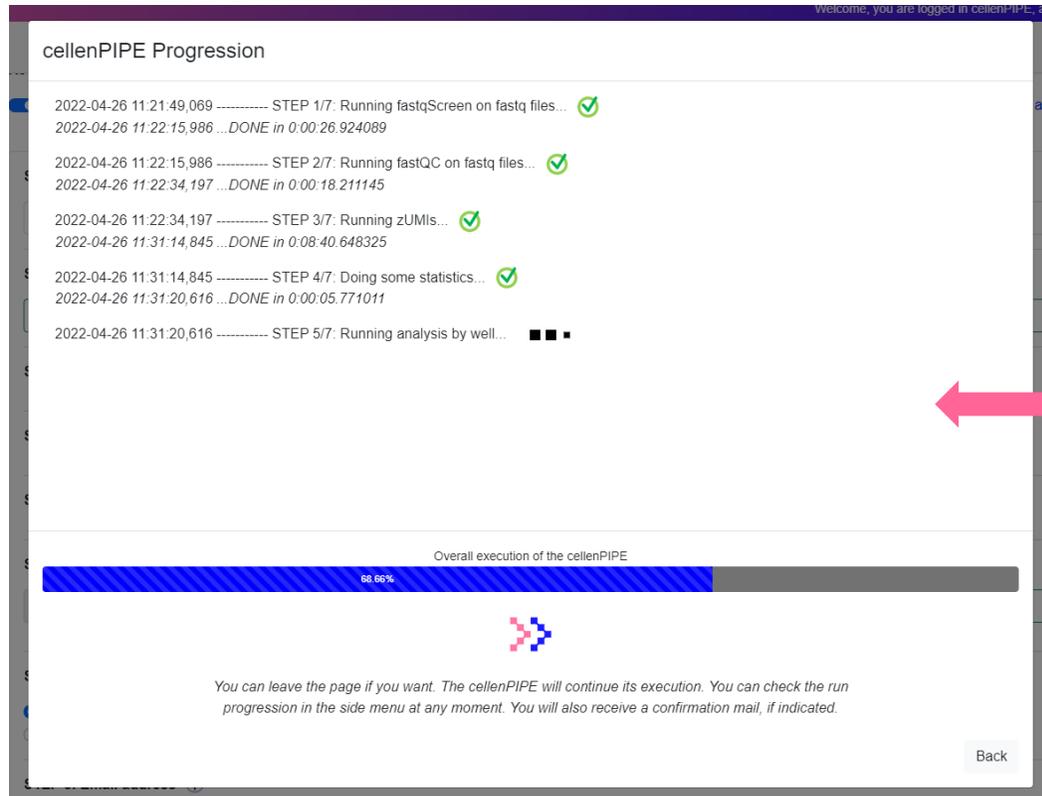
Back

- 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 is a sidebar with a 'BACK' button and a 'ce' logo. It shows 'Remaining uses: 1' and 'Executed runs: 2'. Under 'Your runs', there are two entries: 'scRNA-seq-run1' with a status of 100% and 'scRNA-seq-run2' with a status of 44.63%. Each entry has 'QC report' and 'Download' buttons. The main area is titled 'CREATION OF A NEW' and includes a 'Required: Agreement with the Terms of' section with a checked checkbox 'By using the cellenPIPE application.'. Below are four steps: '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)'.

- 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:

**bzvPwNo1xLyWaloZ6xc**

Remaining uses: 0

Run Summary:

- Creation date: 2022-04-26 11:21:39
- Run Name: scRNAseq-run5
- Species / Reference genome: Human: Homo sapiens / hg38
- Infosamole
- Read 1:
- Read 2:
- 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,

**CELLENION**   
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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

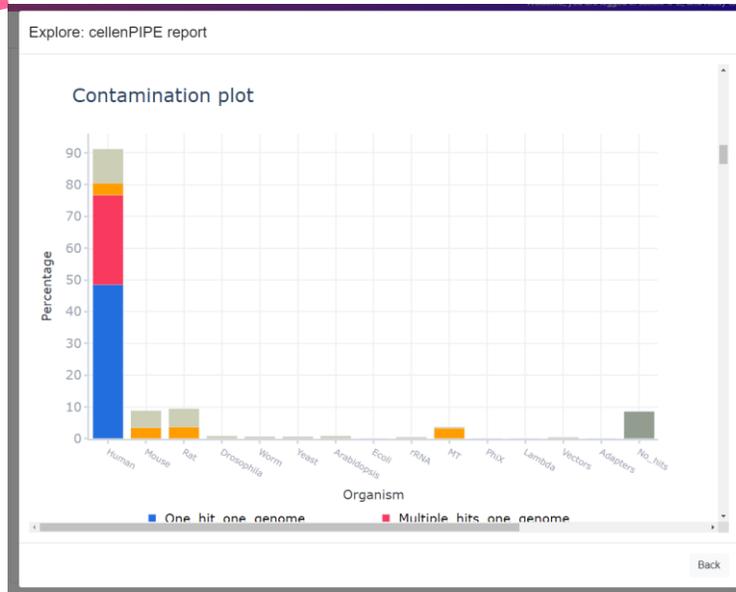


## 7. Explore the cellenPIPE report

scRNAseq-run3 

Status: 100%

 Report  Download

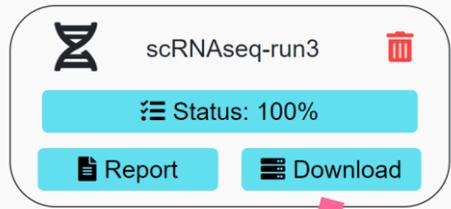


- From the sidebar, manage the cellenPIPE runs
- Explore the cellenPIPE report on your desktop, laptop or tablet computer!

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



## 8. Download the results



scRNAseq-run3

Status: 100%

Report Download

### Results: Download

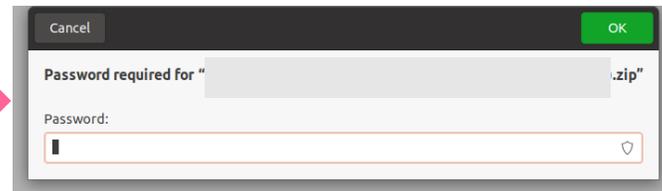
You are downloading the results as a zip folder! It will be locked by the password you received in the email confirming the completion of the run.

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



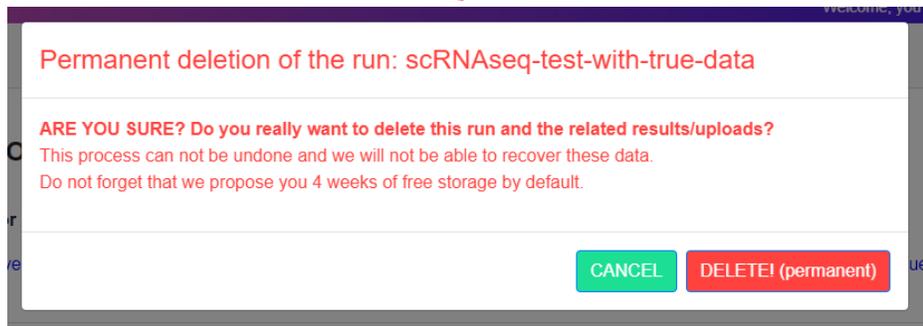
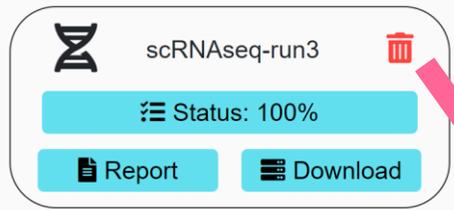
Cancel OK

Password required for " [redacted] .zip"

Password:



## 9. Manage the storage of the cellenPIPE results

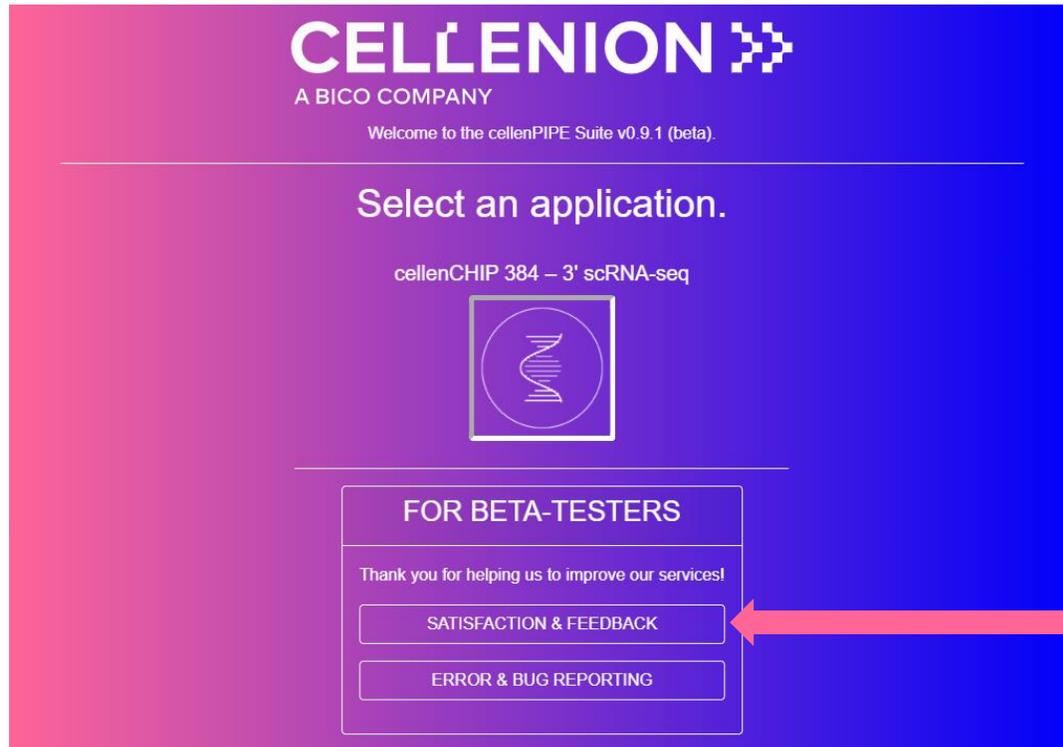


- Permanently delete the results at any moment

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



# 10. Let us know your satisfaction & feedback



**CELLENION** 

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Welcome to the cellenPIPE Suite v0.9.1 (beta).

---

Select an application.

cellenCHIP 384 – 3' scRNA-seq



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**FOR BETA-TESTERS**

Thank you for helping us to improve our services!

[SATISFACTION & FEEDBACK](#)

[ERROR & BUG REPORTING](#)

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



# 11. Report any encountered bug

**CELLENION** 

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Welcome to the cellenPIPE Suite v0.9.1 (beta).

---

Select an application.

cellenCHIP 384 – 3' scRNA-seq



---

**FOR BETA-TESTERS**

Thank you for helping us to improve our services!

SATISFACTION & FEEDBACK

ERROR & BUG REPORTING

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



**JOIN THE  
BIO-CONVERGENCE  
REVOLUTION **