

CELLENION

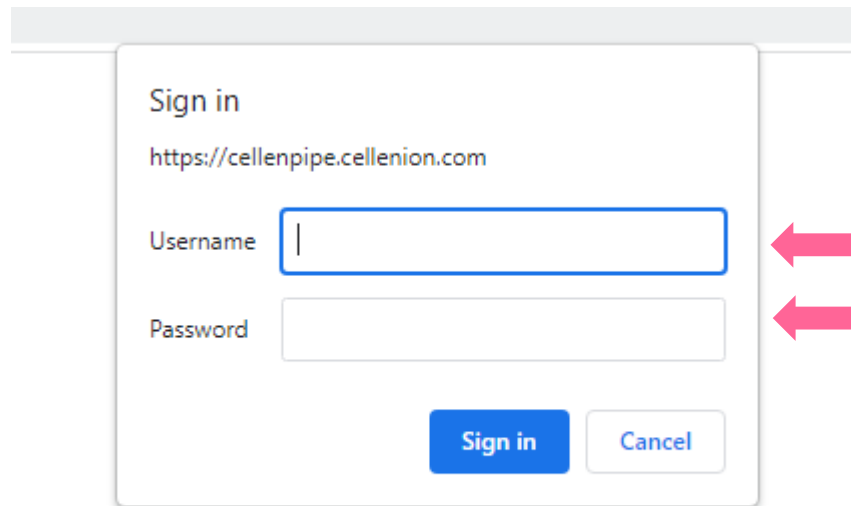
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cellenPIPE
For cellenCHIP 384 3'RNA-seq kit
HOW TO

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.

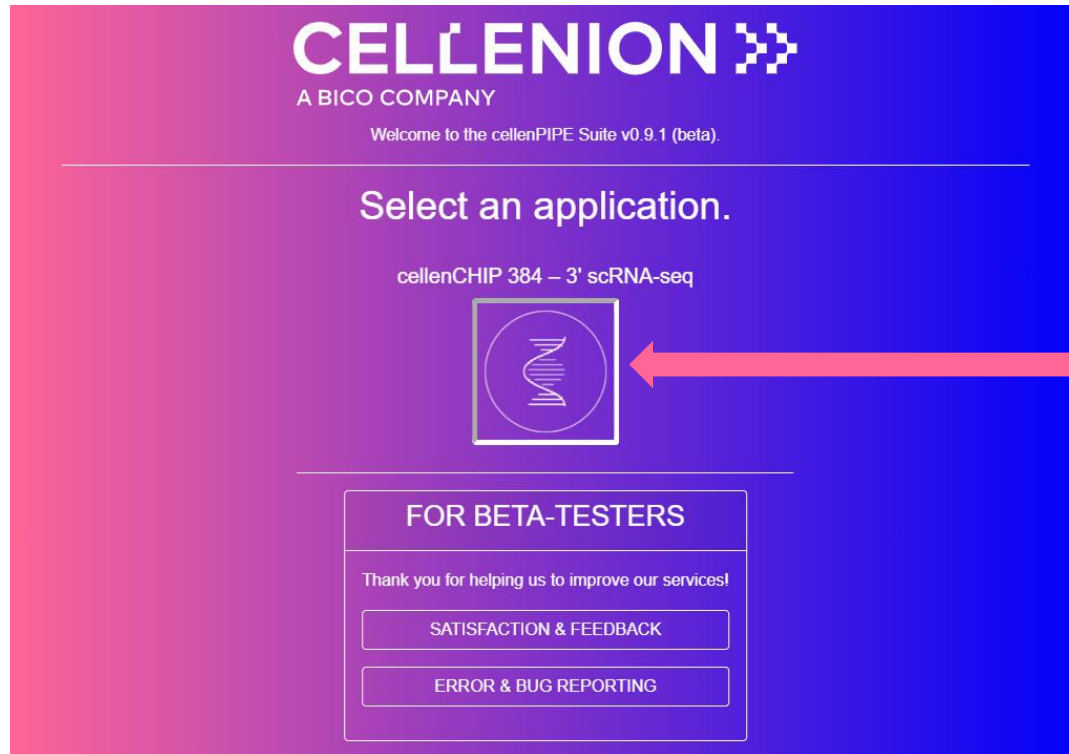
cellenpipe.cellenion.com

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

Dear cellenPIPEadmin, welcome to the cellenPIPE Web App v0.5.1 (beta)

cellenCHIP 384 - 3'scRNA-seq

CREATION OF A NEW RUN

Required: Agreement with the Terms of Services and Privacy Policy ⓘ
By using the cellenPIPE application, I confirm I agree with the related Terms of Services and Privacy Policy.*

STEP 1: Run Name ⓘ
scRNAseq run3 ✓

STEP 2: Species / Reference Genome ⓘ
Human: Homo sapiens / hg38

STEP 3: Infosample (csv; tsv; xls/xlsx) ⓘ
Uploaded: test.xlsx

STEP 4: Read 1 - BC & UMI (fastq.gz) ⓘ
Uploaded: spheror1_5M.fastq.gz

STEP 5: Read 2 - cDNA (fastq.gz) ⓘ
Uploaded: spheror2_5M.fastq.gz

STEP 6: Read Length ⓘ
nt 100 ✓

STEP 7: Storage of the uploaded files ⓘ
☒ 4 weeks of storage (default)
☐ No storage: IMMEDIATE deletion after the cellenPIPE completion

Optional: Email address ⓘ
test@cellenion.com

Launch the cellenPIPE! ⚡

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! ➡

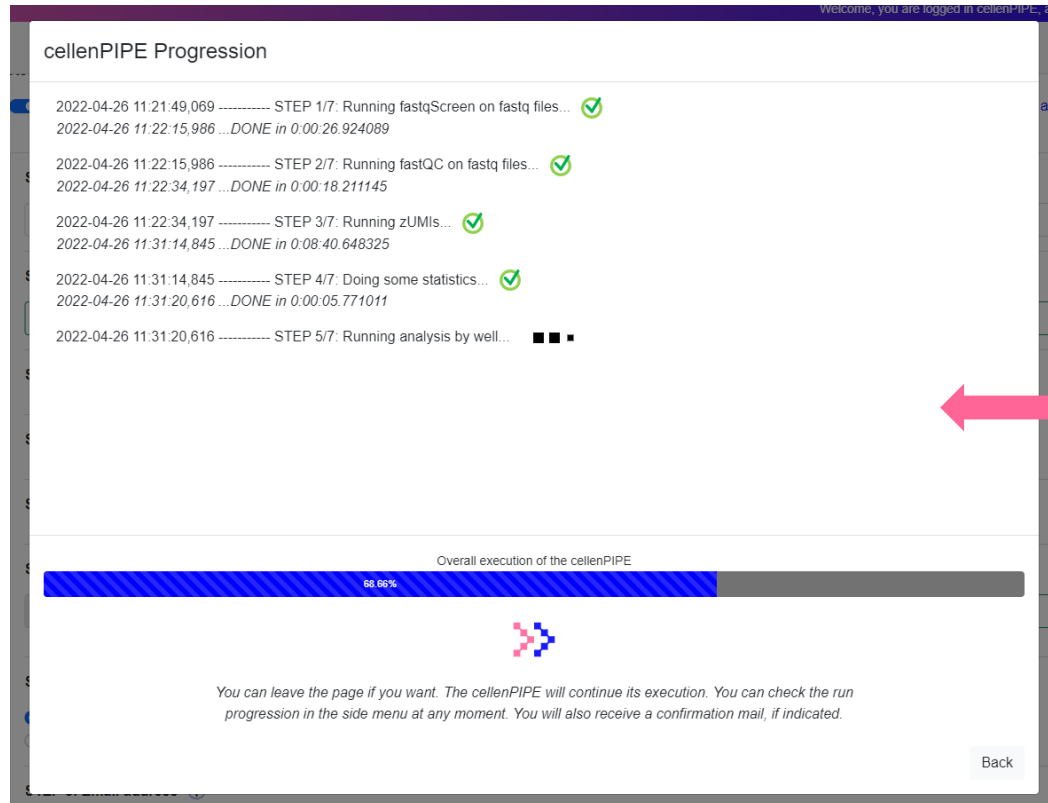
Back

- 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



5. 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 shows the 'CREATION OF A NEW' run process with 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. Email notification when the cellenPIPE run has completed

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:
- 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

See you soon,

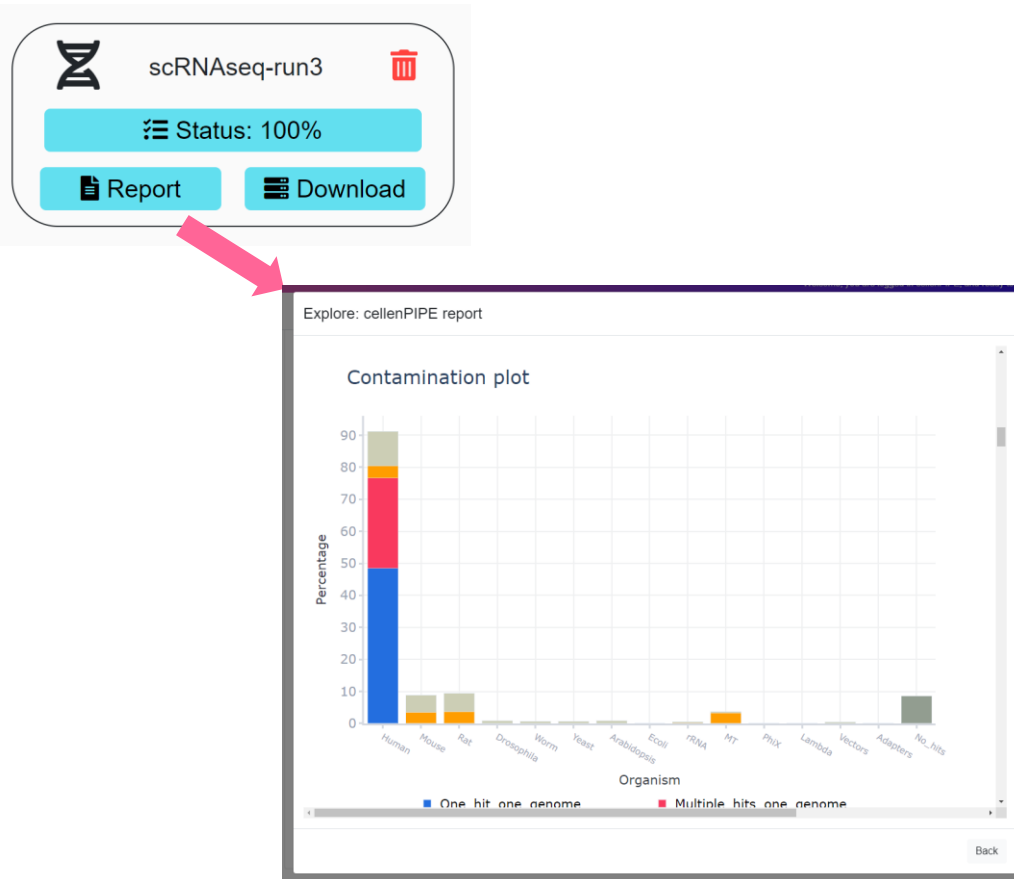
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Warning: this email was sent automatically. Do not reply to this address.

- 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

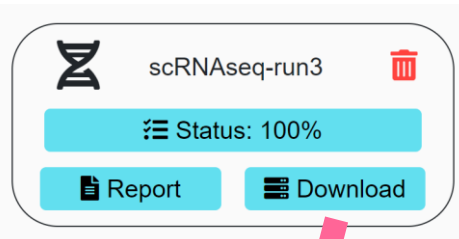


- From the sidebar, manage the cellenPIPE runs
- Explore the cellenPIPE report on your desktop, laptop or tablet computer!

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



8. Download the results



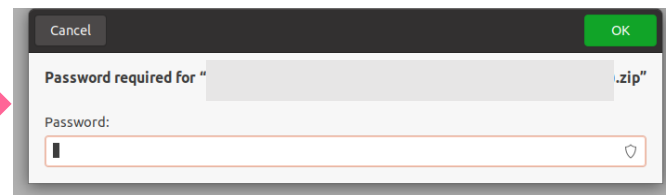
Results: Download

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:

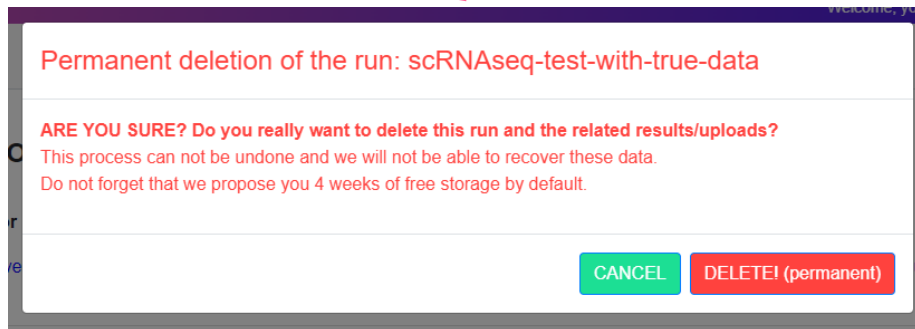
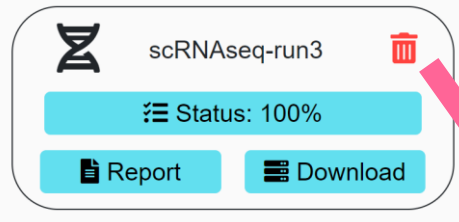
- the cellenPIPE report;
- results regarding quality check: contamination, FastQC, FastQScreen, genebody coverage, reads per cell...
- results regarding gene expression: count matrixes, common genes, clustering and Seurat analysis...
- zUMIs statistics

Back

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



9. Manage the storage of the cellenPIPE results

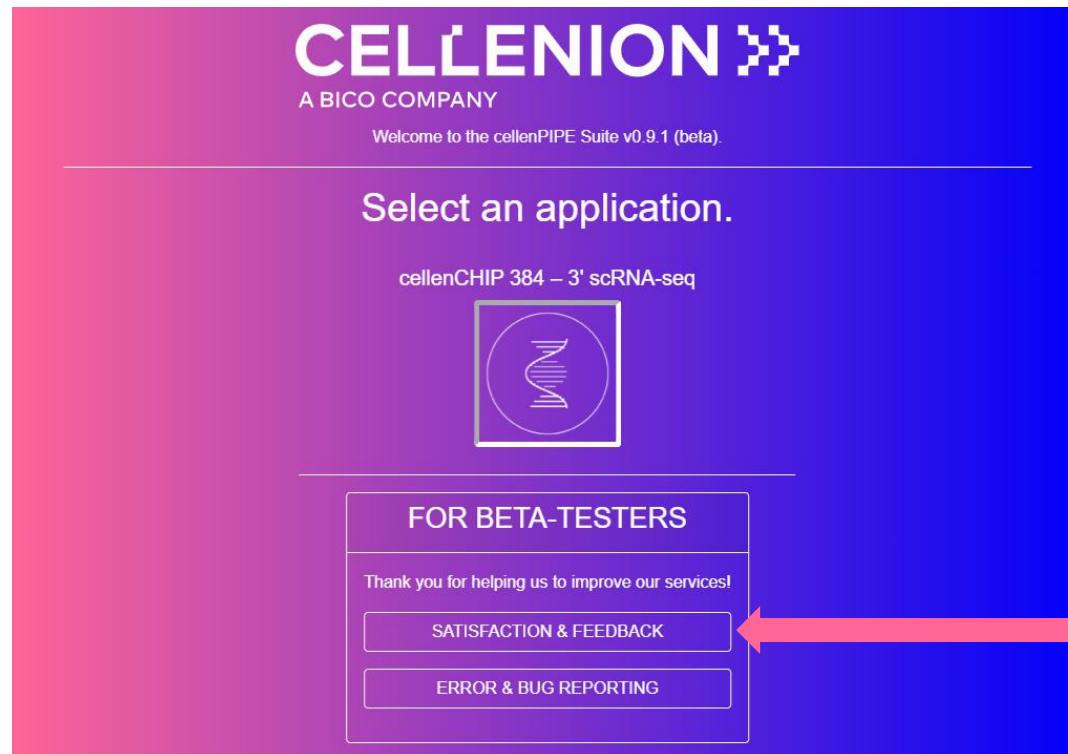


- Permanently delete the results at any moment

Note: the data and results will automatically be deleted after 4 weeks



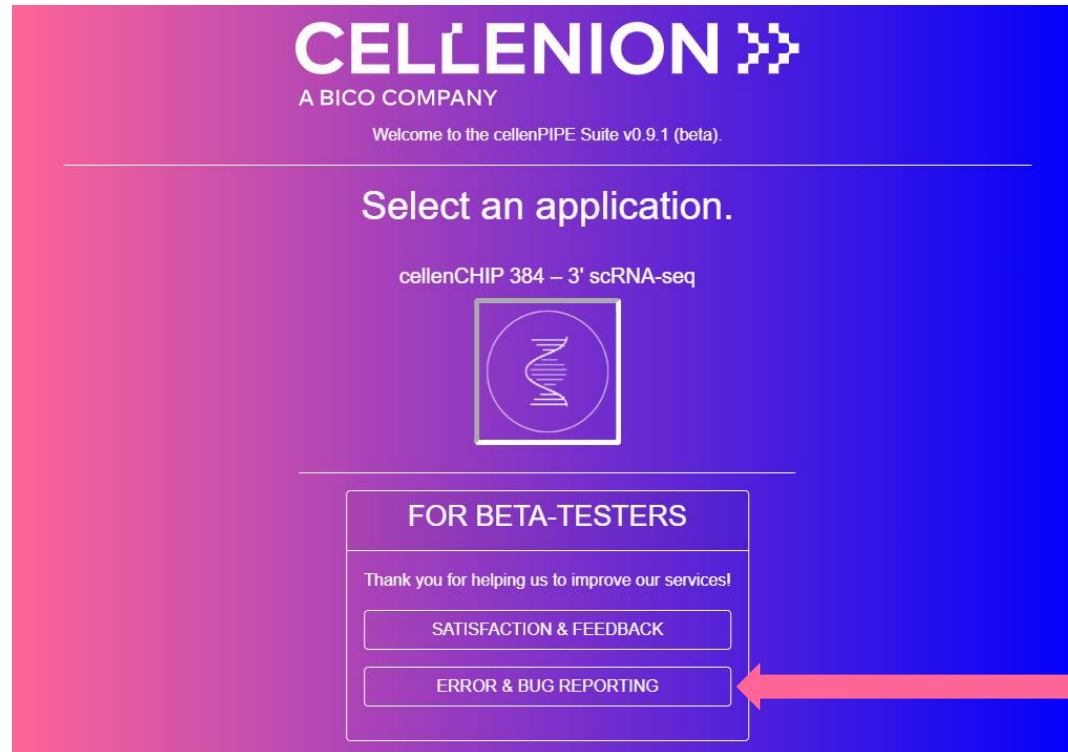
10. Let us know your satisfaction & feedback



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
BIO-CONVERGENCE
REVOLUTION 