

Kangoroo & Lexogen kits

End-to-end solution for your
RNA-Seq experiments.



Kangoroo: Quick step-by-step manual for beginners

Analyze your RNA-Seq data in just a few clicks!

Lexogen's RNA-Seq library prep kits come with a **free voucher code** for data analysis on Kangoroo, our interactive web-based platform for RNA-Seq data analysis. Enjoy our user-friendly complete **workflow for RNA-Seq** experiments - get online and analyze your RNA-Seq data conveniently and quickly on Kangoroo!

Upload your
fastq.gz files

Create a
project

Select
parameters

Run the
analysis

Visualize
your results

Download
your results

Data analysis pipelines

3' seq technologies

- ✓ QuantSeq FWD (with and without UMIs)
- ✓ QuantSeq REV
- ✓ QuantSeq FFPE
- ✓ QuantSeq-Pool*

3' seq single-cell RNA-Seq

- ✓ LUTHOR HD

Whole transcriptome analysis

- ✓ CORALL, including CORALL FFPE

Small RNA analysis

- ✓ miRVEL Profiling
- ✓ miRVEL Discovery

Resources



Check the Video Tutorials



Frequently Asked Questions



Read our LEXICON

Each analysis pipeline includes Differential Gene Expression analysis with DESeq2.

*please make sure that libraries are also demultiplexed for the i1 indices and read our [FAQ](#).

Short Manual for data analysis on Kangooroo

1. Getting started: Registration and Login

Access Kangooroo platform at kangooroo.com.

a) Registration

- Click on "Register" and fill in all required information. To be able to register yourself you will be prompted to agree with the [Terms and Conditions](#).
- Upon registration, you will receive a confirmation email. Verify your registration code matches the email before clicking the verification link.
- You will be notified via email once your account is activated, typically within 1 working day.

b) Login

- If you already have an account, click on "Login" and enter your email address and password.

2. Redeem your voucher code

- With each purchased QuantSeq (FWD, REV, FFPE, Pool), LUTHOR HD, CORALL (standard, FFPE), and miRVel (Profiling, Discovery) kit, you receive a voucher code for free data analysis on Kangooroo.
- Each code allows for the same number of data analysis pipeline runs as the reactions in the kit, including DE analysis. If you need additional quotas, please contact us at sales@lexogen.com to purchase additional codes. Voucher codes are valid for 2 years from the kit (or code) purchase.
- To redeem your code, go to the "Quotas" tab, enter the code and click "Submit". Your quotas will increase. Check your quotas balance any time in the "Quotas" tab in the "Current Quotas Overview" widget.

▶ Video tutorial:

→ [Quotas Voucher Codes](#)

❓ FAQs:

- [What does my voucher code include?](#)
- [How long are my voucher codes valid?](#)

3. Upload your data

Please note that Kangooroo can process only demultiplexed fastq.gz files compressed with gzip software. To upload your files, go to "File Library". You have the option to upload your files either directly from your computer or from your Google Bucket.

ATTENTION: Kangooroo only accepts fully (i5, i7, and - when applicable - i1) demultiplexed FASTQ files. When uploading QuantSeq-Pool files, you must first demultiplex the files for i1 inline barcodes (using Lexogen's [iDemux](#) or an equivalent tool) and then submit the resulting individual FASTQ files for analysis. i1-undemultiplexed files cannot be processed.

ATTENTION: A minimum of **three (3) biological replicates** per condition is required to perform differential gene expression (DGE). If fewer than three replicates are provided, the DGE option in the parameters will be disabled and the analysis will not be executed.

a) Upload from your computer

- Click on "Select files from your computer" and upload the files. You can monitor the upload progress of your files in the "Current Upload" widget.
- Once the upload is complete, you can find the files in the "Uploaded Files" widget of the "File Library" tab.

ATTENTION: Do not close the browser or the tab while the upload is pending! Doing so will cancel the upload.

b) Upload from a Google Bucket

- Click on "use a Google Storage account" and create a Google Connector. To grant us the access rights, make sure to select a Google Account that has permission to access your Bucket. Enter the name of the Google Bucket from which the files will be uploaded.
- Select the files to be uploaded and click "Upload".
- In the "Google Bucket Jobs" widget, you can monitor the upload of your files.

▶ Video tutorial:

→ [File Upload](#)

❓ FAQs:

- [How do I upload my files in the Kangooroo platform?](#)
- [Is there a size limit for the FASTQ file?](#)
- [How do I upload new genome references for my data analysis with Kangooroo?](#)

4. Create a project

- Navigate to "Project" tab and click on the "Create New Project" button.
- Enter a project name and a description.
- Add files and genome/s into "Input-Files" widget.
- Create samples from the files individually or in bulk. Specify a sample name, assign file/s to read/s and set the condition for differential gene expression analysis.

▶ Video tutorial:

- [Project Creation](#)
- [Bulk Sample Creation & Sample Editing](#)
- [Genome file tagging](#)

❓ FAQs:

- [What species are available for my data analysis?](#)
- [How do I fill in my sample file?](#)
- [Can I merge my FASTQ files on Kangooroo?](#)

5. Configure pipeline run

- In the “Project” tab, click on “Configure New Pipeline Run”.
- Enter a name of a pipeline run, select samples, a data analysis pipeline and a relevant genome. Review the parameters in the final summary and initiate the new run by clicking “Start”.
- New entry with the newly setup pipeline run and its details will appear in the “Pipeline Runs” widget. You can monitor the progress of the analysis in the “State” column. Now, you can let Kangooroo analyze the data for you and go back to your experiment or even switch off your computer. Kangooroo will do the data analysis for you.

Video tutorial:

→ [Starting a pipeline run](#)

? FAQs: How is my data analyzed? For...

→ [QuantSeq and LUTHOR HD](#)

→ [CORALL](#)

→ [miRVEL](#)

6. Download your results

- In the “Project” tab, navigate to the “Pipeline Runs” widget and search for the pipeline run you wish to download the results from. In the “Action” column, select “Download Results”.
- Keep in mind that all files, including result files, are stored for 4 weeks only. Please, download your results as soon as the data analysis has finished.

a) Download to your computer

- Click on “Download Bundle to PC” (Please note that trimmed FASTQ files and aligned BAM files will not be included in this download).
- Alternatively, you can choose to download individual result files based on your preferences.

b) Download to Google Bucket

- Select the folders/files you want to download and click on “Download Selected Files to Cloud”.

Video tutorial:

→ [File download](#)

? FAQs:

→ [How do I download my results from the Kangooroo platform?](#)

→ [How long are my data stored in Kangooroo?](#)

→ [What output files do I get with Kangooroo?](#)

7. Inspect your DE data in the interactive visualizations

- Go to the “DE Analysis” tab and select the project and the pipeline run to study.
- There are multiple ways to interact with the plots: select specific datasets, zoom in and out on the chart by holding the SHIFT key, adjust p-values or transparency to reduce overplotting. Highlighting a data point in the table will also highlight the corresponding data point in the chart. Or try to hover over a data point in the chart to view detailed information.

Video tutorial:

→ [Data visualisation](#)

Do you have a question?

Do not hesitate to reach out at support@lexogen.com.



kangooroo.com