



Getting started with nf-core

Last update March 2022

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What is nf-core?

Deploy



Stable pipelines



Centralised
configs



List and update
pipelines



Download
for offline use

Participate



Documentation



Slack workspace



Twitter updates



Hackathons

Develop



Starter template



Code guidelines



CI code linting
and tests



Helper tools

Tutorial



https://nf-co.re/usage/tutorials/nf_core_usage_tutorial

1

Installation

3

Running

2

Listing

4

Troubleshooting



Installation

nf-core tools

nf-core/ tools

```
pip install nf-core
```



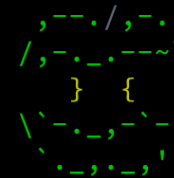
BIOCONDA[®]

```
conda install -c bioconda nf-core
```

nf-core tools

nf-core --help

```

NF-CORE  

```

nf-core/tools version 2.3 - <https://nf-co.re>

Usage: nf-core [OPTIONS] COMMAND [ARGS]...

nf-core/tools provides a set of helper tools for use with nf-core Nextflow pipelines.

It is designed for both end-users running pipelines and also developers creating new pipelines.

Options

--version		Show the version and exit.
--verbose	-v	Print verbose output to the console.
--log-file	-l <filename>	Save a verbose log to a file.
--help	-h	Show this message and exit.

Commands for users

list	List available nf-core pipelines with local info.
launch	Launch a pipeline using a web GUI or command line prompts.
download	Download a pipeline, nf-core/configs and pipeline singularity images.
licences	List software licences for a given workflow.

Commands for developers

create	Create a new pipeline using the nf-core template.
lint	Check pipeline code against nf-core guidelines.
modules	Commands to manage Nextflow DSL2 modules (tool wrappers).
schema	Suite of tools for developers to manage pipeline schema.
bump-version	Update nf-core pipeline version number.
sync	Sync a pipeline TEMPLATE branch with the nf-core template.

A large green arrow pointing to the right, serving as a background for the text.

Listing pipelines

nf-core tools

nf-core list

nf-core/TOOLS version 2.3 - <https://nf-co.re>

Pipeline Name	Stars	Latest Release	Released	Last Pulled	Have latest release?
rnaseq	433	3.6	2 weeks ago	4 months ago	No (v3.4)
viralrecon	61	2.4.1	2 weeks ago	3 weeks ago	No (v2.3.1)
ampliseq	82	2.2.0	1 months ago	—	—
eager	61	2.4.2	2 months ago	—	—
cutandrun	24	1.1	2 months ago	—	—
mhcquant	19	2.2.0	2 months ago	—	—
epitopepre...	18	2.0.0	3 months ago	2 months ago	Yes (v2.0.0)
fetchngs	52	1.5	4 months ago	—	—
nanoseq	68	2.0.1	4 months ago	—	—
mag	81	2.1.1	4 months ago	4 months ago	Yes (v2.1.1)
bacass	33	2.0.0	7 months ago	—	—
airrflow	17	2.0.0	8 months ago	—	—

website

nf-co.re/pipelines

Pipelines

Browse the **62** pipelines that are currently available as part of nf-core.

Available Pipelines

Can you think of another pipeline that would fit in well? [Let us know!](#)

Search keywords

Filter:

Released

33

Under development

24

Archived

5

Sort:

Last Release

Alphabetical

Stars

Display:

Display as blocks

Grid icon

List icon

[nf-core/rnaseq](#) ✓

★ 433

rna rna-seq

[nf-core/viralrecon](#) ✓

★ 61

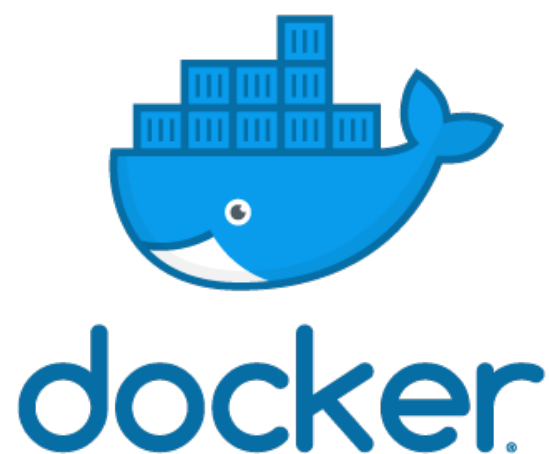
amplicon artic assembly covid-19 covid19 illumina long-read-sequencing

Running pipelines



Software required

nextflow



OR



OR

 CONDA

The Conda logo features a green circular icon with a white geometric pattern, followed by the word "CONDA" in a bold, green, uppercase, sans-serif font.

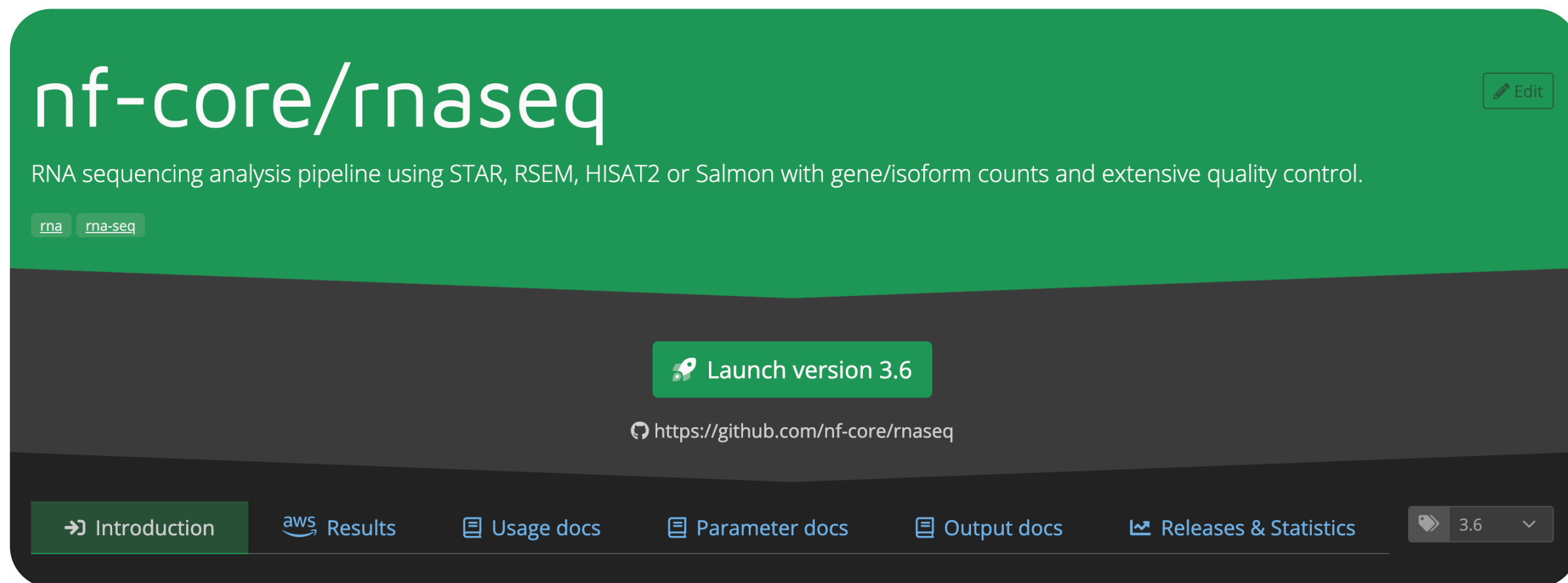
Software required

```
nextflow run nf-core/rnaseq
```

```
-r dev
```

```
nextflow pull nf-core/rnaseq
```

Documentation





The screenshot shows the top section of the nf-core/rnaseq documentation page. It features a green header with the project name 'nf-core/rnaseq' in white, an 'Edit' button, and a description of the pipeline. Below the header is a dark grey section with a 'Launch version 3.6' button and the GitHub repository URL. At the bottom is a navigation bar with links to various documentation sections and a version dropdown menu.

nf-core/rnaseq Edit

RNA sequencing analysis pipeline using STAR, RSEM, HISAT2 or Salmon with gene/isoform counts and extensive quality control.

[rna](#) [rna-seq](#)

 **Launch version 3.6**

 <https://github.com/nf-core/rnaseq>

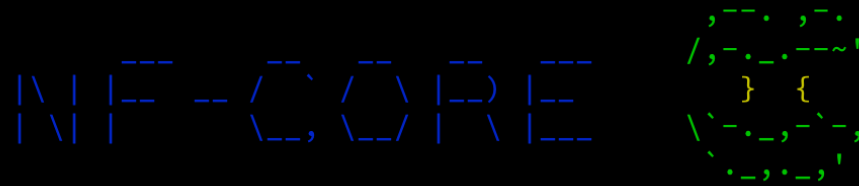
[➔ Introduction](#) [aws Results](#) [Usage docs](#) [Parameter docs](#) [Output docs](#) [Releases & Statistics](#) 3.6 ▼

`https://nf-co.re/PIPELINE-NAME`

Documentation

```
nextflow run nf-core/rnaseq --help
```

```
N E X T F L O W ~ version 21.10.5
Launching `nf-core/rnaseq` [insane_cray] - revision: 964425e3fd [3.4]

-----
NF-CORE 
nf-core/rnaseq v3.4
-----

Typical pipeline command:

    nextflow run nf-core/rnaseq --input samplesheet.csv --genome GRCh37 -profile docker

Input/output options
  --input [string] Path to comma-separated file containing
information about the samples in the experiment.
  --outdir [string] Path to the output directory where the r
results will be saved. [default: ./results]
  --email [string] Email address for completion summary.
  --multiqc_title [string] MultiQC report title. Printed as page he
ader, used for filename if not otherwise specified.
  --save_merged_fastq [boolean] Save FastQ files after merging re-sequen
ced libraries in the results directory.

UMI options
  --with_umi [boolean] Enable UMI-based read deduplication.
  --umitools_extract_method [string] UMI pattern to use. Can be either 'strin
```

Test data

```
nextflow run nf-core/rnaseq -profile test,docker
```

nf-core/  **test-datasets**

Test data

```
nextflow run nf-core/rnaseq -profile test,docker
```

```

Data Type      : Single-End
Strandedness   : None
Trimming       : 5'R1: 0 / 5'R2: 0 / 3'R1: 0 / 3'R2: 0
Aligner        : STAR
Fasta Ref      : https://github.com/nf-core/test-datasets/raw/rnaseq/reference/genome.fa
GTF Annotation : https://github.com/nf-core/test-datasets/raw/rnaseq/reference/genes.gtf
Save prefs     : Ref Genome: No / Trimmed FastQ: No / Alignment intermediates: No
Max Resources  : 6 GB memory, 2 cpus, 2d time per job
Container      : docker - nfcore/rnaseq:1.3
Output dir     : ./results
Launch dir     : /Users/philewels/test
Working dir    : /Users/philewels/test/work
Script dir     : /Users/philewels/.nextflow/assets/nf-core/rnaseq
User           : philewels
Config Profile  : test,docker
Config Description: Minimal test dataset to check pipeline function
[2m-----
[warm up] executor > local
executor > local (14)
[9b/6ab89a] process > get_software_versions [100%] 1 of 1 ✓
[c7/e53c44] process > output_documentation [100%] 1 of 1 ✓
[81/b17819] process > makeBED12 [100%] 1 of 1 ✓
[19/7c5e2e] process > makeSTARindex [100%] 1 of 1 ✓
[53/917cef] process > fastqc [100%] 4 of 4 ✓
[3d/15f1fc] process > trim_galore [100%] 4 of 4 ✓
[2d/9e59bb] process > star [ 0%] 0 of 2
```


Running for real

If you've read the documentation..

```
nextflow run nf-core/rnaseq [...]
```

If not.. (command-line wizard with prompts)

```
nf-core launch rnaseq
```

If you're running offline..

```
nf-core download rnaseq
```

Troubleshooting pipelines

Troubleshoot

- 1 Start small: run pipeline tests first
- 2 Categorise the kind of error
- 3 Read the log, check the work directory
- 4 Check Slack, Google, ask for help
- 5 Report a bug

Exercises 1, 2, 3

Exercise 1 (installation)

- Install nf-core/tools
- Use the help flag to list the available commands

Exercise 2 (listing pipelines)

- Show the `nf-core list` command usage
- List all pipelines
- Sort pipelines alphabetically, then by popularity
- Fetch one of the pipelines using nextflow
- Use `nf-core list` to see if the pipeline you pulled is up to date
- Filter pipelines for any that work with RNA
- Save these pipeline details to a JSON file

Exercise 3 (using pipelines)

- Install software dependencies
- Print the command-line usage for the `nf-core/rnaseq` pipeline
- In a new directory, run the `nf-core/rnaseq` pipeline with the test profile
- Try launching the RNA pipeline using the `nf-core launch` command
- Download the `nf-core/rnaseq` pipeline for offline use using the `nf-core download` command

https://nf-co.re/usage/nf_core_tutorial

Help!



slack

<https://nf-co.re/join>