

# Seqera helps SciLifeLab conduct pioneering research into multi-disciplinary molecular biosciences

## CUSTOMER



<https://www.scilifelab.se/>

## LOCATION

Stockholm, Sweden

## INDUSTRY

Molecular biosciences research

## OBJECTIVES

SciLifeLabs required a comprehensive analysis platform to enable collaborative research in its key focus areas including biomedicine, ecology, and evolution.

## CHALLENGES

- Providing scalable DNA sequencing and analysis
- Complex, diverse pipelines
- Need for reproducible pipelines and faster results
- Need to collaborate and share pipelines and data

## SOLUTION

- Nextflow to manage collaborative workflows
- Open-source nf-core pipelines
- Seqera platform to monitor and share pipelines and seamlessly access multi-cloud capacity

## RESULTS

- Increased productivity
- Improved flexibility
- Enhanced collaboration
- Reduced cloud spending

## Summary

SciLifeLab required a collaborative data analysis platform to provide scalable, reproducible, analysis capabilities across its various facilities. By standardizing on Nextflow and Tower, SciLifeLabs was able to boost productivity, enhance internal collaborations and partnerships with industry, and reduce their monthly cloud spending.

## The business

The Science for Life Laboratory (SciLifeLab), is Sweden's national centre and resource for molecular biosciences. The National Genomics Infrastructure (NGI) division of SciLifeLab provides DNA sequencing and analysis capabilities for research groups across the country. Their vision is for Sweden to be a world-leading nation in life sciences research.

## The challenge

SciLifeLabs provides DNA sequencing and analysis services to its many research groups. This involves supporting diverse, complex pipelines running on-premises and across multiple public clouds.

A key part of SciLifeLab's charter is to foster collaborations with industry, healthcare providers, and domestic and international research organizations.

With growing data volumes, and increased analysis requirements, NGI users were demanding higher throughput analysis and faster time to results. They

also required reproducible and auditable pipeline execution.

To meet these growing requirements, SciLifeLab needed a more scalable research environment to facilitate collaborative research among internal and external partners.

## The solution

SciLifeLab standardized on Nextflow to manage reproducible, collaborative workflows across its various facilities. Key researchers also began contributing to the nf-core project, a community effort to build a curated set of Nextflow-based analysis pipelines across various omics disciplines.

By standardizing on Nextflow, it became easier for scientists at SciLifeLab to share pipelines and research with colleagues and other institutions.

As use of Nextflow became more widespread, several groups began to use Tower, providing users with an intuitive interface to launch pipelines, access datasets and reports, and collaborate on research. Tower's collaborative features made it easier for researchers to partner with external organizations and tap compute resources from various public clouds.

## Results

### INCREASED PRODUCTIVITY

By using fast, high-throughput Nextflow pipelines that maximize parallelism, SciLifeLab has been able to boost their research productivity. Pipelines now run faster and more efficiently, and Tower has made it much easier for non-technical users to launch and monitor data analysis pipelines.

### IMPROVED FLEXIBILITY

Nextflow's extensive library of executors have enabled SciLifeLab to run their analysis workflows across multiple compute environments with virtually no changes to pipeline code. This has provided added

flexibility, enabling researchers to run pipelines on any cloud platform or on-premises cluster environments depending on policy and resource availability.

Improved pipeline portability has also made it easier for SciLifeLab to share pipelines internally and with international partners.

**"Nextflow provides SciLifeLab with automated, reliable, and easy to run data pipelines that yield reproducible results for our team. Nextflow Tower provides us with huge flexibility to deploy genomics workloads anywhere."**

**Phil Ewels, Head of bioinformatics development - NGI Stockholm.**

### ENHANCED COLLABORATION

With Tower, researchers can easily share pipelines, datasets, and compute environments using Tower's intuitive web interface. Features such as Tower Labels have made it easier to search prior runs and find results. Users can even invite external researchers to selected Tower workspaces, facilitating joint research activities with remote users and external organizations.

### LOWER CLOUD SPENDING

By deploying pipeline tasks on scalable cloud infrastructure and optimizing instance selection, Nextflow and Tower have enabled SciLifeLabs to boost analysis capacity while reducing their monthly cloud spend.

Features such as automated resource provisioning and disposal mean that researchers only pay for the resources they use. Pipeline caching and resume functionality allow researchers to resume failed pipelines from where they left off, avoiding unnecessary computation and further reducing resource-related costs.

### LEARN MORE

To learn more, visit [www.seqera.io](https://www.seqera.io)