



## Bioinformatics training and education

Building your bioinformatics expertise  
through advanced education

## Learning Objectives

- To understand DNA replication
- To explain the importance of replication
- To identify similarities and differences bet. PCR and replication



# Introduction

Our portfolio of professional training courses is your pathway to analysing and managing genomic data using bioinformatics tools. The courses are built for all experience levels, including researchers beginning their journey in bioinformatics, seasoned bioinformaticians expanding into new applications, and biomedical professionals who want to advance their careers. Explore training options in our world-class facilities, at your lab, or online.

The bioinformatics professional services team has many years of experience working in the areas of genomics and next-generation sequencing (NGS). Our instructors are trained to deliver in-depth, customised training courses, work with small groups, and adapt the content to reflect the immediate needs of course attendees.

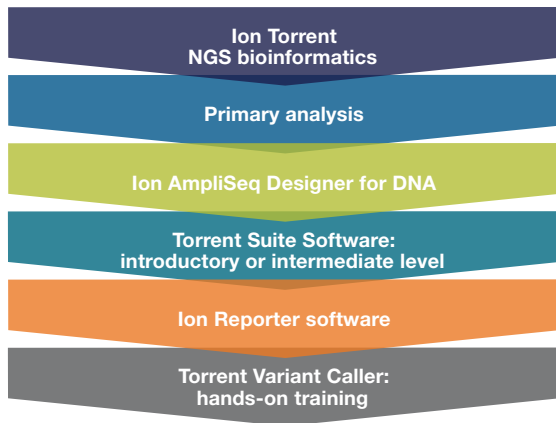
This catalogue is designed to help you select courses to create and personalise your own training program. Four “tracks” have been created around focus areas. Training tracks are recommended, but each class can be purchased independently.



# Training tracks in four key focus areas

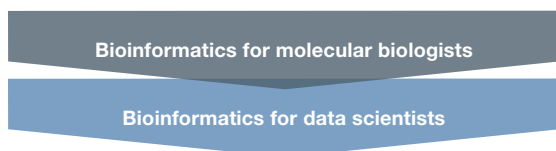
## Targeted DNA sequencing track, Ion Torrent system | 30 hours

From gene panel design through processing and downstream analysis, this track will help develop your expertise in the theory and practice of targeted sequencing. This track begins with an overview of NGS and the Ion Torrent™ data analysis workflow. With interactive modules and sample projects, we move into the core software packages for targeted panel design (Ion AmpliSeq™ Designer), primary analysis (Torrent Suite™ Software), and secondary analysis (Ion Reporter™ software) within the Ion Torrent™ software ecosystem. The track finishes with an in-depth training on the topic of variant calling, one of the hallmarks of a bioinformatician's toolbox.



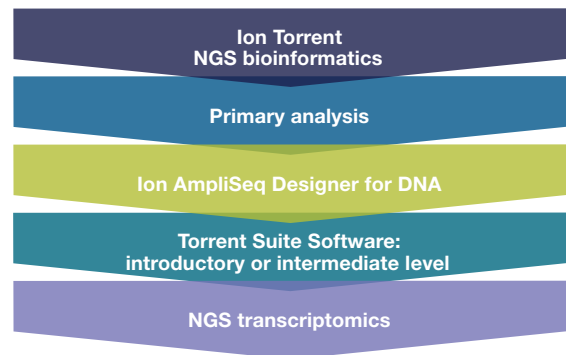
## Career development track for scientists, platform independent | 72 hours

This track provides the foundational steps into bioinformatics, for those with a molecular biology background. You will learn to leverage command-line operations using the Linux™ operating system (OS), leverage relational database (MySQL™) queries, and begin scripting with R, Python™ or Perl™ programming languages. While working on actual datasets and real-life troubleshooting cases, this track will finish with a deeper exposure to the more powerful bioinformatics tools in Linux, Python, and R systems.



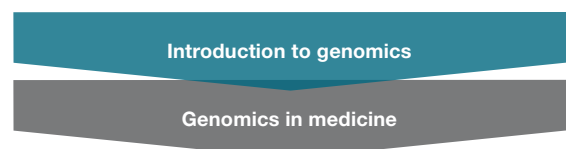
## RNA-Seq and transcriptomics track, Ion Torrent system | 26 hours

From experimental design through processing and downstream analysis, this track will help develop your expertise in the theory and practice of RNA-Seq and transcriptomics. This track begins with an overview of NGS and the Ion Torrent data analysis workflow. With interactive modules and sample projects, we move into the core software packages for RNA panel design (Ion AmpliSeq Designer), primary analysis, and secondary analysis plug-ins (Ion Reporter software within the Ion Torrent software ecosystem). The track ends with an in-depth training on the topics of RNA data preprocessing, quality control (QC), isoform detection, and differential expression featuring open-source tools.



## Career development track for medical practitioners, platform independent | 24 hours

This track provides the foundational steps into genomics for medical practitioners seeking to advance their education in this cutting-edge field. You will gain an understanding of how the human reference genome was built, learn the meaning of genetic variation and how it applies to disease biology, and receive an introduction to NGS and its applications. Application areas in this track focus on the latest advances in genomics as applied to cancer research, the impact of genomics on personalised medicine, an overview of various technologies used in genomics research, and the opportunities and challenges faced in each area of genomics.



# Select the course format and difficulty level that's right for you

These courses are offered in the following three formats:



Online interactive



Customer site



On-site (Thermo Fisher Scientific)

## Courses have been rated with skill levels as follows:

First time

Intermediate

Beginner

Advanced

## Course descriptions, Ion Torrent system

### Ion Torrent NGS bioinformatics | 8 hours



This course will walk you through the key concepts of NGS bioinformatics and data analysis with the Ion Torrent platform.

We will begin the course by reviewing the key points in a sequencing workflow and learn how they can affect the final data. Next, we will review the main approaches to analyse NGS data and discuss the most commonly used metrics that describe these data sets. We will then explain the file types used to store sequence data and variant information, and how to visualize these data with an IGV viewer.

The second half of the course provides an overview of the Ion Torrent data analysis workflow. We will begin with a discussion about primer design for gene panels with the Ion AmpliSeq Designer and will then transition to learning how sequencing data are processed on the Torrent Suite Software, understanding the specific types of files generated by this software, and learning how to manage these data sets. The course covers TVC and is completed with a review of the data analysis workflow implemented by the Ion Reporter Software.

#### Learning objectives

- Understand the main concepts of NGS bioinformatics
- Understand commonly used file formats and visualisation techniques of NGS data

- Build a solid foundation of the Ion Torrent software and data analysis workflow

#### Who should attend?

The course is meant for scientists, biologists, and medical professionals just beginning or planning to step into NGS with the Ion Torrent platform.

### Primary analysis | 3 hours



This course covers data generation and processing workflows on the Ion Torrent sequencers. All steps are covered in detail, beginning from raw data acquisition on the chip and finishing with the final, processed sequence data (BAM file).

#### Learning objectives

- Understand how data are generated using the Ion Torrent technology
- Understand how basic quality metrics are produced
- Understand the data processing steps and how to adjust the data generation workflow for troubleshooting or special application purposes

#### Who should attend?

Ion Torrent users interested in understanding how the sequencing data are generated using the Ion Torrent platforms.

### Ion AmpliSeq Designer for DNA or RNA | 3 hours



This course is about the Ion AmpliSeq™ technology and the Ion AmpliSeq Designer. We will review the technology and the ready-to-use gene panels that are already available on the Ion AmpliSeq platform, and use the Ion AmpliSeq Designer functionality to design custom DNA or RNA panels from scratch. You will also learn to assess the newly designed custom panel, check the coverage achieved, verify the primer placement, and work with the files generated by the designer.

#### Learning objectives

- Understand Ion AmpliSeq technology
- Review available ready-to-use panels
- Use the Ion AmpliSeq Designer to design a custom DNA or RNA gene panel

#### Who should attend?

Ion Torrent users familiar with the Ion Torrent platform who are interested in working with gene panels designed with the Ion AmpliSeq technology. Attending this training is recommended before beginning to work with the Ion AmpliSeq technology, in particular, to clarify some aspects of custom panel design.

### Torrent Suite Software, basics | 1 hour



This course provides an overview of the main features of the Torrent Suite Software—planning a simple sequencing run, tracking the sequencing progress, and finding the sequencing run results.

#### Learning objectives

- Understand how to plan a simple sequencing run
- Understand how to monitor the main quality metrics
- Understand how to perform basic assessment of the sequencing results

#### Who should attend?

First-time or novice users of the Ion Torrent systems interested in a quick introduction to the Torrent Suite Software.

### Torrent Suite Software, advanced basics | 3 hours



In this course, you will learn how the Torrent Suite Software is set up on the Torrent Server. This course provides a detailed look of all the features of the software and tools available to obtain most of your sequencing results. You will learn how to plan and prepare run templates for specific applications, and how to adjust advanced parameter settings. You will also learn how to work with the run reports and examine every metric to understand the insights on data quality and success of the sequencing process.

#### Learning objectives

- Understand the Torrent Suite Software
- Prepare a run template and plan a run
- Assess run reports and quality of sequencing results
- Troubleshoot data analysis results on the Torrent Suite Software
- Configure the Torrent Suite Software for your needs

#### Who should attend?

Ion Torrent users with no previous experience with the Torrent Suite Software and those interested in a software-based course with hands-on experience with the Torrent Suite Software or the Ion Torrent systems; or for existing users who would like a refresher course and more in-depth, hands-on training with the Torrent Suite Software.

### Ion Reporter Software, basics | 1 hour



An introduction to the Ion Reporter Software and how to analyse the data acquired from the Ion Torrent systems. The session will include a lecture and a live demonstration.

#### Learning objective

- Use the Ion Reporter Software to analyse variant data

#### Who should attend?

First-time or novice users of the Ion Torrent system interested in an introduction to the Ion Reporter Software.

## Ion Reporter Software, advanced basics | 3 hours



In this course, you will learn, in depth, about capabilities of the Ion Reporter Software. You will learn about available data analysis workflows and ways to create a custom workflow that best fits your data analysis needs. We will practice running data analysis on samples imported from Ion Torrent sequencers, analyse results, apply filters, and visualize variant data. We will review advanced configurations of the software, create custom annotations, and adjust workflow parameters.

### Learning objectives

- Fully understand Ion Reporter Software capabilities
- Modify and create analysis workflows
- Analyse variant data with help from annotations and filters
- Customise workflows with additional annotation sets and adjusted parameters

### Who should attend?

Ion Torrent users with no previous experience with the Ion Reporter Software, and those interested in a data and software-based course with hands-on experience with the Ion Reporter Software; or Ion Torrent users who are familiar with the Ion Reporter Software, but would like to better understand the Ion Reporter Software functionality and learn how to use the software for their data.

## Torrent Variant Caller | 3 hours



This course explains how the Torrent Variant Caller (TVC) identifies variants in the Ion Torrent data and how to adjust the algorithm in order to get the best results for your application. Participants will review the types of variants that can be detected, the meaning of various quality metrics, and the specifics of hotspot versus novel variants. Additionally, attendees will learn the main parameters used in the algorithm, how to adjust them to optimise variant calling for the desired application, and how to identify and troubleshoot the missed variants.

### Learning objectives

- Understand how variants are called by TVC
- Differentiate between hotspot and novel variants
- Adjust main parameters to achieve the best sensitivity and specificity

### Who should attend?

Ion Torrent users interested in understanding how variants are called by TVC and the main approaches to troubleshoot variant detection.

## Torrent Variant Caller, hands-on training | 16 hours



This advanced course covers TVC in depth. You will learn to work with the TVC, interpret the output of the algorithm, configure parameters, and troubleshoot difficult cases.

The course is heavily hands on with more than 30 exercises. The majority of the course time is spent running the TVC on sample datasets, assessing the results, adjusting the parameters, and discussing example cases of variant detection situations that may occur during analysis of real-time Ion Torrent data.

### Learning objectives

- Work with the main file formats that are used in the TVC
- Create and modify the target regions and hotspot files
- Interpret the variants directly in the output variant call format (VCF) files
- Examine the variants visually with integrative genomic viewer (IGV)
- Understand the input and output data sets of the TVC
- Understand the main TVC parameters and adjust for particular situations
- Identify reasons why some variants are not called and troubleshoot such cases

### Who should attend?

This course is for researchers who have some experience with Ion Torrent data analysis, and an intermediate understanding of the primary analysis workflow and the Torrent Suite Software. The course includes TVC runs and parameter adjustments; however, command-line or programming skills are not required. So, this course is well suited for biologists and clinicians who want to learn about the TVC by practice.

## Data management | 1 hour



This course provides a detailed overview of the data management tools available on the Ion Torrent Suite System. Course topics include: data file categories—sizes, storage capacities, off-board storage solutions, and manual data management; automatic data and disk management—deleting, archiving, exporting, and importing data and protocols for backup.

### Learning objectives

- Manage data types produced by the Ion Torrent system
- Understand your requirements for data management
- Review options and best practices for your data storage and backup

### Who should attend?

This course is for Ion Torrent users who are responsible for managing a Torrent Server and ensuring sufficient space is available on the Torrent Server to handle incoming sequence data.

## Ion Torrent system and data analysis

### overview | 1 hour



This course offers a general overview of library and template preparation, and instrument hardware operations, while providing training on the data analysis workflow and applications of the Ion Torrent™ platforms. At the end of this training, first-time or novice users of the Ion Torrent systems (Ion S5™, Ion PGM™, or Ion Proton™ instruments) will have an understanding of the Ion Torrent system data analysis workflow.

### Learning objectives

- Gain a general understanding of the whole-genome sequencing and data analysis workflow with Ion Torrent platforms

### Who should attend?

First-time or novice users of the Ion S5, PGM, or Proton instruments interested in a high-level overview of the Ion Torrent systems and data analysis workflow.



## NGS transcriptomics | 16 hours



High-throughput sequencing has brought new ways of mapping and quantifying transcriptomes (the set of RNA molecules, including mRNA, rRNA, tRNA, and other noncoding RNA in the cell) beyond microarrays. This course will combine open-source solutions widely used in the field (e.g., Bioconductor, TopHat, Bowtie, SAMtools packages), featuring plug-ins developed for the Ion Torrent software. Training will begin with a basic introduction to RNA-Seq, and will then follow up with data preprocessing and QC, before moving to isoform, differential expression, and alternative expression.

### Learning objectives

- Understand common data formats and standards
- Process NGS data and evaluate QC
- Use relevant tools to run basic analyses (gene quantification, differential expression, etc.), plot, and visualise results

### Who should attend?

This is a course for Ion Torrent users who are using or planning to work with RNA-Seq data. Participants are expected to have a basic understanding of molecular biology (DNA, RNA, gene expression, and PCR).

## Torrent Suite Software application programming interface (API) and plug-in development | 8 hours



This hands-on course is about the Torrent Suite Software representational state (REST)/API and plug-in development. We will familiarize the attendees with the Torrent Suite Software REST/API and its use. The participants will also learn the main steps in developing plug-ins for the Torrent Suite Software and build a basic functional plug-in.

### Learning objectives

- Understand how to use the Torrent Suite Software API resources
- Build a basic Torrent Suite Software plug-in

### Who should attend?

Ion Torrent users who want to understand the Torrent Suite Software API and learn how to develop Torrent Suite Software plug-ins. We recommend that the attendees be proficient with Python and have a general understanding of web development.

First time

Beginner

Intermediate

Advanced

Online interactive

Customer site

On-site (Thermo Fisher Scientific)



## Platform-independent courses

### **Bioinformatics for molecular biologists | 32 hours**



This hands-on course includes an introduction to the Linux OS, MySQL database, and Python (or Perl) programming languages. First, you will learn the basics of the Linux OS and learn how to work on the command line. Then, the focus will shift to relational databases and use of MySQL. You will learn the basic database operations—creating tables, inserting data, and constructing queries. Next, you will learn the main concepts of programming and focus on the Python (or Perl) programming language. In the last part of the course, you will combine all the knowledge to make a script that transforms variant data into a format that can be loaded into the relational database.

### **Learning objectives**

- Become familiar with the Linux OS, relational databases, and programming
- Learn basic command-line skills
- Learn basic database operation skills
- Learn how to write simple scripts

### **Who should attend?**

This course is not limited to Ion Torrent users, and is open to cross-platform data analysis users. Molecular biologists and bench scientists with an interest to go beyond the graphic interface will enjoy this course.

## Introduction to genomics | 16 hours



Clinical researchers interested in genomic technologies will be introduced to state-of-the-art methods and resources through interactive learning and discussion. No specialised knowledge in the fields of genomics and bioinformatics is necessary. Self-reflective learning will be encouraged throughout the different sessions with the use of surveys and demonstrations of results in real time, and the introduction of debate topics covered in the lectures.

### Learning objectives

- Identify the latest advances in genomics applied to cancer research, and understand the challenges to secure effective interventions based on this new area of scientific investigation
- Understand the power and the challenges associated with these technologies and data—how the information can provide a better understanding of disease biology and facilitate informed clinical decisions
- Develop a basic understanding of the current tools available to assist you with genomic-based medicine

### Who should attend?

This course is meant for biomedical practitioners planning to interpret and analyse genomic data, and designed for those wanting to develop a conceptual understanding of the recent developments in genomic medicine.

## Genomics in medicine | 8 hours



The course will be comprised of lectures, panel discussions, question and answer sessions, and will focus on how modern DNA-sequencing technologies are impacting clinical medicine.

### Learning objectives

- Overview NGS platforms and the associated sequencing workflows
- Gain knowledge on the applications of NGS in biomedical research
- Understand the implementation of technologies in explaining disease biology and influencing clinical decisions
- Find out the impact to clinical research of leveraging the power of NGS

- Understand the current limitations of NGS in clinical practice (with some illustrative examples of analysis workflows) alongside other bioinformatics considerations about these types of data
- Present examples of genomics-guided medicine practices (gene panels in oncology)
- Identify the latest advances in genomics applied to cancer research, and the challenges to secure effective interventions based on this new area of scientific investigation

### Who should attend?

Healthcare professionals and medical students interested in learning more about this application area.

## Bioinformatics for data scientists | 32 hours



A balanced combination of lectures and practical sessions will allow you to apply newly acquired skills to a science problem using real data. This course enables participants to gain confidence in their abilities to implement bioinformatics solutions independently. Over four days, this course will show you powerful tools for data exploration and visualization using the R language and bash script.

### Learning objectives

- Understand Linux power scripting (awk, xargs commands)
- Understand fundamentals of data management (assessing data integrity by checksum)
- Handle genomic ranges (BED, SAM, BAM, etc.)
- Explore data and visualise using the R language

### Who should attend?

This course is not limited to Ion Torrent users, and is open to any researchers dealing with large datasets—data scientists and biologists who want to understand the language of bioinformatics and explore their data with an interest to go beyond the graphic interface. Explore the open-source world associated with bioinformatics with the help of our experts.

## Linux for biologists | 8 hours



This course will introduce you to the main concepts and most commonly used commands for the life sciences including file manipulation, pipe facilities, editors, process monitoring, and basic file- and text-searching utilities.

You will be provided with a virtual environment on a USB data stick with real-life datasets, containing the pipelines created throughout the course for use in the lab.

### Learning objectives

- Learn to use the Linux OS to search, retrieve, and manipulate files and directories
- Use remote sessions to connect to servers through the network

### Who should attend?

Researchers who want to learn the Linux OS and feel comfortable working with the command line for analysing large datasets.

## Relational databases—MySQL for scientists | 8 hours



MySQL is an open-source, relational database management system and is both highly reliable and easy to use. It is the open-source database of choice for many biology projects. In this course, you will learn the basics of SQL statements using the MySQL database, and gain practical experience with writing SQL statements using the MySQL client program.

### Learning objectives

- Understand the fundamentals of relational databases to obtain sufficient knowledge for retrieving data from databases
- Perform simple queries
- Create a simple database populated from VCF that is obtained from NGS runs

### Who should attend?

Researchers who want to manipulate data with a widely used relational database management system such as MySQL. Participants should be comfortable working on the command line (e.g., after attending our Linux I course and/or programming in Python).

## Programming in Perl for scientists | 8 hours



Perl (practical extraction and reporting language) is a programming language written by and for working programmers. Perl is easy to use, efficient, and is the language of choice for common gateway interface (CGI) scripting and web development. It features BioPerl, a very useful collection of modules for bioinformatics applications (converting formats, manipulating sequences and alignments).

In this course, you will learn the basic commands in Perl to enable you to manipulate files and write scripts, allowing you to explore the open-source world with our experts.

### Learning objectives

- Understand the fundamentals of Perl
- Write simple Perl scripts to manage data

### Who should attend?

Researchers who want to manipulate data with the widely used language, Perl. Participants should be comfortable working on the command line (e.g., after attending our Linux I course and/or programming in Python).

## Support resources



We are expanding our catalog. If your topic of interest is not listed, please contact us. We may create new courses upon demand.

## Programming in Python for scientists | 8 hours



Python is a high-level programming language often used as a scripting language. Extremely readable with very clear syntax, it has been adopted by bioinformaticians worldwide, making the most of the Biopython project—a set of tools for bioinformatics applications (converting formats, manipulating sequences, and alignments).

In this course, you will learn the basic commands in Python, which will enable you to manipulate files and write scripts, and enable you to explore the open-source world with our experts.

### Learning objectives

- Understand the fundamentals of Python
- Write simple Python scripts to manage data

### Who should attend?

This course is designed for researchers who want to manipulate data with a widely used language, Python. Participants should be comfortable working on the command line (e.g., after attending our Linux I course).

## R programming for bioinformatics— Bioconductor I | 8 hours



R is an integrated software environment for data manipulation, statistical analysis, and graphical display. Bioconductor is a collection of R packages for the analysis of high-throughput genomic data.

In this course, you will learn the basic commands in R, which will enable you to manipulate files and write scripts, and will enable you to explore the open-source world with our experts.

### Learning objectives

- Understand the fundamentals of R and/or Bioconductor
- Write simple scripts to manage data

### Who should attend?

Researchers who want to manipulate data with the widely used language, R and/or Bioconductor. Participants should be comfortable working on the command line (e.g., after attending our Linux I course).

### Benefits of small-group, platform-independent courses

- Courses in this section are limited to 5 participants in order to enhance the learning experience and to minimize the participant-to-instructor ratio.
- Real-life datasets used in interactive sections facilitate knowledge retention.
- Participants will be provided with a virtual environment on a USB stick with the pipelines and scripts created during the course in order to continue learning after returning to the lab.

First time

Beginner

Intermediate

Advanced

Online interactive

Customer site

On-site (Thermo Fisher Scientific)



## What researchers are saying about our training

“Thank you very much for the excellent course—I had a great time and really learned a lot. I have now sketched out a plan to do our analysis and am now really looking forward to implementing it.”

–Dr. Nicholas Wagner, Clinical Molecular Geneticist,  
Laboratoriumsmedizin Köln, Germany

“This was my first dive into programming and bioinformatics, and the level was just perfect. The course gave me the basic background and fundamental resources that I needed to understand how to manipulate large datasets. I think Alessandro (the trainer) was key, making the course entertaining even when there was a lot of things to learn in just a few days. The course was very relevant to my current job is helping me process the large datasets obtained after sequencing our marine microbial samples.”

–Dr. Alejandra Calvo-Díaz, Postdoctoral Researcher,  
Spanish Oceanographic Institute, Spain

### **Do you need help managing or analyzing your laboratory data?**

The global team of over 40 staff members can offer help beyond training, including:

#### **IT infrastructure consulting**

- Rely on us for server management, data migration, and data architecture setup
- Get your lab integrated with Thermo Fisher Cloud, on-premises backup, and LIMS/LIS

#### **Bioinformatics consulting**

- Speed up your sequencing workflow, from experimental design to selection of analysis tools
- Develop a custom pipeline and plug-ins to help analyse your experiments



### Courses can be purchased individually or in track format

Training courses can be scheduled either online or at one of our customer experience centers by registering through our training portal at [learn.thermofisher.com/europe/bioinformatics](http://learn.thermofisher.com/europe/bioinformatics)

### Save on training and IT services

By combining your training course with consultancy and IT services, you'll save on costs. Along with a discount, annual plans with prepurchased hours also include a visit to your institute.

For more information or to request a quote, please contact our training team at [learn-europe@thermofisher.com](mailto:learn-europe@thermofisher.com). You'll be placed in contact with our bioinformatics specialists to help you tailor your individual training track to meet your requirements.

### Ordering information

Service	Duration	Cat. No.
Bioinformatics Consultancy Plan	20-hour maximum	ZGPCSCIONBFX
Bioinformatics Consultancy Plan	10-hour maximum	ZGPCSCBFX10
Web training	1 hour	4477116
On-site training	Half day (minimum 2)	4477125
On-site training	Full day	4485734

Find out more at [thermofisher.com/biofxservices](http://thermofisher.com/biofxservices)

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