

EXATYPE: Sanger HIV

A platform for HIV drug-resistance reporting

INTRODUCTION

HIV genotyping workflow: Three-step process



1

Sample prep



2

Sequencing



3

Analysis

ThermoFisher
SCIENTIFIC

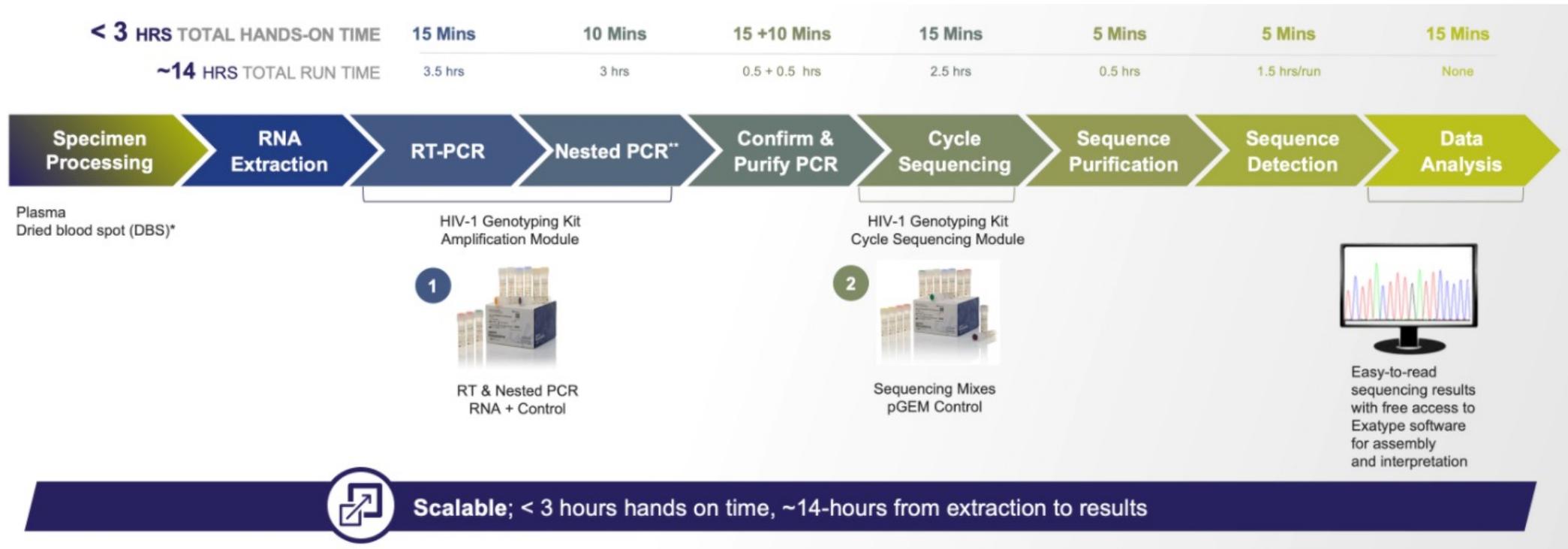


INTRODUCTION

End-to-end solution



Free analysis for
Thermo customers

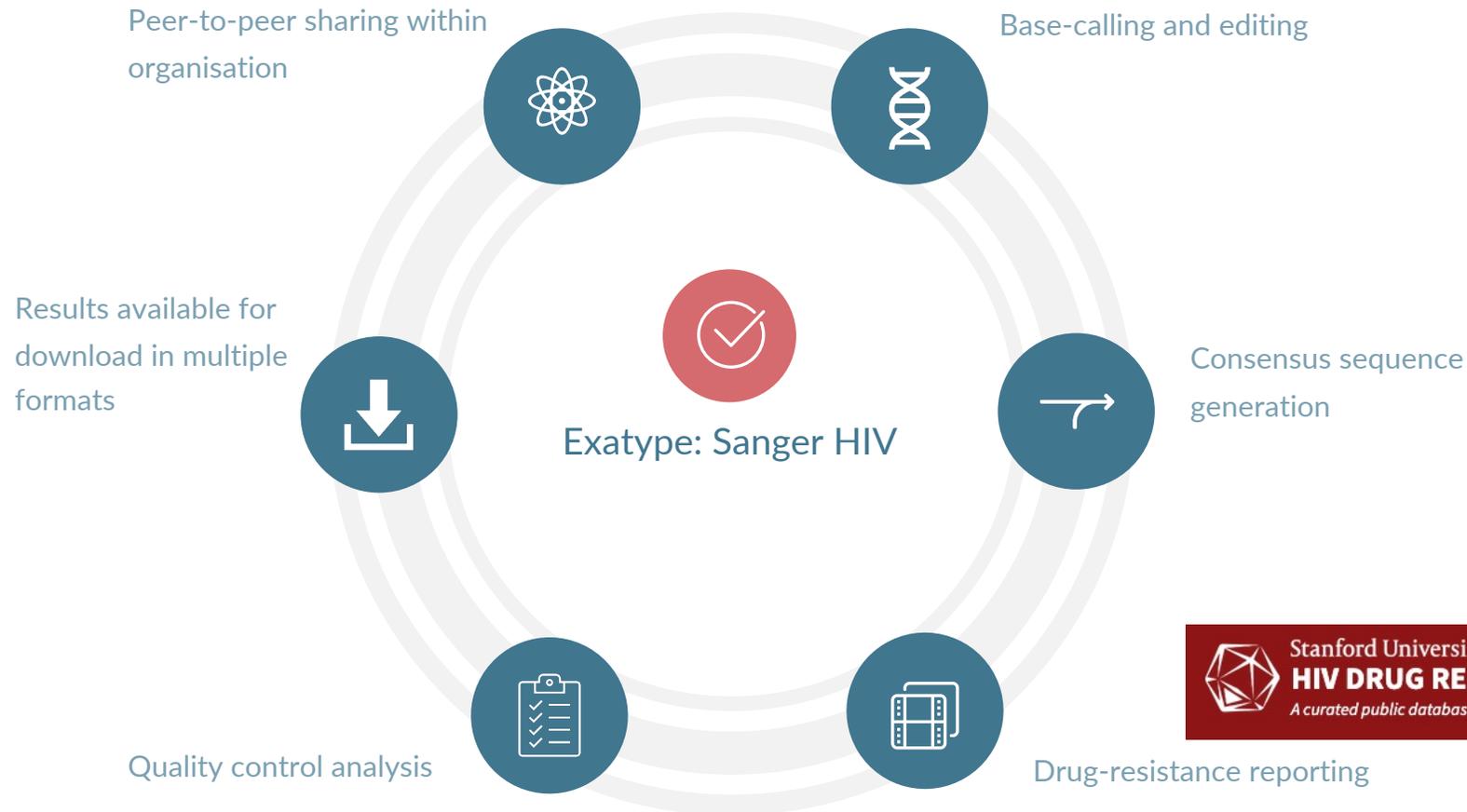


OUT-OF-THE-BOX SOLUTION

HIV drug-resistance analysis

<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC3372133/>

RECall



<https://hivdb.stanford.edu/>

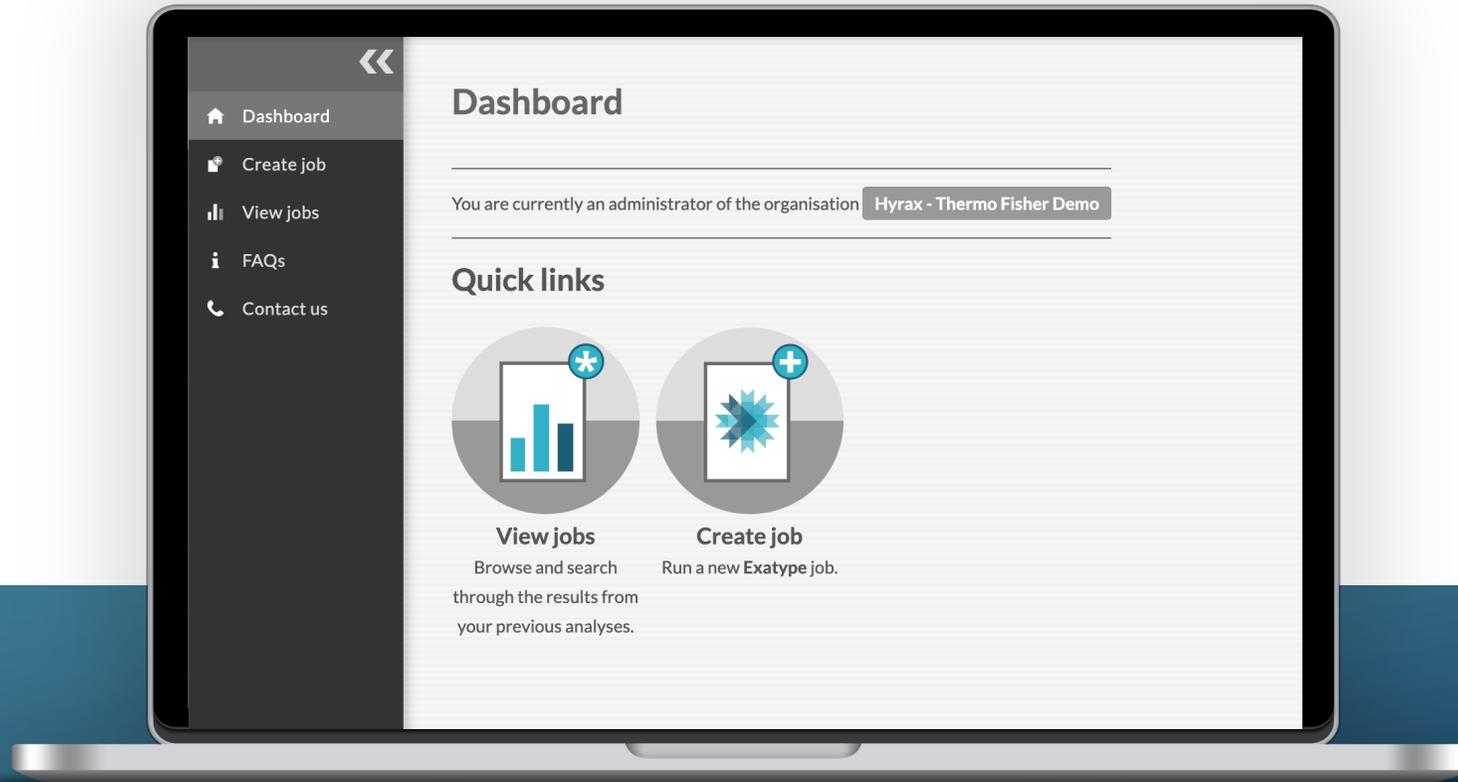
 Stanford University
HIV DRUG RESISTANCE DATABASE
A curated public database to represent, store and analyze HIV drug resistance data.



<https://www.who.int/publications/i/item/978-92-4-000987-5>

DEMO RUN

sanger.exatype.com



PLATFORM FEATURES

Standardisation

Consistent reports and results through automated processes



Automatic data-upload

Hands-off data processing through integration with sequencer software



Secure

Cloud-based analysis
Follow HIPAA and GDPR protocols



Scalable throughput

API for high-throughput users
Upload as many plates/samples as required



HOW TO FIND US AND GET IN TOUCH



EXATYPETM
SANGER

sanger.exatype.com



Information

sanger@hyraxbio.com



Support

support@hyraxbio.com



Partnerships

commercial@hyraxbio.com



Website

hyraxbio.com



Landing page

analyzehiv.com | analyzehiv.com

THANK YOU

KEY BENEFITS



Gold-standard approach for resistance interpretation

- Local installation of the Stanford¹ HIVDB; guaranteed updates within one week of Stanford updates



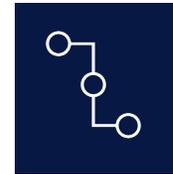
Comprehensive quality-control reporting

- Positive and negative control reports are produced for sequencing quality control
- Surveillance monitoring included through genetic distance, APOBEC and atypical mutation reporting, as recommended by the WHO best practices³



Industry recognised base-calling software

- RECall², University of British Columbia software, is used for base-calling
- No need for separate software that requires regular updates



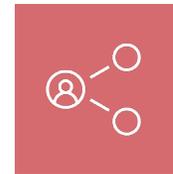
Integration with LIMS

- Push to LIMS system using .tsv/.json file output (additional cost)



Easy-to-use

- Intuitive interface with minimum hands-on time



Peer-to-peer sharing

- Multiple users under a single organisation

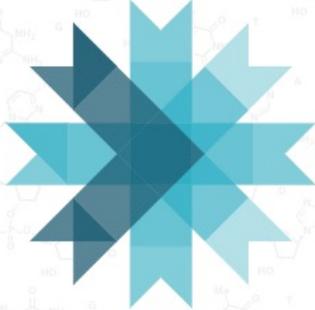
¹<https://hivdb.stanford.edu/>

²<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC3372133/>

³<https://www.who.int/publications/i/item/978-92-4-000987-5>

PRODUCT SCREENSHOTS

<https://sanger.exatype.com/>



EXATYPE™
SANGER

Automated HIV drug-resistance reporting of Sanger-sequencing data

[CREATE AN ACCOUNT](#)

To learn more about Exatype read our [FAQs](#) or contact us at info@hyraxbio.com for any queries you may have.
The Exatype service was developed by Hyrax Biosciences. Visit [our website](#) to learn more about our work.

*Login [here](#) to access data analysed before June 2021

PRODUCT SCREENSHOTS

<https://sanger.exatype.com/signup>

Sign up

Name
Danny Smith ✓

Email
dsmith@youremail.com ✓

Password (Minimum 8 characters)
•••••••• ✓

Confirm password
••••••••| * ✓

Do you agree to the terms and conditions located [here](#)?
 I agree ✓
 I do not agree

I'm not a robot  reCAPTCHA
Privacy - Terms

CREATE MY ACCOUNT

Already have an account? [Log in here.](#)

PRODUCT SCREENSHOTS

Your email account

Please confirm your email External Inbox x Print Share

 **accounts@exatype.com** via amazonses.com 11:57 (0 minutes ago) Star Reply More
to natasha+TF2 ▾



Thank you for signing up to use Exatype.

Please click the button below to confirm your email address. You will then receive an email once your account has been activated by us, at which point you will be able to run samples.

CONFIRM



EXATYPE™

Email confirmed

You may now log in to your Exatype account.

PRODUCT SCREENSHOTS

sanger.exatype.com/login

Login

Email *

Password *

LOG IN

[Forgot your password?](#)

*Login [here](#) to access data analysed before June 2021

PRODUCT SCREENSHOTS

The first time you log in

Create organisation

Please specify the organisation or laboratory where you are running the HIV Drug Resistance (HIV DR) tests.

Organisation name *

Country *

What HIV DR assay do you use? *

I agree that the results from my organisation's data can be used anonymously for surveillance purposes. See our [privacy policy](#) for further information.

Yes
 No

I agree that my organisation's uploaded data can be used anonymously for research purposes other than surveillance. See our [privacy policy](#) for further information.

Yes
 No

CREATE ORGANISATION

PRODUCT SCREENSHOTS

<https://sanger.exatype.com/dashboard>

The screenshot displays the Exatype Sanger dashboard. At the top left is the logo for EXATYPE SANGER. Below it is a dark sidebar with navigation options: Dashboard (selected), Create job, View jobs, FAQs, and Contact us. The main content area is titled 'Dashboard' and includes a user role indicator: 'You are currently an administrator of the organisation Hyrax - Thermo Fisher Demo'. Underneath, there is a 'Quick links' section with two prominent buttons: 'View jobs' (with a bar chart icon) and 'Create job' (with a starburst icon). Each button has a brief description of its function.

EXATYPE
SANGER

Dashboard

You are currently an administrator of the organisation **Hyrax - Thermo Fisher Demo**

Quick links

View jobs
Browse and search through the results from your previous analyses.

Create job
Run a new Exatype job.

PRODUCT SCREENSHOTS

Create a new analysis

The image displays two screenshots of a web application interface for creating a new analysis job. The interface is divided into a dark sidebar on the left and a main content area on the right.

Left Screenshot:

- Sidebar:** Contains navigation links: Dashboard, **Create job** (highlighted with a blue circle), View jobs, FAQs, and Contact us.
- Header:** Includes a breadcrumb trail: Dashboard > Job details > Select data > Filename format > Sample details > Review & submit.
- Main Content:**
 - Job name:** A text input field containing "HIV (Sanger)", which is highlighted with a red box.
 - Which assay are you running?:** A radio button selection area with two options: "Thermo Fisher HIV-1 Genotyping Kit (without Integrase)" and "Thermo Fisher HIV-1 Genotyping Kit (with Integrase)".
 - More options:** A dropdown menu icon is circled in blue. A blue arrow points from this icon to the right screenshot.
 - Next Step:** A "NEXT >" button is visible at the bottom.

Right Screenshot:

- Sidebar:** The same navigation links as the left screenshot.
- Header:** The same breadcrumb trail as the left screenshot.
- Main Content:**
 - Job name:** The same "HIV (Sanger)" text, highlighted with a red box.
 - Which assay are you running?:** The same radio button selection area.
 - More options:** The dropdown is expanded, showing three options for "Evaluation of processed specimens (sequence files):":
 - Review all sequences **i**
 - Review sequences flagged as FAILED and Manual Review by RECall **i** ✓
 - Review only those sequences flagged for Manual Review by RECall **i**
 - Next Step:** A "NEXT >" button is visible at the bottom.

PRODUCT SCREENSHOTS

Create a new analysis

Dashboard | Job details | Select data | Filename format | Sample details | Review & submit

Create job

View jobs

FAQs

Contact us

Create a new job **HIV (Sanger)**

Job details

Job name

 *

Which assay are you running?

Thermo Fisher HIV-1 Genotyping Kit (without Integrase)

Thermo Fisher HIV-1 Genotyping Kit (with Integrase) *

More options ^

Evaluation of processed specimens (sequence files):

Review all sequences ⓘ

Review sequences f

Review only those s

RECall-labelled PASSED (green), FAILED (red), and Manual Review (orange) sequences

NEXT >

PRODUCT SCREENSHOTS

Create a new analysis

The screenshot shows a web interface for creating a new analysis. The top navigation bar includes a back arrow, a 'Job details' tab, and a 'Select data' tab (which is active). Other tabs are 'Filename format', 'Gene region names', 'Sample details', and 'Review & submit'. A left sidebar contains links for 'Dashboard', 'Create job', 'View jobs', 'FAQs', and 'Contact us'. The main content area is titled 'Create a new job' with 'HIV (Sanger)' entered in a text field. Below this is the 'Select data' section, which features a 'Plate 1' input field with a green checkmark and a trash icon. A message states: 'Please select the data files that you would like to analyse. Only ab1 files are accepted.' Below this message is a teal button labeled 'SELECT YOUR AB1 FILES' and a dashed box containing a grey button labeled 'DROP YOUR AB1 FILES HERE'. To the right of the main content is a circular button with a plus sign and the text 'Add a plate'. At the bottom of the main content area are two buttons: '< PREV' and 'NEXT >'. A footer warning reads: '⚠ For Research Use Only. Not for use in diagnostic procedures.'

PRODUCT SCREENSHOTS

Create a new analysis

The screenshot shows a web browser window with the URL analysehiv.com in the address bar. The page is divided into two main columns. The left column, titled "Key benefits", lists three features, each with a checkmark icon: "Gold-standard approach for resistance interpretation", "Industry recognised base-calling software", and "Comprehensive quality-control reporting". The right column, titled "Further information", contains three sections: "Example dataset" (with a "Download zip" link), "Example of a full report" (with a "Download PDF" link), and "Presentation" (with a "Download PDF" link). A red circle highlights the "Example dataset" section in the right column.

analysehiv.com

Key benefits

Hyrax Biosciences is dedicated to providing solutions that meet customer and partner needs.

- Gold-standard approach for resistance interpretation**
Local installation of the Stanford^[1] HIVDB
- Industry recognised base-calling software**
RECall^[2], University of British Columbia software, is used for base-calling. No need for separate software that requires regular updates
- Comprehensive quality-control reporting**
Positive and negative control reports are produced for sequencing quality control Surveillance monitoring included through genetic distance, APOBEC and atypical mutation reporting, as recommended by the WHO best practices^[3]

Further information

Example dataset
Dataset including sample files for the protease, reverse transcriptase and integrase gene regions.

[Download zip](#)

Example of a full report
A full report with sample summary, quality control summary, and sample-specific reports.

[Download PDF](#)

Presentation
Overview of the Exatype: HIV Sanger workflow.

[Download PDF](#)

PRODUCT SCREENSHOTS

Create a new analysis

The screenshot shows a web application interface for creating a new analysis job. The top navigation bar includes tabs for "Job details", "Select data", "Filename format", "Gene region names", "Sample details", and "Review & submit". The "Select data" tab is currently active. On the left, a sidebar menu contains "Dashboard", "Create job", "View jobs", "FAQs", and "Contact us". The main content area is titled "Create a new job" and features a red-bordered input field containing "HIV (Sanger)". To the right of this field are three buttons: "< PREV", "NEXT >", and "CANCEL JOB". Below the job title, the section "Select data" is visible. It includes a text input field with "Plate 1" and a green checkmark, a trash icon, and the text "72 ab1s selected for plate 'Plate 1'". Below this are two buttons: "ADD MORE FILES" and "REMOVE ALL FILES". A large circular button with a plus sign and the text "Add a plate" is positioned to the right of the file list. The file list contains the following items:

- A4_SeqF2_IN_test.ab1
- D1N_SeqF1_IN_text.ab1
- A3_SeqF3_PRRT_text.ab1
- V1cntrl_F3_PRRT_cntrl.ab1
- A1_SeqR2_PRRT_text.ab1
- A2_SeqF3_PRRT_text.ab1
- S2_D_PRRT_text.ab1
- A2_SeqR2_PRRT_text.ab1
- V1cntrl_R1_PRRT_cntrl.ab1
- A1_SeqF3_PRRT_text.ab1
- A1_SeqR12_IN_text.ab1

PRODUCT SCREENSHOTS

Create a new analysis

Job details | Select data | **Filename format** | Gene region names | Sample details | Review & submit

Dashboard | Create job | View jobs | FAQs | Contact us

Create a new job **HIV (Sanger)** < PREV NEXT > CANCEL JOB

Filename format

Sample Primer Gene Region Other + NEW FIELD

Filename format preview

⚠ The filename settings that are currently applied can't work with 72 of the files listed below. Please adjust your settings until this message disappears.

The identifiers in your filenames are coloured according to the specifications provided. Please confirm that the sample name, primer, gene region, and plate name/number (if applicable) identifiers are shown correctly below.

⚠	A4	-	SeqF2_IN_test	-	-	.ab1
⚠	D1N	-	SeqF1_IN_test	-	-	.ab1
⚠	A3	-	SeqF3_PRRT_text	-	-	.ab1
⚠	V1cntrl	-	F3_PRRT_cntrl	-	-	.ab1
⚠	A1	-	SeqR2_PRRT_text	-	-	.ab1
⚠	A2	-	SeqF3_PRRT_text	-	-	.ab1
⚠	S2	-	D_PRRT_text	-	-	.ab1
⚠	A2	-	SeqR2_PRRT_text	-	-	.ab1

PRODUCT SCREENSHOTS

Create a new analysis

Job details | Select data | **Filename format** | Gene region names | Sample details | Review & submit

Dashboard | Create job | View jobs | FAQs | Contact us

Create a new job **HIV (Sanger)** < PREV NEXT > CANCEL JOB

Filename format

Sample Primer Gene Region Other + NEW FIELD

Filename format preview

The identifiers in your filenames are colored according to the specifications provided. Please confirm that the sample name, primer, gene region, and plate name/number (if applicable) identifiers are shown correctly below.

A4	SeqF2	IN	text	.ab1
D1N	SeqF1	IN	text	.ab1
A3	SeqF3	PRRT	text	.ab1
V1cntrl	F3	PRRT	cntrl	.ab1
A1	SeqR2	PRRT	text	.ab1
A2	SeqF3	PRRT	text	.ab1
S2	D	PRRT	text	.ab1
A2	SeqR2	PRRT	text	.ab1
V1cntrl	R1	PRRT	cntrl	.ab1
A1	SeqF3	PRRT	text	.ab1

PRODUCT SCREENSHOTS

Create a new analysis

The screenshot shows a web interface for creating a new job. The top navigation bar includes tabs for 'Job details', 'Select data', 'Filename format', 'Gene region names' (which is the active tab), 'Sample details', and 'Review & submit'. On the left, a sidebar contains links for 'Dashboard', 'Create job', 'View jobs', 'FAQs', and 'Contact us'. The main content area is titled 'Create a new job' with 'HIV (Sanger)' entered in a text field. To the right of this field are three buttons: '< PREV', 'NEXT >', and 'CANCEL JOB'. Below the title is the section 'Gene region names'. A box titled 'Confirm gene regions' contains the text: 'Your filenames contain the following gene region identifiers: IN PRRT . Please confirm that your identifiers and the gene regions of the assay have been matched correctly below.' There are two rows of confirmation: the first row shows 'IN' in an orange box, a dropdown menu with 'Integrase' selected, and a green checkmark; the second row shows 'PRRT' in an orange box, a dropdown menu with 'Protease-Reverse Transcriptase' selected, and a green checkmark. At the bottom of the main content area are two buttons: '< PREV' and 'NEXT >'.

Job details | Select data | Filename format | **Gene region names** | Sample details | Review & submit

Dashboard | Create job | View jobs | FAQs | Contact us

Create a new job **HIV (Sanger)** < PREV NEXT > CANCEL JOB

Gene region names

Confirm gene regions

Your filenames contain the following gene region identifiers: **IN** **PRRT** .
Please confirm that your identifiers and the gene regions of the assay have been matched correctly below.

IN Integrase ✓

PRRT Protease-Reverse Transcriptase ✓

< PREV NEXT >

PRODUCT SCREENSHOTS

Create a new analysis

Job details | Select data | Filename format | Gene region names | **Sample details** | Review & submit

Dashboard | Create job | View jobs | FAQs | Contact us

Create a new job **HIV (Sanger)**

< PREV | NEXT > | CANCEL JOB

Sample details

Please select your **positive** and **negative** controls, or submit the job without controls.

Plate	Sample	Gene region	Positive	Negative
Plate 1	A1	IN	<input type="checkbox"/>	<input type="checkbox"/>
	A1	PRRT	<input type="checkbox"/>	<input type="checkbox"/>
	A2	IN	<input type="checkbox"/>	<input type="checkbox"/>
	A2	PRRT	<input type="checkbox"/>	<input type="checkbox"/>
	A3	IN	<input type="checkbox"/>	<input type="checkbox"/>
	A3	PRRT	<input type="checkbox"/>	<input type="checkbox"/>
	A4	IN	<input type="checkbox"/>	<input type="checkbox"/>
	A4	PRRT	<input type="checkbox"/>	<input type="checkbox"/>
	D1N	IN	<input type="checkbox"/>	<input type="checkbox"/>
	D1N	PRRT	<input type="checkbox"/>	<input type="checkbox"/>
	S1	PRRT	<input type="checkbox"/>	<input type="checkbox"/>
	S2	PRRT	<input type="checkbox"/>	<input type="checkbox"/>
	V1ctrl	IN	<input checked="" type="checkbox"/>	<input type="checkbox"/>
	V1ctrl	PRRT	<input checked="" type="checkbox"/>	<input type="checkbox"/>

< PREV | NEXT >

PRODUCT SCREENSHOTS

Create a new analysis

Job details | Select data | Filename format | Gene region names | Sample details | **Review & submit**

Dashboard | Create job | View jobs | FAQs | Contact us

Create a new job **HIV (Sanger)** [< PREV](#) [CANCEL JOB](#)

Review & submit

Overview

Job name: Demo Product: HIV (Sanger)
Sequencing platform: Sanger Number of samples: 8
Assay: Thermo Fisher HIV-1 Genotyping Kit (with Integrase) Total data quantity: 15.47 MB

[CLICK HERE TO UPLOAD 72 FILES AND RUN YOUR ANALYSIS](#) 0/72 UPLOADED

Sample	Region	Plate	Primer	File name	Size	File status			
A1	IN	Plate 1	SeqR12	A1_SeqR12_IN_text.ab1	0%	226 KB	Selected		
			SeqR11	A1_SeqR11_IN_text.ab1	0%	278 KB	Selected		
			SeqF11	A1_SeqF11_IN_text.ab1	0%	272 KB	Selected		
			SeqF12	A1_SeqF12_IN_text.ab1	0%	252 KB	Selected		
	PRRT	Plate 1	SeqR2	A1_SeqR2_PRRT_text.ab1	0%	244 KB	Selected		
			SeqF3	A1_SeqF3_PRRT_text.ab1	0%	207 KB	Selected		
			SeqR1	A1_SeqR1_PRRT_text.ab1	0%	272 KB	Selected		
			SeqF1	A1_SeqF1_PRRT_text.ab1	0%	272 KB	Selected		
			SeqR3	A1_SeqR3_PRRT_text.ab1	0%	244 KB	Selected		
			SeqF2	A1_SeqF2_PRRT_text.ab1	0%	245 KB	Selected		
			IN	Plate 1	SeqR12	A2_SeqR12_IN_text.ab1	0%	227 KB	Selected
					SeqR11	A2_SeqR11_IN_text.ab1	0%	273 KB	Selected
SeqF11	A2_SeqF11_IN_text.ab1	0%			272 KB	Selected			

PRODUCT SCREENSHOTS

Create a new analysis

Job details | Select data | Filename format | Gene region names | Sample details | **Review & submit**

Dashboard | Create job | View jobs | FAQs | Contact us

Create a new job **HIV (Sanger)** < PREV CANCEL JOB

Review & submit

Overview

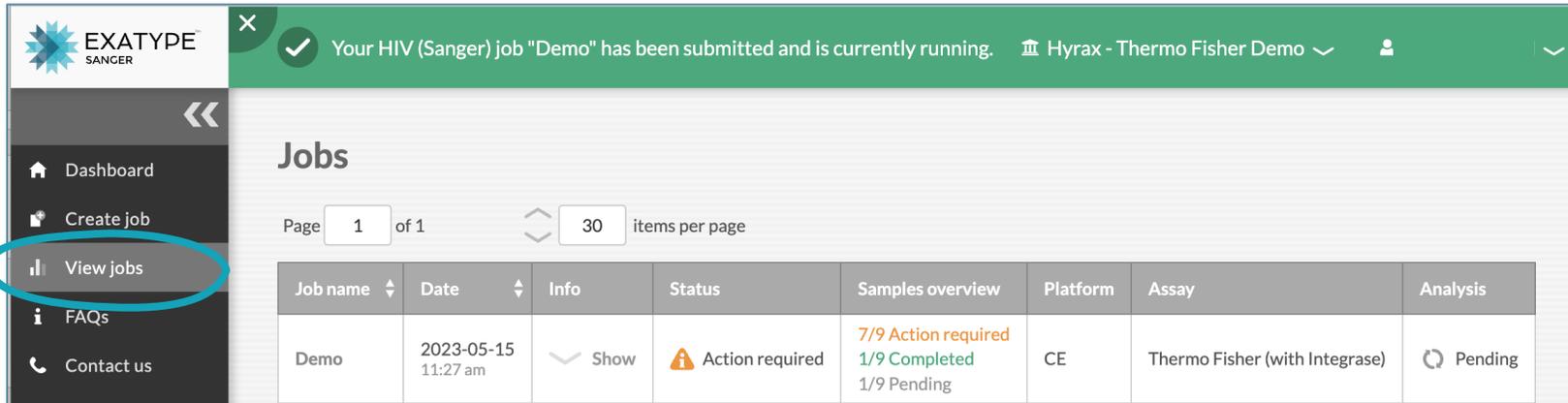
Job name: Demo Product: HIV (Sanger)
Sequencing platform: Sanger Number of samples: 8
Assay: Thermo Fisher HIV-1 Genotyping Kit (with Integrase) Total data quantity: 15.47 MB

5/72 files 3.25 MB/15.47 MB 21%

Sample	Region	Plate	Primer	File name	Size	File status			
A1	IN	Plate 1	SeqR12	A1_SeqR12_IN_text.ab1	43%	226 KB	Uploading		
			SeqR11	A1_SeqR11_IN_text.ab1	0%	278 KB	Queued		
			SeqF11	A1_SeqF11_IN_text.ab1	0%	272 KB	Queued		
			SeqF12	A1_SeqF12_IN_text.ab1	0%	252 KB	Queued		
	PRRT	Plate 1	SeqR2	A1_SeqR2_PRRT_text.ab1	100%	244 KB	Uploaded		
			SeqF3	A1_SeqF3_PRRT_text.ab1	94%	207 KB	Uploading		
			SeqR1	A1_SeqR1_PRRT_text.ab1	30%	272 KB	Uploading		
			SeqF1	A1_SeqF1_PRRT_text.ab1	0%	272 KB	Queued		
			SeqR3	A1_SeqR3_PRRT_text.ab1	0%	244 KB	Queued		
			SeqF2	A1_SeqF2_PRRT_text.ab1	0%	245 KB	Queued		
			IN	Plate 1	SeqR12	A2_SeqR12_IN_text.ab1	43%	227 KB	Uploading
					SeqR11	A2_SeqR11_IN_text.ab1	0%	273 KB	Queued
SeqF11	A2_SeqF11_IN_text.ab1	0%			272 KB	Queued			

PRODUCT SCREENSHOTS

Create a new analysis



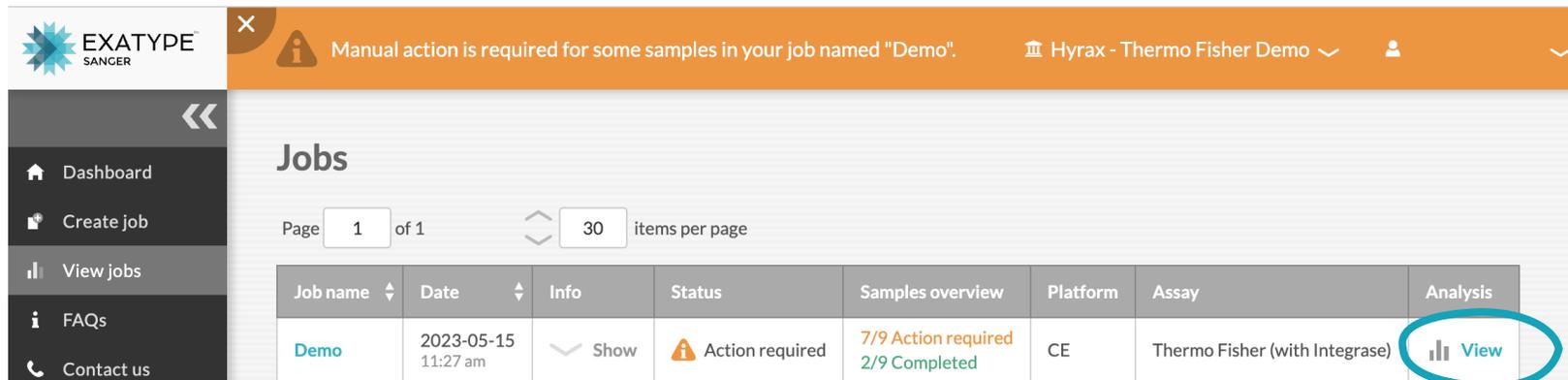
EXATYPE SANGER

Your HIV (Sanger) job "Demo" has been submitted and is currently running. Hyrax - Thermo Fisher Demo

Jobs

Page 1 of 1 30 items per page

Job name	Date	Info	Status	Samples overview	Platform	Assay	Analysis
Demo	2023-05-15 11:27 am	Show	Action required	7/9 Action required 1/9 Completed 1/9 Pending	CE	Thermo Fisher (with Integrase)	Pending



EXATYPE SANGER

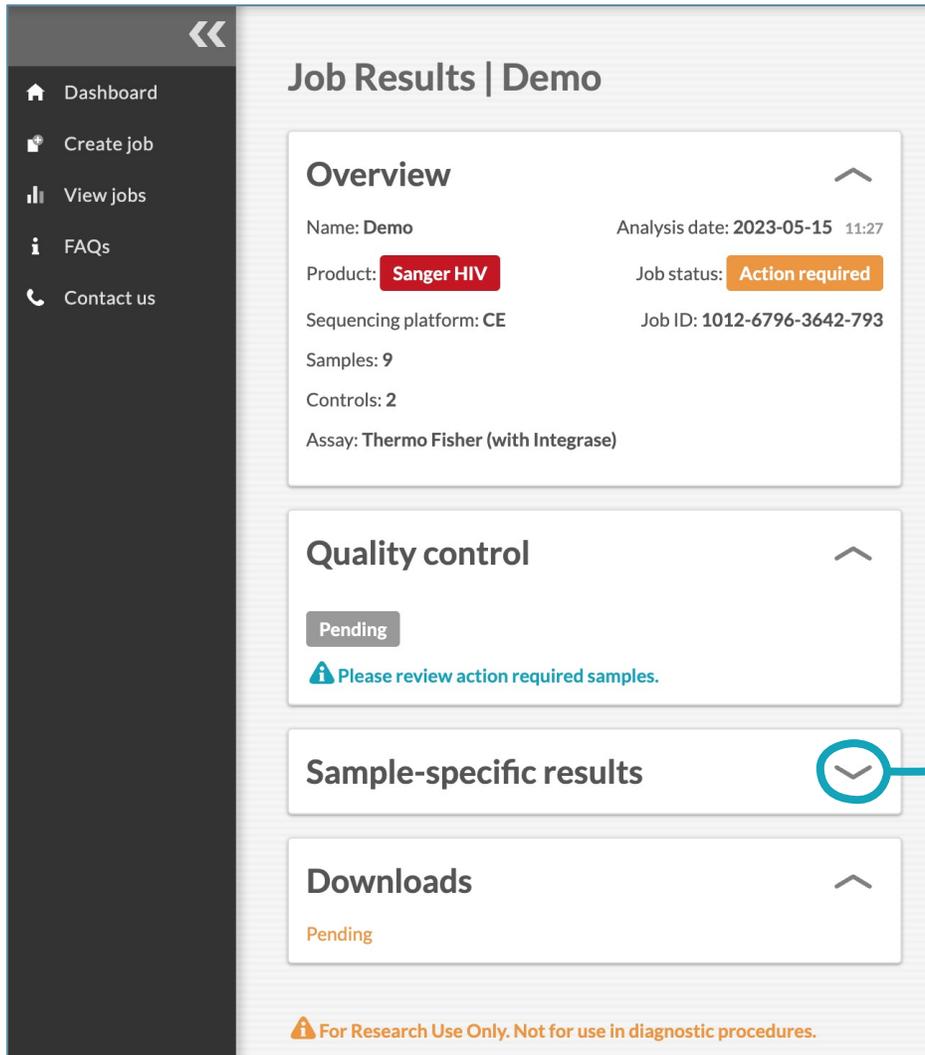
Manual action is required for some samples in your job named "Demo". Hyrax - Thermo Fisher Demo

Jobs

Page 1 of 1 30 items per page

Job name	Date	Info	Status	Samples overview	Platform	Assay	Analysis
Demo	2023-05-15 11:27 am	Show	Action required	7/9 Action required 2/9 Completed	CE	Thermo Fisher (with Integrase)	View

PRODUCT SCREENSHOTS



Job Results | Demo

Overview

Name: Demo Analysis date: 2023-05-15 11:27
Product: **Sanger HIV** Job status: **Action required**
Sequencing platform: CE Job ID: 1012-6796-3642-793
Samples: 9
Controls: 2
Assay: Thermo Fisher (with Integrase)

Quality control

Pending

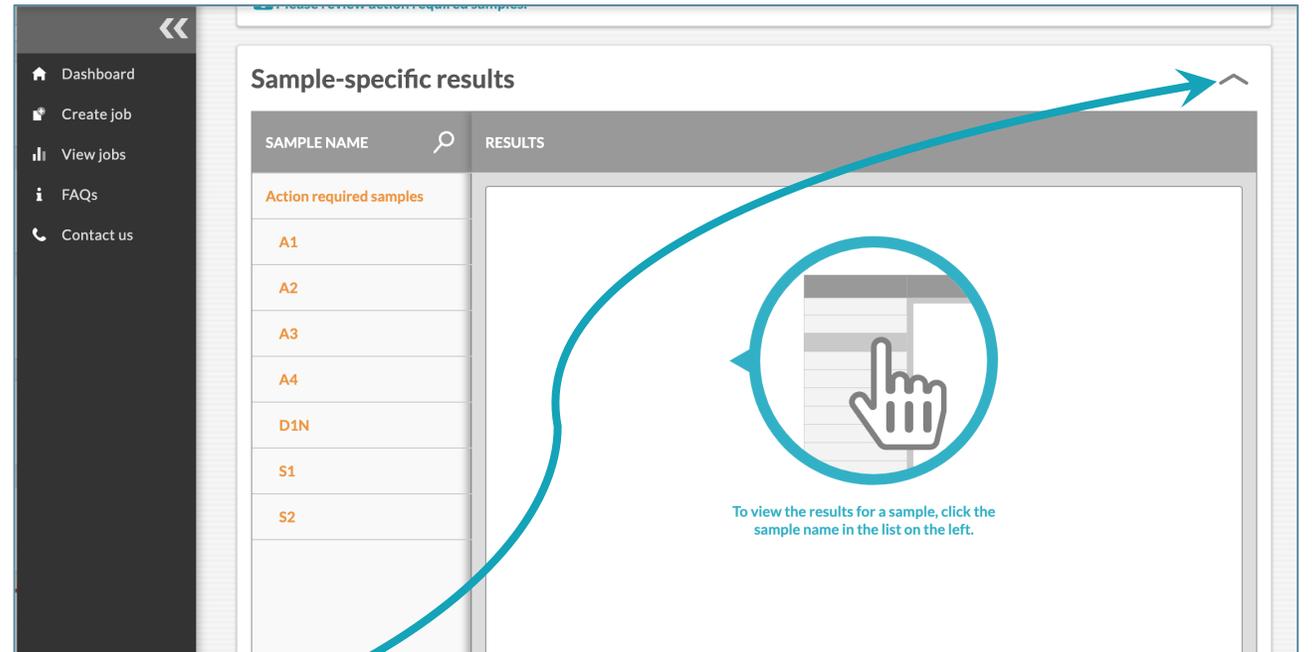
Please review action required samples.

Sample-specific results

Downloads

Pending

For Research Use Only. Not for use in diagnostic procedures.



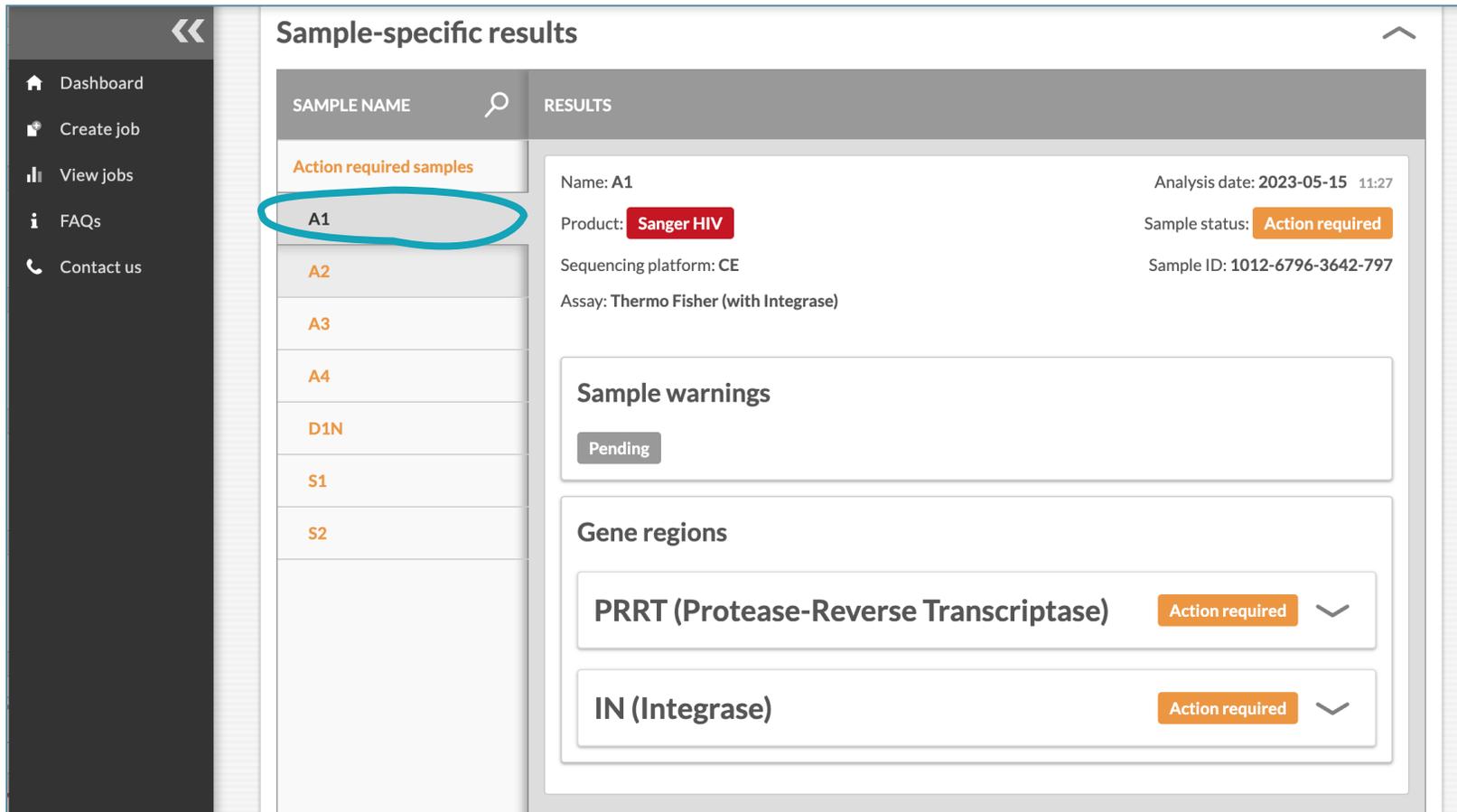
Sample-specific results

SAMPLE NAME	RESULTS
Action required samples	
A1	
A2	
A3	
A4	
D1N	
S1	
S2	

To view the results for a sample, click the sample name in the list on the left.

PRODUCT SCREENSHOTS

Once the first step completes, chromatogram review is required



Sample-specific results

SAMPLE NAME	RESULTS
Action required samples	
A1	Name: A1 Product: Sanger HIV Sequencing platform: CE Assay: Thermo Fisher (with Integrase) Analysis date: 2023-05-15 11:27 Sample status: Action required Sample ID: 1012-6796-3642-797
A2	
A3	
A4	
D1N	
S1	
S2	

Sample warnings

Pending

Gene regions

PRRT (Protease-Reverse Transcriptase) **Action required** ▾

IN (Integrase) **Action required** ▾

PRODUCT SCREENSHOTS

Once the first step completes, chromatogram review is required

The screenshot displays a web application interface for reviewing sample-specific results. On the left is a dark sidebar with navigation links: Dashboard, Create job, View jobs, FAQs, and Contact us. The main content area is titled "Sample-specific results" and features a table of samples. The table has two columns: "SAMPLE NAME" and "RESULTS". Under "Action required samples", the sample "A2" is highlighted with a blue circle. The detailed view for sample A2 shows the following information:

- Name: A2
- Product: Sanger HIV
- Sequencing platform: CE
- Assay: Thermo Fisher (with Integrase)
- Analysis date: 2023-05-15 11:27
- Sample status: Action required
- Sample ID: 1012-6796-3642-800

Below the sample details, there are sections for "Sample warnings" (Pending) and "Gene regions". The "Gene regions" section highlights "PRRT (Protease-Reverse Transcriptase)" with an "Action required" status. The gene region ID is 1012-6796-3642-799. The status is "Action required", and there is a button labeled "EDIT CHROMATOGRAM".

Under "Errors", it states "None detected". Under "Warnings", there are two bullet points:

- Failing primer SeqR2; only 30 acceptable bases
- Note: basecaller passed this sample, however manual review enabled for all samples

PRODUCT SCREENSHOTS

The screenshot displays a web application interface. On the left is a dark sidebar with navigation links: Dashboard, Create job, View jobs, FAQs, and Contact us. The main content area is light gray and contains two job analysis cards. The top card shows a status of 'Action required' and 'None detected' errors. The bottom card, for 'IN (Integrase)', also shows 'Action required' and lists several warnings, including atypical mutations and a need for manual review. Both cards include an 'EDIT CHROMATOGRAM' button.

Navigation sidebar:

- Dashboard
- Create job
- View jobs
- FAQs
- Contact us

Job Analysis Card 1:

Status: **Action required** [EDIT CHROMATOGRAM](#)

Errors

None detected

Warnings

- Failing primer SeqR2; only 30 acceptable bases
- Note: basecaller passed this sample, however manual review enabled for all samples

Job Analysis Card 2:

IN (Integrase) **Action required** [EDIT CHROMATOGRAM](#)

Gene region: IN Gene region ID: 1012-6796-3642-798

Status: **Action required** [EDIT CHROMATOGRAM](#)

Errors

None detected

Warnings

- Suspicious atypical mutation E at codon 197 found.
- Suspicious atypical mutation K at codon 198 found.
- Review key locations
- Manual review required

PRODUCT SCREENSHOTS

Dashboard
Create job
View jobs
FAQs
Contact us

Edit chromatogram

Sample name: **A2 (PRRT)** EXIT **OPEN MAP**

(1) W	(2) Q	(3) R	(4) P	(5 key) L10	(6 key) V11	Reference Protein
W	Q	R	P	L	V	

T	G	G	C	A	A	C	G	A	C	C	C	C	T	C	G	T	Standard Assembled
T	G	G	C	A	A	C	G	A	C	C	C	C	T	T	G	T	

SeqR3_PRRT (reverse)

MIXTURE COMPOSITIONS:
R = A/G Y = C/T K = G/T S = G/C W = A/T
B = C/G/T D = A/G/T H = A/C/T V = A/C/G N = A/C/G/T
M = A/C

USE THE FOLLOWING KEYS TO NAVIGATE:

Next marked base: > Right arrow
Previous marked base: < Left arrow
Next base: ↑ > Shift + right arrow
Previous base: ↑ < Shift + left arrow

KEY LOCATIONS:

Next marked key base: Down arrow
Previous marked key base: Up arrow
Next key amino acid: Ctrl ↑ > Ctrl + Shift + right arrow
Previous key amino acid: Ctrl ↑ < Ctrl + Shift + left arrow

USE THE FOLLOWING KEYS TO MAKE EDITS:

Change base: A C G T N R Y K M S W B D H V
Erase base: - Dash

SAMPLE INFO

Sample name	A2
Sample ID	1725-0977-7372-262
Gene region	PRRT
Gene region ID	1725-0977-7372-264
Upload date	2023-07-29 at 01:18
Status	Manual review
Mixtures	9 (cutoff: 15%)
Marks	4

Basecaller warning: Failing primer SeqR2; only 30 acceptable bases
Note: basecaller passed this sample, however manual review enabled for all samples

JUMP TO LOCATION

Type a base number into the box below, and click Jump to base.

Base number » JUMP TO BASE

Type an amino acid number into the box below, and click Jump to amino acid.

PRODUCT SCREENSHOTS

Dashboard
Create job
View jobs
FAQs
Contact us

Edit chromatogram

Sample name: **A2 (PRRT)** EXIT CLOSE MAP

(1) W | (2) Q | (3) R | (4) P | (5 key) L10 | (6 key) V11 | Reference Protein
W | Q | R | P | L | V | Protein

T G G C A A C G A C C C C T C G T | Standard
T G G C A A C G A C C C C T T G T | Assembled

SeqR3_PRRT (reverse) 1
T G G C A A C G A C C

MIXTURE COMPOSITIONS:
R = A/G Y = C/T K = G/T S = G/C W = A/T
B = C/G/T D = A/G/T H = A/C/T V = A/C/G N = A/C/G/T
M = A/C

SAMPLE INFO

Sample name	A2
Sample ID	1725-0977-7372-262
Gene region	PRRT
Gene region ID	1725-0977-7372-264
Upload date	2023-07-29 at 01:18
Status	Manual review
Mixtures	9 (cutoff: 15%)
Marks	4

USE THE FOLLOWING KEYS TO NAVIGATE:

Next marked base: ➤ Right arrow
Previous marked base: ➤ Left arrow
Next base: ⬆ ➤ Shift + right arrow
Previous base: ⬆ ➤ Shift + left arrow

KEY LOCATIONS:

Next marked key base: ⬇ Down arrow
Previous marked key base: ⬆ Up arrow
Next key amino acid: Ctrl ⬆ ➤ Ctrl + Shift + right arrow
Previous key amino acid: Ctrl ⬆ ➤ Ctrl + Shift + left arrow

USE THE FOLLOWING KEYS TO MAKE EDITS:

Change base:

SAMPLE INFO

Basecaller warning: Failing primer SeqR2; only 30 acceptable bases
Note: basecaller passed this sample, however manual review enabled for all samples

JUMP TO LOCATION

PRODUCT SCREENSHOTS

The screenshot displays a software interface for managing sequencing samples. On the left is a dark sidebar with navigation links: Dashboard, Create job, View jobs, FAQs, and Contact us. The main area is divided into several sections:

- Chromatogram:** A multi-colored line graph at the top showing signal intensity for different bases.
- Navigation Instructions:**
 - USE THE FOLLOWING KEYS TO NAVIGATE:**
 - Next marked base: Right arrow
 - Previous marked base: Left arrow
 - Next base: Shift + right arrow
 - Previous base: Shift + left arrow
 - KEY LOCATIONS:**
 - Next marked key base: Down arrow
 - Previous marked key base: Up arrow
 - Next key amino acid: Ctrl + Shift + right arrow
 - Previous key amino acid: Ctrl + Shift + left arrow
 - USE THE FOLLOWING KEYS TO MAKE EDITS:**
 - Change base: A C G T N R Y K M S W B D H V
 - Erase base: Dash
- SAMPLE INFO:**

Sample name	A2
Sample ID	1725-0977-7372-262
Gene region	PRRT
Gene region ID	1725-0977-7372-264
Upload date	2023-07-29 at 01:18
Status	Manual review
Mixtures	9 (cutoff: 15%)
Marks	4
- Warnings:**
 - Basecaller warning: Failing primer SeqR2; only 30 acceptable bases
 - Note: basecaller passed this sample, however manual review enabled for all samples
- JUMP TO LOCATION:**
 - Type a base number into the box below, and click **Jump to base**.
 - Type an amino acid number into the box below, and click **Jump to amino acid**.
- Actions:** SAVE, SAVE & PASS, FAIL SAMPLE, EXIT

A confirmation dialog box is overlaid on the bottom right, asking: "Are you sure you want to save your edits and pass this sample?". It features two buttons: CONFIRM (green) and CANCEL (white with grey border).

PRODUCT SCREENSHOTS

The screenshot displays a web application interface for sample management. On the left is a dark sidebar with navigation links: Dashboard, Create job, View jobs, FAQs, and Contact us. The main area is divided into a 'SAMPLE NAME' column with a search icon and a 'RESULTS' column. The 'SAMPLE NAME' column lists samples A1 through S2, with A1 through S2 highlighted in orange. The 'RESULTS' column shows details for sample A2: Name: A2, Analysis date: 2023-05-15 11:27, Product: Sanger HIV, Sample status: Action required, Sequencing platform: CE, Sample ID: 1012-6796-3642-800, and Assay: Thermo Fisher (with Integrase). Below this is a 'Sample warnings' section with a 'Pending' status. The 'Gene regions' section shows 'PRRT (Protease-Reverse Transcriptase)' with a 'Completed' status (circled in blue), Gene region: PRRT, Gene region ID: 1012-6796-3642-799, and a 'VIEW CHROMATOGRAM' button. An 'Errors' section shows 'None detected'. A 'Warnings' section lists three items: 'Failing primer SeqR2; only 30 acceptable bases', 'Note: basecaller passed this sample, however manual review enabled for all samples', and 'Passed by manual review'.

SAMPLE NAME

RESULTS

Action required samples

A1

A2

A3

A4

D1N

S1

S2

Name: A2 Analysis date: 2023-05-15 11:27

Product: **Sanger HIV** Sample status: **Action required**

Sequencing platform: CE Sample ID: 1012-6796-3642-800

Assay: Thermo Fisher (with Integrase)

Sample warnings

Pending

Gene regions

PRRT (Protease-Reverse Transcriptase) **Completed**

Gene region: PRRT Gene region ID: 1012-6796-3642-799

Status: **Completed** [VIEW CHROMATOGRAM](#)

Errors

None detected

Warnings

- Failing primer SeqR2; only 30 acceptable bases
- Note: basecaller passed this sample, however manual review enabled for all samples
- Passed by manual review

PRODUCT SCREENSHOTS

Navigation Sidebar:

- Dashboard
- Create job
- View jobs
- FAQs
- Contact us

Top Navigation: A1, A2, A3, A4, D1N, S1, S2

Product Information:

- Product: **Sanger HIV**
- Sample status: **Action required**
- Sequencing platform: CE
- Sample ID: 1012-6796-3642-800
- Assay: Thermo Fisher (with Integrase)

Sample warnings

- Pending

Gene regions

- PRRT (Protease-Reverse Transcriptase)** **Completed**
- IN (Integrase)** **Action required**

IN (Integrase) Details:

- Gene region: IN
- Gene region ID: 1012-6796-3642-798
- Status: **Action required**
- EDIT CHROMATOGRAM**

Errors

- None detected

Warnings

- Suspicious atypical mutation E at codon 197 found.
- Suspicious atypical mutation K at codon 198 found.
- Review key locations
- Manual review required

PRODUCT SCREENSHOTS

SAMPLE NAME **RESULTS**

Action required samples

- A1
- A3
- A4
- D1N
- S1
- S2
- Completed samples**
- A2

Name: A2 **Analysis date:** 2023-05-15 11:27

Product: Sanger HIV **Sample status:** Action required

Sequencing platform: CE **Sample ID:** 1012-6796-3642-800

Assay: Thermo Fisher (with Integrase)

Sample warnings

Pending

Gene regions

PRRT (Protease-Reverse Transcriptase) Completed

IN (Integrase) Completed

Drug calls

● Susceptible ● Intermediate ● Resistant ● No data [PDF REPORT](#)

DRUG CLASS	DRUG	CALL ¹	MUTATIONS
	ABC	S	
	AZT	S	
	D4T	S	

PRODUCT SCREENSHOTS

board
te job
y jobs
s
act us

Edit chromatogram

Sample name: **A1 (IN)**



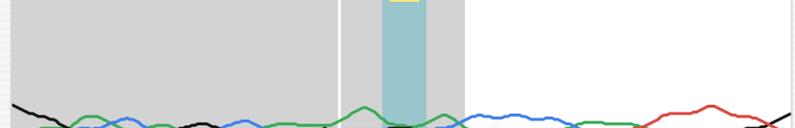
(229)	(230 key)	(231)	(232 key)	(233)	(234)	(235)	(236)	(237)	Reference Protein
D	S230	R	N232	P	L	W	K	G	
D	S	R	D	P	I	W	K	G	

Standard Assembled
 G G G A C A G C A G A G A T C C A C T T T G G A A A G G
 G G G A C A G C A G A G A C C C A A T T T G G A A A G G

SeqF11_IN (forward)
 G A C A G C A G A G A C C C A A T T T

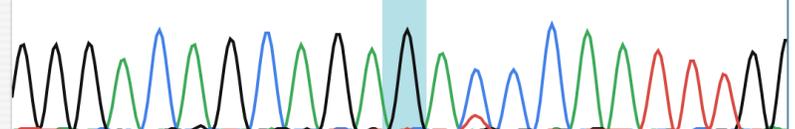
MIXTURE COMPOSITION

R = A/G Y = C/T K =
 B = C/G/T D = A/G/T H =
 M = A/C

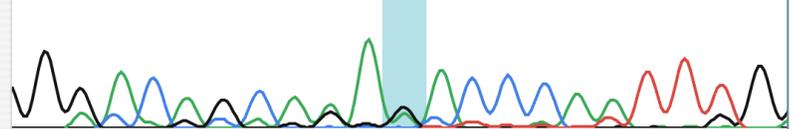


SeqR11_IN (reverse)
 G G G A C A G C A G A G A C C C A A T T T G G

SAMPLE INFO



SeqF12_IN (forward)
 G G A C A G C A G A G A C C C A A T T T G



EDIT HISTORY

*** UNSAVED**

Base	Original	Updated
694	G	R

Edit chromatogram

Sample name: **A1 (IN)**



(229)	(230 key)	(231)	(232 key)	(233)	(234)	(235)	(236)	(237)	Reference Protein
D	S230	R	N232	P	L	W	K	G	
D	S	R	D.N	P	I	W	K	G	

Standard Assembled
 G G G A C A G C A G A G A T C C A C T T T G G A A A G G
 G G G A C A G C A G A R A C C C A A T T T G G A A A G G

SeqF11_IN (forward)
 G A C A G C A G A R A C C C A A T T T

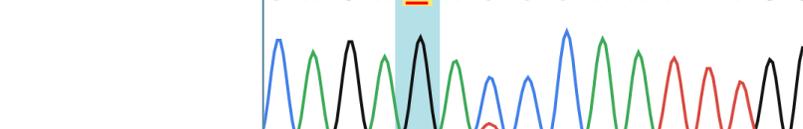
MIXTURE COMPOSITIONS

R = A/G Y = C/T K =
 B = C/G/T D = A/G/T H =
 M = A/C



SeqR11_IN (reverse)
 G G G A C A G C A G A R A C C C A A T T T G G

SAMPLE INFO



C A G A R A C C C A A T T T G

Sample name
Sample ID
Gene region
Gene region ID
Upload date
Status
Mixtures
Marks

PRODUCT SCREENSHOTS

EXATYPE SANGER

All required manual actions are complete for your job "Demo". QC processing is currently underway

Hyrax - Thermo Fisher Demo

Jobs

Page 1 of 1 30 items per page

Job name	Date	Info	Status	Samples overview	Platform	Assay	Analysis
Demo	2023-05-15 11:27 am	Show	Pending 99%	7/9 Completed 1/9 Discordant 1/9 Failed	CE	Thermo Fisher (with Integrase)	Pending

EXATYPE SANGER

Your job "Demo" has completed successfully.

Hyrax - Thermo Fisher Demo

Jobs

Page 1 of 1 30 items per page

Job name	Date	Info	Status	Samples overview	Platform	Assay	Analysis
Demo	2023-05-15 11:27 am	Show	Completed	7/9 Completed 1/9 Discordant 1/9 Failed	CE	Thermo Fisher (with Integrase)	View

PRODUCT SCREENSHOTS

Job Results | Demo

Overview

Name: Demo Analysis date: 2023-05-15 11:27

Product: **Sanger HIV** Job status: **Completed**

Sequencing platform: CE Job ID: 1012-6796-3642-793

Samples: 9

Controls: 2

Assay: Thermo Fisher (with Integrase)

[DOWNLOAD FULL REPORT](#)

Quality control

Sequencing controls

<p>Plate name: Plate 1</p> <p>Sample name: V1cntrl_POS_IN</p> <p>Sample ID: 1012-6796-3642-815</p> <p>Plate ID: 1012-6796-3642-794</p> <p>Sample type: Positive</p> <p>Region: IN</p> <p>Status: Passed</p>	<p>Plate name: Plate 1</p> <p>Sample name: V1cntrl_POS_PRRT</p> <p>Sample ID: 1012-6796-3642-817</p> <p>Plate ID: 1012-6796-3642-794</p> <p>Sample type: Positive</p> <p>Region: PRRT</p> <p>Status: Passed</p>
---	---

Locus	Position	Amino acid	Status
-------	----------	------------	--------

PRODUCT SCREENSHOTS

Quality control

Sequencing controls

Plate name: **Plate 1**

Sample name: V1cntrl_POS_IN
Sample ID: 1012-6796-3642-815
Plate ID: 1012-6796-3642-794
Sample type: Positive
Region: IN
Status: **Passed**

	Locus	Position	Amino acid	Status
✓	IN	61	*	Present
✓	IN	74	M	Present
✓	IN	138	K	Present
✓	IN	140	S	Present
✓	IN	148	K	Present
✓	IN	156	*	Present
✓	IN	263	K	Present

Plate name: **Plate 1**

Sample name: V1cntrl_POS_PRRT
Sample ID: 1012-6796-3642-817
Plate ID: 1012-6796-3642-794
Sample type: Positive
Region: PRRT
Status: **Passed**

	Locus	Position	Amino acid	Status
✓	PR	37	S	Present
✓	PR	41	*	Present
✓	RT	41	L	Present
✓	PR	54	M	Present
✓	RT	65	R	Present
✓	RT	68	*	Present
✓	PR	90	M	Present
✓	RT	103	N	Present
✓	RT	122	E	Present
✓	RT	181	C	Present
✓	RT	183	*	Present
✓	RT	184	V	Present
✓	RT	214	L	Present

Warnings

PRODUCT SCREENSHOTS

The screenshot displays a web application interface. On the left is a dark sidebar with navigation links: Dashboard, Create job, View jobs, FAQs, and Contact us. The main content area is divided into sections. At the top, there are tabs labeled 'K1', 'Z14', 'L', and 'Present'. Below this is a 'Warnings' section with two sub-sections: 'Contamination checks' and 'Unusual mutation checks'. The 'Contamination checks' section lists three categories: 'Samples too similar to positive control' (None detected), 'Samples too similar to selected lab strains' (None detected), and 'Samples too similar to other samples from this job' (S2, S1). The 'Unusual mutation checks' section lists two categories: 'Samples with excess APOBEC mutations' (D1N) and 'Samples with excess atypical mutations' (D1N). At the bottom is a 'Sample-specific results' section with a table header containing 'SAMPLE NAME' and 'RESULTS'.

Navigation sidebar:

- Dashboard
- Create job
- View jobs
- FAQs
- Contact us

Top tabs: K1, Z14, L, Present

Warnings

Contamination checks

- Samples too similar to positive control *i*
None detected
- Samples too similar to selected lab strains *i*
None detected
- Samples too similar to other samples from this job *i*
S2, S1

Unusual mutation checks

- Samples with excess APOBEC mutations *i*
D1N
- Samples with excess atypical mutations *i*
D1N

Sample-specific results

SAMPLE NAME	RESULTS
-------------	---------

PRODUCT SCREENSHOTS

Sample-specific results

SAMPLE NAME **RESULTS**

Completed samples

- A2
- A3
- D1N
- S1
- S2
- A4***

Failed samples

- A1

Sample A4 Details:

Name: A4 Analysis date: 2023-05-15 11:27
Product: **Sanger HIV** Sample status: **Discordant**
Sequencing platform: CE Exatype version: 2.7.5
Assay: Thermo Fisher (with Integrase) Resistance algorithm: Stanford HIVDB v9.4
Sample ID: 1012-6796-3642-806

Sample warnings

None detected

Gene regions

- PRRT (Protease-Reverse Transcriptase) **Completed**
- IN (Integrase) **Failed**

Drug calls

● Susceptible ● Intermediate ● Resistant ● No data

[PDF REPORT](#)

DRUG CLASS	DRUG	CALL ¹	MUTATIONS

PRODUCT SCREENSHOTS

Dashboard

Create job

View jobs

FAQs

Contact us

RT Other: P4T, K11T, V35T, T39N, E40D, K43KR[†], K49KR[†], V60I, K102Q, D121H, K122E, K173R, Q174K, D177E, T200A, Q207E, R211K, V245K, D250E

IN Region

INSTI Major: None

INSTI Accessory: None

IN Other: E11D, R20K, S24N, L101I, T124A, T125A, G134N, I135V, K136T, D167E, Y194YC[†], G197GE[†], E198EK[†], V201I, T206S, I208IM[†], L234I, S283G

[†]Mixed mutation

[†] For Research Use Only. Not for use in diagnostic procedures. For more information please view our terms and conditions at <https://exatype.com/terms-of-use> or contact us at support@hyraxbio.com

*The assay does not cover the entire reverse transcriptase gene region. Therefore, two potential drug-resistance scoring mutations - amino acid position 318 (scoring for DOR, EFV, and NVP) and position 348 (scoring for NVP) - are excluded from the drug-resistance interpretation.

Exatype sample ID: 1725-0977-7372-378

Downloads

Consensus sequences

[Demo.sequences.individual.fasta.zip](#) ⓘ

[Demo.sequences.fasta](#) ⓘ

[Demo.sequences.concatenated.fasta](#) ⓘ

Mutations

[Demo.mutations.csv](#) ⓘ

Summary

[Demo.summary.tsv](#) ⓘ

PRODUCT SCREENSHOTS

[View all your analyses](#)

PRODUCT SCREENSHOTS

Single organisational signup/licence with multiple users

The screenshot displays the Exatype Sanger dashboard for the organization 'Hyrax - Thermo Fisher Demo'. The interface includes a left-hand navigation menu with options: Dashboard, Create job, View jobs, FAQs, and Contact us. The main content area is titled 'Dashboard' and shows the user's role as an administrator. A 'Quick links' section features two primary actions: 'View jobs' (with a refresh icon) and 'Create job' (with a plus icon). On the right, a user profile dropdown menu is open, listing 'Org settings', 'Invite users', 'View invitations', and 'Org users'. The 'Invite users' option is highlighted with a red circle.

EXATYPE
SANGER

Hyrax - Thermo Fisher Demo

Dashboard

You are currently an administrator of the organisation **Hyrax - Thermo Fisher Demo**

Quick links

View jobs
Browse and search through the results from your previous analyses.

Create job
Run a new **Exatype** job.

- Org settings
- Invite users**
- View invitations
- Org users

PRODUCT SCREENSHOTS

Single organisational signup/licence with multiple users

Dashboard

Create job

View jobs

FAQs

Contact us

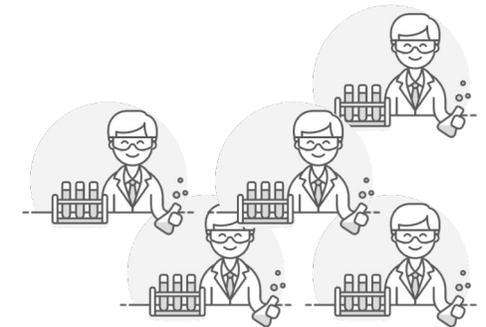
Invite Users

⚠ Please enter the email addresses of the people you would like to invite to your organisation below. You can paste multiple addresses into a field. Spreadsheet columns, as well as comma and tab separated lists are accepted.

Email *

+ ADD ANOTHER INVITATION

INVITE USERS



Invitations

Invitation to join Hyrax - Thermo Fisher Demo

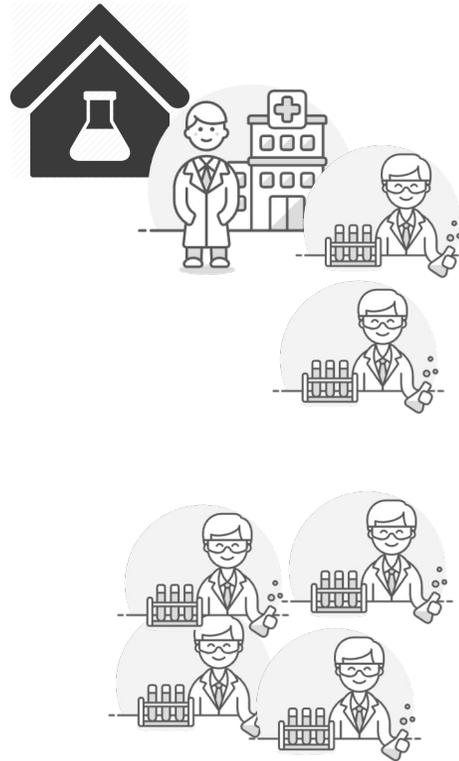
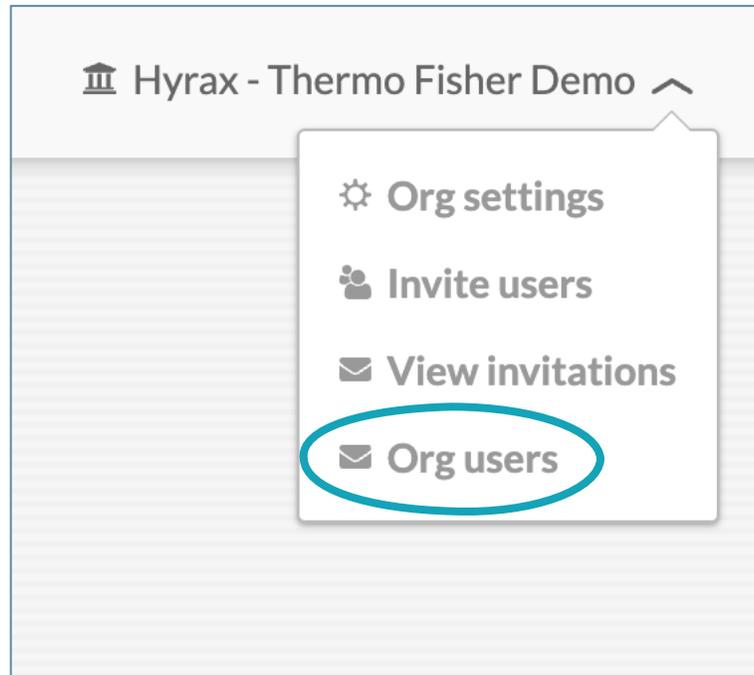
You have been invited to join the organisation Hyrax - Thermo Fisher Demo by natasha+TF2@hyraxbio.com.

✓ ACCEPT INVITATION

✗ REJECT INVITATION

PRODUCT SCREENSHOTS

Single organisational signup/licence with multiple users



User role	Actions
Admin	DEMOTE TO STANDARD USER
Admin	DEMOTE TO STANDARD USER
Admin	DEMOTE TO STANDARD USER
Standard	PROMOTE TO ADMIN USER
Standard	PROMOTE TO ADMIN USER
Standard	PROMOTE TO ADMIN USER
Standard	PROMOTE TO ADMIN USER

PRODUCT SCREENSHOTS

<https://exatype.com/faqs/sanger-hiv-thermofisher/>

 EXATYPE™

Exatype: HIV Sanger - FAQs

[View as plain text](#)