



Exatype: HIV (Sanger)

A platform for HIV drug-resistance reporting

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

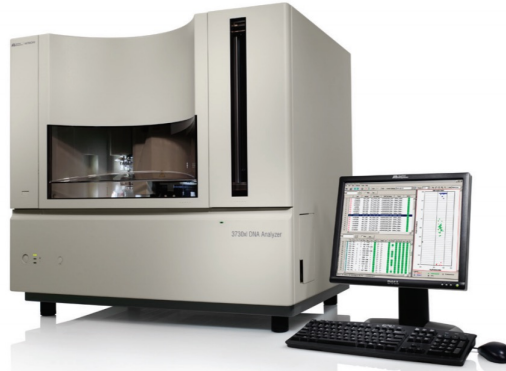
INTRODUCTION

HIV genotyping workflow: Three-step process



1

Sample prep



2

Sequencing

DRUG RESISTANCE REPORT	
DRUG	CALL
	
	
	

3

Analysis

ThermoFisher
SCIENTIFIC

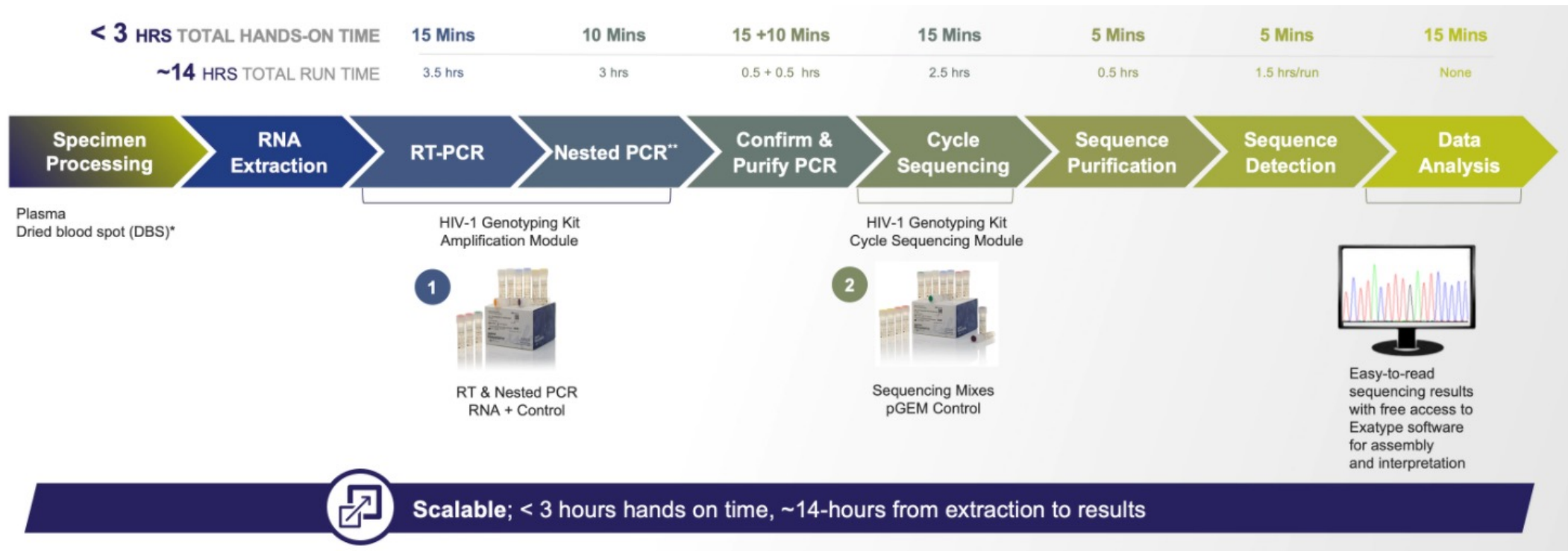


INTRODUCTION

End-to-end solution



Free analysis for
Thermo customers

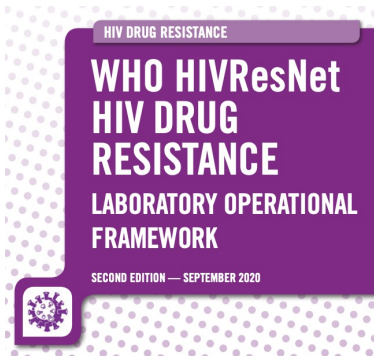
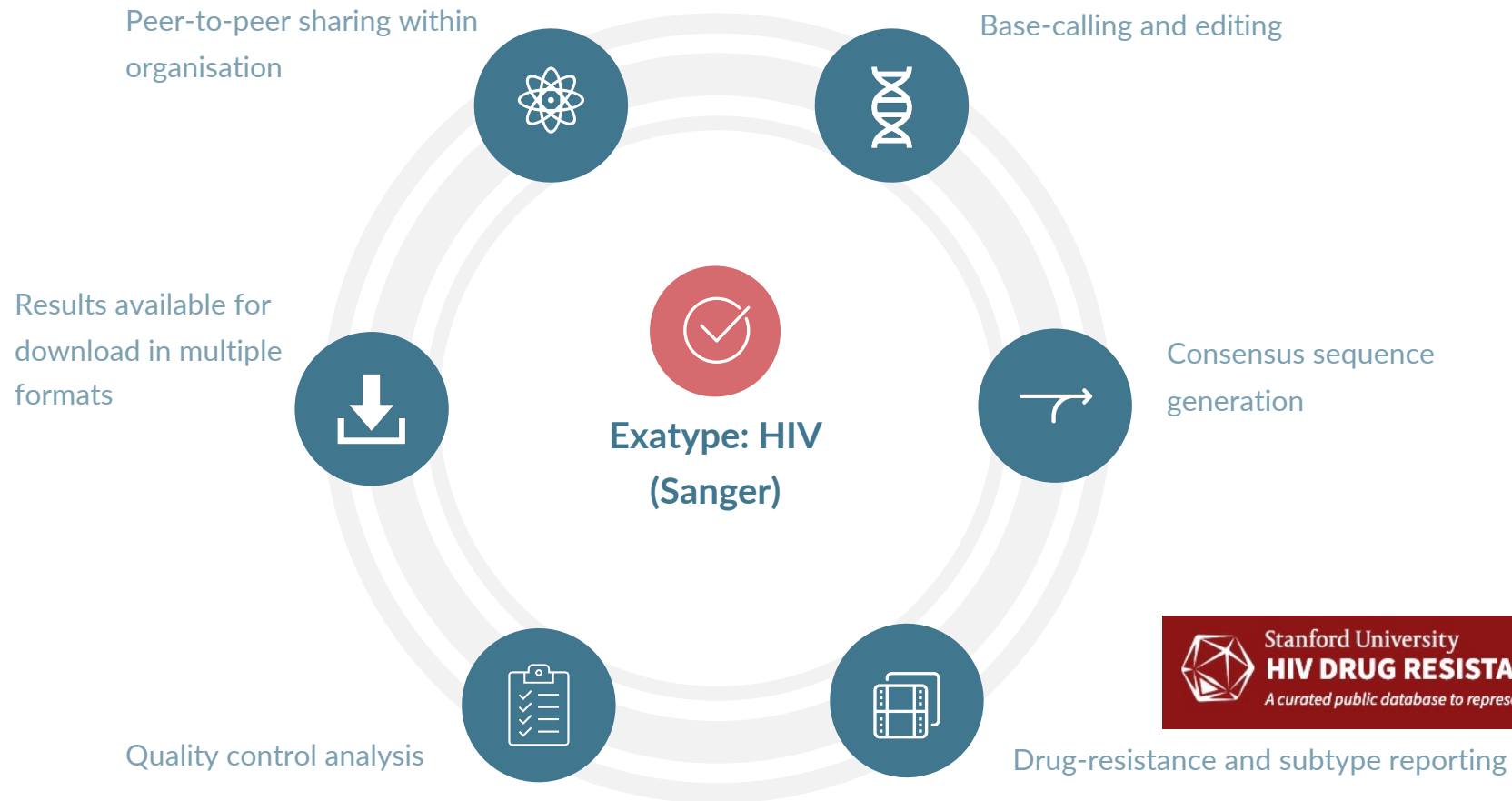


OUT-OF-THE-BOX SOLUTION

HIV drug-resistance analysis

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

RECall



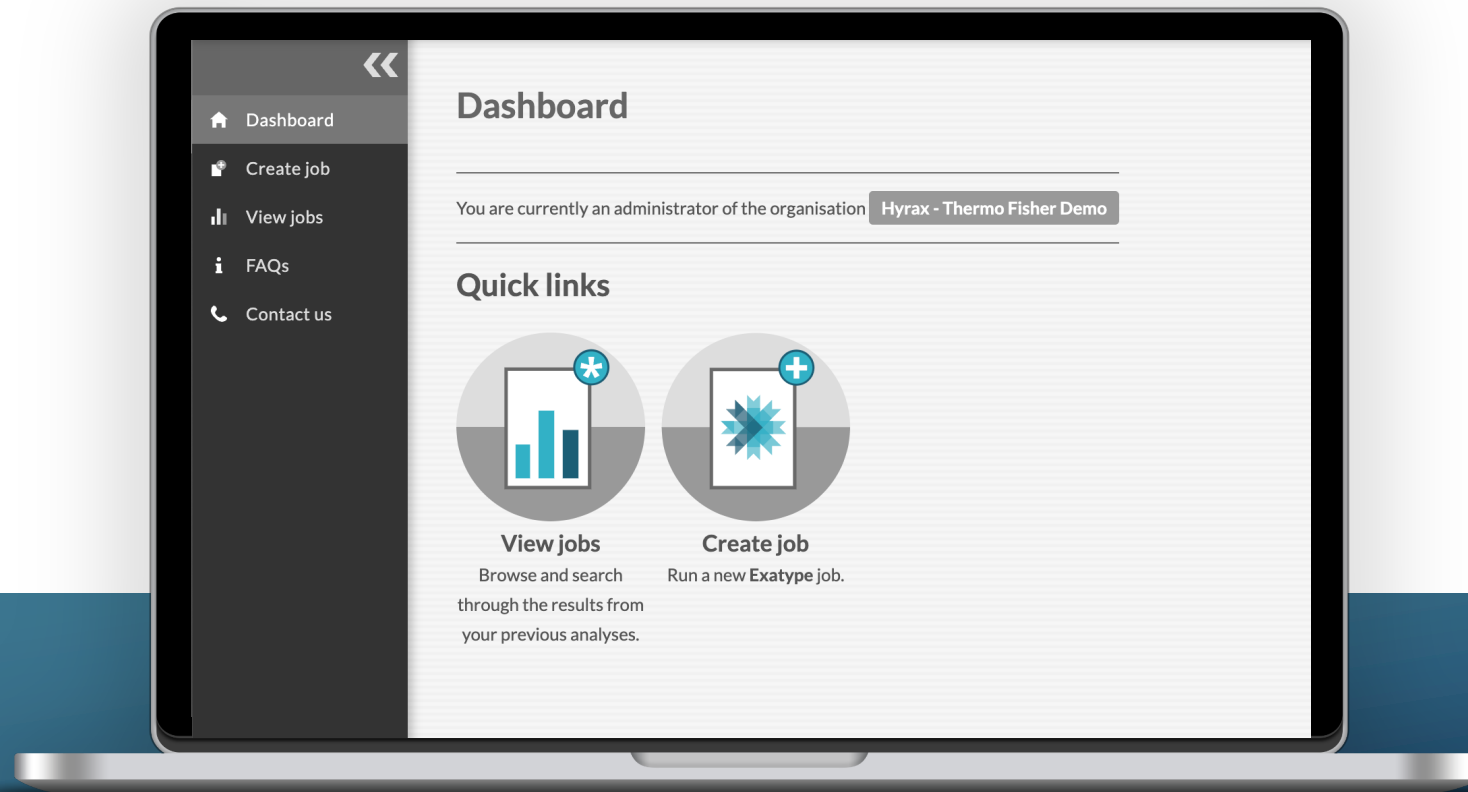
<https://www.who.int/publications/i/item/978-92-4-000987-5>

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



DEMO RUN

sanger.exatype.com



PLATFORM FEATURES

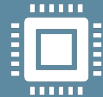
Standardisation

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



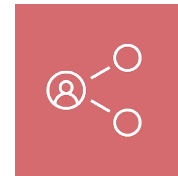
Integration with LIMS

- 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

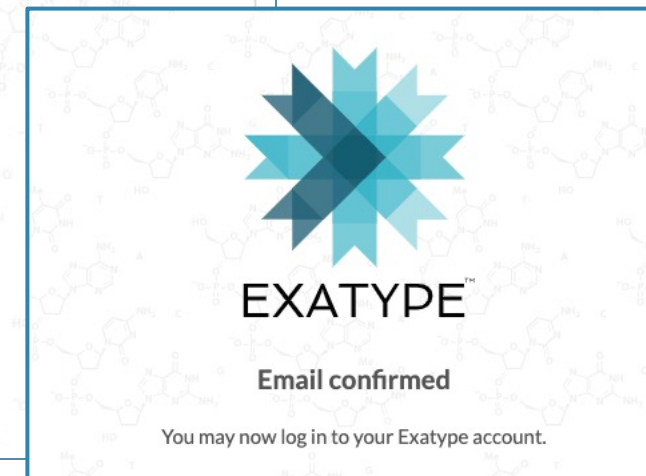
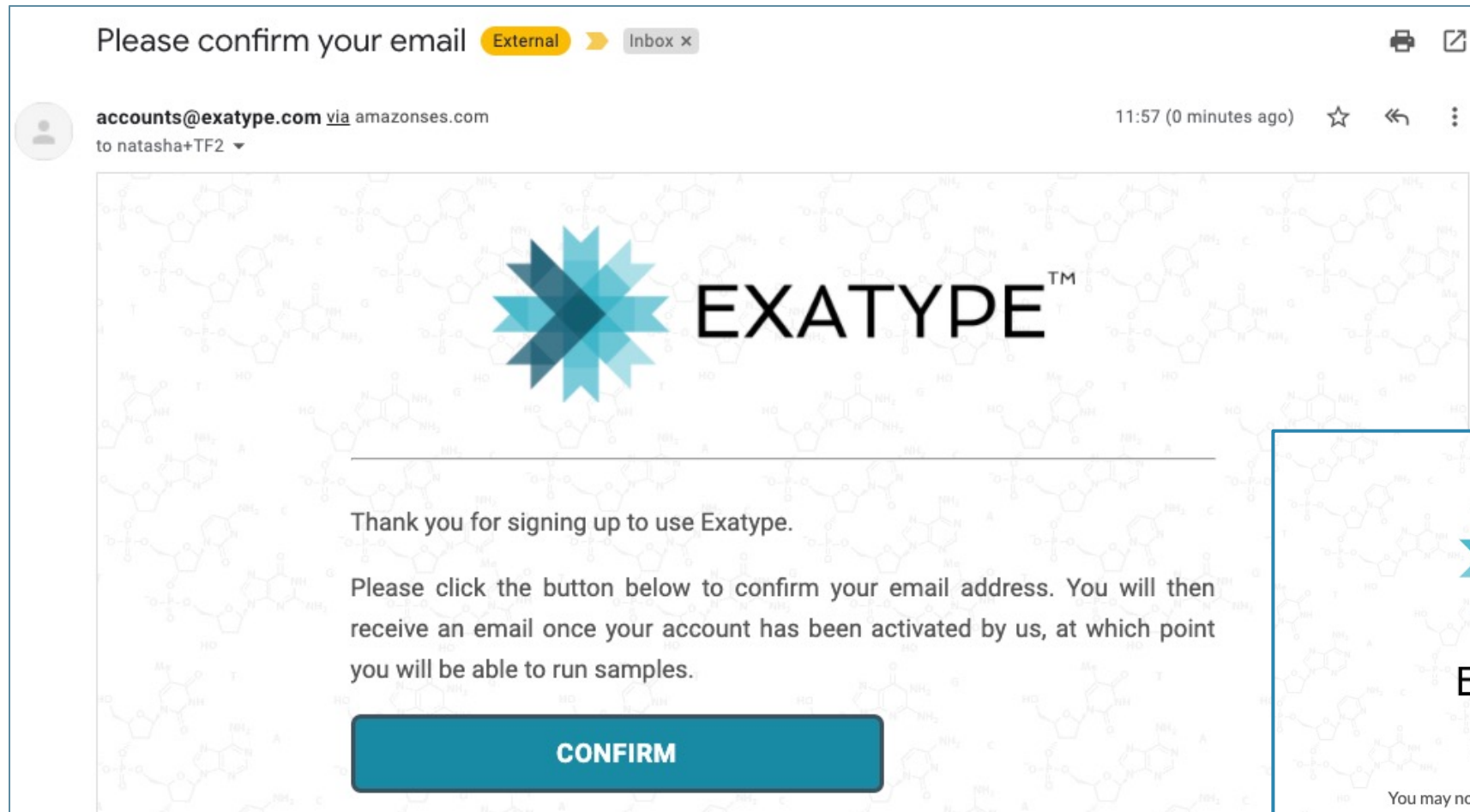

reCAPTCHA
[Privacy](#) - [Terms](#)

CREATE MY ACCOUNT

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

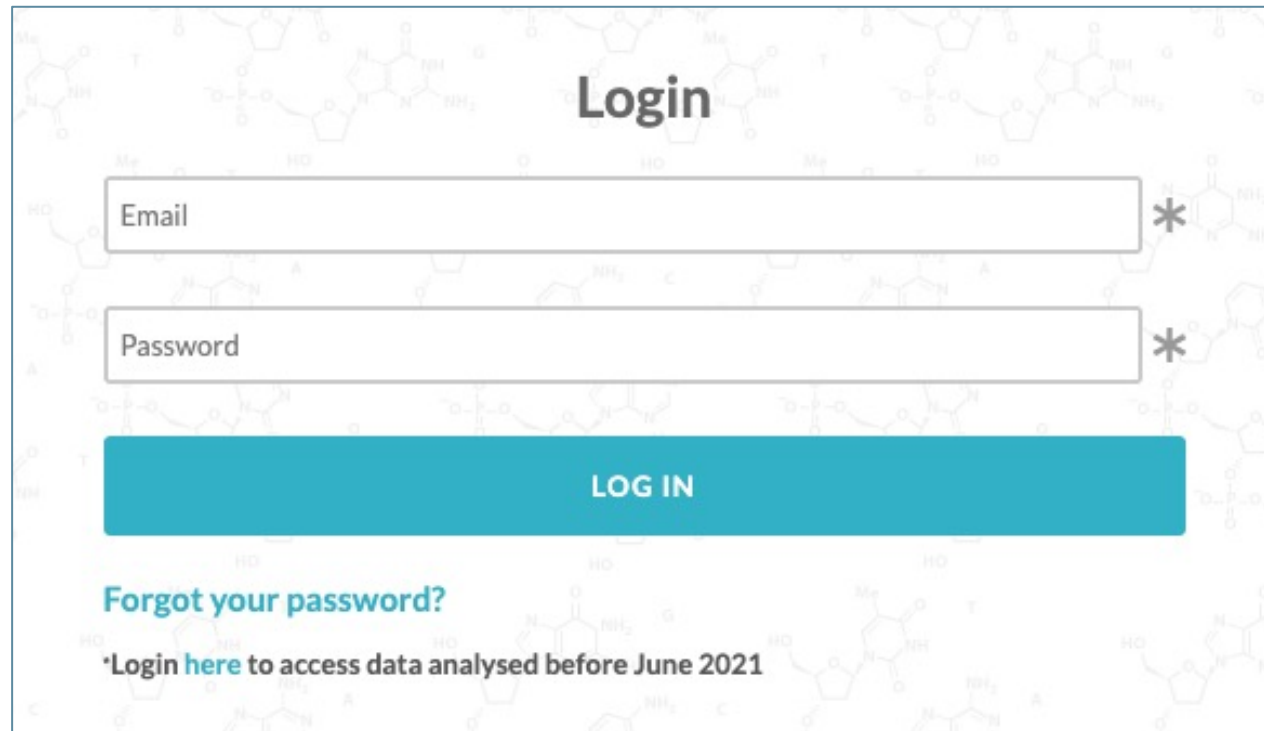
PRODUCT SCREENSHOTS

Your email account



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.

*

Country

Select ▼

 *

What HIV DR assay do you use?

Select ▼

 *

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

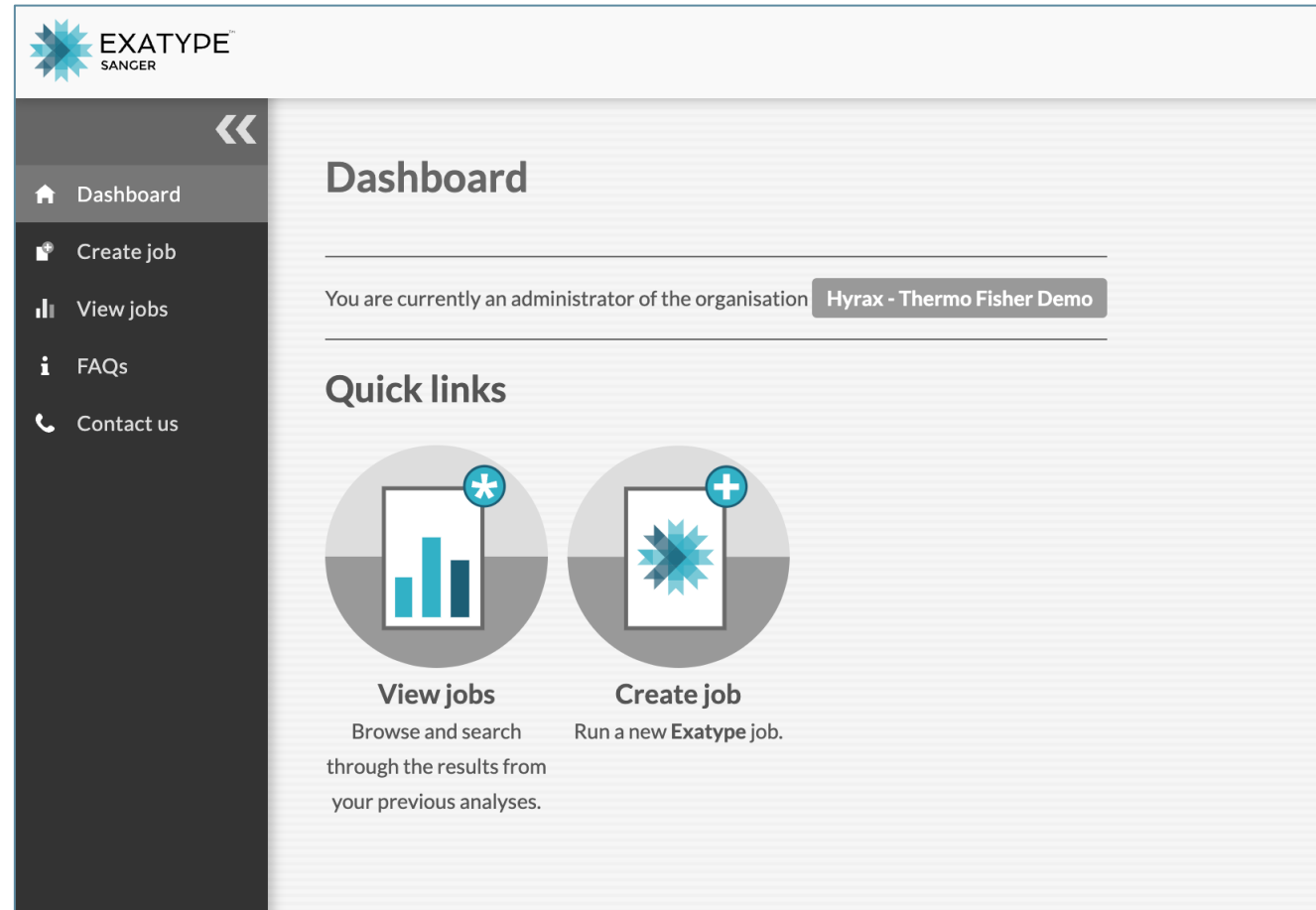
I agree that my organisation's uploaded data can be used anonymously for research purposes other than surveillance. See our [privacy policy](#) for further information.

☐ Yes
☒ No

CREATE ORGANISATION

PRODUCT SCREENSHOTS

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




PRODUCT SCREENSHOTS





Create a new analysis

The image displays two screenshots of a web application interface for creating a new job, specifically for HIV (Sanger) analysis.

Left Screenshot:

- Navigation Menu:** Dashboard, **Create job** (highlighted), View jobs, FAQs, Contact us.
- Tabs:** Job details (selected), Select data, Filename format, Sample details, Review & submit.
- Form Title:** Create a new job **HIV (Sanger)**.
- Job details:**
 - Job name: 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 
- Next Step:** [NEXT >](#)

Right Screenshot:

- Navigation Menu:** Dashboard, Create job, View jobs, FAQs, Contact us.
- Tabs:** Job details (selected), Select data, Filename format, Sample details, Review & submit.
- Form Title:** Create a new job **HIV (Sanger)**.
- Job details:**
 - Job name: 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 
 - ☒ Review all sequences 
 - ☐ Review sequences flagged as FAILED and Manual Review by RECall 
 - ☐ Review only those sequences flagged for Manual Review by RECall 
- Next Step:** [NEXT >](#)

PRODUCT SCREENSHOTS

Create a new analysis

Dashboard

Create job

View jobs

FAQs

Contact us

Job details

Select data

Filename format

Sample details

Review & submit

Create a new job

HIV (Sanger)

Job details

Job name

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

<<

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)**

Select data

Plate 1

Please select the data files that you would like to analyse. Only **ab1** files are accepted.

SELECT YOUR AB1 FILES

DROP YOUR AB1 FILES HERE

+

Add a plate

< PREV

NEXT >

⚠ 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 sections: 'Key benefits' on the left and 'Further information' on the right. The 'Key benefits' section 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 'Further information' section lists three resources, each with a download icon: 'Example dataset', 'Example of a full report', and 'Presentation'. The 'Example dataset' section is circled in blue.


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 displays a web application interface for creating a new analysis. The interface is divided into several sections:

- File Explorer (Left):** Shows a directory structure under 'Downloads'. A folder named 'Sangerv2_DemoDataset' is expanded, revealing a list of files. A red arrow points from the file explorer to the 'DROP YOUR AB1 FILES HERE' area in the 'Select data' section.
- Sidebar (Left):** Contains navigation options: Dashboard, Create job, View jobs, FAQs, and Contact us.
- Main Panel (Right):** Features a series of tabs: Job details, **Select data** (active), Filename format, Gene region names, Sample details, and Review & submit.
- Create a new job:** A dropdown menu is set to 'HIV (Sanger)', which is highlighted with a red box. Navigation buttons '< PREV', 'NEXT >', and 'CANCEL JOB' are visible.
- Select data:** This section includes a 'Plate 1' input field with a green checkmark, a 'SELECT YOUR AB1 FILES' button, and a 'DROP YOUR AB1 FILES HERE' area. A red arrow points from the file explorer to this area.
- Footer:** A warning message states: 'For Research Use Only. Not for use in diagnostic procedures.'

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

Select data

Plate 1

✓

✕

72 ab1s selected for plate "Plate 1"

✓ ADD MORE FILES

✕ REMOVE ALL FILES

✕ 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

+

Add a plate

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 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

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

<<

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"/>
	V1cntrl	IN	<input checked="" type="checkbox"/>	<input type="checkbox"/>
	V1cntrl	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

Sequencing platform: Sanger

Assay: Thermo Fisher HIV-1 Genotyping Kit (with Integrase)

Product: HIV (Sanger)

Number of samples: 8

Total data quantity: 15.47 MB

CLICK HERE TO UPLOAD 72 FILES AND RUN YOUR ANALYSIS0/72 UPLOADED

	Sample	Region	Plate	Primer	File name	Size	File status		
<div><div></div><div>A1</div></div>		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	
		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

Sequencing platform: Sanger

Assay: Thermo Fisher HIV-1 Genotyping Kit (with Integrase)

Product: HIV (Sanger)

Number of samples: 8

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	
<div><div></div><div>A1</div></div>		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  


⏪

 Dashboard


 Create job




 View jobs


 FAQs

 Contact us





Jobs

Page of 1  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  


⏪

 Dashboard


 Create job




 View jobs

 FAQs

 Contact us

Jobs

Page of 1  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

<<

Dashboard

Create job

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Contact us

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.

<<

Dashboard

Create job

View jobs

FAQs

Contact us

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

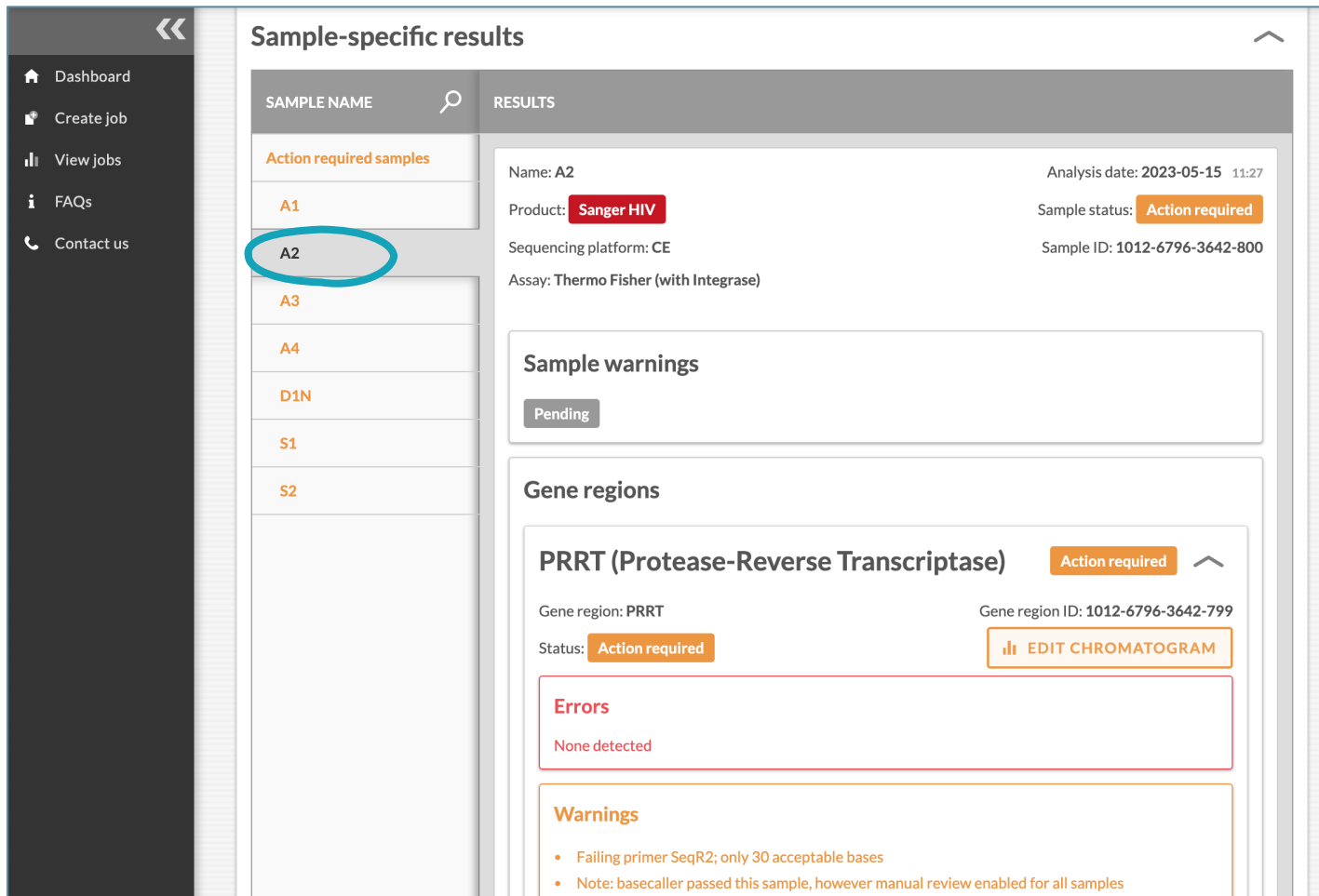
Once the first step completes, chromatogram review is required

The screenshot displays a web application interface for reviewing sample 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 with two columns: 'SAMPLE NAME' and 'RESULTS'. The 'SAMPLE NAME' column lists samples A1, A2, A3, A4, D1N, S1, and S2. Sample A1 is highlighted with a blue circle, and the header 'Action required samples' is shown in orange. The 'RESULTS' column for sample A1 provides detailed information: Name: A1, Analysis date: 2023-05-15 11:27, Product: Sanger HIV (in a red box), Sample status: Action required (in an orange box), Sequencing platform: CE, Assay: Thermo Fisher (with Integrase), and Sample ID: 1012-6796-3642-797. Below this, there are two sections: 'Sample warnings' with a 'Pending' status, and 'Gene regions' which lists 'PRRT (Protease-Reverse Transcriptase)' and 'IN (Integrase)', both marked as 'Action required' with orange buttons and dropdown arrows.

SAMPLE NAME	RESULTS
Action required samples	
A1	<p>Name: A1 Analysis date: 2023-05-15 11:27</p> <p>Product: Sanger HIV Sample status: Action required</p> <p>Sequencing platform: CE Sample ID: 1012-6796-3642-797</p> <p>Assay: Thermo Fisher (with Integrase)</p> <p>Sample warnings</p> <p>Pending</p> <p>Gene regions</p> <p>PRRT (Protease-Reverse Transcriptase) Action required ▼</p> <p>IN (Integrase) Action required ▼</p>
A2	
A3	
A4	
D1N	
S1	
S2	

PRODUCT SCREENSHOTS

Once the first step completes, chromatogram review is required



Sample-specific results

SAMPLE NAME **RESULTS**

Action required samples

SAMPLE NAME	RESULTS
A1	
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)
A3	
A4	
D1N	
S1	
S2	

Sample warnings

Pending

Gene regions

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

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

Status: Action required **EDIT CHROMATOGRAM**

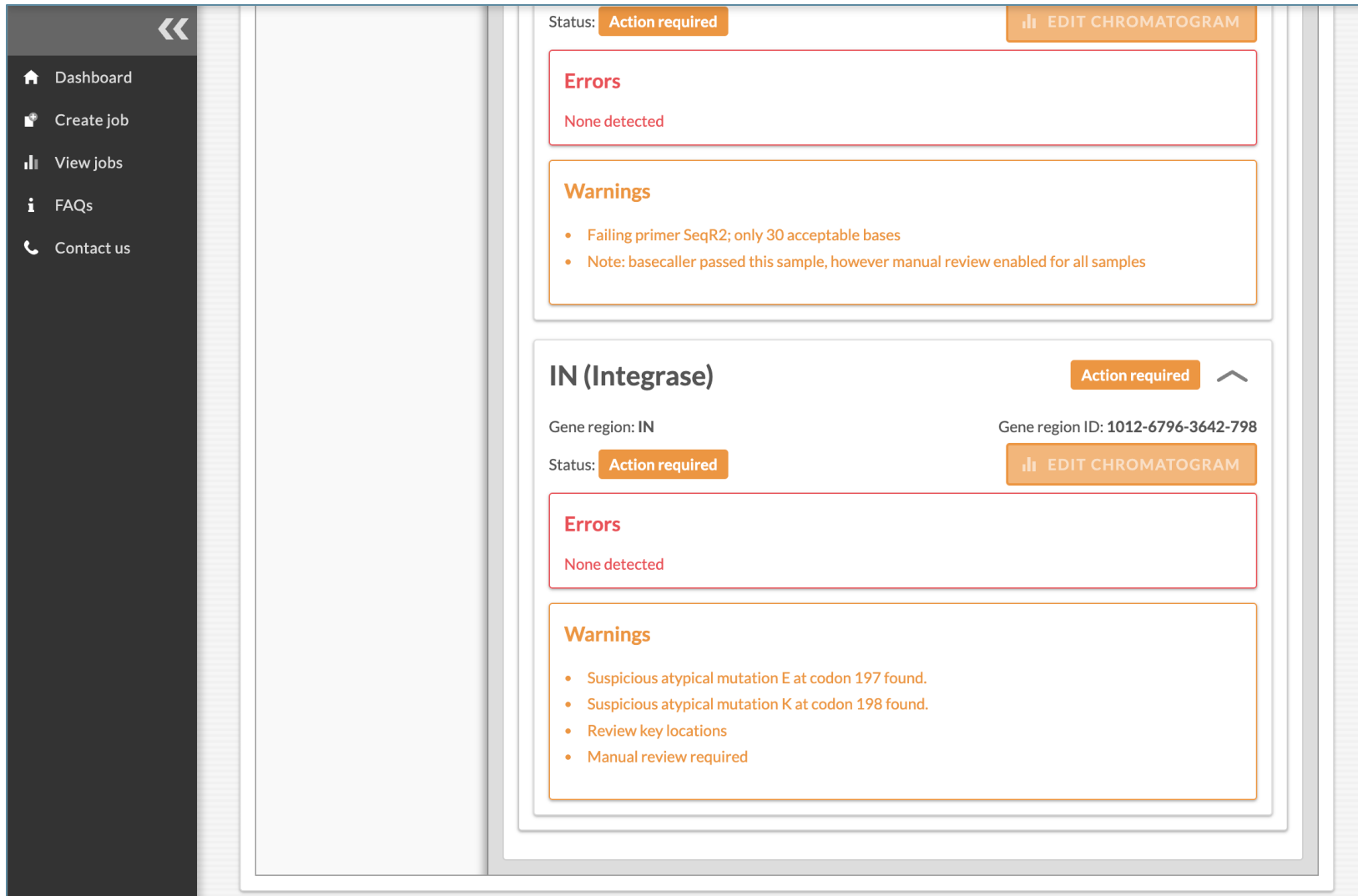
Errors

None detected

Warnings

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

PRODUCT SCREENSHOTS



PRODUCT SCREENSHOTS

Dashboard

Create job

View jobs

FAQs

Contact us

Edit chromatogram

Sample name: **A2 (PRRT)**

EXIT

OPEN MAP

(1) W
W

(2) Q
Q

(3) R
R

(4) P
P

(5 key) L10
L

(6 key) V11
V

Reference Protein

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

Standard Assembled

SeqR3_PRRT (reverse)

1

T G G C A A C G A C 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 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

MIXTURE COMPOSITIONS:

R = A/G
B = C/G/T
M = A/C

Y = C/T
D = A/G/T

K = G/T
H = A/C/T

S = G/C
V = A/C/G

W = A/T
N = A/C/G/T

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

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Edit chromatogram

Sample name: **A2 (PRRT)**

EXITCLOSE MAP

SeqR3_PRRTSeqF1_PRRTSeqR1_PRRTSeqF2_PRRTSeqF3_PRRT

Standard

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

T G G C A A C G A C C C C T C G TStandard

T G G C A A C G A C C C C T T G TAssembled

SeqR3_PRRT (reverse)

1 T G G C A A C G A C 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:

MIXTURE COMPOSITIONS:

R = A/GY = C/TK = G/TS = G/CW = A/T

B = C/G/TD = A/G/TH = A/C/V = A/C/G

M = A/CN = A/C/G/T

SAMPLE INFO

Sample nameA2

Sample ID1725-0977-7372-262

Gene regionPRRT

Gene region ID1725-0977-7372-264

Upload date2023-07-29 at 01:18

StatusManual review

Mixtures9 (cutoff: 15%)

Marks4

⚠ 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

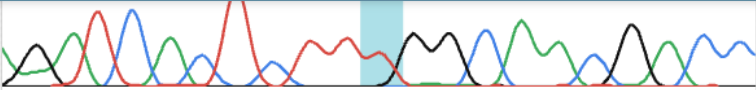
Dashboard

Create job

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Contact us



USE THE FOLLOWING KEYS TO NAVIGATE:

Next marked base:

Previous marked base:

Next base:

Previous base:

Next marked key base:

Previous marked key base:

Next key amino acid:

Previous key amino acid:

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

B = C/G/T
M = A/C

D = A/G/T
H = A/C/T
V = A/C/G
N = A/C/G/T

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.

Amino acid number

» JUMP TO AMINO ACID

SAVE

✓ SAVE & PASS

✗ FAIL SAMPLE

EXIT

Are you sure you want to save your edits and pass this sample?

CONFIRM

CANCEL

PRODUCT SCREENSHOTS

The screenshot displays a web application interface for sequencing 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 divided into two columns. The left column, titled 'SAMPLE NAME', contains a search icon and a list of sample names: A1, A2, A3, A4, D1N, S1, and S2. The right column, titled 'RESULTS', shows details for sample A2. At the top, it lists 'Name: A2', 'Product: Sanger HIV', 'Sequencing platform: CE', and 'Assay: Thermo Fisher (with Integrase)'. To the right of these details are 'Analysis date: 2023-05-15 11:27', 'Sample status: Action required', and 'Sample ID: 1012-6796-3642-800'. Below this is a 'Sample warnings' section with a 'Pending' status. The 'Gene regions' section highlights 'PRRT (Protease-Reverse Transcriptase)' with a 'Completed' status (circled in blue) and a 'VIEW CHROMATOGRAM' button. Below the gene region details are two boxes: 'Errors' (None detected) and 'Warnings' (Failing primer SeqR2; only 30 acceptable bases, Note: basecaller passed this sample, however manual review enabled for all samples, Passed by manual review).

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SAMPLE NAME

SEARCH

Action required samples

A1

A2

A3

A4

D1N

S1

S2

RESULTS

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

Sample warnings

Pending

Gene regions

PRRT (Protease-Reverse Transcriptase)

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

<<

Dashboard

Create job

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A1

A2

A3

A4

D1N

S1

S2

Product: **Sanger HIV**

Sequencing platform: CE

Assay: Thermo Fisher (with Integrase)

Sample status: **Action required**

Sample ID: 1012-6796-3642-800

Sample warnings

Pending

Gene regions

PRRT (Protease-Reverse Transcriptase)

Completed

IN (Integrase)

Action required

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

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SAMPLE NAME

RESULTS

Action required samples

A1

A3

A4

D1N

S1

S2

Completed samples

A2

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

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)

SeqR12_IN

Standard

SeqF11_IN

SeqR11_IN

SeqF12_IN

(229) D

(230 key) S230 S

(231) R

(232 key) N232 D

(233) P

(234) L

(235) W

(236) K

(237) G

Reference Protein

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

Standard Assembled

SeqF11_IN (forward)

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

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

SeqF12_IN (forward)

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

MIXTURE COMPOSITION

R = A/G Y = C/T K =

B = C/G/T D = A/G/T H =

M = A/C

SAMPLE INFO

EDIT HISTORY

* UNSAVED

Base

Original

Updated

694

G

R

Edit chromatogram

Sample name: A1 (IN)

SeqR12_IN

Standard

SeqF11_IN

SeqR11_IN

SeqF12_IN

(229) D

(230 key) S230 S

(231) R

(232 key) N232 D.N

(233) P

(234) L

(235) W

(236) K

(237) G

Reference Protein

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

Standard Assembled

SeqF11_IN (forward)

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

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

SeqF12_IN (forward)

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

MIXTURE COMPOSITIONS

R = A/G Y = C/T K =

B = C/G/T D = A/G/T H =

M = A/C

SAMPLE INFO

Sample name

Sample ID

Gene region

Gene region ID


Upload date

Status


Mixtures


Marks


PRODUCT SCREENSHOTS



×

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

 Hyrax - Thermo Fisher Demo



⌵

⏪

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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



×

 Your job "Demo" has completed successfully.

 Hyrax - Thermo Fisher Demo



⌵

⏪

Dashboard


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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

<<

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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

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

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

Locus	Position	Amino acid	Status

PRODUCT SCREENSHOTS

<<

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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

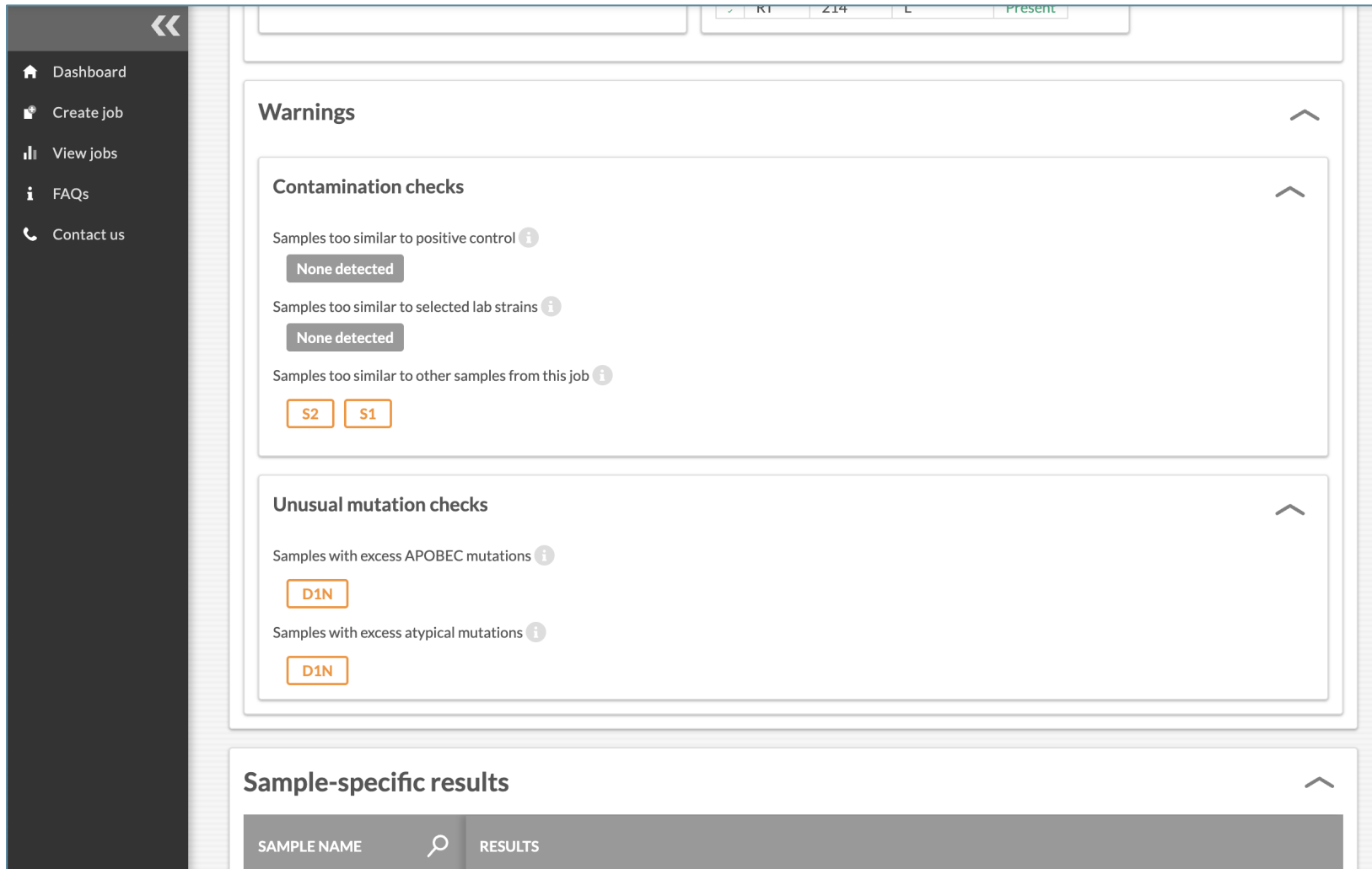
Region: PRRT

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



PRODUCT SCREENSHOTS

<<

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Sample-specific results

SAMPLE NAME

RESULTS

Completed samples

A2

A3

D1N

S1

S2

A4 *

Failed samples

A1

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

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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

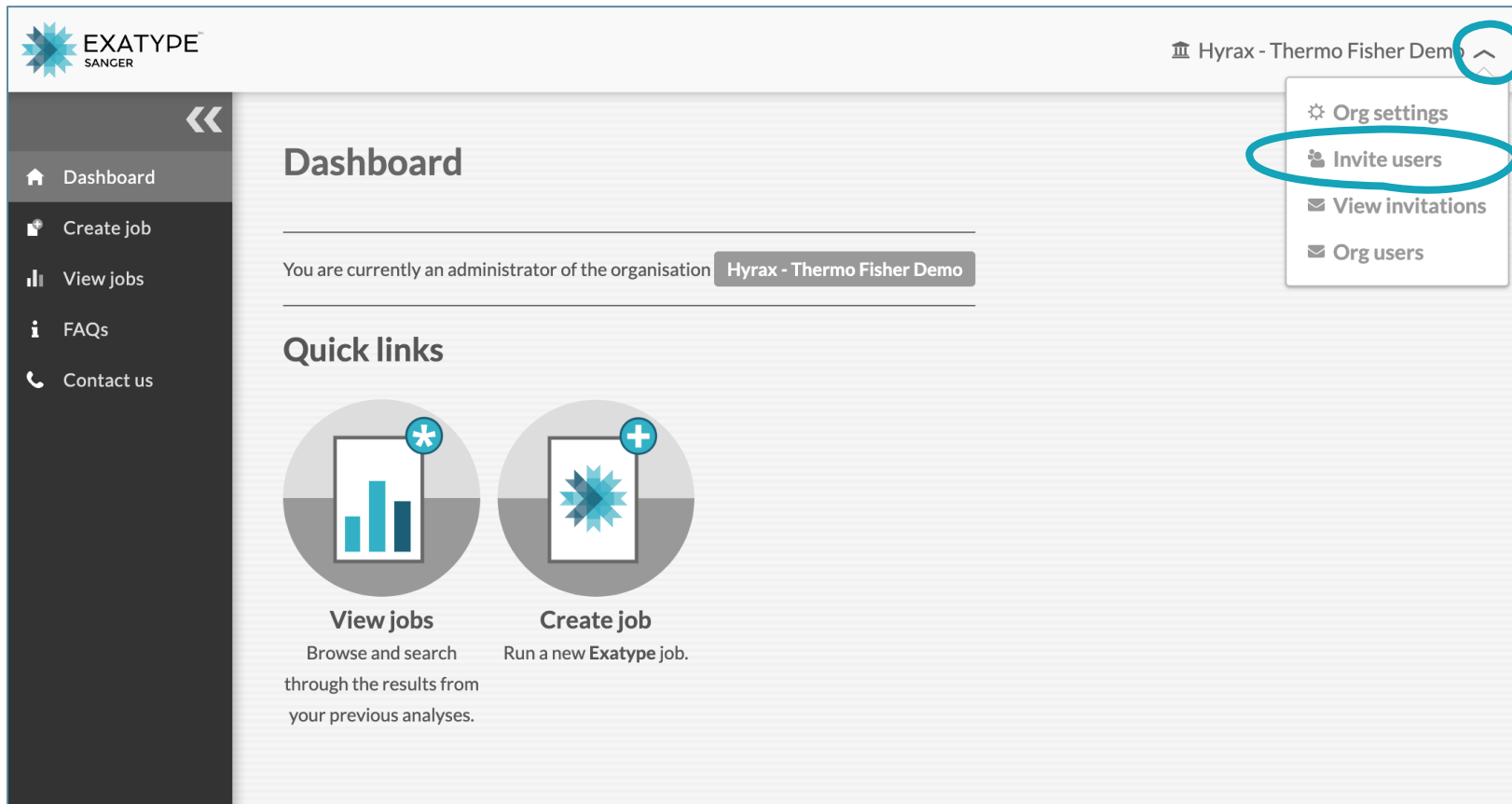
[Demo.summary.tsv](#)

PRODUCT SCREENSHOTS

[View all your analyses](#)

PRODUCT SCREENSHOTS

Single organisational signup/licence with multiple users



The screenshot displays the Exatype Sanger Hyrax dashboard for an administrator. The interface includes a top header with the Exatype Sanger logo and the organization name 'Hyrax - Thermo Fisher Demo'. A left sidebar contains navigation links: 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 offers options to 'View jobs' and 'Create job'. A dropdown menu in the top right corner, triggered by a user icon, lists administrative actions: '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

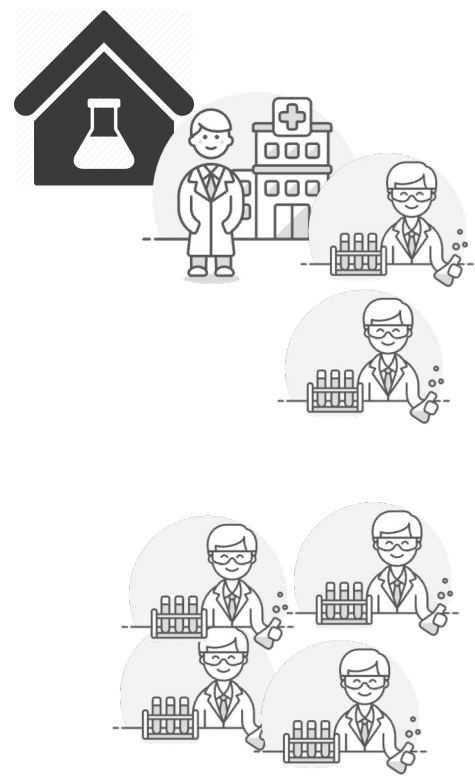
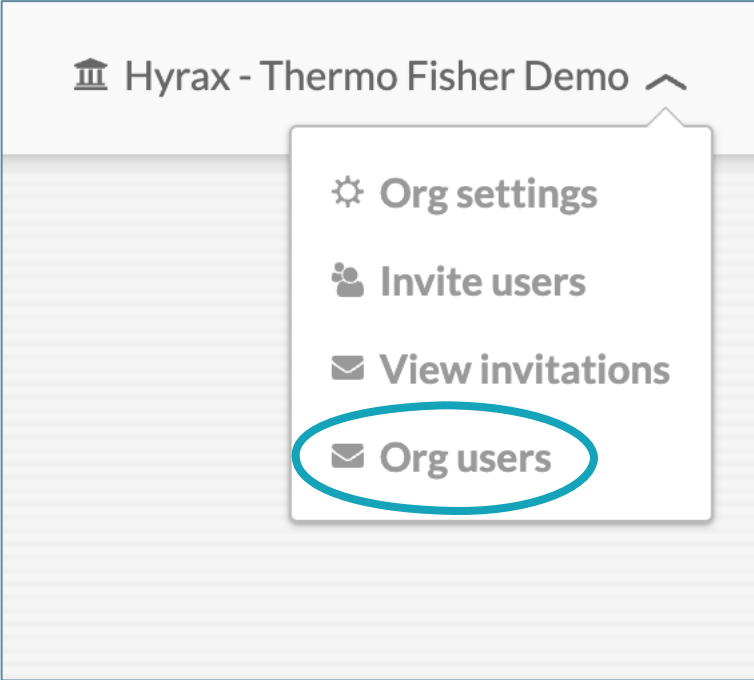
You have been invited to join the organisation Hyrax - Thermo Fisher Demo by natasha+TF2@hyraxbio.com.

✓ 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: HIV Sanger - FAQs

[View as plain text](#)