



How to fill in results
Sexually transmitted diseases
multiplex,
nucleic acid detection

Quick guide for result reporting

1. Start from LabScala home page by choosing My Schemes
→ Fill results → choose correct round.
2. Add Specific Contact, choose Next.
3. Read Instructions, choose Next.
4. Update Sample registration, choose Save & next
5. Reporting results: First report the number of findings identified in the specimen. Then choose correct pos/neg interpretation and test method for each analyte. Fill in the test result and possible further actions.
6. Save as final. Move to next specimen by choosing Next.
7. Finally, validate your results or if needed update them. Choose Accept and send results.

Result reporting

The screenshot shows the LabScala user interface. The top navigation bar includes 'My Orders', 'My Schemes' (highlighted with a red circle), 'My Registry', 'My Documents', and 'Administration'. Below the navigation bar, there are two main sections: 'My EQA & shortcuts' and 'Reports & messages'.

My EQA & shortcuts

SHORTCUTS

- Place orders
- Go to Mainio
- Fill results (Mainio)
- Delivery calendar

MY ROUNDS

Round entry	Closing date	Response Status	Form	Info
Leukocyte differential count, 5-part (18)				
March, 1-2018	06.04.2018	Not sent	LabScala	⚠
Norovirus, nucleic acid detection (2)				
March, 1-2018	12.04.2018	Not sent	LabScala	
Helicobacter pylori, antibodies (2)				
March, 1-2018	12.04.2018	Not sent	LabScala	⚠
Helicobacter pylori, antigen detection in faeces (2)				
March, 1-2018	12.04.2018	Not sent	LabScala	⚠
Synovial fluid crystals (2)				
March, 1-2018	24.04.2018	Not sent	LabScala	

[View all](#)

Reports & messages

MY REPORTS

Report

MESSAGES

Choose correct EQA round on the front page or by choosing My Schemes, Fill results

In the view of the next 5 closing schemes, the closing date and the status of the scheme can be seen

Fill results = eForm open for result filling

Not sent = result filling started but results not sent to Labquality

Sent = results sent to Labquality

Request

- After opening the scheme the request page is opened with the following information
 - **Product:** Here it can be seen what and how much has been ordered (e.g. Sexually transmitted diseases multiplex (2) means 2 sets of samples ordered)
 - **Instructions:** Scheme specific instructions can be read and printed
 - **Pre-analytics:** Sample arrival date, quantity received, sample storage conditions etc.
 - **Analytics:** Analyte specific results can be filled
 - **Postanalytics:** Validate results
 - **Exit:** Back to the front page
- Also the scheme specific contact information is filled here
 - The contact person receives reminders and important scheme specific information
 - **At least one contact person needs to be named!**

Welcome to the round of Sexually transmitted diseases multiplex, nucleic acid detection, April, 1-2018 analysis



[LabScala User instructions](#)

[Request](#)>>[Instructions](#)>>[Pre-analytics](#)>>[Analytics](#)>>[Post-analytics](#)>>[Exit](#)

MY ORDERS



Product	Delivery	Opening	Closing	Status	Form
Sexually transmitted diseases multiplex, nucleic acid detection(2)					
	10.04.2018	11.04.2018	04.05.2018	Ordered	LabScala

MY SCHEME SPECIFIC CONTACTS

Name	Send E-mail notification to	
Test	testi@testmaili.com	 

► Coordinator contact information

By pressing the "Next" button LabScala will automatically move you forward

Pre-analytics

- In Pre-analytics, the following is asked
 - **Sample arrival date**
 - **Quantity received:** How many sample sets were received
 - **Sample storage condition:** How have the samples been stored before analysis (refrigerator, room temperature, freezer, other)
 - **Sample preparation date:** If done, if not, can be left empty
- Comments can be saved if needed

Request>>Instructions>>**Pre-analytics**>>Analytics>>Post-analytics>>Exit

Sample registration

▼ Sample registration

Product	Has eForm	Code	Quantity ordered	Sample arrival date	Quantity received	Sample storage conditions	Sample preparation date
Sexually transmitted diseases multiplex, nucleic acid detection, April, 1-2018	Yes	5302	2	10.04.2018 	2	- Choose - 	

COMMENTS

Save & next

Exit

Pre-analytics – Test selection















- Report the measurement date, test selection (tick the box) and method. This information is transferred automatically to each sample and to the next round.
- You can change this information sample-wise or return to this page in order to change the information for all samples.

Request>>Instructions>>**Pre-analytics**>>Analytics>>Post-analytics>>Exit

Sample registration

Test selection

▼ 5302 - Sexually transmitted diseases multiplex, nucleic acid detection

Measurement date	Analyte	In test selection	Method
16.08.2019 	Chlamydia trachomatis	<input checked="" type="checkbox"/>	Fast-track Diagnostics FTD STD9  
16.08.2019 	Mycoplasma genitalium	<input type="checkbox"/>	
16.08.2019 	Neisseria gonorrhoeae	<input checked="" type="checkbox"/>	Seegene Allplex STI Essential  
16.08.2019 	Trichomonas vaginalis	<input checked="" type="checkbox"/>	Seegene Allplex STI Essential  
16.08.2019 	Ureaplasma urealyticum	<input checked="" type="checkbox"/>	Seegene Allplex STI Essential  

Save & next

Exit

Results – how to start

- If you have ordered multiple sample sets, the sets can be seen on the top of this view
- If the scheme has multiple samples, the samples are listed on top of the result form (e.g. S001, S002, S003 and S004)
- First, report the number of pathogenic findings that were identified from the specimen.

Specimen S001

Specimen S002

Specimen S003

Specimen S004

▼ Results

Number of pathogenic findings

-choose -

-choose -

Negative sample, no pathogens detected

Positive sample, 1 pathogen detected

Positive sample, 2 pathogens detected

Positive sample, 3 pathogens detected

Positive sample, 4 or more pathogens detected

Interpretation cannot be given

* Measurement date	Analyte	* Interpretation	Result and unit
16.08.2019	Chlamydia trachomatis	Seegene Allplex STI Essenl	-choose -
16.08.2019	Mycoplasma genitalium	Seegene Allplex STI Essenl	-choose -
16.08.2019	Neisseria gonorrhoeae	Seegene Allplex STI Essenl	-choose -
16.08.2019	Trichomonas vaginalis	Seegene Allplex STI Essenl	-choose -
16.08.2019	Ureaplasma urealyticum	Seegene Allplex STI Essenl	-choose -

Further action

- Select -

COMMENTS

Results – Interpretations

- Report the interpretation of each pathogen separately and the test result (e.g. Ct value). If you wish, you may copy e.g. interpretation “negative” to all analytes and then change the deviating results. **All interpretations are mandatory to answer.**
 - The analytes which were not ticked as “In test selection” in the Test selection tab are automatically marked as “Not in test selection” in the Analytics page.
 - If the pathogen is routinely tested in your laboratory, but the test has not been performed for one reason or another, please select “**No result**”.
 - If the test has been performed but it is not possible to give an interpretation, please select “**Invalid/unclear test result**”
 - You can give additional information in the comments field at the bottom of the page.

Specimen S001
Specimen S002
Specimen S003
Specimen S004

▼ Results

Number of pathogenic findings

* Interpretation
Negative sample, no pathogens detected ▼

* Measurement date	Analyte	* Method	* Interpretation	Result and unit
16.08.2019	Chlamydia trachomatis	Fast-track Diagnostics FTD	-choose -	
16.08.2019	Mycoplasma genitalium		-choose -	
16.08.2019	Neisseria gonorrhoeae	Seegene Allplex STI Essenl	Negative	
16.08.2019	Trichomonas vaginalis	Seegene Allplex STI Essenl	Weak positive	
16.08.2019	Ureaplasma urealyticum	Seegene Allplex STI Essenl	Positive	
			Invalid/unclear test result	
			No test result	
			Not in test selection	
			-choose -	

Further action
- Select - ▼

COMMENTS

Results

- Finally, select
 - **“Save as final”** if you consider your results as ready. You can still edit your results after saving as final.
 - “Save as draft” if you do not yet want to send in the results.

Analyte			* Interpretation
Number of pathogenic findings			Positive s ▼

* Measurement date	Analyte	* Method	* Interpretation	Result and unit
16.08.2019	Chlamydia trachomatis	Fast-track Diagnostics FTD	Negative ▼	<input type="text"/>
16.08.2019	Mycoplasma genitalium		Not in test selection ▼	
16.08.2019	Neisseria gonorrhoeae	Seegene Allplex STI Essent	Positive ▼	<input type="text"/>
16.08.2019	Trichomonas vaginalis	Seegene Allplex STI Essent	Negative ▼	<input type="text"/>
16.08.2019	Ureaplasma urealyticum	Seegene Allplex STI Essent	Negative ▼	<input type="text"/>

Further action

N. gonorrhoeae would be co... ▼

COMMENTS

[Back to list](#) [Clear all page data](#) [Save as draft](#) [Save as final](#)

Results

- After Save as final you can move to next sample by choosing **Next**
- You can re-open the sample by choosing Edit data or print your results by choosing print

Analyte	* Interpretation
Number of pathogenic findings	Positive sample, 1 pathogen detected

* Measurement date	Analyte	* Method	* Interpretation	Result and unit
16.08.2019	Chlamydia trachomatis	Fast-track Diagnostics FTD STD9	Negative	
16.08.2019	Mycoplasma genitalium		Not in test selection	
16.08.2019	Neisseria gonorrhoeae	Seegene Allplex STI Essential	Positive	
16.08.2019	Trichomonas vaginalis	Seegene Allplex STI Essential	Negative	
16.08.2019	Ureaplasma urealyticum	Seegene Allplex STI Essential	Negative	

Further action
N. gonorrhoeae would be confirmed

COMMENTS

Back to list Edit data Print

Next

Post-analytics

- Next the user is taken to the result validation
 - **Product:** What part of the process is being validated
 - **Sample set:** Which sample set is being validated
 - **Sample:** Which sample is being validated
 - **Errors:** If there are analyte specific validation limit errors these are shown here
 - **Last saved:** The user who has saved the results
 - **Date:** Date of last saving
 - **Status:** Status of the results (**Accepted**, **Draft**, **Error**)

Sexually transmitted diseases multiplex, nucleic acid detection, April, 1-2018 postanalytics

[? LabScala User instructions](#)

Request>>Instructions>>Pre-analytics>>Analytics>>**Post-analytics**>>Exit

Validate results

▼ Validation results

Product	Sample set	Sample	Errors	Last saved	Date	Status
Sexually transmitted diseases multiplex, nucleic acid detection	1	Specimen S001	OK	Elina Tuovinen	09.04.2018 13:49	Accepted
Sexually transmitted diseases multiplex, nucleic acid detection	1	Specimen S002	OK	Elina Tuovinen	09.04.2018 13:52	Draft
Sexually transmitted diseases multiplex, nucleic acid detection	1	Specimen S003	Row "Ureaplasma urealyticum" is incorrect. "Interpretation" is mandatory in form "Results 1".	Elina Tuovinen	09.04.2018 13:51	Error
Sexually transmitted diseases multiplex, nucleic acid detection	1	Specimen S004	OK	Elina Tuovinen	09.04.2018 10:17	Open

Post-analytics

- The results can be edited by selecting the correct sample
- When all of the states are such that the results can be send to Labquality, select "Accept and send results"
- If you wish not to send the results yet, select "Exit"
- The results can be edited as long as the round is open, even if "Accept and send results" has been selected

Validate results

▼ Validation results

Product	Sample set	Sample	Errors	Last saved	Date	Status
Sexually transmitted diseases multiplex, nucleic acid detection	1	Specimen S001	OK	Luiro, Kati	30.08.2019 08:03	Accepted
Sexually transmitted diseases multiplex, nucleic acid detection	1	Specimen S002	OK	Luiro, Kati	30.08.2019 08:03	Accepted
Sexually transmitted diseases multiplex, nucleic acid detection	1	Specimen S003	OK	Luiro, Kati	30.08.2019 08:04	Accepted
Sexually transmitted diseases multiplex, nucleic acid detection	1	Specimen S004	OK	Luiro, Kati	30.08.2019 08:05	Accepted

Accept and send results

Exit

LabScala buttons



Enables you to save changes on the form



Takes you back to the previous view



Enables you to add some information. In tables it adds a row.



Edit button enables you to edit texts and information



Delete button enables you to delete texts and information



Accept button marks something as being accepted or valid



Lookup button marks a search field where you can enter text to be searched for



List button marks a field where you can search from the background register



To the Home page

Questions?

- In case you have questions, please contact:
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