



How to fill in results
Multiplex, nucleic acid detection
schemes (excluding 5191)

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. Pre-analytics: Add measurement date, test selection and method, choose Save & next.
6. Reporting results: First report the number of findings identified in the specimen. Then choose correct interpretation. Fill in the test result (Ct value).
7. Save as final. Move to next specimen by choosing Next.
8. Finally, validate your results or if needed update them. Choose Accept and send results.

Result reporting

The screenshot shows the LabScala user interface. At the top, there is a navigation bar with the following items: My Orders, My Schemes (circled in red), My Registry, My Documents, and Administration. Below the navigation bar, there are two main sections: 'My EQA & shortcuts' and 'Reports & messages'. The 'My EQA & shortcuts' section contains a 'SHORTCUTS' area with links for 'Place orders', 'Go to Mainio', 'Fill results (Mainio)', and 'Delivery calendar'. Below this is a 'MY ROUNDS' section with a table of EQA rounds. The table has columns for Round entry, Closing date, Response Status, Form, and Info. The 'Reports & messages' section contains a 'MY REPORTS' area with a 'Report' button and a 'MESSAGES' area.

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	

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 can be seen which product and how many sample sets has been ordered (e.g. Faecal parasites multiplex, nucleic acid detection (1) means 1 set of samples ordered).
 - **Instructions:** Scheme specific instructions can be read and printed.
 - **Pre-analytics:** Sample arrival date, sample storage conditions, test selection, method 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 Faecal parasites multiplex, nucleic acid detection, May, 2-2023 analysis

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Your results have not been sent to Labquality.

Please note that results that are in draft status or have not been sent, might be excluded from the evaluation.

MY ORDERS

Product	Delivery	Opening	Closing	Status	Information
Faecal parasites multiplex, nucleic acid detection(1)					
	16.05.2023	16.05.2023	08.06.2023	Closed	

MY SCHEME SPECIFIC CONTACTS

Name	Send E-mail notification to	
Test	test@test.com	 

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

Next

Exit

Pre-analytics – Sample registration

- In sample registration, the following is asked:
 - **Sample arrival date.**
 - **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.
- Move forward by selecting "Save & next".

Faecal parasites multiplex, nucleic acid detection, May, 2-2023 pre-analytics

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Sample registration Test selection

▼ Sample registration

Product	Code	Sample arrival date	Sample storage conditions	Sample preparation date
Faecal parasites multiplex, nucleic acid detection, May, 2-2023	5472	19.05.2023	+2 ... +8 C	

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.
- Move forward by selecting "Save & next".

Faecal parasites multiplex, nucleic acid detection, May, 2-2023 pre-analytics












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Sample registration

Test selection

5472 - Faecal parasites multiplex, nucleic acid detection

Measurement date	Analyte	In test selection	Method
19.05.2023 	Giardia lamblia	<input checked="" type="checkbox"/>	BioFire FilmArray Gastrointestinal ( )
19.05.2023 	Cryptosporidium	<input checked="" type="checkbox"/>	BioFire FilmArray Gastrointestinal ( )
19.05.2023 	Entamoeba histolytica	<input checked="" type="checkbox"/>	BioFire FilmArray Gastrointestinal ( )
19.05.2023 	Dientamoeba fragilis	<input type="checkbox"/>	

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 and S003).
- First, report the number of pathogenic findings that were identified from the specimen.

2399: Faecal parasites multiplex, nucleic acid detection, May, 2-2023 - Sample set 1 (Specimen S001)

Help

<<Previous step>>Faecal parasites multiplex, nucleic acid detection>>Next step

SAMPLE SETS

First Previous **1** Next Last

Specimen S001 Specimen S002 Specimen S003

▼ Results

		* Interpretation		
Number of pathogenic findings		-choose -		
* Measurement date	Analyte	* M	Interpretation	Result and unit
19.05.2023	Giardia lamblia	Bio	-choose -	
19.05.2023	Cryptosporidium	Bio	Negative sample, no pathogens detected	
19.05.2023	Entamoeba histolytica	Bio	Positive sample, 1 pathogen detected	
19.05.2023	Dientamoeba fragilis	Bio	Positive sample, 2 pathogens detected	
			Positive sample, 3 pathogens detected	
			Positive sample, 4 or more pathogens detected	
			Interpretation cannot be given	

Norm test selection

Results – Interpretation

- 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 result/s separately.
 - 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.

		* Interpretation		
Number of pathogenic findings		Positive sample, 1 pathogen detected		
* Measurement date	Analyte	* Method	* Interpretation	Result and unit
19.05.2023	Giardia lamblia	BioFire FilmArray Gastroint	-choose -	
19.05.2023	Cryptosporidium	BioFire FilmArray Gastroint	-choose -	
19.05.2023	Entamoeba histolytica	BioFire FilmArray Gastroint	Negative	
19.05.2023	Dientamoeba fragilis		Weak positive	
			Positive	
			Invalid/unclear test result	
			No test result	
			Not in test selection	

COMMENTS FOR YOUR OWN INTERNAL USE ONLY, WILL NOT BE TAKEN INTO ACCOUNT DURING RES

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.

Specimen S001 Specimen S002 Specimen S003

▼ Results

* Interpretation

Number of pathogenic findings: Positive sample, 1 pathogen detected

* Measurement date	Analyte	* Method	* Interpretation	Result and unit
19.05.2023	Giardia lamblia	BioFire FilmArray Gastroint	Positive	Ct 24.30
19.05.2023	Cryptosporidium	BioFire FilmArray Gastroint	Negative	
19.05.2023	Entamoeba histolytica	BioFire FilmArray Gastroint	Negative	
19.05.2023	Dientamoeba fragilis		Not in test selection	

COMMENTS FOR YOUR OWN INTERNAL USE ONLY, WILL NOT BE TAKEN INTO ACCOUNT DURING RESULT PROCESSING.

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.

Specimen S001 Specimen S002 Specimen S003

▼ Results

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

* Measurement date	Analyte	* Method	* Interpretation	Result and unit
19.05.2023	Giardia lamblia	BioFire FilmArray Gastrointestinal (GI) Panel	Positive	Ct 24.30
19.05.2023	Cryptosporidium	BioFire FilmArray Gastrointestinal (GI) Panel	Negative	
19.05.2023	Entamoeba histolytica	BioFire FilmArray Gastrointestinal (GI) Panel	Negative	
19.05.2023	Dientamoeba fragilis		Not in test selection	

COMMENTS FOR YOUR OWN INTERNAL USE ONLY, WILL NOT BE TAKEN INTO ACCOUNT DURING RESULT PROCESSING.

[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).

Validate results

Validation results

Product	Sample set	Sample	Errors	Last saved	Date	Status
Preanalytics		Registration	OK	Jaana Paakkanen	05.10.2023 15:04	Accepted
Faecal parasites multiplex, nucleic acid detection	1	Specimen S001	OK	Jaana Paakkanen	05.10.2023 15:10	Accepted
Faecal parasites multiplex, nucleic acid detection	1	Specimen S002	OK	Jaana Paakkanen	05.10.2023 15:12	Draft
Faecal parasites multiplex, nucleic acid detection	1	Specimen S003	Row "Entamoeba histolytica" is incorrect. "Interpretation" is mandatory.	Jaana Paakkanen	05.10.2023 15:12	Error

Results not sent Accept and send results Exit

Post-analytics

- The results can be edited by selecting the correct sample.
- When all of the statuses are such that the results can be sent 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.

Faecal parasites multiplex, nucleic acid detection, May, 2-2023 postanalytics

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Validate results

Validation results

Product	Sample set	Sample	Errors	Last saved	Date	Status
Preanalytics		Registration	OK	Jaana Paakkanen	05.10.2023 15:04	Accepted
Faecal parasites multiplex, nucleic acid detection	1	Specimen S001	OK	Jaana Paakkanen	05.10.2023 15:10	Accepted
Faecal parasites multiplex, nucleic acid detection	1	Specimen S002	OK	Jaana Paakkanen	05.10.2023 15:13	Accepted
Faecal parasites multiplex, nucleic acid detection	1	Specimen S003	OK	Jaana Paakkanen	05.10.2023 15:13	Accepted

Results not sent

[Accept and send results](#)

[Exit](#)

LabScala buttons



Save

Enables you to save changes on the form



Back

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 the EQA Coordinator responsible of the scheme.