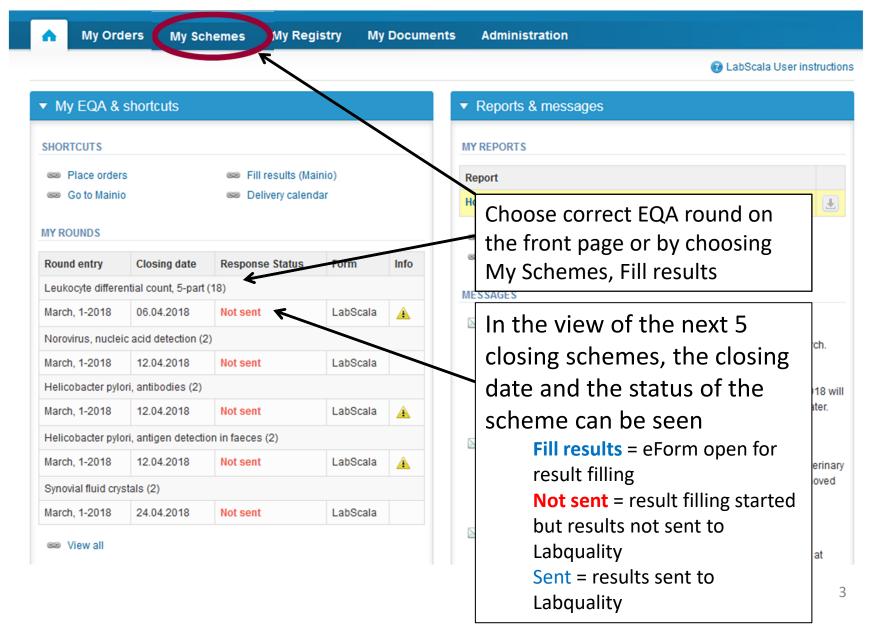


How to fill in results Respiratory infections multiplex, nucleic acid detection

Quick guide for result reporting

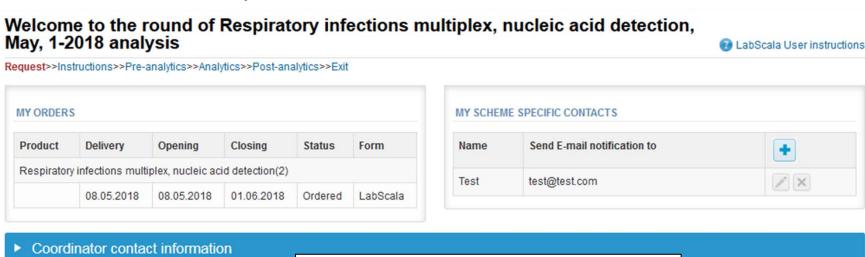
- Start from LabScala home page by choosing My Schemes
 Fill results -> choose correct round.
- 2. Add Specific Contact, choose Next.
- 3. Read Instructions, choose Next.
- 4. Update Sample registration, choose Save & next
- Reporting results: First report the number of findings identified in the specimen. Then choose correct pos/neg interpretation and test method for each analyte. Fill in the test result (Ct value).
- 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



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. Respiratory infections multiplex, nucleic acid detection (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!



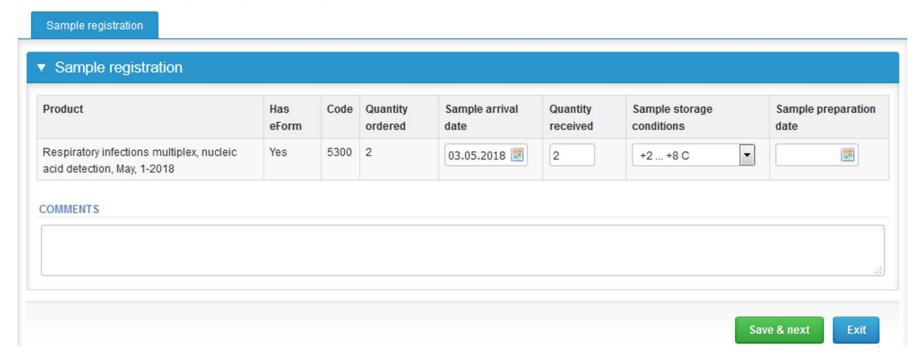
By pressing the "Next" button LabScala

will automatically move you forward

Pre-analytics

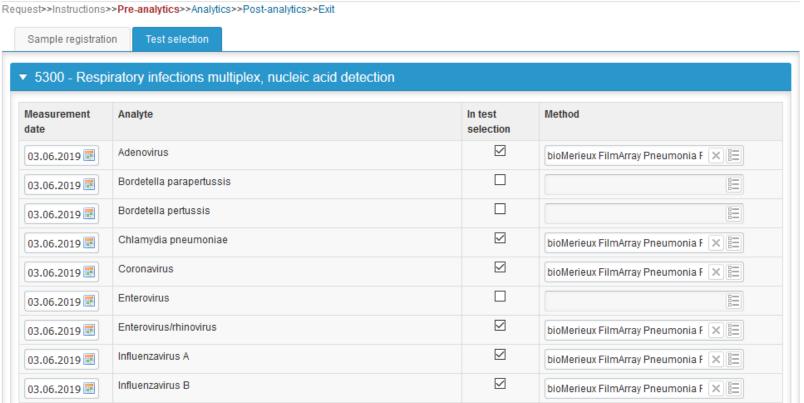
- In Pre-analytics, the following is asked
 - Sample arrival date
 - Quantity received: How many sample sets were received
 - Sample storage condition: How have the samples been stored before analysis (refrigerator, room temperature, freezer, other)
 - Sample preparation date: If done, if not, can be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

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



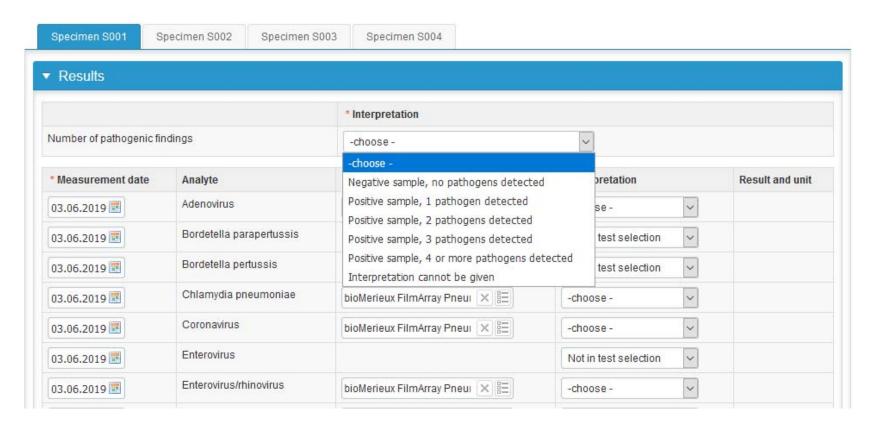
Pre-analytics – Test selection

- 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.



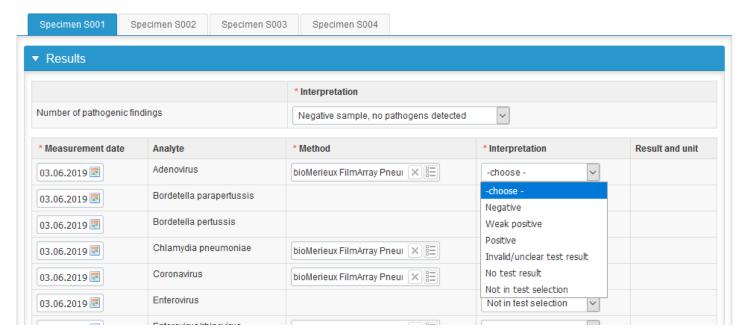
Results – how to start

- 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.



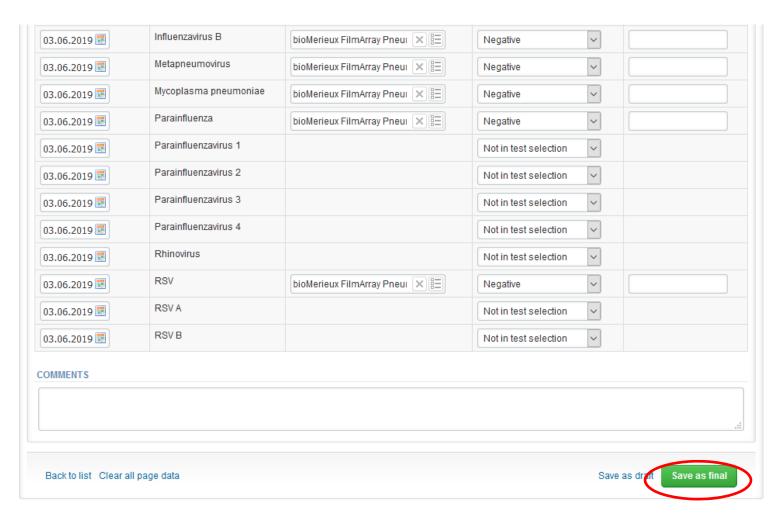
Results – Interpretations

- 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.
 - 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.



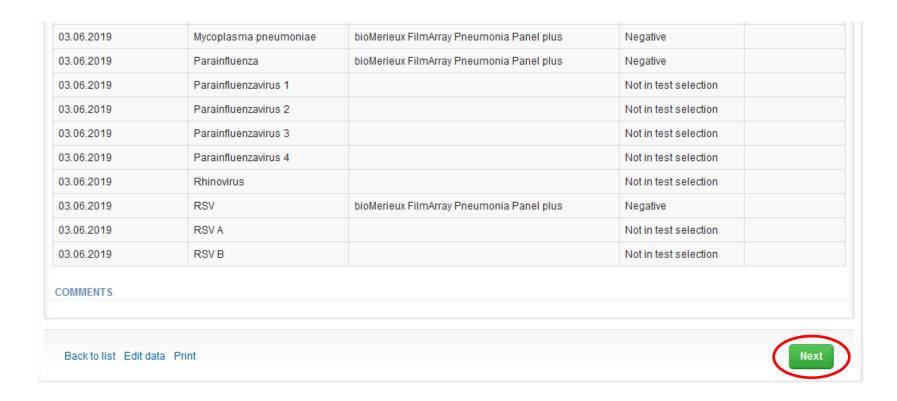
Results

- 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.



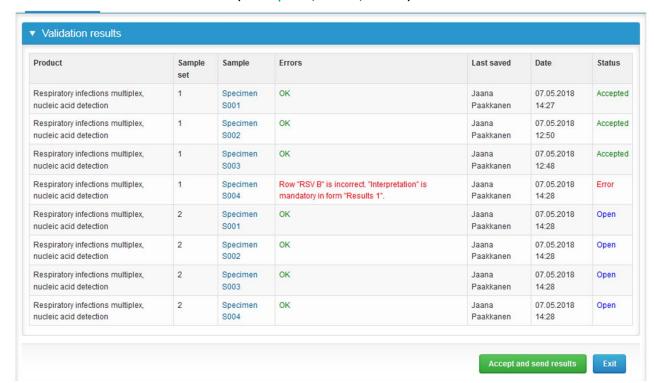
Results

- 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



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)

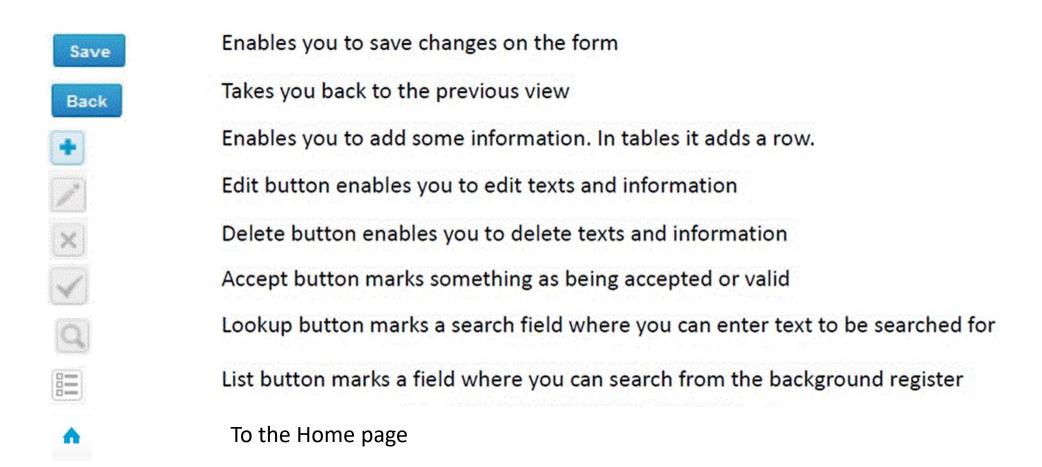


Post-analytics

- The results can be edited by selecting the correct sample
- When all of the states 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

Respiratory infections multiplex, nucleic acid detection	2	Specimen S004	ОК	Jaana Paakkanen	07.05.2018 15:03	Accepted
Respiratory infections multiplex, nucleic acid detection	2	Specimen S003	OK	Jaana Paakkanen	07.05.2018 15:02	Accepted
Respiratory infections multiplex, nucleic acid detection	2	Specimen S002	ОК	Jaana Paakkanen	07.05.2018 14:59	Accepted
Respiratory infections multiplex, nucleic acid detection	2	Specimen S001	OK	Jaana Paakkanen	07.05.2018 14:57	Accepted

LabScala buttons



Questions?

- In case you have questions, please contact:
 - Jaana Paakkanenjaana.paakkanen@labquality.fi+358 50 362 7719