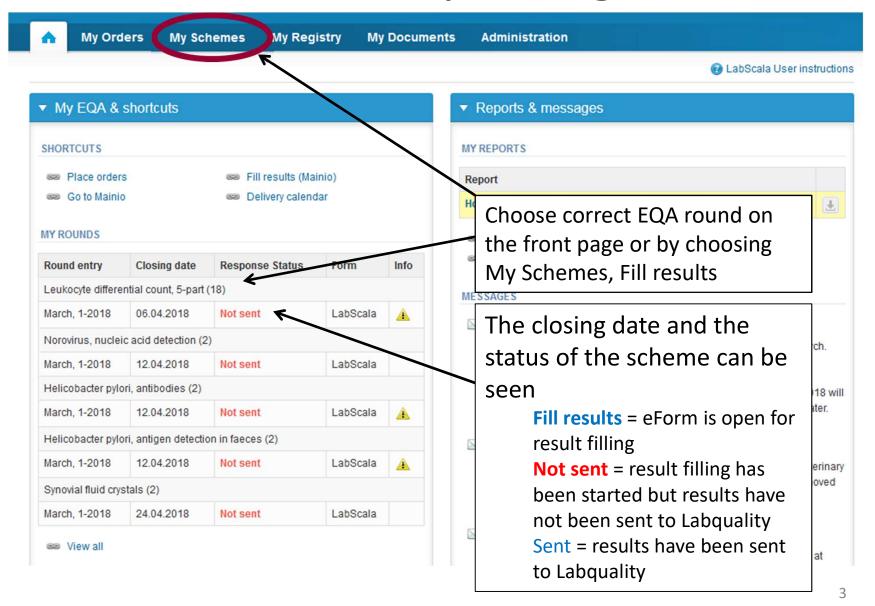


# How to fill in results Meningitis-encephalitis multiplex, nucleic acid detection

## 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) if available.
- 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. Meningitis-encephalitis 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

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

- Also the scheme specific contact information is filled in 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 Meningitis-encephalitis multiplex, nucleic acid detection, April, 1-2019 analysis

MY SCHEME SPECIFIC CONTACTS Send E-mail notification to +



Coordinator contact information

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

Name

test



/ X

LabScala User instructions

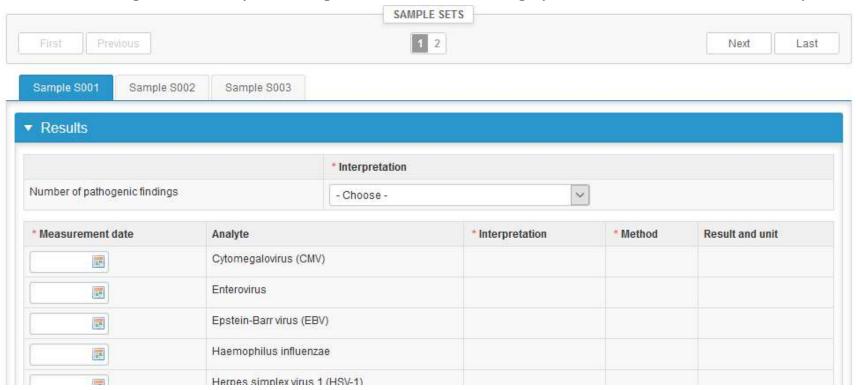
## **Pre-analytics**

- 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
- Move forward by selecting "Save & next"

Request>>Instructions>>Pre-analytics>>Analytics>>Post-analytics>>Exit Sample registration Sample registration Sample storage Sample preparation Product Has Code Quantity Sample arrival Quantity eForm ordered date received conditions date Meningitis-encephalitis multiplex, nucleic 5303 2 H. 02.04.2019 2 +2 ... +8 C acid detection, April, 1-2019 COMMENTS Save & next

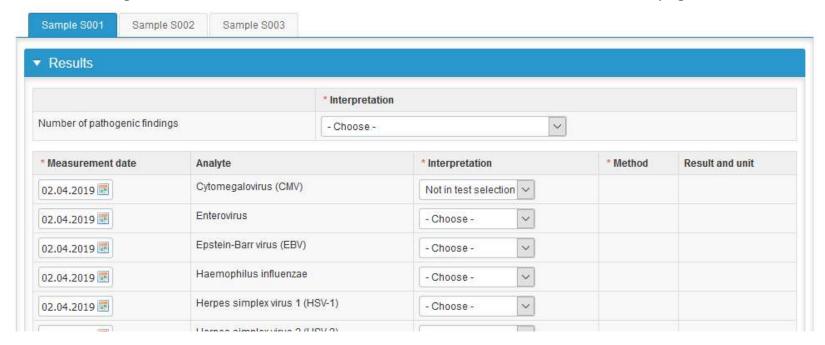
#### Results – how to start

- In "Analytics" the analyte specific results are to be reported
- If you have ordered multiple sample sets, the sets are shown 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)
- Result filling is started by selecting the number of findings you have identified in the sample.



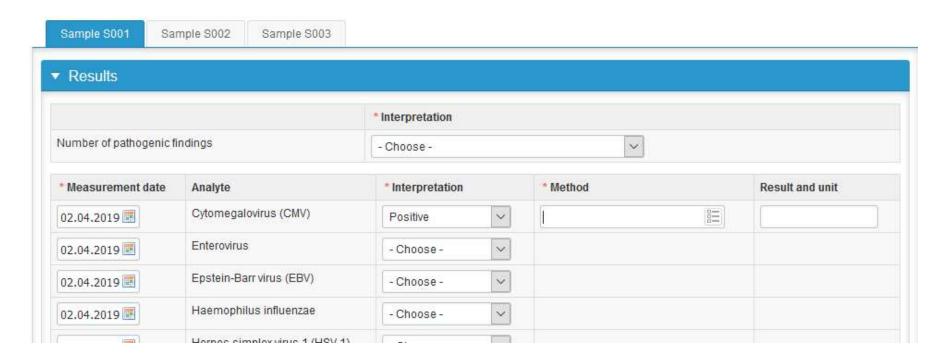
#### Results – Interpretations

- Choose the correct option from the drop-down list. <u>All interpretations are mandatory to</u> answer.
  - If some of the pathogens in the list are not routinely tested in your laboratory, please select the option "Not in test selection"
  - If the pathogen is routinely tested in your laboratory, but the test has not been performed for some reason, 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 comment field at the bottom of the page.



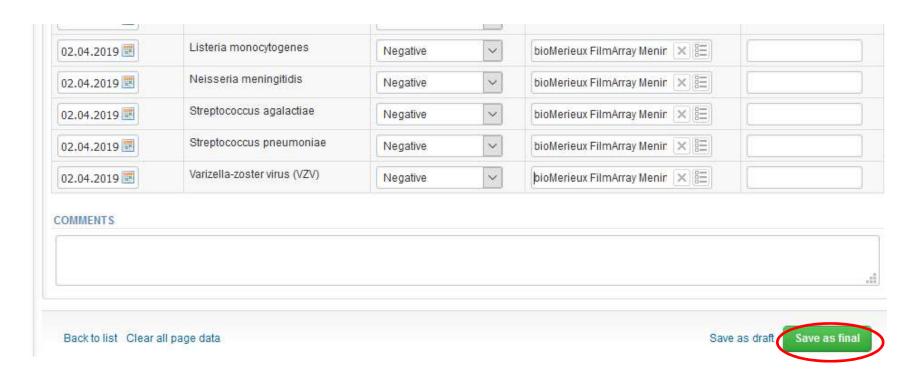
#### Results – Method

• Choose the correct option from the "Method" drop-down list. Please contact the EQA Coordinator as soon as possible (during the round is open) if your method is missing from the list and it will be updated.



#### Results

- Fill in the test result and unit if available (e.g. Ct value).
- 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 submit the results.
- From this page you can return to the front page by selecting "Back to list".



#### Results

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

02.04.2019	Herpes simplex virus 1 (HSV-1)	Not in test selection		
02.04.2019	Herpes simplex virus 2 (HSV-2)	Not in test selection		
02.04.2019	Human herpesvirus 6 (HHV-6)	Not in test selection		
02.04.2019	Listeria monocytogenes	Negative	bioMerieux FilmArray Meningitis/Encephalitis Panel	
02.04.2019	Neisseria meningitidis	Negative	bioMerieux FilmArray Meningitis/Encephalitis Panel	
02.04.2019	Streptococcus agalactiae	Negative	bioMerieux FilmArray Meningitis/Encephalitis Panel	
02.04.2019	Streptococcus pneumoniae	Negative	bioMerieux FilmArray Meningitis/Encephalitis Panel	
02.04.2019	Varizella-zoster virus (VZV)	Negative	bioMerieux FilmArray Meningitis/Encephalitis Panel	

Back to list Edit data Print



#### Post-analytics

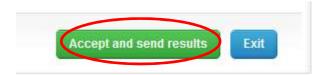
- Next the user is taken to the result validation
  - Product: What part of the process is being validated
  - Sample set: Which sample set is being validated
  - Sample: Which sample is being validated
  - Errors: If there are analyte specific validation limit errors these are shown here
  - Last saved: The user who has saved the results

#### Validate results Validation results Product Sample set Sample Last saved Date Status Errors Preanalytics Registration OK Teija Häkkinen 28.03.2019 11:44 Accepted Meningitis-encephalitis multiplex, nucleic acid detection 1 Sample S001 OK Wonne Björkman 02.04.2019 09:33 Accepted Meningitis-encephalitis multiplex, nucleic acid detection 1 Sample S002 OK Wonne Björkman 02.04.2019 09:38 Draft Meningitis-encephalitis multiplex, nucleic acid detection 1 Sample S003 OK Wonne Björkman 02.04.2019 09:38 Draft Meningitis-encephalitis multiplex, nucleic acid detection 2 Sample S001 OK Yvonne Björkman 02.04.2019 09:37 Open 2 Sample S002 OK Meningitis-encephalitis multiplex, nucleic acid detection Wonne Björkman 02.04.2019 09:37 Open 2 OK Meningitis-encephalitis multiplex, nucleic acid detection Sample S003 Wonne Biörkman 02.04.2019 09:37 Open Accept and send results Exit

## Post-analytics

- The results can be edited by selecting the correct sample
- When all of the states are such that the results can be submitted 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

Sample set	Sample	Errors	Last saved	Date	Status
	Registration	OK	Teija Häkkinen	28.03.2019 11:44	Accepted
1	Sample S001	OK	Wonne Björkman	02.04.2019 09:33	Accepted
1	Sample S002	OK	Yvonne Björkman	02.04.2019 09:42	Accepted
	1	1 Sample S001	1 Sample S001 OK	1 Sample S001 OK Wonne Björkman	1 Sample S001 OK Wonne Björkman 02.04.2019 09:33



#### LabScala buttons

Enables you to save changes on the form Save Takes you back to the previous view Back 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:
  - Yvonne Björkmanyvonne.bjorkman@labquality.fi+358 50 501 4335