

ErbaExpert

Microbiological expert software for evaluation
and interpretation of microorganisms



User manual

Cat n. INS00075

Last revision date: 11/2025, UM/48/25/F



The knowledge provided in this manual is essential for the proper working of the software. Therefore, pay attention to this manual.

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1. General instructions and safety (rules)

1.1 User manual

The User Manual for Evaluation and Interpretation of Microorganisms has been written for the user and provided information about the software routine use and user customization interface.

Before using the software, please read the entire manual. Save the manual so that users can access it whenever it is needed.

1.2 Symbols and signs

These symbols provide you with basic information and warn you of possible danger.



In vitro diagnostics device



Warning: biological alert



Warning: the risk of harming your health
or your immediate surroundings



Producer



Production date



Separate collection of electrical and electronic equipment.

1.3 Software application area

ErbaExpert is an expert microbiological software that allows the interpretation and expert analysis of microbiological samples in accordance with the EUCAST and CLSI international standards.

The software may only be operated by personnel/staff trained in its use.

The software may only be used in accordance with the designated area of use.



Warning: If the user uses a device in other than the producer defined way, the protection afforded by the device may be compromised/ The protection provided by the device may be impaired/ disrupted

The implementation of the software is in line with EU standards.

1.4 CE marking



Based on the directions listed below and the information in the manual, the product is CE marked.

1.4.1 Directive 98/79 / EC on In Vitro Diagnostic Medical Devices

A risk management analysis for this software has been performed. This analysis is part of the ISO documentation of the company and CE software documentation.

2. Introduction

Information system ErbaExpert is a laboratory information system for identification of strains of microorganisms isolated from samples of clinical material, determination of their susceptibility to antibiotics and evaluating results using an expert system based on EUCAST and CLSI standards. The user interface is extremely simple, created in the form of wizards through individual user processes.

For both EUCAST and CLSI, the changes made in 2025 have been implemented.

3. How to use this manual

During system setup, one of the system's operating modes is set up by the administrator. A summary of the processes, supported by each mode, is listed in the [Program Modes](#) chapter. For each mode, a typical workflow is described, including the sequence of the individual processes. For each process, a link to a detailed description of the workflow is included; detailed descriptions of wizards are provided in the [System wizards](#) description chapter.

The manual also contains a description of the user interface control (chapter [User interface control](#)).

4. Start the system

To start the ErbaExpert information system, click the system icon located on your desktop:

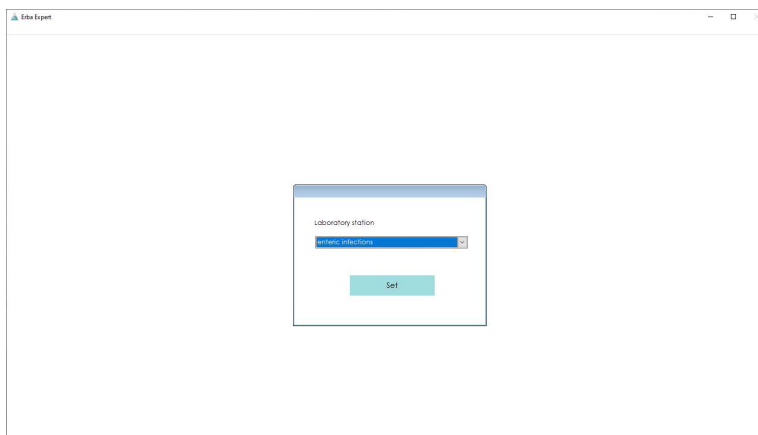


5. Login to the system

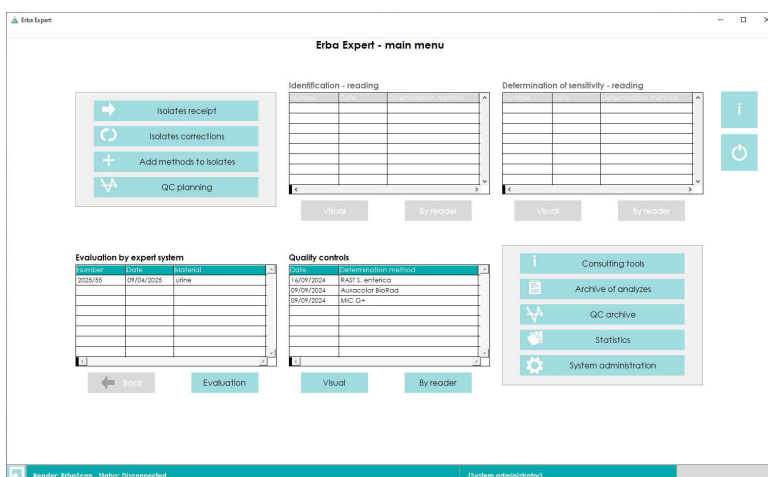
If user login is set up, the user login screen first appears when the system is started.

Select the user whose permissions you access to the system with and enter the password. The system makes all user actions available to the selected user.

If you have the option to work in individual workstations (laboratories) in the system settings, select the laboratory station again.



After login, the system desktop is displayed.





Click the system exit icon at the bottom right to close the system.



You can sign into another user by clicking on the logout icon.



Click the information icon to view system information (version, Product ID)

Switching to another laboratory station can be done by selecting *Material receipt / Station change*.

6. Program Modes

The Administrator presets one of the system following work modes described in this chapter.

6.1 Registration of patients, samples, isolates and examinations

User manually inserts data on accepted samples and patients. The primocultivation of the specimen are determined automatically (based on the set primocultivation rules). The individual isolates for which the required diagnostic methods are determined are recorded in the primoculture count. The results of the diagnostic methods are read automatically by the reader or manually by the user. Finally, the results of all diagnostic methods for a particular sample can be assessed by an expert system.

- User first registers the received samples using the [Sample receipt](#) wizard
- If necessary, user completes / repairs samples in the [Sample corrections](#) wizard.
- Patients can be inserted: **a.** During sample receipt; **b.** Separately using [Patients registration](#)
- Isolates obtained from the [Primoculture reading](#) are further analyzed:
 - o Identification of microorganisms is performed: **a.** Using the [ID – visual evaluation](#) wizard; **b.** [ID - reader evaluation](#) wizard.
 - o Identifications performed by other methods are entered by the Direct identification wizard.
 - o Determination of ATB susceptibility is performed: **a.** Using [ATB – visual evaluation](#) wizard; **b.** [ATB – reader evaluation](#) wizard.
- If necessary to perform further tests, the methods can be added in the [Add methods to isolates](#) wizard.
- Finally, samples are evaluated in the [Expert system](#) wizard.
- Samples, isolates, and examinations can be viewed using the [Statistics and reports](#) form.
- Trial, non-binding identification of microorganisms without impact on stored data of the system is supported by the [Ad-hoc identifications](#) wizard.

6.2 Registration of isolates and assigned examinations

User manually inserts the received isolates data for which the required diagnostic methods are set. The results of the diagnostic methods are read automatically by the reader or manually by the user. Finally, the results of all diagnostic methods can be assessed by an expert system.

- User first registers the received isolates using the [Isolates receipt](#) wizard
- If necessary, user completes / repairs samples in the [Isolates corrections](#) wizard.
- Received isolates are further analyzed:
 - o Identification of microorganisms is performed: **a.** Using the [ID – visual evaluation](#) wizard; **b.** [ID – reader evaluation](#) wizard.
 - o Identifications performed by other methods are entered by the [Direct identification](#) wizard.
 - o Determination of ATB susceptibility is performed: **a.** Using [ATB – visual evaluation](#) wizard; **b.** [ATB – reader evaluation](#) wizard.
- If necessary to perform further tests, the methods can be added in the [Add methods to isolates](#) wizard.
- Finally, samples are evaluated in the [Expert system](#) wizard.
- Samples, isolates, and examinations can be viewed using the [Statistics and reports](#) form.
- Trial, non-binding identification of microorganisms without impact on stored data of the system is supported by the [Ad-hoc identifications](#) wizard.

6.3 Only registration of identifications

User manually registers only the details of the identifications to be performed. The results of the diagnostic methods are read automatically by the reader or manually by the user.

- Identification of microorganisms is performed: **a.** Using the [ID – visual evaluation](#) wizard; **b.** [ID – reader evaluation](#) wizard.
- Samples, isolates, and examinations can be viewed using the [Statistics and reports](#) form.
- Trial, non-binding identification of microorganisms without impact on stored data of the system is supported by the [Ad-hoc identifications](#) wizard.

6.4 Only registration of susceptibility testing

User manually registers only the details of the susceptibility testing to be performed. The susceptibility results are read automatically by the reader or manually by the user.

- Determination is performed: **a.** Using [ATB – visual evaluation](#) wizard; **b.** [ATB – reader evaluation](#) wizard.
- Samples, isolates, and examinations can be viewed using the [Statistics and reports](#) form.
- Trial, non-binding identification of microorganisms without impact on stored data of the system is supported by the [Ad-hoc identifications](#) wizard.

6.5 Import data of isolates from LIS, assigning of respective examinations, export data to LIS

Data from individual isolates for which the required diagnostic methods are set in the system are received from the laboratory information system. The results of the diagnostic methods are read automatically by the reader or manually by the user. Finally, the results are sent back to the LIS.

- Reception of isolates is performed by isolates import from LIS. System receives isolates exported from LIS and puts them into processing
- Received isolates are further analysed:
 - o Identification of microorganisms is performed: **a.** [Using ID – visual evaluation](#) wizard; **b.** [ID – reader evaluation](#) wizard.
 - o Identifications performed by other methods are entered by the [Direct identification](#) wizard.
- Determination of susceptibility to ATB is performed: **a.** Using [ATB – visual evaluation](#) wizard; **b.** [ATB – reader evaluation](#) wizard.
- If necessary to perform further tests, the methods can be added in the [Add methods to isolates](#) wizard.
- Finally, samples are evaluated in the [Expert system](#) wizard.
- Samples, isolates, and examinations can be viewed using the [Statistics and reports](#) form.
- Exporting data back to LIS is started by selecting **Result / Results export to LIS**.
- Trial, non-binding identification of microorganisms without impact on stored data of the system is supported by the [Ad-hoc identifications](#) wizard.

6.6 Import of examination requests from LIS, results export to LIS

The data of the required examinations are received from the laboratory information system. The results of the diagnostic methods are read automatically by the reader or manually by the user. Finally, the results are sent back to the LIS.

- Receiving requests is started by selecting **Material receipt / Isolates import from LIS**. The system accepts the examination requirements exported from the LIS and puts them into processing.
- Received requests are further analysed:
 - o Identification of microorganisms is performed: **a.** Using [ID – visual evaluation](#) wizard; **b.** [ID – reader evaluation](#) wizard.
 - o Determination of ATB susceptibility is performed: **a.** Using [ATB – visual evaluation](#) wizard; **b.** [ATB – reader evaluation](#) wizard.
- Samples, isolates, and examinations can be viewed using the [Statistics and reports](#) form.
- Exporting data back to LIS is started by selecting **Results / Results export to LIS**.
- Trial, non-binding identification of microorganisms without impact on stored data of the system is supported by the [Ad-hoc identifications](#) Wizard.

6.7 Ad-hoc identifications or susceptibility testing only without data saving

The system only allows manual read-out of identifications or susceptibility testing. Data are not stored in system data.

- Trial identification of microorganisms without impact on stored data of the system is supported by the [Ad-hoc identifications](#) wizard.
- Trial susceptibility testing of microorganisms without impact on stored data of the system is supported by the [Ad-hoc susceptibility testing](#) wizard.

7. System Wizards Description

7.1 Material receipt

Using the wizards in this section, sample data, isolates, and patients can be registered into the system.

7.1.1 Sample receipt

The wizard allows to register samples and determine their primocultivation.

In the first step – **Date of sample receipt** – user enters the time of sampling, the system automatically inserts the delivery time when the system is opened.

The sample entry tab is available as a follow-up of the **Sample Receipt** wizard.

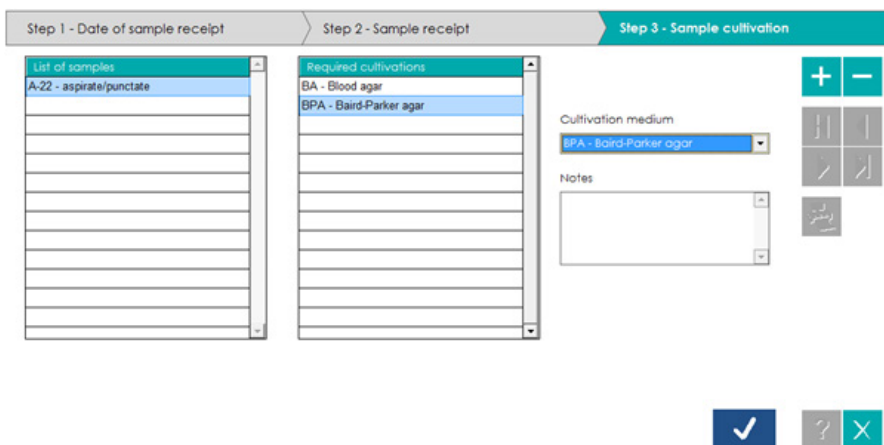
- New samples are added: **a.** Using the **+** button in the form toolbar on the right; **b.** Keyboard shortcut Ctrl + N.
- All the required data for the sample is entered successively. The scale of recorded data has been set by the System Administrator using the **Data Selection** option.
- Required fields are highlighted in yellow.
- Drop-down lists allow incremental search by entering the first few characters of the searched term.
- You can add new records in the *Patient* and *Ward* fields by pressing the button located on the right of the drop-down list:



- The wizard is finished in this step by clicking on the blue storage icon located in the bottom right corner (except the cultivation media settings).



- The system alerts the user to the incompleteness of the data and asks for correcting / completing data by the user.
- When setting the **Sample cultivation** option, the system checks the completeness until this next step and eventually requires correcting / completing data by the user. In this step, the user initializes the primocultivation.



- User selects the individual samples from the *List of Samples* on the left successively and selects the *Required cultivations* for them.
- The system automatically adds to the sample all the culture media defined in the *Primocultivation Patterns*.
- If Primocultivation Patterns are not defined for the material, the system adds a blank Cultivation medium that user fills in.
- The system allows to add any number of additional media: **a.** Using the **+** button in the Forms toolbar on the right; **b.** Keyboard shortcut Ctrl + N.
- The wizard is finished in this step by clicking on the blue storage icon located in the bottom right corner.



- The system checks the completeness of the data entry and, if necessary, requires correcting / adding data by the user.

7.1.2 Sample corrections

The wizard allows to correct sample data including primocultivation.

In the first step of the wizard – **Date of sample receipt** – user selects the sample receipt date from the list to be corrected.

The system only allows to repair those samples whose primocultures have not yet been read!

Next wizard work is identical to the **Sample Receipt** wizard.

7.1.3 Patients registration

The form records patients whose specimens are / were analyzed using the ErbaExpert system.

On the first tab of the record – **Edit Data** – patient identification is kept.

- New patients can be added: **a.** Using the + button in the Forms toolbar on the right; **b.** Keyboard shortcut Ctrl + N.
- All the required data is entered successively. The scale of recorded data has been set using the **Data Selection** option.
- Required fields are highlighted in yellow.

The new record is saved after pressing the Save button located in the toolbar on the right or leaving the form.



The second tab – **Performed examinations** – shows the history of the patient's examination. The record is read-only.

- The list on the left shows a list of samples that have been tested so far.
- In the fields of the tab, information about the identification and ATB susceptibility results is displayed. If need information of a sterile sample or common microflora could be displayed.

Performed examinations

Patient: John Doe

Date of receipt	Material type
09/07/2017	aspirate/puncture
09/07/2017	aspirate/puncture
09/07/2017	aspirate/puncture

Sample nr. A-22

A04 Other bacterial intestinal infections

My hospital - surgery

ENT16 ENTEROtest 16

Edwardsiella tarda

Excellent identification

ATB susceptibility results:

Antibiotic	Result
PIP	S
PIT	R
CTX	R
CAZ	R
CPZ	-
CPS	-
CEP	S
MER	S
ERT	S
TGC	S
NET	S
TOB	S

7.1.4 Isolates receipt

The **Isolates receipt** wizard allows to receive isolates and determine methods of examination (only in Registration of isolates and assigned examinations mode).

In the first step of the **Isolates receipt** wizard, the user enters isolates.

Isolates receipt | Method assigning | Identification - reading | Customization

Isolate number: 2025/25

Material: vomits

Note: vomits

Method: wound surface

Systemic infection: ☐

Local ATB application: ☐

After entering all the isolates, user goes to the next step of the wizard – **Methods assigning**.

When switching, the system automatically checks if the isolate number in the system already exists. If so, the system will not allow you to continue the wizard.

The system verifies duplicate isolates. If user enters the same number for two isolates, the system will not allow the wizard to continue.

The screenshot displays the 'Method assigning' step of the ErbaExpert wizard. It features four main panels:

- Isolates receipt:** A table with columns 'Isolate number' and 'Abbrev.' (partially visible). The first row contains '2025/25'.
- Identification - reading:** A panel with three radio buttons: 'Identification method', 'Susceptibility testing method' (selected), and 'Use only your own ATB methods'.
- Examination method:** A list of diagnostic methods. The selected method is 'MIC G-II (Enterobacteriaceae)'. Other methods include MIC YST, DDM, OMM, SSTR, G-I, G-II, URINE, NIFERM, STAPHY, G+, BP G-I, BP G-II, BP G+, and BP URINE.
- Note:** A text area for additional information.

Navigation buttons are located between the panels: a single right arrow (>), a double right arrow (>>), a single left arrow (<), and a double left arrow (<<). A status bar at the bottom indicates the current step is 'Isolates receipt'.

User assigns a diagnostic method from the *Examination method* table (in the middle) to each isolate.

- Methods can be filtered using a method switch (Identification method/Susceptibility testing Method/Other diagnostic method/Use only your own ATB methods)
- The selected method is moved to the right Examination Method table: **a.** By pressing the > button; **b.** Double clicking on the selected method; **c.** Pressing the Enter key on the selected method; **d.** The selected method is assigned to all isolates in the isolate table by pressing the >> button.
- Methods are removed from the Examination Method list: **a.** By pressing the < button (one method removed); **b.** Pressing << (all methods removed)

If user does not select any configurable methods, the wizard is finished by pressing the blue storage icon located at the bottom right corner.



The system checks whether for each isolate, at least one method is specified. In case of correct status, it saves the data and ends the wizard.

If user chooses a configurable method, the **Customization** tab is available.

Isolates receipt Meth. assigning Customization

Isolate	Examination method	Added test																													
4	MIC single strips	<table border="1"> <thead> <tr> <th>Abbreviat. test name</th> </tr> </thead> <tbody> <tr><td>AMP</td><td>ampicillin (1 - 64 mg/L)</td></tr> <tr><td>AMS</td><td>ampicillin-sulbactam (1/0.5 - 64/32 mg)</td></tr> <tr><td>CAZ</td><td>ceftazidime (0.5 - 32 mg/L)</td></tr> <tr><td>CEP</td><td>cefepime (0.5 - 32 mg/L)</td></tr> <tr><td>CIP</td><td>ciprofloxacin (0.06 - 4 mg/L)</td></tr> <tr><td>CXM</td><td>cefuroxime parenteral (1 - 64 mg/L)</td></tr> <tr><td>ERT</td><td>ertapenem (0.06 - 4 mg/L)</td></tr> <tr><td>GEN</td><td>gentamicin (0.5 - 32 mg/L)</td></tr> <tr><td>IMI</td><td>imipenem (0.12 - 8 mg/L)</td></tr> <tr><td>LIZ</td><td>linezolid (0.25 - 16 mg/L)</td></tr> <tr><td>MER</td><td>meropenem (0.12 - 8 mg/L)</td></tr> <tr><td>NFT</td><td>nitrofurantoin (2 - 128 mg/L)</td></tr> <tr><td>PEN</td><td>benzylpenicillin (0.06 - 4 mg/L)</td></tr> <tr><td>PIT</td><td>piperacillin-tazobactam (2/4 - 128/4 mg)</td></tr> </tbody> </table>	Abbreviat. test name	AMP	ampicillin (1 - 64 mg/L)	AMS	ampicillin-sulbactam (1/0.5 - 64/32 mg)	CAZ	ceftazidime (0.5 - 32 mg/L)	CEP	cefepime (0.5 - 32 mg/L)	CIP	ciprofloxacin (0.06 - 4 mg/L)	CXM	cefuroxime parenteral (1 - 64 mg/L)	ERT	ertapenem (0.06 - 4 mg/L)	GEN	gentamicin (0.5 - 32 mg/L)	IMI	imipenem (0.12 - 8 mg/L)	LIZ	linezolid (0.25 - 16 mg/L)	MER	meropenem (0.12 - 8 mg/L)	NFT	nitrofurantoin (2 - 128 mg/L)	PEN	benzylpenicillin (0.06 - 4 mg/L)	PIT	piperacillin-tazobactam (2/4 - 128/4 mg)
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PIT	piperacillin-tazobactam (2/4 - 128/4 mg)																														

amikacin (1 - 44 mg/L)

clindamycin (0.06 - 4 mg/L)

colistin (0.25 - 16 mg/L)

☒ ☐ ☐

This step provides a set of configurable test methods. For each method (displayed in the left table) user selects a set of tests from the *Added test* table in the middle.

- Tests are moved to the Test list on the right: **a.** By pressing the > button; **b.** Double clicking on the selected test; **c.** Pressing the Enter key on the selected test.
- Tests are removed from the Test list: **a.** By pressing the < button (one test removed); **b.** Pressing << (all tests removed).

The wizard closes by pressing the blue storage icon located at the bottom right corner.



The system checks whether for each method, at least one test is specified and in case of correct status, it saves the data and ends the wizard.

7.1.5 Correcting isolates

You can edit the inserted data using the *Isolates correction* wizard. User goes through a similar wizard as in the case of Isolates receipt; for individual isolates, you can add and remove analysis methods and modify configurable methods.

Only isolates for which the assigned methods have not yet been evaluated can be corrected!

In the first step – ***Date of sample receipt*** – user selects the date of receipt of the sample.

The screenshot shows a wizard interface with four steps: 'Date of sample receipt' (active), 'Isolates', 'Meth. assigning', and 'Customization'. Below the steps, the text 'Select registration date of isolates:' is followed by two input fields. The first field is a date picker showing '29/07/2017'. The second field is a list box titled 'Isolate' containing the number '4' and several empty rows. At the bottom right of the wizard, there are buttons for help (?) and close (X).

After selecting, you can go to the next step – ***Isolates*** – where you can change the label of isolates and add notes.

The isolates can not be removed nor added!

The next steps are the same as in the *Isolates receipt* wizard.

The system does not allow you to remove a method with already read results; you can not modify the test set of already assigned configurable methods!

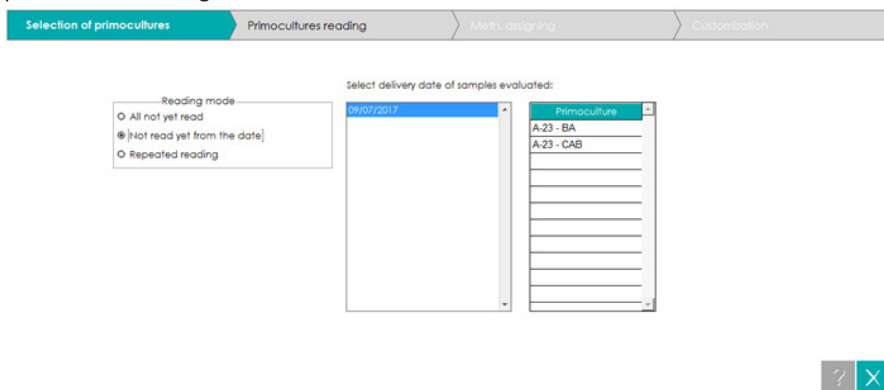
7.2 Analysis

You can use the wizards in this section to enter the sample examination results.

7.2.1 Primocultures reading

The wizard allows the Primocultures reading including the determination of diagnostic methods for individual isolates.

In the first step of the wizard – **Selection of primocultures** – user selects samples for primoculture reading.



By the *Reading mode* switch, user chooses selection of the samples to read: **a.** All isolates that have not been read before; **b.** Isolates not read from a given date; **c.** Repeated reading.

- In case of *Not read yet from the date*, you can select the date of receipt of the sample from the list.
- In the case of *Repeated Reading*, you can also specify a more detailed identification of the sample (sample designation and / or date).

After selecting the Reading mode, you can go to the next step of the wizard – **Primocultures reading**.

The screenshot shows the 'Primocultures reading' step of the ErbaExpert software. The interface is divided into four main sections: 'Selection of primocultures', 'Primocultures reading', 'Meth. assigning', and 'Customization'. The 'Primocultures reading' section is active.

Primoculture	Cultivation medium
A-23 - BA	Blood agar
A-23 - CAB	Columbia agar

Result of primocultivation: isolates found

Isolate number: 11

Note:

Navigation buttons: +, -, <, >, <<, >>, <<<, >>>

For each primoculture, user enters the *Result of primocultivation* from the drop-down list:

- *Isolates found* – the system makes the *Isolate number* list available and adds a new blank field to the *Isolate number* table.
- If more isolates are found in one primoculture, additional isolates can be added:
 - a. Using the + button on the form's right toolbar; b. Keyboard shortcut Ctrl + N.

Once you have entered all the isolates, you can go to the next step of the wizard by clicking **Methods Assigning**.

- The system automatically alerts user to an existing isolate number and prompts to repair.
- The system automatically alerts user to the duplicate isolate number and prompts to repair.
- The system automatically alerts user to unlabeled isolates and prompts to repair.

In the case of a complete assignment, the next step is made available – **Methods Assigning**.

In this step, user assigns diagnostic methods for individual isolates.

User sequentially assigns to each isolate *Examination Method* from the middle table of available methods.

[illegible]

- Methods can be filtered using a Method switch (Identification method/Susceptibility testing method/Other diagnostic method/Use only your own ATB methods)
- The selected method is moved to the assigned *Examination Method* table located on the right: **a.** By pressing the > button; **b.** double click on the selected method; **c.** Pressing the Enter key on the selected method; **d.** The selected method is assigned to all isolates in the isolate table by pressing the >> button.
- Methods can be removed from the Examination Method list: **a.** By pressing the < button (one method removed); **b.** Pressing << (all methods removed).

If user does not select any configurable methods, the wizard is finished in this step by pressing the blue storage icon in the lower-right corner.



The system checks if at least one method is specified for each isolate, and saves the data and terminates the wizard if it is correct.

If user chooses a configurable method, the **Customization** step is available.

Selection of primocultures Primocultures reading Meth. assigning **Customization**

isolate	Examination method	Added test																														
11	MIC single strips	<table border="1"> <thead> <tr> <th>Abbreviated test name</th> <th></th> </tr> </thead> <tbody> <tr><td>AMP</td><td>ampicillin (1 - 64 mg/L)</td></tr> <tr><td>AMS</td><td>ampicillin-sulbactam (1/0.5 - 64/32 mg)</td></tr> <tr><td>CAZ</td><td>ceftazidime (0.5 - 32 mg/L)</td></tr> <tr><td>CEP</td><td>cefepime (0.5 - 32 mg/L)</td></tr> <tr><td>CIP</td><td>ciprofloxacin (0.06 - 4 mg/L)</td></tr> <tr><td>CLI</td><td>clindamycin (0.06 - 4 mg/L)</td></tr> <tr><td>CXM</td><td>cefuroxime parenteral (1 - 64 mg/L)</td></tr> <tr><td>ERT</td><td>ertapenem (0.06 - 4 mg/L)</td></tr> <tr><td>GEN</td><td>gentamicin (0.5 - 32 mg/L)</td></tr> <tr><td>IMI</td><td>imipenem (0.12 - 8 mg/L)</td></tr> <tr><td>MER</td><td>meropenem (0.12 - 8 mg/L)</td></tr> <tr><td>NFT</td><td>nitrofurantoin (2 - 128 mg/L)</td></tr> <tr><td>PEN</td><td>benzylpenicillin (0.06 - 4 mg/L)</td></tr> <tr><td>PIT</td><td>piperacillin-tazobactam (2/4 - 128/4 mg)</td></tr> </tbody> </table>	Abbreviated test name		AMP	ampicillin (1 - 64 mg/L)	AMS	ampicillin-sulbactam (1/0.5 - 64/32 mg)	CAZ	ceftazidime (0.5 - 32 mg/L)	CEP	cefepime (0.5 - 32 mg/L)	CIP	ciprofloxacin (0.06 - 4 mg/L)	CLI	clindamycin (0.06 - 4 mg/L)	CXM	cefuroxime parenteral (1 - 64 mg/L)	ERT	ertapenem (0.06 - 4 mg/L)	GEN	gentamicin (0.5 - 32 mg/L)	IMI	imipenem (0.12 - 8 mg/L)	MER	meropenem (0.12 - 8 mg/L)	NFT	nitrofurantoin (2 - 128 mg/L)	PEN	benzylpenicillin (0.06 - 4 mg/L)	PIT	piperacillin-tazobactam (2/4 - 128/4 mg)
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amikacin (1 - 64 mg/L)

colistin (0.25 - 16 mg/L)

linezolid (0.25 - 16 mg/L)

✓ ? ✕

This step provides a set of configurable test methods. For each examination method from the table located to the left, user selects the required report from the *Added test* table.

- Tests are moved to the Test list on the right: **a.** By pressing the > button; **b.** Double clicking on the selected test; **c.** Pressing the Enter key on the selected test.
- Tests are removed from the Test list: **a.** By pressing the < button (one test removed); **b.** Pressing << (all tests removed).

The wizard closes by pressing the blue storage icon located at the bottom right corner.



The system checks if at least one test has been specified for each method, and saves the data and terminates the wizard if it is correct.

- The result falls into the following categories: **a.** Positive; **b.** Negative; **c.** Dubious (cannot be decided).
- The positive result can be entered: **a.** By pressing the + button; **b.** Pressing 1; **c.** Using a left-click.
- The negative result can be entered: **a.** By pressing the - button; **b.** Pressing 2; **c.** Using a right-click.
- The dubious result can be entered: **a.** By pressing the space bar; **b.** Pressing 0; **c.** Clicking any mouse button on the already-read test with + or - value.
- Tests that are part of the supplied identification kits will be coloured in accordance with the colour of the kit well.

After entering all the isolates, you can go to the next step of the Wizard – **Evaluation**. The system checks whether user entered at least one test result to each isolate; otherwise, it prompts to correct.

25

User goes through the *Isolate* table on the left side and evaluates the identifications.

In the Identified taxon Window, the pre-sorted (using absolute probability limits) taxons are listed. For each taxon you can find two data:

- **Identification score.** It shows the degree of identification exclusivity. Based on the assumption that the identified strain belongs to the given taxon, the identification score indicates the percentage of probability that the strain belongs to this taxon and none other.
- **T-index.** Indicates the typicality of the identified strain relative to the taxa listed. The T index value range is between 1 - 0. The higher the T-index, the more similar is the strain to the „ideal“ of the given taxon.

A final evaluation of the identification is the sum of both the criteria above. The result is reflected in the taxonomy window. In case of very good or excellent identification, the identified taxon is highlighted in dark green. In the case of good or acceptable identification, the taxon is highlighted in light green. In the case of generic or species identification, the taxa are highlighted in yellow.

Obviously, the application-generated identification result must always be verified by the user. There are other auxiliary functions – **Information about taxons**, **List of doubtful results**, and **Differentiation Tests**.

- If important phenotypic groups may exist for a given taxon, a drop-down list of groups will be displayed. The list will only be displayed if ATB susceptibility testing is not scheduled for the isolate.
- User can change assignment to phenotypic group.

If only identification is required, the blue printer icon appears in the lower-right corner. Now you can print the results.



The isolate is then marked as the sent one.

Once you have entered the results for all isolates, you can save the data by pressing the blue wizard exit icon in the lower right corner.



The system checks the completeness of the assignment and prompts the user for any corrections; then the data are saved.

7.2.3 Automated reader identification

The wizard allows the automatic reading to identify the isolates using a reader.

In the first step of wizard – **Isolates selection** – user selects isolates with set identification methods during the primoculture reading.

1 Isolates selection 2 Kit selection 3 Isolates position 4 Reader initializing 5 Plates measuring 6 Tests results 7 Evaluation

Reading mode

☐ All not yet read

☒ Not read yet from the date

☐ Repeated reading

Select date of registration of isolates read:

26/02/2018

Isolate
2802 BA

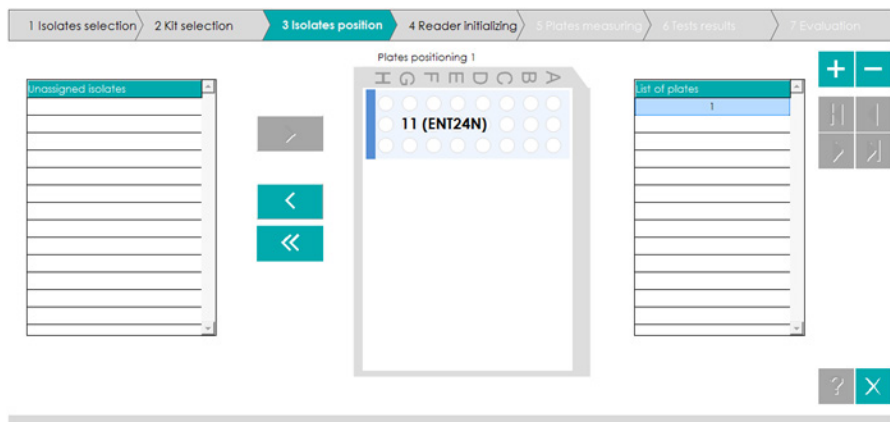
? X

By the *Reading mode* switch, user chooses selection of the isolates to read: **a.** All isolates that have not been read before; **b.** Isolates not read from a given date; **c.** Repeated reading.

- In case of *Not read yet from the date*, you can select the date of receipt of the isolate from the list.
- In the case of *Repeated Reading*, you can also specify a more detailed identification of the isolate (isolate designation and / or date).

After selecting the Reading mode, you can go to the next step of the wizard – **Kit selection**.

User chooses kits from the drop-down list and goes to the next step – **Isolates position**.



The system automatically creates a corresponding number of blank plates to enter the particular number of isolates.

- User sequentially assigns isolates from the *Unassigned isolates* table on the left into the plate: **a.** By pressing the > button; **b.** Double clicking on the selected isolate.
- Once the isolate plate is full, the system automatically goes to the next plate.
- The selected isolate on the plate is marked with a blue stripe on the left.
- Isolates can be removed from the plate: **a.** By pressing < (one isolate); **b.** By pressing << (all isolates).
- To add a new plate to the list: **a.** Press the + right button on the toolbar; **b.** Use the keyboard shortcut Ctrl + N.
- To remove the current plate from the list: **a.** Press the - right button on the toolbar; **b.** Use the keyboard shortcut Ctrl + D.

User assigns the individual isolates to the plates sequentially and goes to the next step **Reader initializing.**

If not done so, user switches the reader on and waits until the reader initialization (autocalibration). The ErbaScan reader signals the autocalibration ending with the permanent green diode on the front panel of the device.

When moving to the **Plates Measuring**, the system ejects plate carrier from the reader and prompts user to insert plate.

- After entering all the isolates, you can go to the next step of the Wizard – **Evaluation**. The system checks whether user entered at least one test result to each isolate; otherwise prompts to correct.

User goes through the Isolate table on the left and evaluates the identifications.

- **Identification score.** It shows the degree of identification exclusivity. Based on the assumption that the identified strain belongs to the given taxon, the identification score indicates the percentage of probability that the strain belongs to this taxon and none other.
- **T-index.** Indicates the typicality of the identified strain relative to the taxa listed. The T index value is between 1 - 0. The higher the T-index, the more similar is the strain to the „ideal” of the given taxon.

A final evaluation of the identification is the sum of both the criteria above. The result is reflected in the taxonomy window. In case of very good or excellent identification, the identified taxon is highlighted in dark green. In the case of good or acceptable identification, the taxon is highlighted in light green. In the case of generic or species identification, the taxa are highlighted in yellow.

Obviously, the application-generated identification result must always be verified by the user. There are other auxiliary functions – **Information about taxons**, **List of doubtful results**, and **Differentiation Tests**. If user requires only identification, the blue printer icon appears in the lower-right corner. Now you can print the results.

- If important phenotypic groups may exist for a given taxon, a drop-down list of groups will be displayed. The list will only be displayed if ATB susceptibility testing is not scheduled for the isolate.
- User can change assignment to phenotypic group.



The isolate is then marked as the sent one.

Once you have entered the results for all isolates, you can save the data by pressing the blue wizard exit icon in the lower right corner.

The system checks the completeness of the assignment and prompts for any corrections; then the data are saved.



7.2.4 Direct identification wizard

The wizard allows you to record isolates directly, as for example, during manual transmission of identification results from other identification methods (typically MALDI).

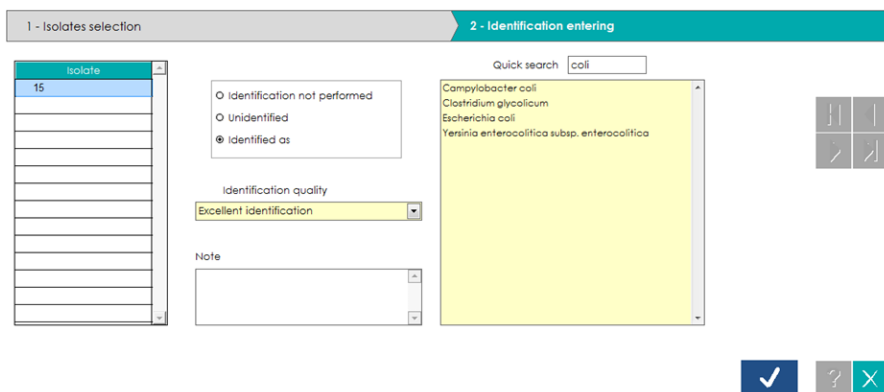
In the first step of the wizard – **Isolates selection** – user selects the isolates for which direct identification methods were entered in the primoculture reading.

[illegible]

By the *Reading mode* switch, user chooses selection of the isolates to read: **a.** All isolates that have not been read before; **b.** Isolates not read from a given date; **c.** Repeated reading.

- In case of *Not read yet from the date*, you can select the date of receipt of the isolate from the list.
- In the case of *Repeated Reading*, you can also specify a more detailed identification of the isolate (isolate designation and / or date).

After selecting the Reading mode, you can go to the next step of the wizard – **Identification entering**. In this step, user goes through the list of isolates in the Isolate table located on the left and selects the identification result for from the taxa list.



- The identification result switch can be selected: **a.** *Identification not performed*; **b.** *Unidentified*; **c.** *Identified as*
- In case of *Identified as*, the user selects the *Identification Quality* and the identified taxon from the taxon list.
- For quicker orientation, *Quick Search* can be used. After entering any text, the system selects from the taxon list that one in which the text appears anywhere in the genus or generic name of the taxon.

After entering the results for all isolates, the data is saved by pressing the blue wizard exit icon in the lower right corner.



The system checks the completeness of the assignment and prompts the user for any corrections; then the data are saved.

7.2.5 ATB – visual evaluation

The wizard allows manual reading of the antibiotics susceptibility.

In the first step of the Wizard – **Isolates selection** – user selects the isolates to which the susceptibility testing methods were assigned in the primoculture reading.

1 - Isolates selection 2 - Kit selection 3 - Strains reading

Reading mode

☐ All not yet read

☒ Not read yet from the date

☐ Repeated reading

Select date of registration of isolates read:

12/04/2025
09/04/2025

Isolate
2025/25
2025/25
2025/25
2025/985



By the *Reading mode* switch, the user chooses selection of the isolates to read: **a.** All isolates that have not been read before; **b.** Isolates not read from a given date; **c.** Repeated reading.

- In case of *Not read yet from the date*, you can select the date of registration of the isolates from the list.
- In the case of *Repeated reading*, you can also specify a more detailed identification of the isolate (isolate designation and / or date).

After selecting the reading mode, you can go to the next step of the wizard – **Kit selection**.

From the drop-down list (*Select the kit to measure*), the user selects the kit (or all of them in the case of the *Read All Kits* option) to read.

Select the kit to measure:

- Disc diffusion method
- MIC G-I (Enterobacteriaceae)
- Other MIC methods
- RAST *S. enterica*

[Read all kits](#)

In the next step – **Strains reading** - the user looks through individual isolates and their determination and visually reads the individual kits.

In the case of MIC kits, the results are entered by clicking on the strip well, in which inhibition of growth is first observed in the row. In case of growth in all wells, the user selects the R field:

[illegible]

		I	G	T	M	C	S	A	
1	<input type="checkbox"/>	○	●	●	●	●	●	●	ampicillin
2	<input type="checkbox"/>	○	●	●	●	●	●	●	ampicillin-sulbactam
3	<input type="checkbox"/>	●	●	●	○	○	○	○	cefazolin
4	<input type="checkbox"/>	○	○	○	○	○	○	○	cefuroxime
5	<input type="checkbox"/>	○	○	●	●	○	○	○	meropenem
6	<input type="checkbox"/>	○	○	○	○	○	○	○	gentamicin
7	<input type="checkbox"/>	○	○	○	○	○	○	○	amikacin
8	<input type="checkbox"/>	●	●	●	○	○	○	○	trimethoprim-sulfamethoxazole
9	<input type="checkbox"/>	●	○	○	○	○	○	○	norfloxacin
10	<input type="checkbox"/>	○	○	○	○	○	○	○	ciprofloxacin
11	<input type="checkbox"/>	○	●	○	○	○	○	○	tigecycline
12	<input type="checkbox"/>	○	○	●	○	○	○	○	nitrofurantoin

 Growth in a well Growth inhibition

Determine the MIC value by clicking into the certain well in the plate



Proteus vulgaris

1 - Isolates selection 2 - Kit selection 3 - Strains reading

Escherichia coli

When reading the disk diffusion method according to the RAST methodology, the user also selects the reading date (4, 6 or 8 hours):

Salmonella enterica

When reading another MIC method, the user enters the MIC for each antibiotic directly:

[illegible]

If only susceptibility determination for the isolate is required, the blue printer icon appears in the lower-right corner. Now you can print the results



The isolate is then marked as the sent one.

Once you have entered the susceptibility testing results for all isolates, you can save the data by pressing the blue wizard exit icon in the lower right corner.



The system checks the completeness of the assignment and prompts for any corrections; then the data are saved.

7.2.6 ATB – reader evaluation

The wizard allows automated susceptibility testing reading.

In the first step of wizard – **Isolates selection** – user selects isolates that have set susceptibility determination methods during the primoculture reading.

[illegible]

By the *Reading mode* switch, user chooses selection of the isolates to read: **a.** All isolates that have not been read before; **b.** Isolates not read from a given date; **c.** Repeated reading.

- In case of *Not read yet from the date*, you can select the date of registration of the isolates from the list.
- In the case of *Repeated reading*, you can also specify a more detailed identification of the isolate (isolate designation and / or date).

After selecting the reading mode, you can go to the next step of the wizard – **Kit selection**, where the user chooses a kit to be read.

- ?

- During inserting the plate, follow the order of the inserts (for better plate orientation, in the table in the right column, the number of the first isolate on the plate is always indicated at the plate number).
- Ensure that the plate is oriented correctly when inserted into the carrier (marking of the A-H positions on the carrier must match the plate markings).
- Press the **Measuring** button to start the plate readout.
- The system prompts to insert another plate.
- The system informs user about the last plate measured and goes to the next step of the wizard – **Test results**.

For MIC sets, the results are presented in a strip form. The strip well, in which inhibition of growth is first observed in the row, is grayed out. In case of growth in all wells, the reader selects the R field.

1 Isolates selection
2 Kit selection
3 Isolates position
4 Plates measuring
5 Tests results

Plate	Isolate	Method
1	2026/25	G-I

1 ☐ R

2 ☐ R

3 ☐ R

4 ☐ R

5 ☐ R

6 ☐ R

7 ☐ R

8 ☐ R

9 ☐ R

10 ☐ R

11 ☐ R

12 ☐ R

I

Q

T

M

U

C

B

>

ampicillin

ampicillin-sulbactam

cefazolin

cefuroxime

aztreonam

gentamicin

amikacin

colistin

trimethoprim-sulfamethoxazole

ciprofloxacin

chloramphenicol

tetracycline

☐ Growth in a well

☒ Growth inhibition

☐ Suspicious growth - review

Determine the MIC value by clicking into the certain well in the plate

✓

?

✕

Escherichia coli

User checks the results of all tests on selected isolates. Also in this case, you can change the results - by clicking in the well you can set the MIC value.

If only susceptibility determination for the isolate is required, the blue printer icon appears in the lower-right corner. Now you can print the results.



The isolate is then marked as the sent one.

Once you have entered the susceptibility testing results for all isolates, you can save the data by pressing the blue wizard exit icon in the lower right corner.

The system checks the completeness of the assignment and prompts for any corrections; then the data are saved.



7.2.7 Other methods

The wizard allows to read other diagnostic methods.

In the first step – **Isolates selection** – user selects the desired isolate / isolates, which shall be analyzed by Other diagnostic methods.

The screenshot shows the '1 - Isolates selection' step of the wizard. At the top, a progress bar indicates the current step. Below it, the 'Reading mode' section has three radio buttons: 'All not yet read', 'Not read yet from the date' (which is selected), and 'Repeated reading'. To the right, there is a label 'Select date of registration of isolates read:' followed by a date picker showing '28/02/2018'. Further right is a table with the header 'Isolate' and one row containing the number '2802'. On the far right, there are several icons for navigation and help. At the bottom right, there are buttons for '?' and 'X'.

By the Reading mode switch, user chooses selection of the isolates to read: **a.** All isolates that have not been read before; **b.** Isolates not read from a given date; **c.** Repeated reading.

- In case of *Not read yet from the date*, you can select the date of registration of the isolates from the list.
- In the case of *Repeated reading*, you can also specify a more detailed identification of the isolate (isolate designation and / or date).

After selecting the reading mode, you can go to the next step of the wizard – **Method selection**, where the user chooses a kit to be read.

1 - Isolates selection

2 - Method selection

3 - Strains reading

Which method will you read?

Haemolysis - Staphylococci



In the next step – **Strains reading** – user visually reads individual isolates and enters the results into dedicated form (numeric or other format).

1 - Isolates selection

2 - Method selection

3 - Strains reading

Isolate	Examination method
2802	HEM

HEM (Haemolysis -)

betd



Once you have entered results for all isolates, you can save the data by pressing the blue wizard exit icon in the lower right corner.



The system checks the completeness of the assignment and prompts for any corrections; then the data are saved.

7.2.8 Add methods to isolates wizard

The wizard allows to add other required methods of examination to the already-processed isolates.

In the first step – **Isolates Selection** – user selects the desired isolate / isolates by specifying the isolate number and / or the isolate reading data. In the next step – **Analysis Methods**, user assigns additional diagnostic methods to individual isolates. The hitherto unread methods can be removed at this step. Otherwise, the methods are read-only.

User assigns to each isolate from the table on the left the examination methods available in the *Method assigning* table.

- Examination methods can be filtered using a method type switch Identification method / Susceptibility testing method / Other diagnostic method / Use only your own ATB methods)
- The selected method from the *Examination Method* Table can be moved to the Assigned Examination Method Table on the right: **a.** By pressing the > button; **b.** Double clicking on the selected method; **c.** Pressing the Enter key on the selected method.
- Methods could be removed from the *Examination Method* list by pressing the < button (one method removed).

If user did not choose any of the configurable methods, the wizard is finished in this step by pressing the blue storage icon in the bottom right corner.



The system checks if at least one method is specified for each isolate, and saves the data and terminates the wizard if it is correct.

If user chooses a configurable method, the **Customization** step is available.

This step provides a set of configurable test methods. User goes through the table of isolates with the methods assigned in the form on the left. User assigns for each isolate in the table on the left a method from the *Added tests* table.

- Tests are moved to the Test list on the right: **a.** By pressing the > button; **b.** Double clicking on the selected test; **c.** Pressing the Enter key on the selected test.
- Tests are removed from the Test list: **a.** By pressing the < button (one test removed); **b.** Pressing << (all tests removed).

The wizard closes by pressing the blue storage icon located at the bottom right corner.



The system checks if at least one test has been specified for each method, and saves the data and terminates the wizard if it is correct.

7.2.9 Ad-hoc identifications wizard

The wizard allows to perform any identification using system identification methods without the need to enter isolates. The results of these identifications are not stored in the data and are not logged by the system.

In the first step of the wizard – **Kit selection** – user chooses the identification kit. Then you can go to the next step – **Strains reading**.

1 - Kit selection
2 - Strains reading
3 - Tests results

Strip tests

Supplementary tests

+	+	-	-	+	-	-	-
URE	ARG	ORN	LYS	H2S	SCI	MAL	ONP
+	+	-	-	-	-	+	+
SAL	SOR	MLB	CEL	LAC	TRE	MAN	GLR
-	-	-	+	-	-	+	-
DUL	ADO	ART	SUC	INO	RAF	ESL	BXY

-	-	-
OXI	IND	VPT

?
X

44

User gradually puts the results of each test into the appropriate box fields.

- The result falls into the following categories: **a.** Positive; **b.** Negative; **c.** Dubious (cannot be decided).
- The positive result can be entered: **a.** By pressing the + button; **b.** Pressing 1; **c.** Using a left-click.
- The negative result can be entered: **a.** By pressing the - button; **b.** Pressing 2; **c.** Using a right-click.
- The dubious result can be entered: **a.** By pressing the space bar; **b.** Pressing 0; **c.** Clicking any mouse button on the already-read test with + or - value.
- Tests that are part of the supplied identification kits will be coloured in accordance with the colour of the kit well.

After entering all the tests, you can go to the next step of the Wizard – **Evaluation**. The system checks whether at least one test was specified; otherwise prompts to correct.

1 - Kit selection
2 - Strains reading
3 - Tests results

Identified taxon	Identification score	T - index	List of doubtful results
Edwardsiella tarda	100.0	1.000	
Salmonella enterica subsp. enterica	0.00	0.045	IND 1 SOR 90 MAN 98
Escherichia coli	0.00	- 115	H2S 1 SOR 88 TRE 95
Morganella morganii subsp. morganii	0.00	- 082	H2S 20 IYS 1 URE 96

Strain is excellently differentiated.
Edwardsiella tarda - strain is typical
Excellent identification

Information about taxons List of doubtful results

Edwardsiella tarda Edwardsiella tarda **Differentiation**

Taxons are listed in the Identified taxon Window, which were pre-sorted using absolute probability limits. For each taxon you can find two data:

- **Identification score.** It shows the degree of identification exclusivity. Based on the assumption that the identified strain belongs to the given taxon, the identification score indicates the percentage of probability that the strain belongs to this taxon and none other.
- **T-index.** Indicates the typicality of the identified strain relative to the taxa listed. The T index value is between 1 - 0. The higher the T-index, the more similar is the strain to the „ideal“ of the given taxon.

A final evaluation of the identification is the sum of both the criteria above. The result is reflected in the taxonomy window. In case of very good or excellent identification, the identified taxon is highlighted in dark green. In the case of good or acceptable identification, the taxon is highlighted in light green. In the case of generic or species identification, the taxa are highlighted in yellow.

Obviously, the application-generated identification result must always be verified by the user. There are other auxiliary functions – **Information about taxons**, **List of doubtful results**, and **Differentiation Tests**.

Identification result can be printed by pressing the blue printer icon in the lower right corner. Data are not longer stored in the system.



All current identifications are always printed. For each set, results are listed on a new page. Isolates are numbered in the order in which they are inserted. However, if you need to enter your own isolate numbers, it is more appropriate to use another mode of program work.



The wizard closes by pressing the form's exit button in the lower-right corner.

7.2.10 Ad-hoc susceptibility testing wizard

The wizard allows the user to perform any sensitivity determination using the system's ATB methods without having to enter isolates. The results of these determinations are not stored in the data and are not logged by the system.

We will start the free sensitivity determination using the *Tools and Reports / Consulting Tools / Ad-hoc susceptibility testing* procedure.

In the first step of the wizard - **Material, methods** - the user selects the ATB kit and the sample material:

Material, methods

Customization

Identification - reading

MIC / zones

Evaluation

Output report

Material

blood

☐ Local ATB application
 ☒ Systemic infection

☒ Susceptibility testing method
 ☐ Use only your own ATB methods

Abbrev.	Examination method
MIC YST	MIC YST Diagnostics
DDM	Disc diffusion method
OMM	Other MIC methods
STR	MIC single strips
G-I	MIC G-I (Enterobacteriaceae)
G-II	MIC G-II (Enterobacteriaceae)
URINE	MIC URINE
NEFERM	MIC NEFERM
STAPHY	MIC STAPHY
G+	MIC G+
BP G-I	SENGLAtest G-I
BP G-II	SENGLAtest G-II
BP G+	SENGLAtest G+
BP URINE	SENGLAtest URINE

>

<

<<

Examination method

MIC G-I (Enterobacteriaceae)

Disc diffusion method

☐ Použití metodu RAST

?

X

The user further assigns the test methods available to the isolate in the middle table of the Test Methods. Examination methods can be filtered using the method type switch (Susceptibility testing methods / Only own ATB methods).

- The selected method from the Test methods table can be moved to the table of assigned isolate examination methods on the right by pressing the > button, double-clicking on the selected method or pressing the Enter key on the selected method.
- Examination methods can be removed from the list of assigned methods by pressing the < (one method removed) or << (all methods removed) button.

If a configurable method has been selected, the user proceeds to the **Customization** step:

Material methods

Customization

Identification - reading

AMC / zones

Evaluation

Output report

Acute

Examination method

Disc diffusion method

Added test

Abbrev.

Test name

AMK

amoxicillin

AMC

amoxicillin-clavulanic acid

AMB

amphotericin B

AMP

ampicillin

AMS

ampicillin-sulbactam

ANM

azithromycin

AZI

aztreonam

AZA

aztreonam-avibactam

BEI

benzylpenicillin

CFP

caspofungin

CEC

cefazolin

CFR

cefadroxil

LEX

cefalexin

FAM

cefamandole

CFZ

cefazolin

CDR

ceftriaxone

amikacin

⏮

⏪

⏩

⏭

>

<

<<

?

✕

User assigns for each isolate in the table on the left a method from the Added tests table.

- Tests are moved to the Test list on the right either by pressing the > button or double clicking on the selected test or pressing the Enter key on the selected test.
- Tests are removed from the Test list either by pressing the < button (one test removed) or pressing << (all tests removed).

Next, the user goes to the step **Identification – reading**:



Quick search:

Acinetobacter baumannii
 Acinetobacter baumannii complex



The user selects an identified taxon from the list of taxa.

Quick search can be used for easier orientation. After entering any text in this field, the system selects from the list of taxa where the text occurs anywhere in the genus or species name of the taxon.

After entering the identification result for the isolate, it is possible to go to the **MIC / zones** step.



Isolate	Examination method
1	CR
2	
3	
4	
5	
6	
7	
8	
9	
10	
11	
12	

	1	2	3	4	5	6	7	8	9	10	11	12	
1	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	ampicillin
2	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	ampicillin-sulbactam
3	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	cefazolin
4	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	cefuroxime
5	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	aztreonam
6	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	gentamicin
7	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	amikacin
8	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	colistin
9	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	trimethoprim-sulfamethoxazole
10	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	ciprofloxacin
11	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	chloramphenicol
12	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	tetracycline

☐ Growth in a well ☒ Growth inhibition

Determine the MIC value by clicking into the certain well in the plate



- In the case of MIC kits, the results are entered by clicking on the strip well, in which inhibition of growth is first observed in the row. In case of growth in all wells, the user selects the R field.
- When the disc diffusion method is read, user enters directly the inhibition zones diameter for individual antibiotics.
- When reading another MIC method, the user directly enters the MIC value for each antibiotic.

After entering the sensitivity results, it is possible to go to the Evaluation step:

- The result details (MIC/zone diameter, kit used, change of standard, use of PK/PD breakpoints, etc.) will be displayed when the mouse is moved above the given result.
- Click on the Evaluation comments button to get the report for the laboratory staff to help interpret the results, recommend the next steps, and show any discrepancies in the analysis results (atypical resistance profiles).
- Click on the Therapeutic recommendation button to get report for acceptable treatment (sensitive or intermediate results). The button is displayed only if the List the recommended ATB dosage during evaluation is selected.
- By clicking on the Switch Standard and evaluate button, it is possible to change the interpretation rules to the second standard (EUCAST or CLSI) and evaluate results based on the second one.
- You can change the strain identification by selecting the result from the drop-down list of taxa. You can use the filter in the Quick search field to select taxa.
- The results can be changed by clicking on the result field and overwriting it. Changed results are marked with an orange stripe at the bottom of the result and text.
- Warning to the right appears in case of atypical resistance phenotypes (intrinsic resistance results)

The next step of the wizard – **Output report** can be accessed after verification and eventual modifications of the isolate / sample.

In this step, you can edit the output for the end user (clinician). Moving to this step, you will see an editable list of all the analyzed antibiotics with the end-user reports and a field for a possible *Final comments*:

[illegible]

The Expert System Rating for the current isolate / sample can be printed by clicking on the blue printer icon.



All currently performed determinations are always printed. For each strain, the results are listed on a new page. Isolates are numbered according to the order in which they are inserted. However, if you need to enter your own isolate numbers, it is better to use another mode of program operation (isolate registration).

The wizard is closed by pressing the form exit button in the lower right corner.

7.3 Results

7.3.1 Expert System

The expert system evaluates the analysis of samples and isolates. The expert system evaluates only isolates for which both identification and antibiotic susceptibility results are available.

In the first step – ***Isolates selection*** – user selects isolates to be evaluated:

Isolates selection	Evaluation	Output report													
<p>Mode of samples evaluation:</p> <ul style="list-style-type: none"> <input type="radio"/> [All completed and not yet evaluated'] <input checked="" type="radio"/> Completed and not yet evaluated from the date <input type="radio"/> Preliminary evaluation (including Incompleted) <input type="radio"/> Repeated evaluation of the results 	<p>Select registration date of isolates evaluated:</p> <div> <input type="text" value="09/07/2017"/> <table border="1"> <thead> <tr> <th>isolate</th> </tr> </thead> <tbody> <tr><td>4</td></tr> <tr><td>11</td></tr> <tr><td>16</td></tr> <tr><td>17</td></tr> <tr><td> </td></tr> <tr><td> </td></tr> <tr><td> </td></tr> <tr><td> </td></tr> <tr><td> </td></tr> <tr><td> </td></tr> <tr><td> </td></tr> <tr><td> </td></tr> </tbody> </table> </div>	isolate	4	11	16	17									
isolate															
4															
11															
16															
17															

By switching the *Mode of samples evaluation* switch, user selects the selection of isolates:

- a. All completed and not yet evaluated; b. Completed and not yet evaluated from the date;
 - c. Preliminary evaluation (including incompleting); d. Repeated evaluation of the results.
- In the case *Completed and not yet evaluated from the date*, you can select from the list the date of receipt of the isolates.
 - In the case of *Repeated evaluation of the results*, you can specify a closer identification of isolates (isolate designation and / or date).

After selecting the Reading mode, you can go to the next step of the wizard – **Evaluation**, and gradually evaluate individual samples / isolates. The system based on identification and MICs or disk zone diameters values determines susceptibility to analyzed antibiotics (using EUCAST or CLSI standards):

- The result details (MIC/zone diameter, kit used, change of standard, use of PK/PD breakpoints, etc.) will be displayed when the mouse is moved above the given result.
- Click on the *Evaluation comments* button to get the report for the laboratory staff to help interpret the results, recommend the next steps, and show any discrepancies in the analysis results (atypical resistance profiles).
- Click on the *Therapeutic recommendation* button to get report for acceptable treatment (sensitive or intermediate results). The button is displayed only if the List the recommended ATB dosage during evaluation is selected.
- By clicking on the *Switch Standard and evaluate* button, it is possible to change the interpretation rules to the second standard (EUCAST or CLSI) and evaluate results based on the second one.
- You can change the strain identification by selecting the result from the drop-down list of taxa. You can use the filter in the *Quick search* field to select taxa.
- The results can be changed by clicking on the result field and overwriting it. Changed results are marked with an orange stripe at the bottom of the result and text.
- Warning to the right appears in case of atypical resistance phenotypes (intrinsic resistance results)


If the user does not wish to have any ATB in the end report, it can be removed. We do this by right-clicking on the sensitivity result and selecting Remove ATB from report. The deleted ATB changes the background and font colour.

[illegible]

Both basic and derived ATB can be removed. If a user deletes a basic ATB, all ATBs derived from that ATB are also deleted.

The next step of the wizard – **Output report** can be accessed after verification and eventual modifications of the isolate / sample.

[illegible]

- The range of antibiotics listed is controlled by the selection of an expert system standard.
-  By clicking the *Switch Standard and evaluate* button the results of the second standard can be evaluated.
- If important phenotypic groups may exist for a given taxon, a drop-down list of groups will be displayed.
- If the strain corresponds to an important phenotypic group, it is designated as this group. The user can change the phenotypic group assignment.

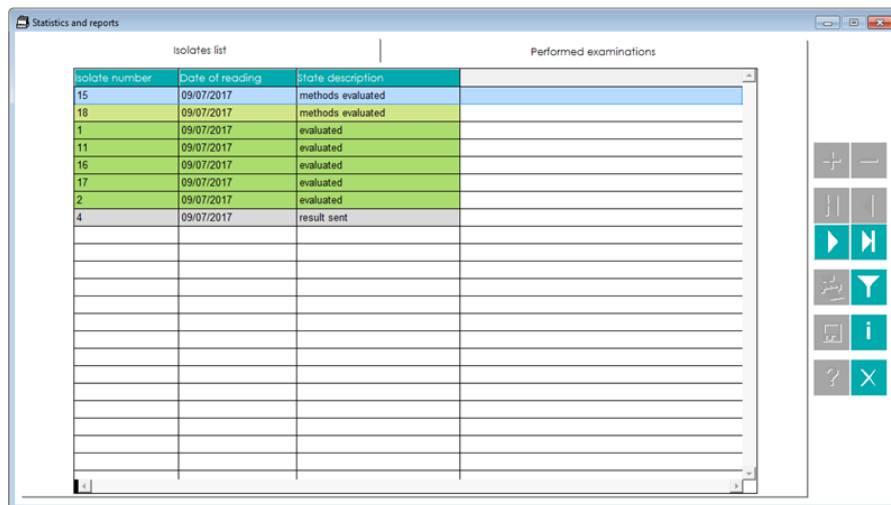



If the current sample / isolate was the last one not evaluated, the wizard is terminated after saving the data.

7.3.2 Statistics and reports

The form allows you to view all of the isolates / samples that have been received in the system so far. For each sample / isolate it is possible to list all used diagnostic methods and their results, including evaluation by an expert system.

The *Isolates / Samples* list (depending on the system mode set – see [Program Modes](#)) is displayed when the form is started.



- The list of Isolates is colour-coded by status (from received to sent).
-  You can search for samples / isolates using the *Records Selection* tool in the toolbar on the right.
- In the **Performed examinations** tab, user finds the examinations of the specimen / isolate.

All examinations for the given isolate / sample are listed in the table on the left side. Evaluation of the expert system (if any) is always listed the first. After you move to the appropriate record, the results are displayed.

Evaluation of the expert system as well as all comments are available by the buttons on the right.



Statistics and reports

Isolates list

Performed examinations

Isolate number: 11 Date of reading: 09/07/2017 Status: evaluated

Isolates	Kit
11	ENT24N
11	SSTR

ENT24N ENTEROtest 24 N

Morganella morganii subsp. morganii - Very good identification

S S S

AMC COL LIZ

...

...

The identification result is displayed, including the results of all tests:

Statistics and reports

Isolates list

Performed examinations

Isolate number: 11 Date of reading: 09/07/2017 Status: evaluated

Isolates	Kit
11	ENT24N
11	SSTR

ENT24N ENTEROtest 24 N

Morganella morganii subsp. morganii - Very good identification

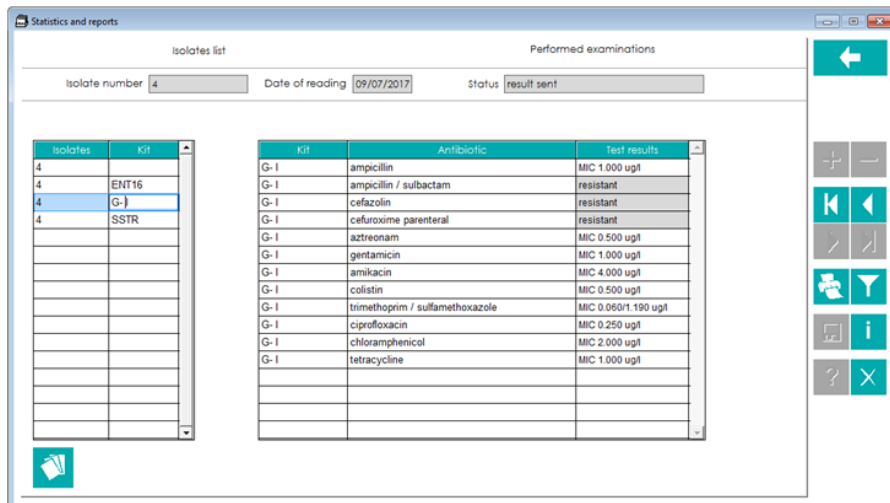
Strip tests

URE	ARG	ORN	LYS	H2S	SCI	MAL	ONP
SAL	SOR	MLB	CEL	LAC	TRE	MAN	GLR
DUL	ADO	ART	SUC	INO	RAF	ESL	BXY

Supplementary tests

IND	VPT	OXI
-----	-----	-----

The ATB susceptibility is listed as MIC / disc zone diametres:



Isolates	KIT
4	
4	ENT16
4	G-I
4	SSTR

KIT	Antibiotic	Test results
G-I	ampicillin	MIC 1.000 ugt
G-I	ampicillin / sulbactam	resistant
G-I	cefazolin	resistant
G-I	ceftiofur parenteral	resistant
G-I	aztreonam	MIC 0.500 ugt
G-I	gentamicin	MIC 1.000 ugt
G-I	amikacin	MIC 4.000 ugt
G-I	colistin	MIC 0.500 ugt
G-I	trimethoprim / sulfamethoxazole	MIC 0.060/1.190 ugt
G-I	ciprofloxacin	MIC 0.250 ugt
G-I	chloramphenicol	MIC 2.000 ugt
G-I	tetracycline	MIC 1.000 ugt

The form is closed by pressing the *Close the form* button in the right side toolbar.



7.3.2.1 Printing the results

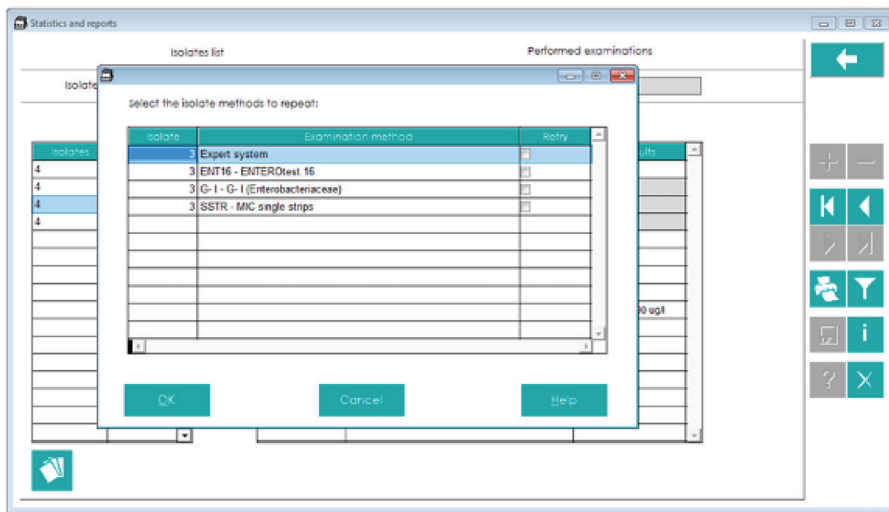
You can print results from the **Statistics and Reports** form, even repeatedly, by clicking on the printer icon in the right side toolbar:



7.3.2.2 Select the sample/isolate methods to repeat

The conversion form is started by pressing the conversion button with the back arrow icon in the upper right corner:





In the *Retry* column, the user chooses the examination to repeat.

- If only the Expert system evaluation returns, the system converts the sample / isolate to the *Methods evaluated* state.
- If the user also returns one of the identification or ATB susceptibility testing methods, the system returns the method to the *Registered* state, the sample to the *Primocultures deducted* state, and the isolate to the *Registered* state.
- If the user returns a sample without isolates, the system returns both the sample and the primocultures to the *Registered* state.

7.3.2.3 Sample / isolate removal

To remove the sample / isolate, press the - button in the toolbar on the right. Only a sample / isolate that has not yet been submitted can be removed.

Once deleted, the record is marked as invalid and is included at the end of the sample / isolate list. An invalidated record is not included in report and statistic processing.

7.4 Statistics

Due to the scope, a separate ErbaExpert documentation is available for the statistics module.

7.5 Daily statistics

The form will allow you to view a daily overview of the laboratory work.

The user selects the date of the statistics. Then it can view both the overview of performed diagnostic methods and the number of isolates of individual taxa.

[illegible]

7.6 Quality control

Quality control means verification of the correct functioning of the kits (identification and MIC) with the help of standard control strains.

The quality control module is accessible from the top menu line. For a given user role, the quality control module must be made available by the ErbaExpert system administrator.

7.6.1 Check strains

In the Check strains list, all control strains that are ready for use in quality control processes can be viewed. The list is read-only.

Strain ID	Collection number	Alternative strain	Strain description
2	ATCC 49619	CCM 4501	Streptococcus pneumoniae ATCC 49619
3	ATCC 25922	CCM 3954	Escherichia coli ATCC 25922
4	ATCC 27853	CCM 3955	Pseudomonas aeruginosa ATCC 27853
5	ATCC 35218	CCM 4225	Escherichia coli ATCC 35218
1	ATCC 29212	CCM 4224	Enterococcus faecalis ATCC 29212
7	ATCC 29213	CCM 4223	Staphylococcus aureus ATCC 29213
9	ATCC 13880	CCM 303	Serratia marcescens subsp. marcescens ATCC 13
10	CCM 1799		Proteus spp. CCM 1799
11	ATCC 15947	CCM 2238	Edwardsiella tarda ATCC 15947
12	CCM 2531		Klebsiella aerogenes CCM 2531
13	CCM 4043		Streptococcus constellatus subsp. constellatus CC
14	CCM 4617		Streptococcus uberis CCM 4617
15	ATCC 29503	CCM 1911	Aerococcus viridans ATCC 29503
16	ATCC 49331	CCM 4296	Staphylococcus cohnii subsp. urealyticum CCM 42
17	ATCC 43198	CCM 3659	Enterococcus cecorum ATCC 43198
18	ATCC 49427	CCM 4216	Enterococcus raffinosus ATCC 49427
19	ATCC 10556	CCM 4047	Streptococcus sanguinis ATCC 10556
20	ATCC 11700	CCM 1875	Enterococcus faecalis ATCC 11700
21	CCM 2699		Kytococcus sedentarius CCM 2699
22	ATCC 12228	CCM 4418	Staphylococcus epidermidis ATCC 12228
23	ATCC 35539	CCM 3572	Staphylococcus gallinarum ATCC 35539
24	CCM 4069		Staphylococcus lugdunensis CCM 4069
25	CCM 7046		Staphylococcus nepalensis CCM 7046
26	ATCC 700061	CCM 4657	Staphylococcus sciuri subsp. rodentium ATCC 700

7.6.2 Acceptable QC results

This form indicates which control strains can be used to check each kit. Standard results are also shown for each strain and kit.

Acceptable QC results

Edit data | List

Metoda: MIC G+ | Check strain: Enterococcus faecalis ATCC 29212

☒ Use this strain

Diagnostic tests	Acceptable MIC (mg/L)
PEN - benzylpenicillin (0.06 - 8 mg/L)	1 - 4
AMP - ampicillin (0.12 - 16 mg/L)	0.5 - 2
ERY - erythromycin (0.06 - 8 mg/L)	1 - 4
CLI - clindamycin (0.12 - 16 mg/L)	4 - 16
LIZ - linezolid (0.12 - 16 mg/L)	1 - 4
CMP - chloramphenicol (0.25 - 32 mg/L)	4 - 16
TET - tetracycline (0.25 - 32 mg/L)	8 - 32
T_S - trimethoprim-sulfamethoxazole (0.03/0.6 - 4/76 mg/L)	<=0.5
GEN - gentamicin (0.25 - 128 mg/L)	4 - 16
VAN - vancomycin (0.12 - 16 mg/L)	1 - 4
TEC - teicoplanin (0.12 - 16 mg/L)	0.25 - 1
NFT - nitrofurantoin (2 - 128 mg/L)	4 - 16

Navigation icons: +, -, <, >, <=, >=, ?

Use this strain - if the field is selected, the strain is included in the set of check strains of the selected kit. Thus, the user can limit the number of strains used to check the kit.

7.6.3 QC plans

The form is used for scheduling kit checks. The user selects the one for which he will plan checks and switches to the Data Editing tab:

1 - Kit selection | 2 - Check strains | 3 - Schedule control

Which kit will you read?

☐ Identification method
☐ Susceptibility testing method
☐ Use only your own ATB methods

Autacolor BioRad
 ENTEROtest 16
 ENTEROtest 24
 ENTEROtest 24 N
 ENTERO-Screen
 ENTERO-Rapid 24
 STAPHYtest 16
 STAPHYtest 24
 STREPTOtest 16
 STREPTOtest 24
 NEFERMtest 24
 CANDIDA-Screen
 CANDIDAtest 21

Navigation icons: ?

[illegible]

1 - Kit selection

2 - Check strains

3 - Schedule control

Auxacolor BioRad

☒ Generate requests

Testing frequency

☐ ad-hoc quality control
☐ daily quality control
☒ weekly quality control
☐ two-week quality control
☐ monthly quality control

Check (day of week):

tuesday

Last examination

/ /

Last batch No.

Medium last batch No.

✓

?

✗

Testing frequency – you can choose how often the check of this kit will be performed. If the user chooses ad-hoc checks, they will have to schedule each check separately. This mode is used e.g. when checking new batches of kits.

Generate requests – If the user selects an option other than ad-hoc as the test frequency, scheduled checks can be generated automatically based on the entered date.

Last batch No. – new batch number can be entered when changing the batch of the kit.

After you schedule a check (or automatically generate a check), a warning icon appears in the lower right of your control board the day before your scheduled date:

After the check is scheduled, the scheduled checks appear in the Quality Check table in the ErbaExpert main dashboard.

7.6.4 IDE – visual control

The wizard will allow visual controls of identification kits.

In the first step of the wizard – Selection of controls – the user selects the checks scheduled for this or previous days and which will be read.

1 - Selection of controls

2 - Kit selection

3 - Strains reading

4 - Evaluation

Reading mode

☐ All not yet read

☒ Not read yet from the date

☐ Repeated reading

Select a scheduled QC date:

26/11/2019

Method	Strain label
ENTERotest 16	ATCC 15947
ENTERotest 16	CCM 2531
ENTERotest 16	ATCC 13880
ENTERotest 16	CCM 1799

?

X

By the *Reading mode* switch, user chooses selection of the isolates to read: **a.** All controls that have not been read before; **b.** Controls not read from a given date; **c.** Repeated reading.

- In case of *Not read yet from the date*, you can select the date of registration of the isolates from the list.
- In the case of *Repeated Reading*, you can also specify a more detailed identification of the control (date).

After selecting the reading mode, you can go to the next step of the wizard – **Kit selection**. User chooses one kit from the list.

1 - Selection of controls

2 - Kit selection

3 - Strains reading

4 - Evaluation

Select the kit to measure:

ENTEROtest 16

Batch number
445/78-88

Medium batch No.
123-456

Batch number – here it is possible to add the marking of the tested batch.

Medium batch No. - here it is possible to add the designation of the tested batch of suspension medium.

In the next step – **Strains reading** – all the strains listed in the Strain table are item-by-item scanned. User goes through the individual kit tests, reads all the strains and inserts the results into the appropriate fields.

1 - Selection of controls

2 - Kit selection

3 - Strains reading

4 - Evaluation

Strain

ATCC 13880

OCM 1799

ATCC 15947

CCM 2531

Strip tests

H2S

LYS

IND

ORN

URE

PHE

ESL

SCI

MAL

INO

ADO

CEL

SUC

SOR

TRE

MAN

?

×

- The result falls into the following categories: **a.** Positive; **b.** Negative; **c.** Dubious (cannot be decided).
- The positive result can be entered: **a.** By pressing the + button; **b.** Pressing 1; **c.** Using a left-click.
- The negative result can be entered: **a.** By pressing the - button; **b.** Pressing 2; **c.** Using a right-click.
- The dubious result can be entered: **a.** By pressing the space bar; **b.** Pressing 0; **c.** Clicking any mouse button on the already-read test with + or - value.
- Tests that are part of the supplied identification kits will be coloured in accordance with the colour of the kit well.

After entering all the strains, you can go to the next step of the Wizard – **Evaluation**. The system checks whether user entered at least one test result to each strain; otherwise, it prompts to correct.

1 - Selection of controls
2 - Kit selection
3 - Strains reading
4 - Evaluation

Strain	Diagnostic tests	Result	Acceptable
ATCC 13880	hydrogen sulfide production	-	-
COM 1799	lysine decarboxylase	+	+
ATCC 15947	indole production	-	-
CCM 2531	ornithine decarboxylase	+	+
	urea hydrolysis	-	-
	phenylalanine deaminase	-	-
	aesculine hydrolysis	+	+
	citrate utilization	+	+
	malonate utilization	-	-
	acid from myo-inositol	+	+
	acid from adonitol	+	+
	acid from cellobiose	-	-
	acid from saccharose	+	+
	acid from sorbitol	+	+
	acid from trehalose	+	+

The user scans the table of read strains on the left and evaluates the controls.

- Tests complying with the requirements are highlighted in green.
- Non-compliant tests are orange.
- Unrated tests are greyed out.

The blue printer icon appears in the lower-right corner. Now you can print the results.



The control is then marked as the sent one.

Once you have entered the results for all controls, you can save the data by pressing the blue wizard exit icon in the lower right corner.



The system checks the completeness of the assignment and prompts the user for any corrections; then the data are saved.

7.6.5 IDE - automated reader control

The wizard allows the automatic reading to perform the controls using a reader.

In the first step of wizard – Selection of controls – user selects controls planned for this or previous days.

1 Selection of control 2 Kit selection 3 Isolates position 4 Reader initializing 5 Plates measuring 6 Tests results 7 Evaluation

Reading mode

☐ All not yet read

☒ Not read yet from the date

☐ Repeated reading

Select a scheduled QC date:

26/11/2019

Method	Strain label
ENTERotest 16	ATCC 15947
ENTERotest 16	CCM 2531
ENTERotest 16	ATCC 13880
ENTERotest 16	CCM 1799

?
✕

By the Reading mode switch, user chooses selection of the isolates to read: a. All controls that have not been read before; b. Controls not read from a given date; c. Repeated reading.

- In case of Not read yet from the date, you can select the date of registration of the isolates from the list.
- In the case of Repeated Reading, you can also specify a more detailed identification of the control (date).

After selecting the reading mode, you can go to the next step of the wizard – Kit selection. User chooses one kit from the drop-down list.

Selection of controls Kit selection Isolates position Plates measuring Tests results Evaluation

Select the kit to measure:

ENTERotest 16

Batch number

445/78-9

Medium batch No.

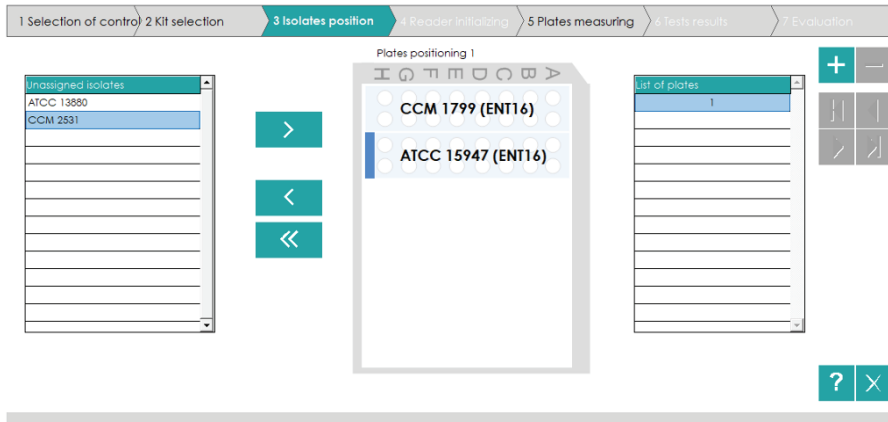
123-456

?
✕

Batch number – here it is possible to add the marking of the tested batch.

Medium batch No. - here it is possible to add the designation of the tested batch of suspension medium.

In the next step – **Isolate Position** – the user assigns the control strains to the plates.



The system automatically creates a corresponding number of blank plates to enter the particular number of strains.

- User sequentially assigns strains from the Unassigned strains table on the left into the plate: **a.** By pressing the > button; **b.** Double clicking on the selected strain.
- Once the isolate plate is full, the system automatically goes to the next plate.
- The selected strain on the plate is marked with a blue stripe on the left.
- Strains can be removed from the plate: **a.** By pressing < (one strain); **b.** By pressing << (all strains).
- To add a new plate to the list: **a.** Press the + right button on the toolbar; **b.** Use the keyboard shortcut Ctrl + N.
- To remove the current plate from the list: **a.** Press the - right button on the toolbar; **b.** Use the keyboard shortcut Ctrl + D.

User assigns the individual strains to the plates sequentially and goes to the next step **Reader initializing**.

If not done so, user switches the reader on and waits until the reader initialization (autocalibration). The ErbaScan reader signals the autocalibration ending with the permanent green diode on the front panel of the device.

When moving to the **Plates Measuring**, the system ejects plate carrier from the reader and prompts user to insert plate

1 Selection of control 2 Kit selection 3 Isolates position 4 Reader initialising 5 Plates measuring 6 Tests results 7 Evaluation

Plate number	Isolate number
1	ATCC 13880

Insert plate nr. 1 into the reader and press Measure:

Measuring

? X

- During inserting the plate, follow the order of inserts (for better plate orientation, the number of the first strain on the plate is always indicated at the plate number)
- Ensure that the plate is oriented correctly when inserted into the carrier (marking of the A-H positions on the carrier must match the plate markings).
- Press the **Measure** button to start the plate readout.
- The system prompts you to insert another plate when reading finishes.
- The system informs user about the last plate measured and goes to the next step of the wizard – **Test results**.

1 Selection of control 2 Kit selection 3 Isolates position 4 Reader initialising 5 Plates measuring 6 Tests results 7 Evaluation

Plate	Strain
1	ATCC 13880
1	CCM 1799
1	ATCC 15947
1	CCM 2531

Strip tests

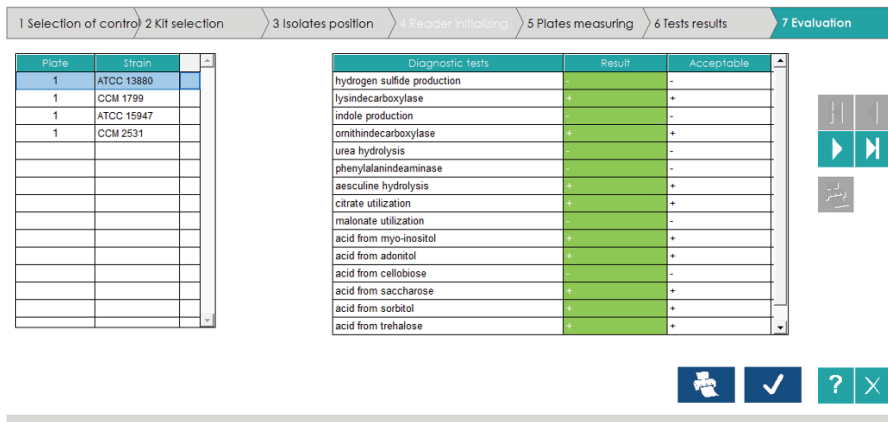
H2S	LYS	IND	ORN	URE	PHE	ESL	SCI
MAL	INO	ADO	CEL	SUC	SOR	TRE	MAN

? X

In this step, all isolates listed in the left table can be reviewed. For each isolate, user verifies the evaluation of each test.

- The positive result can be entered: **a.** By pressing the + button; **b.** Pressing 1; **c.** Using a left-click.
- The negative result can be entered: **a.** By pressing the - button; **b.** Pressing 2; **c.** Using a right-click.
- The dubious result can be entered: **a.** By pressing the space bar; **b.** Pressing 0; **c.** Clicking any mouse button on the already-read test with + or - value.
- Tests that are part of the supplied identification kits will be coloured in accordance with the colour of the kit well.

After entering all the isolates, you can go to the next step of the Wizard – **Evaluation**. The system checks whether user entered at least one test result to each isolate; otherwise prompts to correct.



The user scans the table of read strains on the left and evaluates the controls.

- Tests complying with the requirements are highlighted in green.
- Non-compliant tests are orange.
- Unrated tests are greyed out.

The blue printer icon appears in the lower-right corner. Now you can print the results.



The control is then marked as the sent one.

Once you have entered the results for all controls, you can save the data by pressing the blue wizard exit icon in the lower right corner.



The system checks the completeness of the assignment and prompts the user for any corrections; then the data are saved.

7.6.6 ATB – visual control

The wizard allows manual reading of the controls of antibiotics kits.

In the first step of wizard – ***Selection of controls*** – user selects ATB controls planned for this or previous days.

1 - Selection of controls **2 - Kit selection** **3 - Strains reading** **4 - Tests results**

Reading mode:

- ☐ All not yet read
- ☒ Not read yet from the date
- ☐ Repeated reading

Select a scheduled QC date:

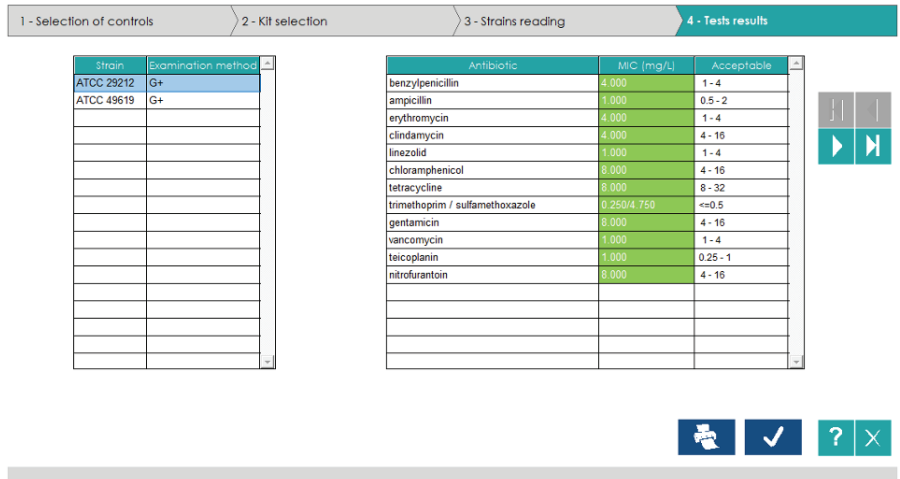
28/11/2019

Method	Strain label
MIC G+	ATCC 49619
MIC G+	ATCC 29212

By the Reading mode switch, the user chooses selection of the isolates to read: **a.** All isolates that have not been read before; **b.** Isolates not read from a given date; **c.** Repeated reading.

- In case of Not read yet from the date, you can select the date of registration of the isolates from the list.
- In the case of Repeated reading, you can also specify a more detailed identification of the isolate (isolate designation and / or date).

After selecting the reading mode, you can go to the next step of the wizard – **Kit selection**.



The user scans the table of read strains on the left and evaluates the controls.

- Tests complying with the requirements are highlighted in green.
- Non-compliant tests are orange.
- Unrated tests are greyed out.

The blue printer icon appears in the lower-right corner. Now you can print the results.



The control is then marked as the sent one.

Once you have entered the results for all controls, you can save the data by pressing the blue wizard exit icon in the lower right corner.



The system checks the completeness of the assignment and prompts the user for any corrections; then the data are saved.

7.6.7 ATB – reader control

The wizard allows automated reading of the controls of antibiotics kits using reader.

In the first step of wizard – **Selection of controls** – user selects ATB controls planned for this or previous days.

1 Selection of controls 2 Kit selection 3 Isolates position 4 Reader initializing 5 Plates measuring 6 Tests results 7 Evaluation

Reading mode

☐ All not yet read

☒ Not read yet from the date

☐ Repeated reading

Select a scheduled QC date:

25/11/2019

Method	Strain label
MIC G+	ATCC 49619
MIC G+	ATCC 29212



By the Reading mode switch, the user chooses selection of the isolates to read:

a. All isolates that have not been read before; **b.** Isolates not read from a given date; **c.** Repeated reading.

- In case of Not read yet from the date, you can select the date of registration of the isolates from the list.
- In the case of Repeated reading, you can also specify a more detailed identification of the isolate (isolate designation and / or date).

After selecting the reading mode, you can go to the next step of the wizard – **Kit selection**.



Select the kit to measure:

MIC G+

Batch number

789-456

Medium batch No.

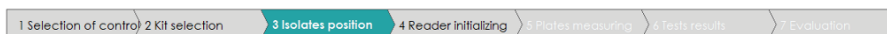
123-456



Batch number – here it is possible to add the marking of the tested batch.

Medium batch No. - here it is possible to add the designation of the tested batch of suspension medium.

In the next step – **Isolate Position** – the user assigns the control strains to the plates.

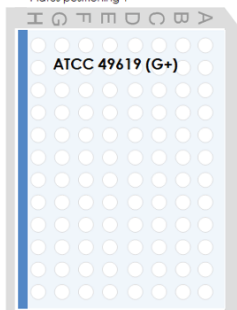


Unassigned isolates

Isolate	Examination method
ATCC 29212	G+



Plates positioning 1



List of plates

1
2



The system automatically creates a corresponding number of blank plates to enter the particular number of strains.

- User sequentially assigns strains from the Unassigned strains table on the left into the plate: **a.** By pressing the > button; **b.** Double clicking on the selected strain.
- Once the isolate plate is full, the system automatically goes to the next plate.
- The selected strain on the plate is marked with a blue stripe on the left.
- Strains can be removed from the plate: **a.** By pressing < (one strain); **b.** By pressing << (all strains).
- To add a new plate to the list: **a.** Press the + right button on the toolbar; **b.** Use the keyboard shortcut Ctrl + N.
- To remove the current plate from the list: **a.** Press the - right button on the toolbar; **b.** Use the keyboard shortcut Ctrl + D.

User assigns the individual strains to the plates sequentially and goes to the next step **Reader initializing.**

If not done so, user switches the reader on and waits until the reader initialization (autocalibration). The ErbaScan reader signals the autocalibration ending with the permanent green diode on the front panel of the device.



When moving to the **Plates Measuring**, the system ejects plate carrier from the reader and prompts user to insert plate.

1 Selection of control **2 Kit selection** **3 Isolates position** **4 Reader initializing** **5 Plates measuring** **6 Tests results** **7 Evaluation**

List of plates

Plate number	Isolate	Examination method
1	ATCC 49619	G+
2	ATCC 29212	G+

Insert plate nr. 1 into the reader and press Measure:

- During inserting the plate, follow the order of inserts (for better plate orientation, the number of the first strain on the plate is always indicated at the plate number)
- Ensure that the plate is oriented correctly when inserted into the carrier (marking of the A-H positions on the carrier must match the plate markings).
- Press the **Measure** button to start the plate readout.
- The system prompts you to insert another plate when reading finishes.
- The system informs user about the last plate measured and goes to the next step of the wizard – **Test results**.

In the case of MIC kits, it is possible to change results by clicking on the strip well, in which inhibition of growth is first observed in the row. In case of growth in all wells, the user selects the R field:

1 Selection of control > 2 Kit selection > 3 Isolates position > 4 Reader initializing > 5 Plates measuring > **6 Tests results** > 7 Evaluation

Plate	Strain	Method
1	ATCC 49619	G+
2	ATCC 29212	G+

	A	B	C	D	E	F	G	H	
<input type="checkbox"/> R	White	White	White	White	White	White	White	White	benzylpenicillin
<input type="checkbox"/> R	White	White	White	White	White	White	White	White	ampicillin
<input type="checkbox"/> R	White	White	White	White	White	White	White	White	erythromycin
<input type="checkbox"/> R	White	White	White	White	White	White	White	White	clindamycin
<input type="checkbox"/> R	White	White	White	White	White	White	White	White	linezolid
<input type="checkbox"/> R	White	White	White	White	White	White	White	White	chloramphenicol
<input type="checkbox"/> R	White	White	White	White	White	White	White	White	tetracycline
<input type="checkbox"/> R	White	White	White	White	White	White	White	White	trimethoprim-sulfamethoxazole
<input type="checkbox"/> R	White	White	White	White	White	White	White	White	gentamicin
<input type="checkbox"/> R	White	White	White	White	White	White	White	White	vancomycin
<input type="checkbox"/> R	White	White	White	White	White	White	White	White	teicoplanin
<input type="checkbox"/> R	White	White	White	White	White	White	White	White	nitrofurantoin

☐ Growth in a well
 ☒ Growth inhibition
 ☐ Suspicious growth - review

Determine the MIC value by clicking into the certain well in the plate

User checks the results of all tests on selected isolates and goes to the next step of the wizard – **Evaluation**. The system checks if at least one result has been entered for all isolates; otherwise, prompts to correct.




7.6.8 Archive of controls

The form will allow you to view all the checks that have been processed so far in the system. For each control, it allows you to list all strains and their results, including compliance with expected values.

When you run the form, a list of isolates is displayed.

[illegible]

- Controls in different states (from scheduled to invalid) are differentiated in colour.
- For checks in the Evaluated state, the checks are distinguished from the following checks (green tinted) and unsatisfactory (orange tinted).
-  Checks can be searched using the Record Selection tool in the right toolbar.
- In the tab *Performed examinations* the user will find individual strains of the control.

In the tab *Performed examinations*, all strains analysed for the given control are listed in the table on the left. When you navigate to the entry, the results for that strain are displayed.

Overview of quality controls

Isolates list

Examination date: 28/11/2019

Batch number: 12-22/99

Strain	Result
ATCC 49619	compliant
ATCC 29212	not compliant

MIC G+ ATCC 49619

Diagnostic tests	MIC (mg/L)	Acceptable
benzylpenicillin	0.250	0.25 - 1
ampicillin	0.250	0.06 - 0.25
erythromycin	0.120	0.03 - 0.12
clindamycin	<=0.120	0.03 - 0.12
linezolid	1.000	0.25 - 2
chloramphenicol	8.000	2 - 8
tetracycline	0.500	0.06 - 0.5
trimethoprim / sulfamethoxazole	0.500/9.500	0.12 - 1
gentamicin	4.000	not evaluated
vancomycin	0.500	0.12 - 0.5
teicoplanin	2.000	not evaluated
nitrofurantoin	8.000	4 - 16



You can exit the Overview of Quality Controls form by clicking the Close Form button in the right toolbar.

7.6.8.1 Printing the results



You can print results from the *Overview of Quality Controls* form, even repeatedly, by clicking on the printer icon in the right side toolbar:

Overview of quality controls

Isolates list

Examination date: 28/11/2019

Batch number: 12-22/99

Report print - Overview of quality controls

Output report

Output destination

☒ screen

☐ printer

Copies count: 1

Report scope

☒ All records of file

☐ Current selection

☐ Current record

Printer setup

Preview Back Help

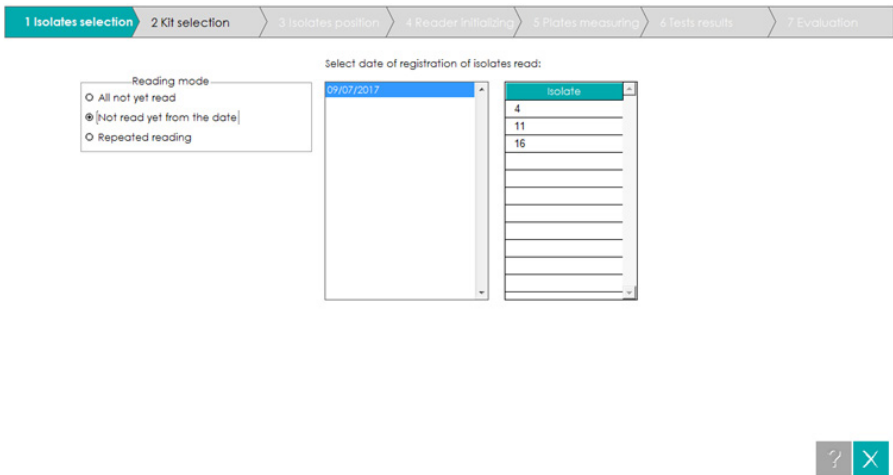
In the *Output Report* list, a list of all the tests that can be performed for the respective control (with respect to already performed examinations) is displayed. After selecting the report and clicking the *Print (Preview)* button, the report is printed / displayed.

8. User interface control

8.1 Wizards

The most important forms of the ErbaExpert system are the wizards. They are adapted to support individual processes while working in the lab. A process is understood to be an activity with a defined start and end usually performed without interruption.

The wizard is divided into individual steps between which you can move by clicking on the progress bar at the top of the wizard.



1 Isolates selection 2 Kit selection 3 Isolates position 4 Reader initializing 5 Plates measuring 6 Tests results 7 Evaluation

Reading mode

☐ All not yet read

☒ Not read yet from the date


☐ Repeated reading

Select date of registration of isolates read:

09/07/2017

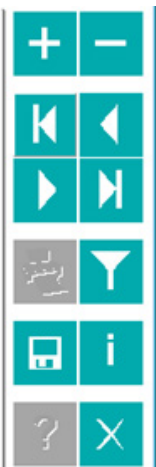
Isolate	
4	
11	
16	

? X

- The current step of the wizard is displayed in green with white writing.
- The wizard steps that can be instantly moved from the current step are shown in gray with black writing.
- The currently unaccessible wizard steps are shown in grey colour with white writing.
-  You can terminate the wizard at any time without saving the data by pressing the form exit button in the toolbar at the bottom right corner.
- Save data, or print and save data, is usually available in the last step of the wizard by clicking on the corresponding blue buttons located in the lower right corner.

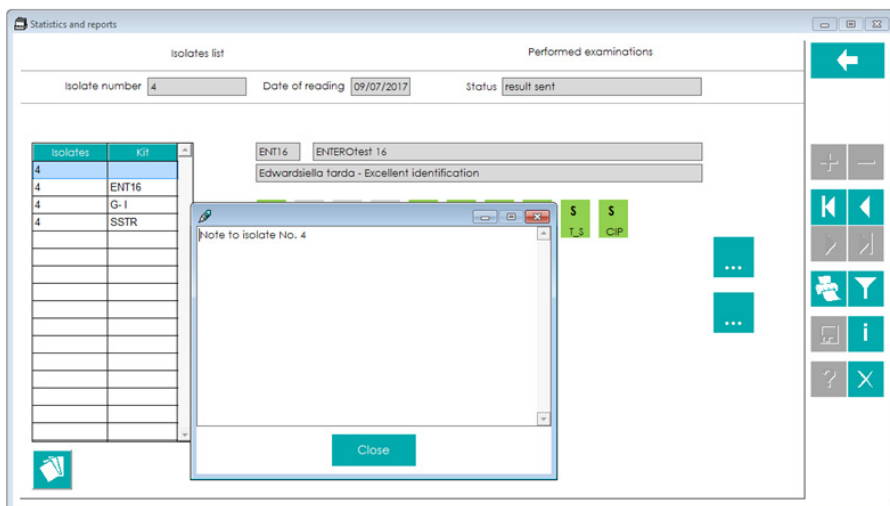
8.2 Toolbars

The working toolbar allows the most common data file operations. By default, it is anchored at the right edge of the form. The accessibility of the taskbar buttons may vary from application to application; it depends on the type of application and access rights.



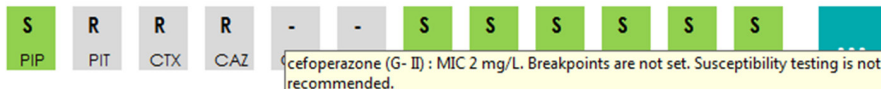
8.3 Notes

When you go through the wizards, you can write user notes to the current steps. Notes are kept by the system; if an object (sample, isolate, method) with existing notes is processed in subsequent follow-up wizards, notes can be displayed by clicking the notes button at the bottom left:



8.4 Tooltips

Tooltips are light yellow information boxes appearing when moving the mouse over a defined object. They are typically displayed above buttons in toolbars and above text boxes when entering test results. Not all the objects have tooltips.



8.5 Data forms

Data forms are used to input data into application data files, as for example a patient form.

The screenshot shows a software window titled 'Patient'. It contains three tabs: 'Edit data', 'Performed examinations', and 'List'. The 'Edit data' tab is selected. Inside this tab, there are several input fields and a dropdown menu. The fields are labeled: 'Patient internal code' (value: JD01), 'Name' (value: John), 'Surname' (value: Doe), 'Personal ID' (value: 1), 'Year of birth' (value: 1959), 'Gender' (radio buttons for 'woman', 'man', and 'unknown'), and 'Health insurance' (dropdown menu showing 'First Insurance Company'). To the right of the form is a vertical toolbar with icons for adding (+), deleting (-), and editing (pencil) records, as well as a help (?) icon.

8.5.1 Working with records in data forms

It is possible to add, modify, and delete records in data files using data forms, if the user possesses the administrator rights. These operations can be done in the following ways:

- Use the **shortcut menu**, right-click the form and select the action.
- Use the button in the toolbox on the form on the right.

You can move between the text input fields and other controls inside the data form using the mouse or the Tab key.

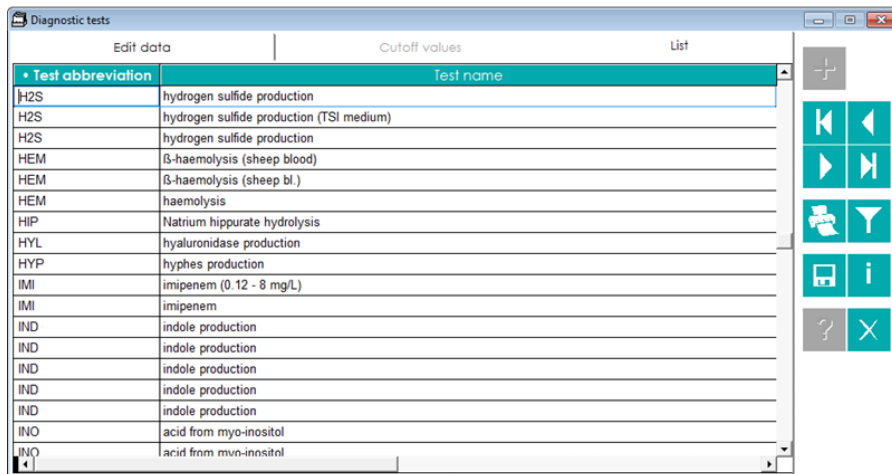
8.5.2 Table data display

In most data forms, the Data Browsing is the last tab of the form. It allows you to view the records of the data file in a spreadsheet. By going to the appropriate line, the user goes to the file record.

In spreadsheet view, you can edit the column width and column order by dragging the mouse after the column dividing line (width) or after the column header (order). The system saves the settings and displays the data according to the last edition.

8.5.3 Data files sorting

To sort the records in a spreadsheet view (Data Browsing tab), you can click on the column header to sort the file. The selected sorting will be done by changing the header font to bold and adding a • mark before the header (see the example below).



• Test abbreviation	Test name
H2S	hydrogen sulfide production
H2S	hydrogen sulfide production (TSI medium)
H2S	hydrogen sulfide production
HEM	β-haemolysis (sheep blood)
HEM	β-haemolysis (sheep bl.)
HEM	haemolysis
HIP	Natrium hippurate hydrolysis
HYL	hyaluronidase production
HYP	hyphes production
IMI	imipenem (0.12 - 8 mg/L)
IMI	imipenem
IND	indole production
IND	indole production
IND	indole production
IND	indole production
IND	indole production
INO	acid from myo-inositol
INO	acid from muo-inositol



Click the filter button to display the data selection form.



9. Terms and abbreviations

9.1 Used terms

Data file – a file that stores the results of analyzes of individual samples and isolates. It changes during working with the program.

Diagnostic method, diagnostic kit – a user-defined or predefined set of diagnostic tests used to analyze isolates; also a commercially available set of diagnostic tests.

Diagnostic test – traceable property or taxa characteristics in the identification matrix; then also the procedure, used to detect the occurrence of given property in the studied strain.

Identification matrix – databases distributed along with the program that includes the occurrence frequencies of observed properties (diagnostic tests) in observed taxa. Identification matrix data are not changed during the analyses procedure.

Strain, isolate – specific bacterial culture, with specific properties. Isolates are examined using diagnostic methods.

Data file field – unit of the data file structure, carrying information about the identified isolate or sample.

Product ID – unique SW key identifier used for activation of the ErbaExpert during installation.

Software key – unique series of letters and numbers, used during ErbaExpert software installation.

Taxon – taxonomic unit contained in an identification matrix. It can be a species, subspecies, biovar or pathovar. The properties of the taxa are defined in the identification matrix by the frequencies of the individual diagnostic tests.

Sample – material of biological (clinical) origin, analyzed for the presence of microorganisms.

Backup file – a security copy of the data file created on the backup media (other network hard drive, tape, etc.).

9.2 Abbreviations

ATB	Antibiotic
LIS	Laboratory Information system
MALDI	Matrix-Assisted Laser Desorption/Ionization
MIC	Minimal Inhibition Concentration



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