

SynReport Cloud - Instructions

Recommendations



The use of a Chromium-based browser (e.g. Microsoft Edge, Google Chrome) is strongly recommended, as the software is mainly tested with Chromium-based browsers.

Report Manager

In the report manager you can create new reports and manage your existing reports (e.g. re-open, change status). The reports and the corresponding data will be saved for the duration of the project and can be accessed by the project manager of RCPA (participants can only access their own reports).

Creating a new report



Upon entering the report manager, you will be asked to specify a report identifier (e.g. the specimen / accession number) and the number of pots/containers (if more than one). You can then select the appropriate form template and upon opening the form in one of the three views described below, the new report will be added to the list. No longer required reports can be assigned the status 'invalid' – data of these reports will be excluded from statistical data exports.

Opening forms

Depending on your requirements, you can select between three reporting views upon opening the form:



- Full form: opens the entire form, i.e. all form sections are displayed by default.
- Micro: opens the section 'Microscopic report' and all subsequent sections (-> Filling in forms). Clinical and specimen information as well as microscopic report are hidden by default.
- Macro: opens the first four main sections of the reporting template (i.e the sections 'Scope',
 'Clinical information', 'Specimen information' and 'Macroscopic report') in the touch mode,
 optimised for gross reporting. The section 'Microscopic report' and subsequent sections are
 hidden by default.

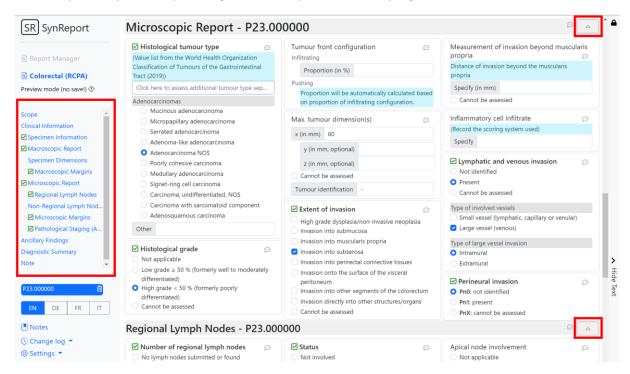


Filling in forms

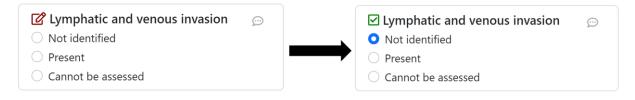
The forms are divided into different sections, representing steps in the pathology workflow. The main sections usually present in a typical SynReport histopathology reporting form are:

- Scope (optional, restricts the questions asked by specimen type, e.g. lymph nodes only)
- Clinical Information
- Specimen information
- Macroscopic Report
- Microscopic Report
- Ancillary Studies
- Diagnostic Summary
- Note (overarching comment)

Depending on the reporting mode in which the form has been opened, certain sections are hidden/collapsed by default (-> Opening forms / reporting modes). Individual sections can be accessed via the navigation bar on the left of the screen. Upon selection in the navigation bar, previously collapsed sections are automatically expanded. Sections can also be manually accessed by scrolling and collapsed/expanded by clicking the arrow symbol at the top right corner of each section.



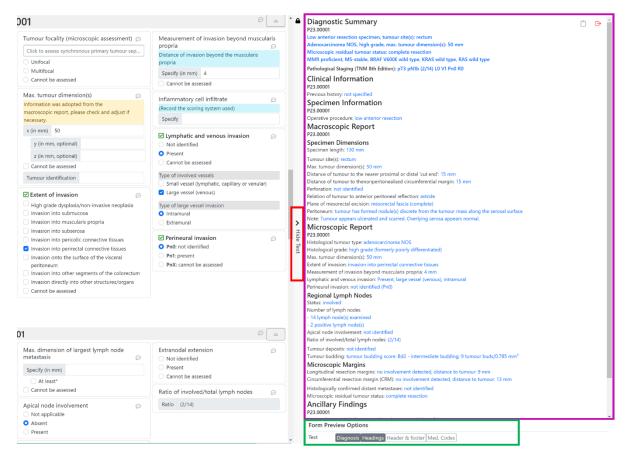
Mandatory questions are indicated by a bold question name and an icon in the upper left corner of the question (when a question is completed, the initial red symbol changes to a green symbol).



V1.03, 21.01.2023 Author: Claudio Molina Page **2** of **8**

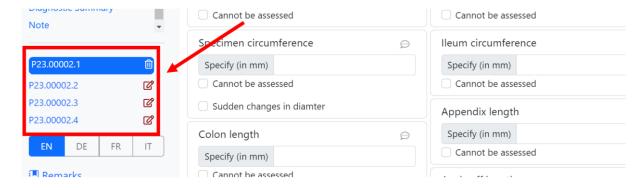


Upon answering the questions, the report text is continuously generated on the right side of the screen (see purple box below). The preview of the report text can be hidden or displayed by clicking 'Hide Text' / 'Display Text' (see red box below). By default, the report text includes a short summary as well as the headings of the different form sections and the specimen identifier. If preferred, the summary text and the headings can individually be deactivated. Additionally, a header and a footer including name, version and incorporated guideline of the form can be added to the text (see green box below).



Multiple pots/containers

If you have initially specified that the sample consists of several pots (-> Creating a new report), the corresponding number of forms is automatically provided. Each pot/form is listed in the sidebar on the left (labelled according to the scheme 'Report ID/Accession number.1', 'Report ID/Accession number.2' etc., see below). This way, each pot can be assessed individually and yet a combined report can be created. To switch between the pots/forms you can click on the respective pot label in the list.



V1.03, 21.01.2023 Author: Claudio Molina Page **3** of **8**

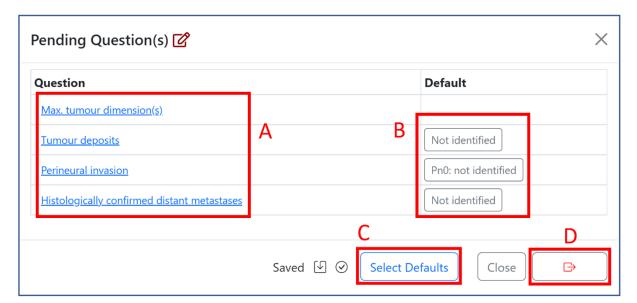


Completeness check, saving and closing

Below the form questions, there is a tool bar including three buttons:



- 'Pending Question(s)'
 - o Displays the number of unanswered mandatory questions (given that there are any)
 - Upon clicking this button, a panel appears, in which the individual unanswered mandatory questions are listed (see below, A)
 - By clicking on any displayed question name listed in the panel, the software jumps to the corresponding question in the form, where it can be completed
 - Certain questions have predefined standard values (e.g. for the question 'Histologically confirmed distant metastasis' the standard value is 'Not identified').
 - In the 'Pending question(s)' panel, the standard values can be selected individually (B) or all at once (C) (if all standard values have been selected at once, individual values can also be de-selected manually afterwards within the panel)



- 'Save'
 - Saves the current state of the form / report
 - Once there are no more unanswered mandatory questions, the button switches from white to green, while the 'Pending Question(s)' button disappears



- 'Save and Close'
 - Exits the report after saving all previously unsaved changes
 - Unless all mandatory questions have been completed, this button will also prompt the 'Pending Question(s)' panel at first instance
 - The pending questions can be ignored by again clicking the save and close symbol in the 'Pending Question(s)' panel (see screenshot above, D)
 - This button can also be found in the top right corner of the screen



Copying report to clipboard

The report can be directly copied to the clipboard with the corresponding button at the top right corner of the screen. The report text can subsequently be pasted into the laboratory information system or into a Word document.



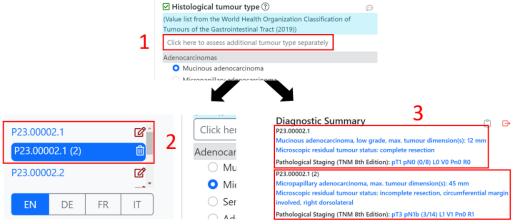
Additional functionalities

- Changing form template
 - It may occur that you wish to manually change the form template once the report has already been opened because:
 - The submission consists of several pots, and not all pots contain specimens that are to be reported with the same form template
 - The wrong form template has been selected upon creating the report
 - The form template can be switched by clicking on the title of the currently loaded form template in the top left corner (see below) and selecting the desired form in the appearing panel. After switching the form template, all previously entered data that can be unambiguously assigned is automatically transferred to the newly loaded form.



Multiple tumours

- o In case of multifocal tumours, the relevant tumour properties can be specified separately for each tumour within the same form.
- In case of multiple (synchronous) primary tumours or additional metastasis, a separate form can be opened for any additional tumour, by clicking the correspondingly named button in the form (see below, 1). This will open an additional form (2, not to be confused with an additional form representing a separate pot) resulting in a combined but subdivided report with two separate staging's (3).



V1.03, 21.01.2023 Author: Claudio Molina Page **5** of **8**



- Remarks (bottom left corner of screen, see screenshot below):
 - Remarks can be added to the report (e.g. to inform a colleague that ancillary studies are still pending). These remarks do not appear in the report text but can optionally be displayed to the reporting user upon opening the pre-existing report.
- Change log:
 - Via the change log, all previously saved states of the report can be viewed
- Settings:
 - Nested within the settings toolbar, there are several options
 - 'Touch mode': switches to and from touch mode
 - 'Table design' / 'Card design': allows switching between design
- Manual:
 - Allows you to access the user manual
- Reporting issues:
 - o In the bottom left corner of the screen (see below), as well as on the right side of any question (see screenshot below 'Supplementary information', B), there is a button which allows the communication of errors and suggestions to our development team.



- Supplementary information:
 - Many questions (as well as certain form sections) have supplementary information attached. This information can be accessed by clicking the question mark next to the form element (see below, A).



V1.03, 21.01.2023 Author: Claudio Molina Page **6** of **8**



Example report created with SynReport

Diagnostic Summary

P23.00001

Low anterior resection specimen, tumour site(s): rectum
Adenocarcinoma NOS, high grade, max. tumour dimension(s): 50 mm
Microscopic residual tumour status: complete resection
MMR proficient, MS-stable, BRAF V600E wild type, KRAS wild type, RAS wild type
Pathological Staging (TNM 8th Edition): pT3 pN1b (2/14) L0 V1 Pn0 R0

Clinical Information

P23.00001

Previous history: not specified

Specimen Information

P23.00001

Operative procedure: low anterior resection

Macroscopic Report

P23.00001

Specimen Dimensions

Specimen length: 130 mm Tumour site(s): rectum

Max. tumour dimension(s): 50 mm

Distance of tumour to the nearer proximal or distal 'cut end': 15 mm Distance of tumour to thenonperitonealised circumferential margin: 15 mm

Perforation: not identified

Relation of tumour to anterior peritoneal reflection: astride Plane of mesorectal excision: mesorectal fascia (complete)

Peritoneum: tumour has formed nodule(s) discrete from the tumour mass along the serosal surface

Note: Tumour appears ulcerated and scarred. Overlying serosa appears normal.

Microscopic Report

P23.00001

Histological tumour type: adenocarcinoma NOS

Histological grade: high grade (formerly poorly differentiated)

Max. tumour dimension(s): 50 mm

Extent of invasion: invasion into perirectal connective tissues Measurement of invasion beyond muscularis propria: 4 mm

Lymphatic and venous invasion: Present, large vessel (venous), intramural

Perineural invasion: not identified (Pn0)

V1.03, 21.01.2023 Author: Claudio Molina Page **7** of **8**



Regional Lymph Nodes

Status: involved

Number of lymph nodes
- 14 lymph node(s) examined
- 2 positive lymph node(s)

Apical node involvement: not identified Ratio of involved/total lymph nodes: (2/14)

Tumour deposits: not identified

Tumour budding: tumour budding score: Bd2 - intermediate budding; 9 tumour buds/0.785 mm²

Microscopic Margins

Longitudinal resection margins: no involvement detected, distance to tumour: 9 mm

Circumferential resection margin (CRM): no involvement detected, distance to tumour: 13 mm

Histologically confirmed distant metastases: not identified Microscopic residual tumour status: complete resection

Ancillary Findings

P23.00001

Mismatch repair (MMR) immunohistochemistry: MMR proficient

BRAF V600E mutation testing: wild type

MLH1 promoter methylation testing: not tested

MMR status by microsatellite instability (MSI) testing: MS-stable

KRAS mutation testing: wild type RAS mutation testing: wild type

Contact

Celerato AG
Chimligasse 4
8603 Schwerzenbach, Switzerland
www.celerato.ch
info@celerato.ch
0041 44 527 71 57

List of Changes

Version	Changes	Date	Edited by	Validated by
0.10	Creation initial version	09.12.2022	Claudio Molina	Norbert Wey
0.20	Finishing first draft	10.12.2022	Claudio Molina	-
0.30	Addition of missing points	06.01.2023	Claudio Molina	Norbert Wey
0.40	Wording	06.01.2023	Claudio Molina	Norbert Wey
0.50	Addition of missing points	20.01.2023	Claudio Molina	-
0.60	Addition of screenshots	20.01.2023	Claudio Molina	-
0.70	Addition of screenshots	20.01.2023	Claudio Molina	Norbert Wey
0.80	Changes in structure and wording	20.01.2023	Norbert Wey	Claudio Molina
0.90	Addition of screenshots, ex. report	20.01.2023	Claudio Molina	-
1.00	Addition of last points, screenshots	20.01.2023	Claudio Molina	Norbert Wey
1.01	Position screenshot, layout	21.01.2023	Norbert Wey	-
1.02	Copy to clipboard before Additional Features, Ref.	22.01.2023	Claudio Molina	Norbert Wey
1.03	Added crossed-out Safari Logo	23.01.2023	Claudio Molina	Samuel Merki

V1.03, 21.01.2023 Author: Claudio Molina Page **8** of **8**