

Project: Lab results in FHIR Tips and Tricks in addition to the Implementation Guide for Receivers

(work in progress)

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Context of this document

- Out of scope
 - Lab Requests > Referral prescription project <https://github.com/hl7-be/referral>
 - Publication to hubs
 - Roll-out in production to all labs and receivers, o.a. implementation of a centralized repository of which receivers are able to receive in FHIR and to what extend (e.g. not yet structured microbiology)

Links to documentation & visualiser

FHIR Profiles

- [BeLaboratoryReport](#)
- [BeSpecimenLaboratory](#)
- [BeLaboratoryreportComposition](#)
- [BeObservationLaboratory](#)

FHIR Implementation Guide

- For textual guidance <https://build.fhir.org/ig/hl7-be/lab/guidance.html>
- Questions and remarks and history of previous questions <https://github.com/hl7-be/lab/issues>
- All sources <https://github.com/hl7-be/lab>

Reference tables

- Loinc & Albert2 Codes:
<https://www.ehealth.fgov.be/standards/kmehr/en/page/retam-exports>
- UCUM units

<https://www.health.belgium.be/nl/ucum>

Test plan & test files (in json, pdf and html)

- <https://github.com/hl7-be/hl7-be-fhir-laboratory-report/blob/master/testing/Test%20Plan.MD>

Visualizer

- <https://vizapp.icure.dev/>

Attention points

1. These attention points are additions to the above documentation, specific for the receiving software.
2. The visualiser is meant to check the validity and content of the FHIR message. It is not a reference for how the results must/should be displayed in receiving software. But do think about how you will handle validation errors.
3. Test case/sample 815333049 is a good starter case. In the end all test cases should be handled. Each test case also has a PDF version, all info on that PDF should also be visible in the receiving software.
4. Titles, subtitles, comments, footer info, conclusion, interpreter (biologist), status are not transferred as fictive results and/or in free text anymore. The corresponding specific FHIR elements (e.g. .note, .conclusion, .resultsInterpreter, ...) must be correctly handled.
5. Several elements support hierarchies and grouping (e.g. using .hasMember). Handling of these (e.g. indentation) must be implemented, as it can be important for a correct interpretation.
6. For each observation, the receiving software must use the Loinc/Albert2/.. code to find the corresponding label in the Retam reference table, in the user's language. So not just display the "text" attribute of the observation>code element.
7. Units should be displayed based on the content of "unit" in FHIR (and not of "code").
8. New lines should be displayed for /r/n ou /r (e.g. in reference range)
9. Formatted text should be displayed using a non proportional font
10. HTML formatted text must be displayed properly ?
11. The result can contain text indicating the reason of a missing result, e.g. "sample not received", "result pending", ... these texts are not standardized across laboratories, but should be displayed.

12. For patients without NISS, a local identifier can be used (put in FHIR by the lab).
13. There are significant additions compared to the older formats like the possibility to:
- a. add detailed information + note about specimen(s) and link between specimens and observations/results
 - b. include images on report and observation level (e.g. by linking an observation to a media resource, for example for electrophoresis charts)
 - c. include pdf version (in presented form)
 - d. include a conclusion at the report level
 - e. information about the interpreter (biologist) or external performer for an observation
 - f. specify an status per observation
 - g. specify a different request or performer for certain observations (vs the general ones specified at report level)
 - h. specify an observation is derived from another observation
(check the FHIR implementation guide for details about all these additions)
14. Structured microbiology results should be presented in a table ?
15. The eHealthbox messages carrying lab results in FHIR should have the meta tag HC-FunctionalType="fhir-lab". They could also have CM-GeneratingSoftware and CM-GeneratingSoftwareVersion tags intended for easing troubleshooting.
16. The service request identifier in FHIR is not necessarily the identifier of the initial request by the caregiver. To be improved in a prescription referral project ?
17. The narrative should be empty. But should it contain something, this should not be displayed to users, as it should only be used for debugging purposes.