Logical Observation Identifier Names and Codes (LOINC®) Users' Guide

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This and other relevant documents are available via

FTP/Gopher:www.mcis.duke.edu/standards/termcode/loinclab/
World Wide Web: http://www.mcis.duke.edu/standards/termcode/loinc.htm

List of Files:

Description	Format	File Name
LOINC database	ASCII	LOINDBT1.TXT
LOINC database	ASCII ZIP	LOINDBT1.ZIP
LOINC database	MDB ZIP	LOINCMDB.ZIP
LOINC database printout	RTF	LOINDBW1.RTF
LOINC database printout	RTF ZIP	LOINDBW1.ZIP
LOINC Users' Guide	WP 6/7/8	LOINMAN1.WPD
LOINC Users' Guide	Word 6/95	LOINMAN1.DOC
LOINC Introduction	ASCII	LOININTR.TXT
LOINC Read Me	ASCII	LOINRDME.TXT
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>
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>
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>
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>
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Preface and Introduction

The LOINC databases provide sets of universal names and ID codes for identifying laboratory and clinical test results.[1] The purpose is to facilitate the exchange and pooling of results, such as blood hemoglobin, serum potassium, or vital signs, for clinical care, outcomes management, and research. Currently, many laboratories are using ASTM 1238 or its sister standard, HL7, to send laboratory results electronically from producer laboratories to clinical care systems in hospitals. Most laboratories identify tests in these messages by means of their internal (and idiosyncratic) code values. So the receiving medical informatics systems cannot fully "understand" the results they receive unless they either adopt the producer's laboratory codes (which is impossible if they receive results from multiple source laboratories, e.g.; the hospital lab, the local commercial lab, and a nursing home lab), or invest in work to map each laboratory's code system to their internal code system.[2]

If medical information producers who wish to communicate with each other used the LOINC codes to identify their results in data transmissions, this problem would disappear. The receiving system with LOINC codes in its master vocabulary file would be able to understand and properly file HL7 results messages that identify clinical observations via LOINC codes. Similarly, government agencies would be able to pool results (within limits) for tests from many sites if they were reported electronically using the LOINC codes. The LOINC codes (and names) for test observations should be of interest to hospitals, clinical laboratories, doctors' offices, state health departments, governmental health care providers, third-party payers, and organizations responsible for quality assurance and utilization review.

The LOINC codes are not intended to transmit all possible information about a test or observation. They are only intended to *identify* the test result or clinical observation. Other fields in the message can transmit the identity of the source laboratory and very detailed information about the sample. (For instance, the result code may identify a *blood* culture, but the message source code can be more specific and identify the sample as pump blood.) The level of detail in the LOINC definitions was intended to distinguish tests that are usually distinguished as separate test results within the master file of existing laboratory systems. Indeed, we used the master files from seven U.S. laboratories to shape this effort.

Each LOINC record corresponds to a single test result. (A current project is to invent names and codes for batteries of tests such as electrolytes.) The record includes fields for specifying:

1)   Component (analyte) — e.g., potassium, hemoglobin, hepatitis C antigen.
2)   Property measured — e.g., a mass concentration, enzyme activity (catalytic rate).
3)   Timing - i.e., whether the measurement is an observation at a moment of time, or an observation integrated over an extended duration of time — e.g., 24-hour urine.
4)   The type of sample — e.g., urine, blood.
5)   The type of scale — e.g., whether the measurement is quantitative (a true measurement) ordinal (a ranked set of options) or nominal (E Coli; Staph Aureus).
6)   Where relevant, the method used to produce the result or other observation.

It also contains information about the amount, route, and timing of physiologic or pharmacologic challenges (e.g., oral glucose tolerance test, which would be expressed in LOINC as GLUCOSE^1H POST 100 DL GLUCOSE PO[i]) The LOINC identifiers do not usually include the method in the name for chemistry tests, where tests are more often standardized to normalized methods, but do include it for most serological tests and coagulation studies. This same principle is usually reflected in the master files of existing laboratories. Of course, the method can always be reported as a separate item of information in a result message regardless of whether it is part of the test name.

We used many sources for constructing the database, including the Silver Book from the International Union of Pure and Applied Chemistry (IUPAC) and the International Federation of Clinical Chemistry (IFCC),[3] textbooks of clinical pathology (e.g. Henry[4] and Tietz[5]), the expertise and work of the LOINC members, and EUCLIDES. We have also reviewed the master test files of seven sources (Indiana University/Regenstrief, University of Utah, Association of Regional and University Pathologists (ARUP), Mayo Medical Laboratories, LDS Hospital in Salt Lake City, the Department of Veterans Affairs, Quest Diagnostics, and University of Washington). This has been an empirical effort. Our

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[i]In the United States, PO (an abbreviation for *per ora*) is used to identify medications taken by mouth.

goal is to provide codes to which laboratories (and clinical departments) could map to their master files.

The database includes fields for each of the six parts of the name. In addition, it may also contain EUCLIDES codes (for the component/analytic part of the name), IUPAC/IFCC codes, and ASTM codes, as well as related words, synonyms, and comments. Related words ("synonyms") are included to facilitate searches for individual laboratory test and clinical observation results.

Laboratories and managers of medical records systems should record the LOINC codes as attributes of their existing test/observation master files and use the LOINC codes and names in the OBSERVATION ID field (OBX-3) of the ASTM and HL7 OBX segment and the corresponding CEN TC251 and DICOM messages to identify laboratory results.

The print version of the LOINC database is presented to you as an electronic document grouped by "sensible" categories to make it easier to find general areas of interest. It is divided into two main categories, "lab" and "clinical." (This split is recorded in Field #38, CLASSTYPE.) The laboratory portion of the LOINC database contains the usual categories of chemistry, hematology, serology, microbiology (which includes parasitology and virology), and toxicology; we also have categories for drugs and the cell counts you would find reported on a complete blood count or a cerebrospinal fluid cell count. We have separated antibiotic susceptibilities into their own category. The clinical portion of the LOINC database contains entries for vital signs, hemodynamics, intake/output, EKG, obstetric ultrasound, and other clinical observations. Table 18 (in Appendix A) lists all of these classes in detail. There is nothing sacred about these categories. You will be able to sort the database by whatever class is convenient for your application when you get the electronic version.

We have defined fields in the database for a number of data elements, e.g., typical units, sample normal ranges, but most of those fields are not yet filled in. In a few cases, we have suggested standard answer lists for tests whose results are usually reported as codes. The database is an ongoing project. We have established guidelines for users who wish to request additions and changes to LOINC, which are detailed in Appendix C.

For some kind of tests and observations, the database provides several ways to report values. For example, blood cell antigens might be presented as a "panel" with separate "tests" which report each possible antigen as present or absent if the test is to establish paternity; for cross matching, the result would be reported as a list of antigens found. We try to provide for both methods of reporting in the LOINC databases by including codes for both types of test identifiers.

The Regenstrief Institute and the LOINC committee will maintain the database while grant support is available (at least until January 1, 2001). We expect to find longer-term support or another home for the database before then. The LOINC database (which identifies over 13,000 different lab tests and clinical observations) and supporting documentation is available through the Duke standards Internet site. Anonymous FTP and Gopher access is available at **www.mcis.duke.edu**. The LOINC database and accompanying files are in the directory **standards/termcode/loinclab**.

The World Wide Web URL **http://www.mcis.duke.edu/standards/termcode/loinc.htm** provides links to all the LOINC files.

The LOINC databases are stored in a number of file formats. In each of them, the first part of the file contains the copyright notice with permission to use the database for any purpose without charge or written permission. We have copyrighted the databases and this document to assure that multiple variants of the codes do not emerge. Having many variants would defeat the purpose of a universal identifiers for test results.

✔ **Tab Delimited ASCII:**

Each record of the database is on a separate line. Each record is terminated by CR/LF, and each field is delimited by a tab character. Non-null text fields are enclosed in double quotes ("). Spreadsheet and database programs can import such files easily. This is the format you will use if you want to inport into your own data base. It contains all of the content of the data base. The tab delimited ASCII file is the "database of record" -- unlike the word processing versions, it will always contain all implemented fields. This file is available in a zipped and unzipped version.

✔ **RTF file:**

This file is formatted to print landscape in a Courier 6 point font and is intended to provide an easy to read print version. The LOINC records are sorted in alphabetic order by class and then by full LOINC name within class. The print version <u>does not</u> include all of the LOINC fields. Some of the longer fields float vertically. The size of the printed page makes it impossible to display all database fields in this file.

   The following files are available either zipped and unzipped. (PKUNZIP v. 2.04 or compatible required)

✔ **ACCESS database:**

The LOINC database is also available as a ACCESS (MDB) file. This database, which is indexed, is available as LNC1MDB.ZIP. The database was created using Microsoft Access™ 2.0.

✔ **The LOINC Users' Guide** is also available both as a WordPerfect 6.0 or Word 95 file. The Users' Guide (this document) explains the structure of the database, its rationale, and the rules we used for naming test results. It is not compressed.

✔ **Brief Users' Guide**

The introduction to the Users' Guide is available as a separate ASCII text file.

✔ **RELMA**

In addition to the basic LOINC files, we also produce a Windows-based mapping utility called the Regenstrief LOINC Mapping Assistant (RELMA™). This program is also available for free use and may be downloaded from

   http://www.mcis.duke.edu/standards/termcode/relma.zip

The RELMA package includes the LOINC table in the database plus several large index tables. Zipped, the program and database files exceed 12M, not including the manual. Note that you must unzip the LOINC database after running the SETUP.EXE program. All of the RELMA files will need almost 80 meg of disk space.

✔ **RELMA Users' Guide**

There is a separate Users' Guide documenting the RELMA program, which is included in this ZIP file.

We welcome corrections or extensions to the database. We are not interested in adding terms that *might* be needed in some future situation but we are interested in adding test observations that are actively being reported today. Appendix C provides instructions about submitting new terms.

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1   Goals

The goal of this project is to create universal identifiers (names and codes) to be used in the context of existing ASTM E1238, HL7, CEN TC251, and DICOM observation report messages employed in the various subdomains of healthcare informatics such as Clinical Laboratory Information Management Systems and Computer-Based Patient Record Systems.[6,7] Specifically, we want to create identifiers that can be used as the coded value of the "Observation Identifier" field (# 3) of the OBX segment of an ORU HL7 (HL7 Vs 2.2 and 2.3[8] or ASTM 1238-94[9]) message, or in a similar context in future versions of these HL7/ASTM standards. The LOINC codes will be identified in HL7 as code system "LN". The ultimate goal is that these "universal" identifiers, when used in the context of the messaging standards, will allow the exchange of clinical laboratory data between heterogeneous computing environments.

To facilitate this process, each identifier needs a fully specified name that is created in a standard way so that users can create long names for their tests that can be linked to the universal test identifier using semi-automated methods. We have either begun, or plan, to link other code systems for tests observations such as the IUPAC/IFCC2, ASTM E1238-94, SNOMED[10], and Euclides[11] codes to the LOINC codes. You will see a field in the LOINC database labeled for each of these related codes.

We decided to focus on creating names for results of reportable tests or clinical measurements rather than requestable batteries as our first effort, because the issues involved in naming results of tests are less complex than those involved in naming the batteries. Furthermore, defining the individual results is a prerequisite for defining the batteries that contain these individual tests. In addition, we can begin the process of transferring (and pooling) results once we have created unique identifiers for results. We do have a proposed approach to some orderable test batteries.

Our goal is to create a "universal" master file of elected "test" names that will cover most of the entries in master files of operational laboratory systems, so that the terms in these operational master files could be mapped directly into universal codes and names. The names we create correspond most closely to the "long test descriptions" seen in test master files. We want to create "fully specified" names. That is, if a person wanted to map her local test dictionary to the LOINC codes, all information needed to map a local test name to one of the fully specified names should be present in the LOINC name. This means that the names created will usually be longer than those used in lab reports today. The fully specified LOINC name is not meant to be used on clinical reports. It is assumed that shorter, more convenient abbreviated names and synonyms will be created and maintained by the local computer system. We have had many requests to create standardized "short" names (that could serve as reportable names) and will consider defining such names as a future project.

We want to achieve a level of detail in the definition of a test that will map one-to-one to the separately reported observations on a clinical laboratory report. If a test has its own column on a clinical report, or has a reference range that is different from other tests, or has clinical significance distinct from other closely related tests, it will usually be assigned a separate name. We deliver these fully specified names, their codes, and their related names as a database in which each line corresponds to a unique type of test.

1.1   Successes

The LOINC codes have been greeted enthusiastically since they were released to the Internet in April of 1996. Since then we have released ten revisions of the LOINC data base and it now includes nearly 14,000 observation concepts. The LOINC codes have been endorsed by the American Clinical Laboratory Association (ACLA) and recommended for adoption by its members, and by the informatics committee of the College of American Pathologists. The ACLA is the association of large referral laboratories, and its members are responsible for more than 60% of US outpatient laboratory volume. Quest Diagnostics (formerly Corning MetPath) and LabCorp, two of the largest commercial laboratories have adopted LOINC as their code system for reportable test results, as has LifeChem and ARUP (Associated Regional and University Pathologists). In addition, University of Colorado, Intermountain Health Care, Promedica, Kaiser Permanante, Clarian Partners (Indiana University, Methodist Hospital, and Riley Hospital), Partners Healthcare System of Boston (Brigham and Women's and Mass General Hospital), Care Group of Boston, and the United States Navy are adopting the LOINC codes for laboratory reporting. Insurance carriers such as Empire Blue Cross are also adopting LOINC for internal purposes. Internationally, LOINC has also met success. Geneva, Switzerland, is adopting LOINC in a trial preliminary to country-wide adoption. The province of Ontario, Canada, is adopting LOINC codes for a pilot study of a province-wide laboratory data base, and both Newfoundland and British Columbia are considering following in its footsteps.

The LOINC codes have are being incorporated into the National Library of Medicine's ULMS. They are the basis for HCFA's ICD10-PCS laboratory codes. They have been incorporated in HCFA's quality assurance testing pilot programs, and they have been adopted by the Center for Disease Control and Preventions/State and Territorial Epidemiologist's project for reporting/transmitting communicable diseases electronically.

SNOMED collaboration

LOINC and SNOMED are supporting a collaboration that will ensure a consistent, unambiguous clinical reference terminology that builds upon the strengths of each. The SNOMED Editorial Board and the LOINC Committee have agreed on the following method for linking the SNOMED and LOINC terminologies in a synergistic way and preventing overlap:

▸ The detailed names of laboratory tests provided by LOINC will all be incorporated into the P3 SNOMED axis. These codes will retain the full LOINC code (number and check digit) but will include a prefix to identify the SNOMED axis. The LOINC committee will continue to have editorial control over these terms and will continue to distribute them on the Internet for public use.

▸ SNOMED will not define laboratory test names that overlap in meaning with fully specified LOINC names. The SNOMED Editorial Board can create hierarchical concepts in the SNOMED P3 (Laboratory Procedures) axis that combine any one or two LOINC relationships. However, if one of the relationships is the LOINC component relationship, SNOMED can NOT combine it with the LOINC system relationship. When the SNOMED Editorial Board has the need to use more than two LOINC relationships, the Editorial Board will work with the LOINC Committee to create a mutually acceptable solution. Any concept in the SNOMED P3 axis that currently does not meet these criteria will be retired and/or given to the LOINC Committee for consideration. LOINC will not define codes for entities that would be stored as values for its observations, including those that are listed as text in the answer field of the LOINC database.

▸ The components of LOINC names will be mapped to their corresponding atomic SNOMED elements. The entire mapping (along with the LOINC copyright requirement) will be published in a future release of SNOMED. Contact the CAP if you are interested in examining a pre-release version of this mapping. SNOMED version 3.4 contains numerous additions to the SNOMED chemicals, functions, living organisms, and other (atomic) axes that are referred to by the LOINC mapping.

1.2   What is not part of the name

Certain parameters and descriptions pertaining to test performance are specifically excluded from the fully specified test name. These parameters will typically be reported in separate fields (attributes) of a test/observation report message, not as part of the observation name. Attributes that we explicitly exclude from the fully specified name are:

> ▸ the instrument used in testing
> ▸ fine details about the sample or the site of collection such as "right antecubital fossa"
> ▸ the priority of the testing, e.g., whether stat or routine
> ▸ who verified the result
> ▸ the size of the sample collected
> ▸ the place of testing (e.g. home, bedside, clinical lab)

In the case of laboratory tests, the name does include information that identifies the type of sample (or specimen). However, the "sample" part of the name is not meant to carry all possible information about the sample, but only enough to indicate significant differences in the result *and* to reflect current usage in test names. For example, laboratories usually define urine sodium, sweat sodium, and serum sodium as different tests because each of these has a different normal range. But laboratories do not define different tests to distinguish the concentration of arterial serum sodium from venous serum sodium, though the lab may report that the sample was venous or arterial in another part of the report. We are guided by the pragmatics of conventional usage. If laboratories define separate tests for the same measurements done on different specimens (this usually implies a well defined normal range difference), we will define different "resultable" tests in our dictionary. If they do not, we will not.

The extent to which we include methods as part of the name is also guided by pragmatics. We distinguish

tests/observations by the method used to produce the results only if the method has a significant effect on the interpretation of the result. This is a complex subject and it is difficult to fully describe our rationale in this report. Where laboratories do not tend to include the method in the name -- e.g., most of chemistry -- we do not include the method in the name. Where they tend to -- e.g., in immunochemistry -- we do. For some tests, this can be justified by the standardization of methods to produce "equivalent" results, and sometimes by the many variables (method, reagent) that one could never hope to represent fully in a single name. However, even when we do distinguish these cases, we distinguish by method *class*, not the most detailed possible method distinction. (See section 2.7 for more details.)

The College of American Pathologists produces statistical summaries of the results for measurements of standard samples broken down by laboratory and by instrument or procedure. (These are called CAP surveys.) We explored the feasibility of using this CAP survey data to decide empirically when test names should be distinguished by method. This was not feasible because many of the apparent differences in method obtained with the standard samples were artifacts of the sample matrix and did not apply to serum specimens. In addition, the variation among laboratories was often of the same magnitude as the variation among methods within laboratories for the same method.

We do not mean to underrate the importance of method differences. The result message will still include information about the normal range for that particular test, the source laboratory and, if the laboratory wishes, specific information about the method (e.g., OBX 17 can carry very specific method information). However, such information is reported in separate fields in the HL7 message. It is not embedded in the names of the test.

We have a cooperative agreement with CAP and SNOMED to provide copies of the LOINC codes and names for distribution with the SNOMED codes in the P3 AXIS. The LOINC committee will continue to have editorial control and to distribute the LOINC database via the WG SNOMED and add hierarchies to the LOINC data base.

1.3   Scope of this document

The current scope of the existing laboratory portion of the LOINC database includes all observations reported by clinical laboratories, including the specialty areas: chemistry, including therapeutic drug monitoring and toxicology; hematology; serology; blood bank; microbiology; cytology; surgical pathology; and fertility.In the most current release, a modest number of terms used in veterinary medicine have been included, and more are planned for the near future. In addition, the scope includes those non-test measurements that are commonly required to interpret test results and are usually included as part of the report with the laboratory observations. Examples include:

> ‣   for cervical pap smears, the phase of menstrual cycle use of estrogens
> ‣   for arterial blood gases, inspired dioxygen
> ‣   for drug concentrations used in pharmacokinetics, the dose
> ‣   for a blood bank, the number of units dispensed

The clinical portion of the LOINC database covers the areas of blood pressure, heart and respiratory rates, critical care measures, cardiac output, body dimensions, body temperature, intake and output, electrocardiography, obstetric ultrasound, urologic ultrasound, and the major headings of history and physical, discharge summary, and operative note reports. Work on gastroenterology, mechanical ventilator management, and obstetrics is underway.

To each name, we have assigned a unique permanent code that we call the LOINC code. This is the code that systems should use to identify test results in electronic reports. The LOINC code has no intrinsic structure except that the last character in the code is a mod 10 check digit. The algorithm to calculate this check digit is given in Appendix B. All of the structure associated with a single LOINC entity is stored in other fields in the LOINC database.

2   Major "Parts" of a Test/Observation Name

The fully specified name of a test result or clinical observation has five or six main parts including: the name of the component or analyte measured (e.g. glucose, propranolol), the property observed (e.g. substance concentration, mass, volume), the timing of the measurement (e.g. is it over time or momentary), the type of sample (e.g. urine, serum), the scale of measurement (e.g., qualitative vs. quantitative), and where relevant, the method of the measurement (e.g.,

radioimmune assay, immune blot). These can be described formally with the following syntax.

<Analyte/component>:<kind of property of observation or measurement>:<time aspect>: <system (sample)>:<scale>:<method>

The colon character, ":", is part of the name and is used to separate the main parts of the name.

The first part of the name can be further divided up into three subparts, separated by carats (^). The first subpart can contain up to three levels of increasing taxonomic specification, separated by dots (.). The hierarchical structure is outlined in Table 1, with references to the section numbers where each item is explained in detail.

We used Tietz[4], Henry[3], IUPAC[2], EUCLIDES[10], diagnostic microbiology textbooks such as Mahon and Manuselis[12] the American Association of Blood Banking[14], and other sources as well as the expertise of the individuals or the committee to choose preferred names.

Examples of fully specified LOINC names:

> SODIUM:SCNC:PT:SER:QN
> SODIUM:SCNC:PT:UR:QN
> SODIUM:SRAT:24H:UR:QN
> CREATININE.RENAL CLEARANCE:VRAT:24H:UR:QN
> GLUCOSE^2H POST 100 G GLUCOSE PO:MCNC:PT:PLAS:QN
> GENTAMICIN^TROUGH:MCNC:PT:SER/PLAS:QN
> CALCIUM.FREE:SCNC:PT:SER/PLAS:QN
> ALBUMIN:MCNC:PT:SNV:QN

2.1   General naming conventions

2.1.1   Abbreviations in names of component/analyte

Except for enumerated exceptions (Table 2), abbreviations should not be used in the component (analyte) of the name. We require the use of "total" not "tot," "Fraction" not "frac," "alpha" not "A-," "Beta not B-" (and so on for any Greek letter), oxygen, not O_2 and so on.

2.1.2   General naming rules for the component (analyte) part of the fully specified name

2.1.2.1 <u>Place the identifier of the substance being measured first</u>. This means "Hepatitis A antibodies (AB)" not "Antibodies, Hepatitis A."

2.1.2.2 <u>Use the generic name of a drug</u>, not the brand name, when referring to drug concentrations and minimum inhibitory concentrations (MICs), e.g., Propranolol, not Inderal. For concentrations of drugs and to antibiotic susceptibility, we will usually include the brand or trade names in the field "related name".

Table 1:	
Subpart Name	**Section**
Component/analyte	2.2
Name and modifier	2.2.1
Component/analyte name	2.2.1.1
Component/analyte subname	2.2.1.2
Component/analyte sub-sub-name	2.2.1.3
Information about the challenge (e.g., 1H post 100 gm PO challenge)	2.2.2
Adjustments/corrections	2.2.3
Kind of Property (mass concentration, mass)	2.3
Time Aspect (point or moment in time vs. time interval)	2.4
System/Sample type (urine, serum)	2.5
"Super System" (patient, donor, blood product unit)	
Type of Scale (nominal, ordinal, quantitative)	2.6
Method Type	2.7

2.1.2.3 <u>Use full taxonomic name of an organism or virus name</u> (not the disease) when describing a test that diagnoses that disease. Say "rickettsia rickettsii AB" not "Rocky mountain spotted fever AB". Say "herpes simplex virus AB" not "HSV AB." The disease name should be included as a synonym in the Related Term field.

2.1.2.4 <u>Species and groups of species</u>: SP identifies a single species whose identity is not known. SPP identifies the set of species beneath a genus. We have a third case, however. In some tests, antibodies apply to different strains of species. In rickettsial diseases, the antibodies are then against groups of species, e.g. the spotted fever group or the typhus group. The convention remains the same: we name the immunochemical (serologic) test by the organism, so it becomes Rickettsia SPP.Spotted fever group, or Rickettsia SPP.Typhus group.

When the test measures an antigen to a specific species of organism but cross-reactivity is such that other organisms are identified, the name should be the principal organism which is targeted by the test.

2.1.2.5 Avoid "direct" and "indirect" except as parts of synonym names. Avoid conjugated and unconjugated when a more precise term is available. For instance, use bilirubin glucuronide instead of bilirubin conjugated. Bilirubin conjugated becomes the synonym.

2.1.2.6 Use "platelets," not "thrombocytes."

2.1.2.7 <u>Name vitamins by their chemical name.</u> E.g., use thiamin not Vitamin B1, The name containing "Vitamin" will be included as a synonym. This is the only reasonable approach because all vitamins have a chemical name but not all vitamins have a "numbered" vitamin name.

2.1.2.8 <u>Always specify whether serology tests measure the antigen or antibody</u>, using the abbreviation "AB" for antibody and "AG" for antigen. Remove the "anti" from "ANTI X AB." It is redundant and obscures the most significant word in the name. Thus, "anti-smooth muscle AB" becomes "Smooth muscle AB."

Table 2: Allowable Abbreviations in Component (analyte) Names	
Abbreviation	**Full Name**
AB	antibody
AG	Antigen
AGGL	Agglutination
CFU	colony forming unit
DNA	deoxyribonucleic acid
HIV	human immunodeficiency virus
HLA	human histocompatibility complex derived antigens
HTLV-1	human t-cell lymphotropic virus-1
Igx	immunoglobulins (e.g., IGG for immune globulin G, IGM for immune globulin M)
RNA	ribonucleic acid
RRNA	ribosomal nucleic acid

2.1.2.9 VDRL will be named Reagin AB because that is what it is. We will have to depend upon synonyms and aliases to equate our "standardized" names with the old names.

2.1.2.10 <u>Use the noun form of the target of the antibody</u>, e.g., Myocardium AB, not Myocardial AB.

2.1.2.11 <u>Anion vs acid</u>: Always use the anionic name for chemicals, not the acid name, e.g., lactate, citrate, and urate, not lactic acid, citric acid, and uric acid. The acid form of the name will be included in the synonym field of the database.

2.1.2.12 <u>Alcohols</u>: Always use the single-word names for alcohols: methanol, not methyl alcohol; ethanol, not ethyl alcohol, and so on.

2.1.2.13 Always spell out OH as Hydroxy, or as - ol, with no space or hyphen between Hydroxy and the next word.

2.1.2.14 Greek letters, alpha, beta, gamma, etc., are always spelled out (e.g., alpha tocopherol, not A-tocopherol), with a space between the spelled out Greek letter and the rest of the chemical name.

2.1.2.15 Use pH, not log(H+).

2.1.2.16 When naming allergenic materials of plant or animal origin, order the common name to reflect the Linnaean taxonomy of "genus species," e.g., for specific species of the maple, genus *Acer*, the LOINC analyte names would be MAPLE RED (*Acer rubrum*); MAPLE SILVER (*Acer saccharinum*); MAPLE SUGAR (*Acer saccharum*). Whenever available, the Latin name will be stored in the RELATED NAMES field.

2.1.2.17 Avoid use of the word "total" in laboratory test names, except when denoting the denominator of a fraction. Thus it is ALKALINE PHOSPHATASE, NOT ALKALINE PHOSPHATASE.TOTAL, but ALKALINE PHOSPHATASE.BONE/ALKALINE PHOSPHATASE.TOTAL.

2.1.3   Punctuation in analyte names

A number of analyte names include punctuation characters such as commas, for example, to identify the position of multiple alkyl groups in a carbon chain. We will avoid special characters, e.g., commas, dashes, and parentheses, except where they are included in the name specified by IUPAC, the Chemical Abstract Service (CAS) convention, or another international convention. So commas *will* appear in multiple substitutions of alkyl chains per the CAS standard, dashes will appear in HLA antigen names, and parentheses (i.e. round brackets) will appear in the names of red blood cell antigens.

2.1.4   Case insensitivity

All names are case insensitive. We use upper case in our example, but senders and receivers could use upper, lower or

mixed case. However, the meanings should not be sensitive to case conversions to avoid any possibility of confusion when the information is sent over networks that may apply case conversion. To identify parts of the few names that by international convention *are* case sensitive, such as red blood cell antigens, we use the word 'LITTLE' in front of the letter that is lower case. We use a similar convention to indicate superscripts with the word SUPER. See examples in Table 3.

Since some systems are capable of distinguishing upper and lower case, we provide mixed case names in the EXT_CP_SY (Exact Component Synonym) field (Field #33). However, the available character set does not permit direct representation of superscripts; these are recorded in the EXT_CP_SY field as a carat ("^"), e.g., Lu^a.

Table 3: Case Specifying Conventions	
Our conventions	**Standard mixed case**
A LITTLE U (LITTLE A) AB	Au(a) AB
L LITTLE U LITTLE SUPER A	Lu^a
LITTLE I -1 AB	I-1 AB

2.1.5   Roman numerals vs. arabic numerals

Whenever possible, numerals shall be represented in their arabic form. However, when the conventional name uses Roman numerals as is the case for clotting factors such as factor VIII, the LOINC primary name will use Roman numerals and we define a synonym containing Arabic numerals.

2.2   Component/analyte (1st part)

The first main part consists of three subparts: (1) the principal name (e.g. the name of the analyte or the measurement); (2) the challenge or provocation, if relevant, including the time delay, substance of challenge, amount administered, and route of administration; and (3) any standardization or adjustment.

The three subparts of the first part follow this syntax:

>   <[analyte].[subclass].[sub-subclass]> ^
>   <[time delay] post [amount] [substance] [route])> ^
>   <adjustment>

In the above syntax, the carat (^) is a required delimiter and the "dot" (.) separates the analyte name from its subspecies.

This convention also implies that dots (.) and carats (^) cannot be a formal part of any of the words that are connected by these delimiters.

These subparts are described in greater detail below, Sections 2.2.1 through 2.2.3.

2.2.1   Analyte Name (1st subpart)

The first subpart names the analyte, including any relevant sub-classifications, separated from the main analyte name by dots.

2.2.1.1   Class/Subclass/Sub-subclass

The principal name (the first subpart) can be divided further by subclass (e.g. calcium (II) is one component, calcium.ionized is another test that measures a subclass of calcium.) Subclasses are separated by dots. Bound and free, and bioavailable, components, ionized and unionized components, and antibody subtypes are all subclasses. Note that bio-available is distinguished from free by including both free and partially bound moieties. Use total as a modifier sparingly, in in denominators of mass and substance fractions, e.g. the fraction of Prealbumin over Protein.total.

.

If the antibody is from a particular subclass of antibodies specify the subclass (IGM, IGG, IGA, or IGD) e.g., Hepatitis A AB.IGG, Hepatitis A AB.IGM

If more than one species is included in the measurement, all are listed in the subclass, e.g. "Hepatitis A AB.IGM+IGG" with a plus sign (+) to separate the subspecies. There should be no spaces between the plus sign and the words it connects. If two constituents are measured as one quantity, both should be named and the component separated by a plus sign (+), e.g., Alprozolam + Metabolites.

2.2.2   Challenge test (2nd subpart)

The second subpart contains information necessary to interpret "challenge" (or loading or tolerance) tests. Variables that report the result of a measurement taken a certain amount of time post challenge (e.g. glucose after an oral glucose tolerance test) must be distinguished according to the challenge and the time post challenge. Thus, the second subpart has a substructure that identifies the time interval or time difference and the challenge, using the following syntax, where the word "post" (or base line) is required.

<time delay> "post" <challenge>

where the challenge can be further characterized as

<amount given> <substance/treatment given> <route given>

The time difference follows the syntax: n<S|M|H|D|W> where n is a number (possibly a decimal); S denotes seconds; M denotes minutes; H denotes hours; D denotes days; and W denotes weeks. The time delay can be preceded by a 'greater than' (>) sign, e.g. >4H.

Table 4 lists some possible values for time difference, but any time specification that follows the above syntax would be legal.

The second subpart can also be used to specify the ordering of specimens, e.g., ^1ST SPECIMEN 1, ^2ND SPECIMEN. Use this syntax to indicate pre- and post-immunization specimens, acute and convalescent specimens, or a series of specimens for which no more detailed information is available.

More general terms, of the form <analyte>^POST CHALLENGE, are available to transmit information about challenges for which pre-coordinated terms do not exist in the LOINC database.

The second subpart is also used to describe measurements taken at a specified point after the beginning of an ongoing treatment, such as peritoneal dialysis, e.g., CREATININE^12H POST PERITONEAL DIALYSIS

Table 4: Time Delay Post Challenge			
BS	Baseline (time just before the challenge)		
PEAK	The time post drug dose at which the highest drug level is reached (differs by drug)		
TROUGH	The time post drug dose at which the lowest drug level is reached (varies with drug)		
RANDOM	Time from the challenge, or dose not specified. (random)		
n minutes/hours/days/weeks/months/etc. after challenge begun:			
1M	1 minute post challenge	6H	6 hours post challenge
2M	2 minutes post challenge	7H	7 hours post challenge
3M	3 minutes post challenge	8H	8 hours post challenge
4M	4 minutes post challenge	8H SHIFT	8 hours allligned on nursing shifts
5M	5 minutes post challenge	12H	12 hours post challenge
6M	6 minutes post challenge	24H	24 hours post challenge
7M	7 minutes post challenge	2D	2 days
8M	8 minutes post challenge	3D	3 days
9M	9 minutes post challenge	4D	4 days
10M	10 minutes post challenge	5D	5 days
15M	15 minutes post challenge	6D	6 days
20M	20 minutes post challenge	7D	7 days
25M	25 minutes post challenge	1W	1 week
20M	30 minutes post challenge	10D	10 days
1H	1 hour post challenge	2W	2 weeks
2H	2 hours post challenge	3W	3 weeks
2.5H	2 1/2 hours post challenge	4W	4 weeks
3H	3 hours post challenge	1MO	1 month (30 days) post challenge
4H	4 hours post challenge	2MO	2 months (60 days) post challenge
5H	5 hours post challenge	3MO	3 months (90 days) post challenge

2.2.2.1   Reporting the baseline measure as part of a challenge test

We define one baseline term for different challenge batteries when the challenge is given by the same dose and route. So we define one baseline test for the 100 gm oral glucose tolerance test regardless of the number of separate measurements defined in the battery. For example, the baseline serum glucose for 100 g oral glucose by mouth would be:

GLUCOSE^BS 100 G GLUCOSE PO

A laboratory could use this same test identifier to identify the baseline result of a 2 h glucose tolerance and a 3 h glucose tolerance, for example.

We would define different baseline measurements for challenges with different substances. The baseline serum glucose before a challenge with 50 U insulin challenge would be defined as a different test from the baseline glucose for an oral glucose tolerance test. These different baseline tests are defined to accommodate laboratories that conventionally do the same. However, a baseline glucose for any challenge is not affected by the challenge and could in principle be reported as a glucose without specifying the relation to a coming challenge.

We denote the route of the challenge by HL7 Version 2.2 "abbreviations for medication routes" (Table 5). An oral route of administration would be denoted by "PO," an intravenous route by "IV."

Table 5: Route Abbreviations for Challenge Part			
(from HL7 vs. 2.3, chapter 4)			
AP	Apply Externally	MM	Mucous Membrane
B	Buccal	NS	Nasal
DT	Dental	NG	Nasogastric
EP	Epidural	NP	Nasal Prongs
ET	Endotrachial Tube	NT	Nasotrachial Tube
GTT	Gastronomy Tube	OP	Ophthalmic
GU	GU Irrigant	OT	Otic
IMR	Immerse (Soak) Body Part	OTH	Other/Miscellaneous
IA	Intra-arterial	PF	Perfusion
IB	Intrabursal	PO	Oral
IC	Intracardiac	PR	Rectal
ICV	Intracervical (uterus)	RM	Rebreather Mask
ID	Intradermal	SD	Soaked Dressing
IH	Inhalation	SC	Subcutaneous
IHA	Intrahepatic Artery	SL	Sublingual
IM	Intramuscular	TP	Topical
IN	Intranasal	TRA	Tracheostomy
IO	Intraocular	TD	Transdermal
IP	Intraperitoneal	TL	Translingual
IS	Intrasynovial	UR	Urethral
IT	Intrathecal	VG	Vaginal
IU	Intrauterine	VM	Ventimask
IV	Intravenous	WND	Wound
MTH	Mouth/Throat		

Examples

GLUCOSE^BS 100 G GLUCOSE PO:MCNC:PT:SER:QN
GLUCOSE^30M POST 100 GM GLUCOSE PO:MCNC:PT:SER:QN
GLUCOSE^2H POST 100 GM GLUCOSE PO:MCNC:PT:UR:QN
GENTAMICIN^TROUGH:MCNC:PT:SER:QN

For drug peak (obtained at a time presumed to reflect the highest concentration) and trough (obtained at a time presumed to reflect the lowest concentration) measures the nature of the substance loaded is the same as the analyte name, and need not be included.

2.2.2.2   Physiologic challenges

Some challenges are defined in terms of a physiologic stress, not a dose of a chemical substance. The LOINC names currently cover calorie fasts (no calorie intake), exercise, and fluid restrictions. These challenges are denoted by codes given in Table 6.

In the case of such challenges, the syntax also includes the duration of the challenge.

E.g., <duration> POST <duration><physiologic challenge>
E.g., CHOLESTEROL^POST 12H CFST

Table 6: Nature of Challenge	
CFST	Calorie fast. No caloric intake (food) for the period specified in the time part of the term, e.g., POST 12H CFST
EXCZ	Exercise undertaken as challenge (can be quantified)
FFST	Fluid "fast." No fluid intake for the period specified

The naming structure is an exact analogous structure to that of chemical challenges. A test for glucose after 12 hours of an energy fast would be represented as:

GLUCOSE^BS POST 12H CFST:MCNC:PT:SER:QN

In all physiologic challenges (fasting, fluid deprivation), the duration of the physiologic challenge must be stated.

A test for osmolality after fluid restriction would be

OSMOLALITY^POST 12H FFST:OSMOL:PT:UR:QN

A test for triglyceride after an 18 h for energy fast would be:

TRIGLYCERIDES.TOTAL^POST 12H CFST:MCNC:PT:SER:QN

Two durations can appear in one specification, e.g.:

CORTISOL^1.5H POST 0.05-0.15 U INSULIN/KG IV POST 12H CFST:MCNC:PT:SER:QN

Our rules for naming challenge tests work well only when there is a single intervention followed by a test for one or more components over time. Complex challenge tests involving more than one intervention or complicated sampling techniques need a unique name, but the name may not be a complete description of all of the test parameters.

2.2.2.3   Reporting characteristics of challenge as separate observations

Because we cannot anticipate every type of challenge and route of administration, and because some challenge tests have no usual dose, some challenge tests will not contain a dose. Challenge observations that do not include a specific dose in the name have the word "DOSE" where a numeric dose would otherwise appear. The general form is:

<analyte>^<time> post dose <route>

Examples:

GLUCOSE^1H POST DOSE PO:MCNC:PT:SER:QN

The actual dose might then be sent as a comment or as a separate "test" that carries the dose as its value. To accommodate laboratories that wish to transmit the relevant challenge dose as a separate observation, we also define separate test names (and codes) for reporting such doses. This dose could then be sent by the reporting service as a separate result in a separate OBX segment.

The name of the observation that identifies the value of the dose would have the form:

<drug or challenge substance>: <time> post dose <challenge substance>

Examples:

GLUCOSE^PO:MASS:PT:DOSE:QN
GENTAMICIN^IV:MASS:PT:DOSE:QN

Thus we distinguish a drug concentration from the drug dose by means of the system (sample), 4th part, of the test name (see Section 2.5). You can find the observations that carry the dose of drugs or challenges grouped in the class DRUG within the LOINC database. This approach has the advantages of parsimony and practicality. It also provides an observation ID for the piece of information that must be transmitted along with the request for the observation.

Another example would be:

> OXYGEN:PRES:PT:BLDA:QN
> OXYGEN INHALED:VRAT:PT:IHG:QN (liters/minute or milliliters/second)
> OXYGEN INHALED MECHANISM:TYPE:PT:DOSE:NOM (to report kind of delivery mechanism, e.g., nasal cannula)

An analogous approach is used for reporting many kinds of associated variables when the variables are not conventionally embedded in the name, in part because there are too many levels of the variables and it is not feasible.

2.2.2.4 Generic challenge specifications

We allow for very specific challenges, and less specific challenge designs:
> a) 30M post challenge
> b) 1st specimen post challenge

Some challenges will be specified fully as described above, e.g. 30M post 100 gm glucose pc. We will also include challenges without the amount specified, e.g. 30M xxx glucose and those that do not specify the exact time, e.g., 1st specimen post xxx glucose pc, or even more generic, 1st specimen post challenge. These latter varients are needed to accommodate the submissions to reference laboratories that do not fit any common protocol (and do not report the details of the study protocol to the referenc laboratory).

2.2.2.5 Acute and convalescent, pre & post immunization specimens.

To assess the efficacy of immunizations by measuring antibody titres before and after the immunization, we obtain evidence for acute infection by assessing acute and convalescent screens. Both of these cases are assessed by the 1st specimen, 2nd specimen option, e.g.:

> STREPTOCOCCUS AB^1ST SPECIMEN:ACNC:PT:SR:QN

2.2.3 Adjustments/corrections (3rd subpart)

The third subpart of the data element contains calculations that adjust or correct some measured value. We use this subpart to distinguish corrected or adjusted values from the uncorrected measurement, e.g., corrected cell counts from the raw cell counts. Since these attributes are unique to each measurement, they will be short phrases of text rather than a controlled vocabulary to define the content of the third subpart. However when defined, such a test will have a unique LOINC code and the meaning will be fixed by the text in the third part.

Examples:

> CALCIUM.FREE^^PH ADJUSTED TO 7.4:SCNC:PT:SER/PLAS:QN

> CREATININE.RENAL CLEARANCE^^NORMALIZED TO 1.72 BODY SURFACE AREA:VRAT:24H:UR:QN

> LEUKOCYTES^^CORRECTED FOR NUCLEATED ERYTHROCYTES:NCNC:PT: BLD:QN

Note that the actual pH of the sample would be sent as a separate OBX segment in the test result message analogous to the approach described in Section 2.2.2.1.

2.3   Kind of Property (also called kind of quantity) (2nd part)

The second part of the fully specified name distinguishes between different kinds of quantities relating to the same substance, e.g., the mass versus the concentration of sodium in a urine sample, a molar concentration versus a mass concentration, or the absolute eosinophil count versus the percent of the total white count that are eosinophils. The type of property (kind of quantity) is an IUPAC concept described in the Silver Book.[6] We include most of the relevant IUPAC types of property in Table 7. (See Appendix E for detailed examples.)

Analytes reported with masses (mgs, gms, etc.) in the numerator of the units of measure are associated with one of the properties that begin with the word mass, e.g., mass content, mass concentration, etc. Analytes reported as moles or millequivalents in the numerator of units of measure are associated with properties that begin with the word substance, e.g., substance amount, substance concentration. Counts are associated with properties that begin with "number," e.g., a white blood cell count reported as number of WBCs divided by volume of blood, would have a property of Number Concentration. Measures of enzymatic activity are all associated with properties beginning with "catalytic."

Each of these four major property categories has five derivatives: content, concentration, concentration ratio, fraction, and rate. Measures of an amount (of mass, substance amount, catalytic activity, or number) divided by volume are concentrations. Measures of the total amount measured per mass of sample are reported as contents (mass content, substance content, etc.). These have units such as kg/gm sample. "Mass fraction" is used when grams of a component measured as a subcomponent of another component, e.g., CKMB/TOTAL CK. These are almost always reported as percents (%).

A mass ratio is the ratio of the mass of two chemical components in one system (or sample). If the ratio refers to components in a single system, the ratio of the mass concentrations is also a mass ratio because the denominators cancel out. So, a mass of serum creatinine to mass of serum urea nitrogen within the same specimen (system) would be a mass ratio. Amount of substance (molar amount) would give a different ratio: SRTO. If the measures come from different specimens, e.g., PT patient/PT control, it is a relative ratio.

IUPAC describes an entitic quantity. This refers to measure per entity by number of entities (e.g. cells, receptors, molecules).

Entetic quantities usually have units that include the name of some entity, e.g. red blood cells ("per 10^6 RBCs). One must be careful about measures of constituants of red blood cells because they can be expressed as an amount "per mass of hemoglobin" or "per red blodd cell". The former is a mass content, the latter is a mass per entity.

All clearances have the property of volume rate, but "Clearance" will be included in analyte name to clarify meaning:

> SODIUM RENAL CLEARANCE:VRAT:24H:UR:QN
> CREATININE RENAL CLEARANCE:VRAT:12H:UR:QN

Use "PRID" (presence or identity) as the type of property field when a specimen is sent for culture, and the result can be the presence of any organism (especially as an initial result) and later the organism is identified. The same rule applies to toxicology screens or other observations that report the identity of one or more classes of entities as the result. For example:

> MICROORGANISM IDENTIFIED:PRID:PT:ISLT:NOM:BACTERIAL SUBTYPING
> MICROORGANISM IDENTIFIED:PRID:PT:ISLT:NOM:VIRAL SUBTYPING

Table 7: Kind of Property

Enzymatic Activity		Other Properties	
CACT	*Catalytic Activity	ABS	Absorbance
CCNC	*Catalytic Concentration	ACT	*Activity
CCRTO	Catalytic Concentration Ratio	ANAT	Anatomy
CCNT	*Catalytic Content	ANGLE	Angle
CFR	*Catalytic Fraction	APER	Appearance
CRAT	*Catalytic Rate	ARB	*Arbitrary
CRTO	*Catalytic Ratio	AREA	Area
		ASPECT	Aspect
Entitic		BIB	Bibliographic Citation
ENT	*Entitic	CIRC	Circumference
AENT	*Arbitrary Entitic	CLAS	*Class
ENTSUB	*Entitic Substance of Amount	CNST	*Constant
ENTCAT	*Entitic Catalytic Activity	COEF	*Coefficient
ENTLEN	Entitic Length	COLOR	Color
ENTMASS	Entitic Mass	COMPLX	Complex
ENTNUM	*Entitic Number	CONS	*Consistency
ENTVOL	*Entitic Volume	DEN	Density = Mass/Volume
		DEV	Device
Mass		DIFF	*Difference
MASS	Mass	ELAS	Elasticity
MCNC	*Mass Concentration	ELPOT	Electrical Potential (Voltage)
MCRTO	Mass Concentration Ratio	ELPOTRAT	Voltage Rate (=Amperage)
MCNT	Mass Content	ELRES	Electrical Resistance
MFR	*Mass Fraction	ENGRAT	Power = Energy/Time
MINC	*Mass Increment	ENGRTO	Energy Ratio
MRAT	Mass Rate	ENRG	Energy
MRTO	Mass Ratio	EQL	*Equilibrium
RLMCNC	*Relative Mass Concentration	EQU	Equation
THRMCNC	*Threshold Mass Concentration	FCN	Function
Counts		FIND	Finding
ACNT	Arbitrary Count	FORCE	Mechanical Force
NUM	*Number	FREQ	Frequency
NARIC	Number Areic (number per area)	IMP	Impression/interpretation of study
NCNC	*Number Concentration (count/vol)	ID	Identifier
NCNT	Number Content = Count/Mass	HX	History
NFR	*Number Fraction	KINV	*Kinematic Viscosity
NRAT	Number Rate = Count/Time	LEN	Length
NRTO	Number Ratio	LENRTO	Length Ratio
Substance Amount (Moles/Millequivalents)		LINC	*Length Increment
RLSCNC	*Relative Substance Concentration	LIQ	*Liquifaction
SUB	*Substance Amount	METHOD	Method
SCNC	*Substance Concentration	MGFLUX	Magnetic flux
SCRTO	*Substance Concentration Ratio	MORPH	Morphology
SCNT	*Substance Content	MOTIL	Motility
SCNTR	*Substance Content Rate	OD	Optical density
SFR	*Substance Fraction	OSMOL	*Osmolality
SCNCIN	*Substance Concentration Increment		
SRAT	*Substance Rate	PCT	Percent
SRTO	*Substance Ratio	PRCTL	Percentile
THRSCNC	Threshold Substance Concentration	PRID	Presence or Identity
Volumes		PPRES	*Pressure (partial)
VOL	*Volume	PRES	Pressure
VCNT	*Volume Content	PRESRTO	Pressure Ratio
VFR	*Volume Fraction	RANGE	Ranges
VRAT	*Volume Rate	RATIO	Ratios
VRTO	*Volume Ratio	RDEN	Relative Density
ARENRG	Energy/Area	REL	*Relative
ARRESIS	Resistance/Area	ROUTE	Route of RX
ARVOL	Volume/Area	SATFR	*Saturation Fraction
ARVOLRT	Volume Rate/Ratio	SHAPE	Shape
ARVRAT	Volume Rate/Area	SMELL	Smell
Arbitrary Unit Measures		SUSC	Susceptibility
ACNC	Concentration, Arbitrary Substance	TASTE	Taste
ACNT	Arbitrary Content	TEMP	*Temperature
AFR	Arbitrary Fraction	TEMPDF	*Temperature Difference
THRACNC	Threshold Arbitrary Concentration	TEMPIN	*Temperature Increment
ARAT	Arbitrary Rate	TEXT	Text

Table 7: Kind of Property

Time		THRESHOLD	*Thresdhold
DATE	Date	TITR	Dilution Factor (Titer)
TIME	Time (e.g. seconds)	TYPE	Type
TMSTP	Time Stamp -- Date and Time	VEL	*Velocity
TRTO	Time Ratio	VELRAT	*Velocity Rate
RCRLTM	*Reciprocal Relative Time	VELRTO	*Velocity Ratio
RLTM	*Relative Time	VISC	Viscosity
*Starred items are adopted from the IUPAC Silver Book,[2] non-starred items are extensions.			

Properties tend to be the most foreign to new users of LOINC. Appendix E provides more explanation and many detailed examples.

2.4 Time Aspect (Point or moment in time vs. time interval) (3rd part)

One can measure a property at a moment (point) in time or over a time interval and integrate, in the mathematical sense, over time. In the latter case, we aggregate a "series" of physiologic states into a single scalar value that reflects some "average" property measured over the specified time interval. Intervals also have relevance for rate measurements such as excretion (substance rate or mass rate) or clearances (volume rates). The amount over an interval is often expressed as a mass rate (MRAT) or a substance rate (SRAT, e.g., mol/24h). Interval measurements often apply to urine and stool (e.g., collection over 24 h and calculation of a concentration, total amount, or clearance). They also apply to clinical measurements such as urine outputs where we have shift totals and 24 h totals, and event counts on physiologic monitors such as the number of premature ventricular contractions (PVCs) over 24 h on a Holter monitor.

The allowed values are defined as a syntax exactly like the syntax for the times in challenge tests, e.g., <numeric value><S|M|H|W> The most common one is 24H. Table 8 gives some other examples.

For 24H urine collection is the "standard" integrated measure and these are almost always reported as mass (MRAT), amount of substance (SRAT), or catalytic (CRAT) rates. These would contrast with spot or random urines which are represented as point (PT) measures in our nomenclature and usually reported as concentrations -- MCNC, CCNC, or SCNC for mass, catalytic, and substance concentrations respectively. However, we can also report the average concentration on a 24 hour specimen and a 24 hour average concentration must be distinguished from the point concentration.

The designation of 24 h collection is maintained for tests that traditionally have reference ranges based on amount of substance of a component cleared or excreted in 24 h. However, a given specimen could have a 23 h collection time and would still be called as a 24 h study. Depending upon the policies and procedures of the lab, they might extrapolate the reported value to what it would have been if the collection was the full 24 hours and report it as moles per day.

We allow indirect specifications of a time window. STDY identifies the duration of the Study (without specifying an exact time). ENCTR identifies the Encounter (ER visit, hospital stay, etc).

Drug doses (as required to report the mass or amount of substance of a drug given) would be identified by recording "DOSE" as the system (sample) and "MASS" as the kind of quantity. A point dose would be the dose given at a single point in time (e.g., 250 mg of ampicillin). To represent the total amount of a drug given in 24 h, one would record "24H" in the third subfield, and "MASS RAT" as the property.

Example:

    GENTAMICIN:MASS:PT:DOSE:QN
    GENTAMICIN:MRAT:24H:DOSE:QN

Sample volumes reported for timed measurements are carried in other fields or as separate "test" results in other OBX segments.

Table 8: Duration Categories					
PT	To identify measures at a point in time. This is a synonym for "spot" or "random" as applied to urine measurements.				
	.				
	.				
STDY	Duration of the study				
ENCTR	Duration of an encounter (hospital stay, visit).				
PROCEDURE	Duration of the procedure (surgery, etc.)				
XXX	Not specified; time will be reported in another part of the electronic message				
* (star)	Life of the "unit." Used for blood products.				
1M	1 minute	7H	7 hours		
5M	5 minutes	8H	8 hours	2W	2 weeks
10M	10 minutes	9H	9 hours	3W	3 weeks
15M	15 minutes	10H	10 hours	4W	4 weeks
20M	20 minutes	12H	12 hours	1MO	1 month (30 days)
30M	30 minutes	18H	18 hours	2MO	2 months
45M	45 minutes	24H	24 hours	3MO	3 months
90M	90 minutes	72H	72 hours		
1H	1 hour	1D	1 day		
2H	2 hours	2D	2 days		
2.5H	2½ hours	3D	3 days		
3H	3 hours	4D	4 days		
4H	4 hours	5D	5 days		
5H	5 hours	6D	6 days		
6H	6 hours	1W	1 week		

Table 9 shows the allowable time aspect codes. The second and optional subpart of the time component allows an indication of some sub selection or integration of the measures taken over the defined period of time, so 8H^MAX heart rate would be the highest heart rate observed over 8H (Shift). MIN, MAX, FIRST, LAST, MEAN are the other possible values for this subpart. When nothing is stored in this subpart, we assume a mean value over the time period in questions.

Table 9: Time Aspect Codes	
Time	**Definition**
MIN	Minimum value over interval
MAX	Maximum value over interval
FRST	First value observed during an interval
LAST	Last value observed during an interval
MEAN	Mean of all of the values observed on the interval (This is the default selection)

2.5 System (Sample) Type (4th part)

System (sample) type is the fourth part of the fully specified test name. It consists of two subparts; the first names the system, the optional second (delimited with a "^") indicates the super system source of the sample if it is not the patient, e.g., fetus, blood product unit, donor, etc. Sample type should be represented with the abbreviations in Table 10 (which include most of the sample types defined in ASTM E1238, and HL7).

We define different tests for the combination of component (analyte) and type of system (sample) that are commonly reported. In practice, laboratories include a relatively small range of sample types in the their test names. Chemical tests commonly distinguish between serum, urine, blood, and cerebrospinal fluid. Microbiology cultures tend to distinguish between a greater number of sources. The list in Table 10 was defined for reporting sample type in a field of the HL7/ASTM message that is quite independent of the test/measure name, and we do not imply that all such types will find their way into distinct LOINC names. However, when a distinction by type of system *is* required in the name, it should be represented by one of the codes given in Table 10.

When should we lump a variety of specimen types under the unspecific code FLU and when we should give a body material its own unique name for a given component? The decision depends upon the degree to which laboratories have reported the system-component pair as a separate "result" and the degree to which the normal ranges for a given component-system have been standardized. By this rule, we will always define different tests for serum and for urine, when a component can be measured in both. We define sweat sodium as a distinct test because it is a standardized test used to diagnose cystic fibrosis. We did not define duodenal fluid sodium as a separate LOINC code because this measure has not been standardized. This does not mean that the specifics about the system would be ignored. It just means that this information would be recorded in another field of the message (the specimen field of the HL7 OBR segment), not in the name.

For many chemistry tests we have included in the LOINC database a test name for identifying miscellaneous types of body fluid (FLU), to provide a way to distinguish tests that are performed on fluid types that are not explicitly represented in the database. We use the code XXX to identify a material that is not specified — it could be solid or fluid, for example.

For many types of tests, the distinction between plasma and serum is irrelevant. When testing on serum or plasma is clinically equivalent, the system should be recorded as SER/PLAS. Sometimes the test can only be run on either plasma or serum; the component will then be associated with either SER or PLAS in one observation. If the test can be run on either but the results are different and standardized (a very rare circumstance), two separate tests will be defined in our file, one with a system PLAS and one with a system SER. The current LOINC database includes some SER tests and some PLAS tests that should really be SER/PLAS. As we determine that a SER or PLAS test really should have been designated SER/PLAS, we will change the designation.

If the test is run on a combination of types of system (such as a ratio of substance found in CSF and plasma) the codes are joined with a "+" : CSF+PLAS, CSF+SER, etc.

We will be specific about the type of system to distinguish at least among blood, urine, cerebrospinal fluid, pleural fluid, synovial fluid, and peritoneal fluid.

Details about the exact source and collection method (e.g. blood drawn from the right arm and maintained on ice) are not a proper part of the test name and are reported in other parts of the message, e.g., OBX and OBR of the HL7 definition.

Table 10: System/Sample Type Codes								
Abbrev	**Name**		**Abbrev**	**Name**		**Abbrev**	**Name**	
ABS	Abcess		FLU	Body fluid, unsp		SKN	Skin	
AMN	Amniotic fluid		FOOD	Food sample		SKM	Skeletal muscle	
ANAL	Anus		GAS	Gas		SPRM	Spermatozoa	
ASP	Aspirate		GAST	Gastric fluid/contents		SPT	Sputum	
BPH	Basophils		GEN	Genital		SPTC	Sputum - coughed	
BIFL	Bile fluid		GENC	Genital cervix		SPTT	Sputum - tracheal aspirate	
BLDA	Blood arterial		GENF	Genital fluid		STON	Stone (use CALC)	
BBL	Blood bag		GENL	Genital lochia		STL	Stool = Fecal	
BLDC	Blood capillary		GENM	Genital Mucus		SWT	Sweat	
BLDCO	Blood - cord		GENV	Genital vaginal		SNV	Synovial fluid (Joint fluid)	
BLDMV	Blood- Mixed Venous		HAR	Hair		TEAR	Tears	
BPU	Blood product unit		IHG	Inhaled Gas		THRT	Throat	
BLDV	Blood venous		IT	Intubation tube		THRB	Thrombocyte (platelet)	
BON	Bone		ISLT	Isolate		TISS	Tissue, unspecified	
BRAIN	Brain		LAM	Lamella		TISG	Tissue gall bladder	
BRTH	Breath (use EXG)		WBC	Leukocytes		TLGI	Tissue large intestine	
BRO	Bronchial		LN	Line		TLNG	Tissue lung	
BRN	Burn		LNA	Line arterial		TISPL	Tissue placenta	
CALC	Calculus (=Stone)		LNV	Line venous		TSMI	Tissue small intestine	
CDM	Cardiac muscle		LIQ	Liquid NOS		TISU	Tissue ulcer	
CNL	Cannula		LIVER	Liver		TRAC	Trachea	
CTP	Catheter tip		LYM	Lymphocytes		TUB	Tube, unspecified	
CSF	Cerebral spinal fluid		MAC	Macrophages		ULC	Ulcer	
CVM	Cervical mucus		MAR	Marrow (bone)		UMB	Umbilical blood	
CVX	Cervix		MEC	Meconium		UMED	Unknown medicine	
COL	Colostrum		MBLD	Menstrual blood		URTH	Urethra	
CNJT	Conjunctiva		MLK	Milk		UR	Urine	
CUR	Curettage		MILK	Breast milk		URC	Urine clean catch	
CRN	Cornea		NAIL	Nail		URT	Urine catheter	
CYST	Cyst		NOS	Nose (nasal passage)		URNS	Urine sediment	
DENTIN	Dentin		ORH	Other		USUB	Unknown substance	
DIAFP	Peritoneal Dialysis fluid		PAFL	Pancreatic fluid		VITF	Vitreous Fluid	
DIAF	Dialysis fluid		PAT	Patient		VOM	Vomitus	
DOSE	Dose med or substance		PEN	Penis		BLD	Whole blood	
DRN	Drain		PCAR	Pericardial Fluid		BDY	Whole body	
DUFL	Duodenal fluid		PRT	Peritoneal fluid /ascites		WAT	Water	
EAR	Ear		PLC	Placenta		WICK	Wick	
EARW	Ear wax (cerumen)		PLAS	Plasma		WND	Wound	
ELT	Electrode		PLB	Plasma bag		WNDA	Wound abscess	
ENDC	Endocardium		PLR	Pleural fluid (thoracentesis fld)		WNDE	Wound exudate	
ENDM	Endometrium		PMN	Polymorphonuclear neutrophils		WNDD	Wound drainage	
EOS	Eosinophils		PPP	Platelet poor plasma		XXX	To be specified in another	
RBC	Erythrocytes		PRP	Platelet rich plasma			part of the message	
EYE	Eye		PUS	Pus				
EXG	Exhaled gas (=breath)		SAL	Saliva				
FIB	Fibroblasts		SMN	Seminal fluid				
FLT	Filter		SMPLS	Seminal plasma				
FIST	Fistula		SER	Serum				

These abbreviations are used in the laboratory LOINC codes. Systems in clinical LOINC terms are spelled out in full and should be easily understood.

2.5.1   Super system (2nd subpart)

The second subpart of the system distinguishes observations on the patient (or samples taken from the patient or donor) from observations on non-patient materials that relate to the patient, e.g. a blood product unit (BPU). We refer to this as the super system. When the super system is not included in a name, it can be assumed to be the patient. This subpart can take on the values in Table 11:

Table 11: Super System	
CONTROL	Control
PATIENT	Patient
DONOR	Donor
BPU	Blood Product Unit (Pack)
FETUS	Fetus
POPULATION DISTRIBUTION	Population Distribution
NEWBORN	Newborn

For instance, an example of representing a coagulation study which uses measures on both patient and a control might be:

> COAGULATION REPTILASE INDUCED:TIME:PT:PPP^PATIENT:QN:TILT TUBE
> COAGULATION REPTILASE INDUCED:TIME:PT:PPP^CONTROL:QN:TILT TUBE

Blood banks often report red blood cell antigens for the patient and for each blood product pack assigned to that patient. So we have:

> RHESUS NOS AG:ACNC:PT:SER^PATIENT:ORD:AGGL
> RHESUS NOS AG:ACNC:PT:SER^BPU:ORD:AGGL

The super system does not have to be valued (and usually is not). Assume patient when the super system is null.

Note - the inclusion of the super system as part of the system represents a change from an earlier version of LOINC. Earlier versions included this information in the 3 subparts of the component.

2.6   Type of Scale (5th part)

The fifth data part of the test name specifies the scale of the measure, and is a required part. The abbreviation of the type of scale (previously called precision), given in Table 12, should be used in the fully specified name. Note we have changed the codes for these from SQ to ORD and from QL to NOM to more accurately identify the meaning.

We have five kinds of scales. Quantitative (QN) identify scales that can be tied to some physical quantity through a linear equation. This means that if we have two reports for the same quantity one with a value of 5 and the other a value of 10 we know that the two are related in amount through the linear equation $Y=aX+b$. When the intercept, b, is non zero we have a difference scale. Fahrenheit temperature is a difference scale. When it is zero we have a ratio scale (Kelvin temperature is a ratio scale).[13]   A QN value may be reported as a value for a "continuous" scale, as is the case for serum sodium, or it may be reported from a series of discretevalues, as is the case for titers, e.g., 1:16, 1:32.

Some observations have values that are well ordered, e.g., 1+, 2+, 3+, or negative, intermediate, positive, but the values have no linear relationship to one another. We do not know that positive is two or three times as much as intermediate, we just know that positive is more than intermediate. These kinds of observations have an ordinal scale (ORD).

Some observations take on values that have no relative order. Think of the numbers on football jerseys. These simply identify the players, they do not provide quantitative information or rank ordering of the players. We refer to these as nominal (NOM) in scale. Blood culture results provide a good example. The value can be E.coli (or a code for E.coli) or staph aureus. Other examples are admission diagnoses, discharge diagnoses. Any tests or measure that looks broadly at patient or specimen and reports the name of what it finds, is a NOM scale. The values of nominal scaled observations are assumed to be taken from a predefined list of codes or from a restricted vocabulary.

Some observations are reported as free text narrative,. The content is not drawn from a formal vocabulary or code system. A dictated present illness would be an example of a scale of narrative (NAR). Many clinical LOINC codes will come in two versions one for the nominal (coded) version and one for a narrative (free text) version.

We strongly encourage all reporting to be at the most granular level of detail. That is if three numbers are reported they would each be reported under a unique LOINC code and transmitted in a separate HL7 in separate OBX segment.

Occasionally reporting systems are not able to comply with this dictum. For example some chromatography instruments can identify chemicals from the entire spectrum of known chemicals (CAS identifies more than 10 million distinct chemicals) and we may not have specific LOINC codes for reporting out these details. We have designated the scale of MULTI to identify results that include many separately structured results as one text "glob" with or without imbedded (display formatting). Some laboratories report all of the details of many multiple measure tests under such globs with test names that correspond to their order name. We strongly discourage such reporting. It defeats the very purpose of individual codes to tag content.

Table 12: Type of Scale		
Type of Scale	**Abbr.**	**Description**
Quantitative	QN	The result of the test is a numeric value that relates to a continuous numeric scale. Reported either as an integer, a ratio, a real number, or a range. The test result value may optionally contain a relational operator from the set {<=, <, >, >=}. Valid values for a quantitative test are of the form "7", "-7", "7.4", "-7.4", "7.8912", "0.125", "<10", "<10.15", ">12000", 1-10, 1:256
Ordinal	ORD	Ordered categorical responses , e.g. 1+, 2+, 3+ ; positive, negative; reactive, indeterminant, nonreactive. (Previously named SQ)
Quantitative or Ordinal	ORDQN	Test can be reported as either ORD or QN, e.g., an antimicrobial susceptibility which can be reported as either resistant, intermediate, susceptible or as the mm diameter of the inhibition zone. (Previously named SQN)
Nominal	NOM	Nominal or categorical responses that do not have a natural ordering. e.g. names of bacteria (reported as answers); categories of appearance that do not have a natural ordering, e.g., yellow, clear, bloody. (Previously named QL)
Narrative	NAR	Text narrative, such as the description of a microscopic part of a surgical papule test.
"Multi"	MULTI	Many separate results structured as one text "glob," with or without imbedded display formatting.

2.7   Type of Method (6th part)

The method by which the test was performed is the sixth part of the test name. Methods need only be expressed as part of the name when they provide a distinction between tests that measure the same component (analyte) but which have different clinical significance or have a different clinical reference ranges. For instance, whole blood glucose tested with a chemstrip might be distinguished in the method field.

The list of methods given in Table 13 is not exhaustive; we have included only those methods which are abbreviated in the database or which otherwise require explanation or clarification. Most methods are fully spelled out in the database and should be self-explanatory.

Laboratories do not include the method as part of the name for most common chemical and hematological tests. They often need the freedom to choose the instrument according to time of day, urgency of the request for service, availability of the instruments and so on, even though the instruments may employ different methods. The laboratories then adjust each of the "interchangeable" instruments to produce equivalent results even though the instruments may use different methods. So, we do not want to distinguish too finely on the basis of methods. Though method is rarely significant for many chemical and hematological tests, it is often important to immunochemical/serology testing, because the sensitivity and specificity of some tests varies greatly with the method. So you will commonly see methods included in microbiology tests and coagulaiton tests within the LOINC database.

This does not mean that information about the method is irrelevant, but that it is not always a meaningful part of the test name. It is an essential element of the internal quality assurance of laboratories. Remember that both reference range and

method can be sent in other fields of ASTM, HL7, and CEN TC251 result messages.

Table 13: Methods		
Method	**Abbr**	**Comment**
AGAR DIFFUSION	AGAR	Bacterial sensitivity (Kirby-Bauer)
AGGLUTINATION	AGGL	
LATEX AGGLUTINATION	LA	
AGGLUTINATION -- RED BLOOD CELL	AGGL RBC	Blood bank typing
COMPLEMENT FIXATION	CF	
COAGULATION ASSAY	COAG	To distinguish coagulation assays based on coagulation
DNA NUCLEIC ACID PROBE	DNA PROBE	Nucleic acid amplification - PCR is one of several methods.
TARGET AMPLIFICATION & PROBE	PROBE.AMP.TAR	
SIGNAL AMPLIFICATION & PROBE	PROBE.AMP.SIG	
ENZYME IMMUNOASSAY	EIA	Subsumes variants such as ELISA
ENZYMATIC ASSAY	ENZY	To distinguish coagulation assays based on enzymatic activity
FLOCCULATION ASSAY	FLOC	
HEMAGGLUTINATION INHIBITION	HAI	
IMMUNE BLOT	IB	
IMMUNE DIFFUSION	ID	
IMMUNE FLUORESCENCE	IF	
IMMUNE STAIN		Cells "stained" with immune enzyme.Also called Cyto immune enzyme.
LEUKOCYTE HISTAMINE RELEASE	LHR	
MINIMUM LETHAL CONCENTRATION	MLC	Also called MB (bactericidal) C
MINIMUM INHIBITORY CONCENTRATION	MIC	Antibiotic susceptabilities
NEUTRALIZATION	NEUT	
RADIOIMMUNOASSAY	RIA	
SERUM BACTERICIDAL TITER	SBT	Antibacterial susceptabilities

Stain methods which are modifications of a basic method are named using a <basic>. <modification> syntax, e.g., METHENAMINE SILVER STAIN.JONES.

2.7.1 DNA/RNA probes/measures

We will distinguish three kinds of DNA probe methods.

Probe (without amplification)

Probe with signal amplification (PROBE.AMP.SIG)
See Table 14A for a list of methods that would be identified as PROBE.AMP.SIG in a LOINC method

Probe with target amplification (PROBE.AMP.TAR)
See Table 14B for a list of methods that would be identified as PROBE.AMP.TAR in the method part of the LOINC term.

Table 14A: Examples of specific methods that would be classed as target amplified DNA/RNA (not an exhaustive list)		
PROBE.TAR.AMP (includes nucleic acid signal amplification and probe)		
PCR	Polymerase Chain Reaction	Applies to: DNA, RNA Roche Molecular Systems (thermal cycler) Requires repeated cycles of heating and cooling - each cycle doubles the target
TMA	Transcription Mediated Amplification	Applies to DNA, RNA Genprobe, Inc. (isothermal)
NASBA	Nucleic Acid Sequence Based Analysis	Applies to RNA, DNA Organon-Tenika Corp (isothermal)
SDA	Strand Displacement Amplification	Applies to DNA Beckon Dickenson (isothermal)
LAT	Ligation-Activated Transcription	
3SR SR	3 Self-Sustaining Sequence Replication	Applies to RNA, DNA Bartel's Diagnostic (isothermal)
LCR	Ligase Chain Reaction	Also probe amplification category method Abbott Laboratories (thermal cycler)
QBR	Q-Beta Replicase or probe amplification category method	Applies to DNA RNA Gene Track Systems. (isothermal)
Table 14B: Examples of specific methods that would be defined in LOINC as signal amplification methods		
PROBE.AMP.SIG		
HPA	Hybridization Protection Assay	Applies to _____
BdnA	Branched Chain DNA	Applies to DNA, RNA Chiron Corp (isothermal)
---------	Hybrid Capture	Applies to _____

2.7.2 Immune fluorescent (IF)

We do not distinguish among many variants of immune fluorescent tests. DFA, ACIF, are all classed as immune fluorescent (IF).

2.7.3 Immune Tissue Stain (Cyto IE)

We classify Peoxidase and all other immune stains of tissue under the method category immune stains

2.7.4 Enzyme Immune Assay

We classify many variants of enzymes under EIA, including ELISA, CEIA, etc.

2.7.5 Coagulation

We distinguish among three kinds of coagulation method. Coagulation, which measures the coagulation activity, immune - which measures the coagulation constituant, and enzymatic -- which measures the coagulaiton factor via enzyme rate methods.

2.7.6 Stains

We provided very detailed distinctions among various tissue stains.

2.7.7 Clinical measures

We distinguish reported from estimated and measured values; so reported body weight would be the stated weight from a patient or surrogate. Estimated would be the body weight estimated by an observer, and measured body weight.

2.7.8 Imaging studies

We distinguish among the major imaging modalities for most measures derived from such imaging studies (e.g., cardiac output from a muga scan, vs angiography).

3 Special Cases

3.1 Findings viewed as variables or as values

For some complex tests there are two ways to organize the results into a report.

3.1.1 Value

Assume a set "X" is made up of five "results" that can have a scale of (absent present) or (0 1). These results could be reported as:

Finding 1 =	Present or as	1
Finding 2 =	Absent	0
Finding 3 =	Present	1
Finding 4 =	Absent	0
Finding 5 =	Absent	0

Each finding is then considered a binary variable. This is sometimes called a "panel" approach.

3.1.2 Variable (Multiple Choice) Approach

The alternative would be to report this information as a single variable (or multiple-choice question) with many possible values:

Variable X - Finding 1, Finding 3

In this case the findings are the values of a variable called Variable X; only the positive findings are reported as values. Many laboratory tests, e.g., those that test for HLA antigens, red blood cell antigens, or screens for toxic substances, could in theory be presented either way. The microscopic part of the differential count and urinalysis could also be described either way. History and physical findings and (given a real stretch) even culture results could be structured in the panel or multiple choice/multiple answer format.

A single lab may report red blood cell antigens in either way, as a binary panel or a multiple-choice result, depending upon the purpose of the test. The routine cross and type are reported out in the multiple choice pattern format (only positives from a modest fixed set of tested antigens are reported). But if the tests are being used to prove fatherhood, the results are usually reported as a binary panel.

Blood cultures could in theory be regarded as panels:

Test Name	Value
E.Coli	absent
Staph aureus	present
Diptheroids	absent
Pneumococcal pneumonia	absent
Pseudomonas	present

although in practice such tests are almost always reported in the multiple choice/multiple answer format, as follows:

Test Name	Values
Blood culture	*Pseudomonas, Staph aureus*

We bring up these issues to explain why we use a somewhat different data format for some types of tests, and why we sometimes provide for both reporting methods (e.g., HLA blood cell antigen tests) in the LOINC database. When a binary scale is used, the kind of property will usually be arbitrary concentration (ACNC). When the multiple-choice multiple-answer approach is used, the scale will be nominal and the type of property will be presence or identification (PRID).

3.2   Blood bank

Red cell antigens will be named in accordance with the American Association of Blood Banking (A/AB/B) naming standards.[14] In addition to the antigen or antibody, a modifier would be included in the fourth subfield of the first field, to indicate whether testing was performed on the patient, donor, or blood pack. Unless explicitly stated, testing is assumed to have been on a material collected from a patient. Additional information about the person identified in the fourth subpart, such as the donor's name or relationship to patient, should be placed in other OBX segments, or comment segments of the message, and would *not* be part of the test name.

Examples of blood bank related names:

    ANTIBODIES IDENTIFIED:PRID:PT:SER^PATIENT:ORD
    B AB:ACNC:PT:SER^DONOR:NOM:AGGL RBC

Each reportable antigen must have its own test, so that each element in a full set of binary tests could be reported as (negative positive) or (0 1).

The fully specified names of A, AB, and O blood types (as observations) would be as follows:

Measure of serum antibody against type A blood of donor:

    A AB:ACNC:PT:SER^DONOR:NOM:AGGL RBC

Presence of A antigen on donor's red blood cells:

    A AG:ACNC:PT:RBC^DONOR:NOM:AGGL RBC

Presence of A antigen on the blood cells in a pack of blood given to the patient:

    A AG:ACNC:PT:RBC^BPU:NOM:AGGL RBC

Blood bank reporting illustrates the need for a method of reporting by panel *and* by multiple-answer mechanism. The LOINC database provides observation names for both kinds of reporting.

    B AG:ACNC:PT:RBC^BPU:ORD:AGGL RBC
    ANTIGENS ABSENT:PRID:PT:BBL^BPU:ORD

The LOINC database provides other "observations" for reporting: the status of each blood pack (e.g. held, given, discarded), and for reporting that information when HIS and medical records systems want it; how much of each type of blood product was given at a moment in time; the type of each pack; any adverse reaction to that pack; and the pack number to accommodate laboratories that send this information as discrete observations.

    BLOOD PRODUCT DISPOSITION:TYPE:PT:BPU:NOM
    BLOOD PRODUCT TYPE:TYPE:PT:BBL:NOM

3.3   Immunocompetence studies

The T-cell markers in the LOINC database include all of the single markers and the most commonly reported combinations, e.g. "CD10+CD20+". Most of these are really measuring the number or percent of lymphocytes which bear the specific T-cell marker pattern. So they should be specified as a subtype of a lymphocyte, e.g., Lymphocytes,CD10+CD20

Two kinds of measures are of interest. The "absolute" number of such cells per cubic millemeer. These are represented as number concentrations, e.g.,:

      Lymphocytes.CD10+CD20+NCNC:PT:BLD:QN

The other quantity of interest is the percent of these cells per 100 lymphocytes. These are represented as number fractions, e.g.:

      Lymphocytes.CD10+CD20+100 lymphocytes:NFR:PT:BLD:QN

The database also includes fully specified names for all of the commonly reported HLA antigens. These are grouped in the class HLA. Experimental methods can define many subtypes of many antigens, so this list is not exhaustive, and is also likely to expand with time.

Example:

      HLA-A1:ACNC:PT:BLD^PATIENT:ORD

3.4   Naming results of microbiological culture

The inherent complex structure of results of microbiological culture presents unique challenges for standard names. Result Status (Preliminary, Final) will be indicated in the OBR segment of HL7 segment with the Result Status field (OBR-25), not as part of the name.

Specimen Type (Serum, Blood, Urine, etc.) will be indicated in the HL7 OBR segment with the Specimen Source field (OBR-15), but may also be represented in the name.

Details of specimen collection will usually be noted as OBX segments or comment segments that accompany the culture result message. The observation identifier for the OBX segment will have the fully specified name of "Specimen Collection Description:NOS:NOMS" and the Observation Sub-ID field will be used to order or group sets of observations. That is, if the material was collected by swabbing a wound of the right upper arm, multiple OBX segments would be created, each with the name "Specimen Collection Description:NOS:NOMS," and the Observation Results fields of the OBX segments would contain respectively "Swab," "Right," "Arm," and "Wound." (The granularity of the actual terms used in the specimen description is at the discretion of the user. Thus, "Right Arm Wound" as the value of a single OBX segment could be used in place of the three codes described in the previous sentence.)

Descriptions of measurement and culture growth will be noted as separate OBX segments that accompany the culture result message. The name of the observation identifier will provide the context of the observation. For instance, the name for a quantitative test of bacteria in a specimen would be:

      COLONY COUNT:NUM:PT:XXX:QN:VC

Descriptions of Gram stain findings will be noted as OBX segments that accompany the culture result message. The name of the observation identifier will be:

      MICROSCOPIC OBSERVATION:PRID:PT:XXX:NOM:GRAM STAIN

The result values that could be reported with this test (which is a multiple-choice, multiple answer type or observation) might include one or more of the following:

Epithelial cells
Gram positive cocci in chains
Many Gram negative diplococci

The organisms identified in a culture will be sent as result values in OBX segments. A separate table of allowable organism names will need to be identified. Bergey's Manual of Determinative Bacteriology[15] or some other authoritative source (SNOMED is an appropriate source for these organism names/codes) may be used as the standard. The names for the result identifiers will be created using the same strategy as for other identifiers but with particular emphasis on the method. While "Throat Culture" is the source of the culture inoculum, it is also a label that indicates what kind of media was inoculated and the other techniques used in the laboratory. So, it is a short hand for a kind of method and such will be recorded as the method part of the name. Thus, "Throat Culture," and "Blood Culture," and "*Clostridium difficile* Culture," all represent labels for how a culture was performed. Examples of names of culture results are:

MICROORGANISM IDENTIFIED:PRID:PT:BLD:NOM:BLOOD CULTURE
MICROORGANISM IDENTIFIED:PRID:PT:BRN:NOM:DIRECT BURN CULTURE
MICROORGANISM IDENTIFIED:PRID:PT:STL:NOM:STOOL CULTURE

Names of methods of staining directly on a sample/material (where many descriptive observations are possible):

MICROSCOPIC OBSERVATION:PRID:PT:XXX:NOM:GRAM STAIN
MICROSCOPIC OBSERVATION:PRID:PT:XXX:NOM:ACID FAST STAIN.KINYOUN
MICROSCOPIC OBSERVATION:PRID:PT:XXX:NOM:DRY MOUNT
MICROSCOPIC OBSERVATION:PRID:PT:XXX:NOM:INDIA INK PREPARATION
MICROSCOPIC OBSERVATION:PRID:PT:XXX:NOM:TRICHROME STAIN
MICROSCOPIC OBSERVATION:PRID:PT:XXX:NOM:GIEMSA STAIN

Names for results of staining procedures performed on organisms that are growing in culture will use Isolate (ISLT) as the system/sample type. For example:

MICROORGANISM IDENTIFIED:PRID:PT:ISLT:NOM:FUNGAL SUBTYPING

Names for organism-specific cultures:

BRUCELLA SP:PRID:PT:BLD:NOM:ORGANISM SPECIFIC CULTURE
BORDETELLA PERTUSSIS:ACNC:PT:THRT:ORD:ORGANISM SPECIFIC CULTURE
CHLAMYDIA SP:PRID:PT:GEN:NOM:ORGANISM SPECIFIC CULTURE
LEGIONELLA SP:PRID:PT:SPT:NOM:ORGANISM SPECIFIC CULTURE

Names for method for general class of organism:

FUNGUS IDENTIFIED:PRID:PT:WND:NOM:ROUTINE FUNGAL CULTURE
MICROORGANISM IDENTIFIED:PRID:PT:CSF:NOM:STERILE BODY FLUID CULTURE

Again, the Result Value of these tests would be either organism names or other statements of culture outcome. Table 15 contains valid values of the culture result OBX segment:

Table 15: Example Culture Results
No growth
Gram-positive cocci
Small Gram negative rod
Escherichia coli
Normal flora
Candida albicans

Note if a test applies to a specific species of organism, the component should include the genus AND species (at least). If

the measure applies to a series of species in the same family the string "SP" must be included. If it applies to as subgroup of the genus, then that subgroup should be named.

PRID as a property should be used when the value of a test can identify one set of alternative infectious agents. If the culture is for herpes virus and the culture can have results of herpes virus 1, herpes virus 2, etc., then PRID is the right property. If the culture is for herpes virus and the answer is positive/negative or yes/no, then the property should be ACNC and the scale ordinal (ORD).

3.5   Drug susceptibilities

Drug-susceptibility tests will be named according to the generic name of the drug tested and the methodology used in testing, with the property SUSC, with values that are either QN or ORD. Thus, appropriate names would be:

> AMPICILLIN:SUSC:PT:ISLT:QN:MIC
> AMPICILLIN:SUSC:PT:ISLT:ORD:AGAR DIFFUSION
> TICARCILLIN+CLAVULANATE:SUSC:PT:ISLT:QN:MBC

Table 16 lists methods in drug-susceptibility tests.

Table 16: Drug Susceptibility Methods	
AGAR	Bacterial sensitivity (Kirby-Bauer) via agar diffusion
MIC	Minimum inhibitory concentration
MLC	Minimum lethal concentration
SBT	Serum bactericidal titre
GRADIENT STRIP	Susceptable by E-Test or gradient strip method

The drug susceptibility tests are all grouped together in the LOINC database under the class ABXBACT.

3.6   Alternate representation of microscopic examinations

Because of the alternative representation of microscopic observations (see discussion in 1.1 of LOINC and item 21) the following convention will be used for the alternate representation of microscopic examinations:

> WBC CASTS:ACNC:PT:URNS:ORD:MICROSCOPY.LIGHT
> RBC CASTS:ACNC:PT:URNS:ORD:MICROSCOPY.LIGHT
> EPITHELIAL CELLS:ACNC:PT:URNS:ORD:MICROSCOPY.LIGHT

3.7   Cell counts

The following convention will be used to represent microscopic examinations:

> WBC CASTS:ACNC:PT:URNS:SQ:MICROSCOPY.LIGHT
> RBC CASTS:ACNC:PT:URNS:SQ:MICROSCOPY.LIGHT
> EPITHELIAL CELLS:ACNC:PT:URNS:SQ:MICROSCOPY.LIGHT

Counts of various entities and cells in urinalysis and CSF and other body fluids may be performed and reported in one of three ways.

They may be reported as absolute counts per unit volume, then they have the property of NCNC, or as percents of a general cell type, e.g., percent eosinophils, then they have the property of NFR. Blood cells are usually reported in such a manner, via a manual or automated count method.

Counts on urine and other body fluids can also be done as direct counts and reported as NCNC or NFR. However, they are more often reported as the number of entities or cells per microscopic high power or low power field, e.g., 5-10 cells per

high power field. These are really numbers per area (NARIC). E.g., the number of erythrocytes per low power field would be reported as follows

ERYTHROCYTE CASTS:NARIC:PT:URNS:QN:MICROSCOPY.LIGHT.LPF

Note that even though the values are reported as a range, the scale is still QN, because the values can be related through a ratio. We use HPF or LPF to identify high power and low power fields respectively. Large entities (such as casts) are usually reported per low power fields, smaller entities per high power fields.

The other way such entities are reported is as a pure ordinal, e.g., none, few, moderate, loaded. These would be specified as ACNC properties with ordinal scale, e.g.

ERYTHROCYTES:ACNC:PT:URNS:ORD:MICROSCOPY.LIGHT

3.8   Skin tests

These follow the pattern of a challenge test. For a TB skin test it would be:

TUBERCULOSIS REACTION WHEAL^3D POST 25 U TU ID:LEN:PT:SKN:QN

Where TU means tuberculin units, ID means intradermal, LEN indicates a measure of length (the diameter of the wheal) and so on.

4   Clinical observations and measures

4.1   Introduction

For most of the measures we include separate observations for summary data, e.g., shift and twenty four hour urine output totals. We also provide varying degrees of pre-coordination for the observation, the body site at which it was obtained, and the method. E.g., a cardiac output based on the Fick method is distinguished from a cardiac output computed from 2D cardiac echo data.

Physiologic measures are often monitored continuously over time, and the instrument reports summary "statistics" over that reporting period. For vital signs these can include minimum, maximum, and mean value over a time period. For intake and output the total is the summary statistic usually reported. When we address measures taken over time, we usually include 1 hour, 8 hour, 10 hour, 12 hour, and 24 hour intervals to cover the varying lengths of work shifts within and across institutions. The LOINC names of these correspond to the form of a 24H urine specimen. The times are recorded in the duration (3rd part) of the name.

The parts of clinical measurement names are the same as for laboratory measures. Parts 2, 3, 5 and 6 (type of property to method) correspond exactly in meaning between laboratory and clinical LOINC codes. Part 4, body system, has the same general meaning for clinical and laboratory measures, but in the case of laboratory tests the system usually identifies a fluid and a body compartment by implication, e.g., serum, cerebral spinal fluid. For clinical terms, the system is usually a body part (e.g., chest), organ (e.g., cardiac ventricle), or part of an organ (cardiac In the case of laboratory tests, the component usually identifies some chemical moiety that is distributed in the system (glucose, or HIV antibodies).

In the case of clinical terms, the component usually identifies a particular projection of a three or four dimension space to a measure of a particular feature (e.g., QRS interval, systolic) of a time changing measure. ventricle.left.outflow tract). In some cases the system may be an instrument or device attached to the system.

The component includes such things as the special kinds of length (whether circumference, or diameter, or radius) when length is the property, and the specific level and axis on which a measure of a body part is taken, e.g. circumference taken at the nipple line. The component should remove all ambiguity as to what projection or axis or specific subtime frame is being measured. So if one is measuring the diameter of the kidney, the system would have to specify the kidney.right (or

kidney.left), and the component would identify the axis and level at which the diameter was measured (e.g., crossectional at level of pelvis). For a measure of chest circumference the system = chest, the property = circumference at nipple line, and the property = length. Areas, lengths, and volumes of organs all have to be specified enough in the component to distinguish a particular area or length that is being measured. When a measure changes over some cycle (e.g., inspiration, expiration, diastole, systole), then that should also be specified in the component. (Duration is used to identify the duration of an over all study)

Table 17 Subjects covered to date in clinical LOINC
Blood pressure (systolic, diastolic, and mean)
Heart rate (and character of the pulse wave)
Respiratory rate
Critical care measures
Cardiac output, resistance, stroke work, ejection fraction, etc.
Body weight (and measures used to estimate ideal body weight)
Body height
Body temperature
Circumference of chest, thigh, legs
Intake and output
Major headings of history and physical
Major headings of discharge summary
Major headings in operative note
Electrocardiographic measures
Obstetric ultrasound imaging
Urology ultrasound imaging

In general the component is used to distinguish the various points or ranges, or inflections of a physiologic tracing, and to define precisely which of a number of possible dimensions of length or area are being measured in imaging.

For most clinical measurements, the component is an attribute of a patient or an organ system within a patient. However, attributes of non-patient systems are also often of interest. For example, we might want to know the class of instrument used to obtain the measurement: i.e., the vendor model number or institutional inventory number of an endoscopy. Such identification numbers have a property of ID. Infection control might want the latter reported in order to track nosocomial infections.

When attributes of an instrument or device are being reported, the system is the name of instrument. The same is true when we report characteristics of tubes used to move fluid in and out of body cavities. For example, we might want to report the size and type of a nasogastric tube.

To accommodate the special dimensions of clinical observations we have introduced new options for the kind of property, The new kinds of property are what you might expect from the new kinds of dimensions being measured (e.g., resistance, voltage, work per beat). However we have also introduced three important new properties:

ANAT is a special case of PRID (or taxon) which applies to anatomic sites only.

IMP (impression) is a diagnostic statement, always an interpretation or abstraction of some other observation (a series of test results, an image, a total patient), and almost always generated by a professional. (We could also consider the EKG cart's automated diagnoses as impressions.) Impressions are used in laboratory medicine as well as clinical medicine, so you will see them appearing there as well.

FIND Finding is an atomic clinical observation, not a summary statement as an impression. Physical, historical, review of systems and other such observations have a property of Finding. These may have a scale of NOM (for coded findings) or NAR for findings reported in narrative text.

In clinical measures, super systems (the second subpart of the system component) is widely used. For example, we distinguish a head circumference of the patient versus a fetus as follows:

    CIRCUMFERENCE:LEN:PT:HEAD
    CIRCUMFERENCE:LEN:PT:HEAD^FETUS:QN

4.2   Atomic versus molecular (pre-coordinated names)

With clinical terms we almost always have two ways of reporting. Using the first, we can report an observation by reporting a number of atomic variables which together fully describe the observation. For example, we have the following atomic observations for circumference measures. These variables let us deal with all of the odd ball kinds of circumferences for which we have not yet defined a pre-coordinated term

CIRCUMFERENCE:LEN:PT:BODYPART.XXX:QN	The actual measure of some circumference
CIRCUMFERENCE SITE:ANAT:PT:*:QL	Identifies the body part measured (specifies the system)
CIRCUMFERENCE METHOD:TYPE:PT:BODY PART.XXX:*	Identifies the measuring technique used to obtain the circumference (answers = tape measure, derived, imaging)

We also provide pre-coordinated terms that combine some of the atomic variables into one LOINC code. For example we have

8279-2 CIRCUMFERENCE.AT NIPPLE LINE:LEN:PT:CHEST:QN

and

8290-2 CIRCUMFERENCE^INSPIRATION:LEN:PT:CHEST:QN

which provide more specificity and permit the key components of the measure to be expressed as one variable as is the convention in many clinical systems. We call these pre-coordinated codes "molecular" variables.
Within the LOINC database molecular variables will vary with respect to how many atomic components are aggregated. As is true in some laboratory areas, methods often not included as part of a name, nor are they always reported. The commonest molecular aggregation is between functional measure and a particular site of measurement. (E.g., the many different intravascular sites for blood pressure measurements.) But in some cases the molecular variables represent combinations of specific measures and particular methods (e.g., the cardiac output measures). Please note that most molecular variables could also be accompanied by one or more atomic measures to provide special information about the measure, e.g., special circumstances of the measure, or the vendor model number or institutional inventory number of the measuring instrument.

We have introduced one more convention in this release. When we have a variable that really reports what would have been contained in the name in a fully pre-coordinated term, will have an asterisk placed in the part that will be reported as a value. For example, a variable that is used to report the anatomic site as an atomic variable, would have an asterisk (*) in the system part of the name. The variable used to report the method of a particular measure would have a asterisk (*) in the method part of the name.

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Appendix A -- LOINC Database Structure

#	Field Name	Type	Width	Description
1	LOINC_NUM	Char	7	The unique LOINC Code. This is a numeric code with a mod 10 check digit. (The algorithm for calculating a mod 10 check digit is given in Appendix B.)
2	COMPONENT	Char	150	Fields 2-7 contain the six parts of the name. The fully specified name for a given LOINC code would be constructed by printing out the contents of these fields (2-7), inserting a colon (:) between the contents of each of these fields.
3	PROPERTY	Char	10	
4	TIME_ASPCT	Char	10	
5	SYSTEM	Char	50	
6	SCALE_TYP	Char	30	
7	METHOD_TYP	Char	50	
8	RELAT_NMS	Char	254	One or more synonyms, separated by semicolons (;). This field is intended to make it easier to find a given observation by providing other names by which the observation may be known. For a drug level, for example, we include the trade names of that drug under the related names.
9	CLASS	Char	20	An arbitrary classification of the terms for grouping related observations together. The current classifications are listed in Table 18. We present the database sorted by the class field within class type (see field 10). Users of the database should feel free to re-sort the database in any way they find useful, and/or to add their own classifying fields to the database.
10	SOURCE	Char	8	Field 10 - Source, is for our internal use, and should be ignored by database users.
11	EUCLIDE_CD	Char	10	EUCLIDES analyte code. The Euclides code identifies the analyte (the first subpart of the first part of the name).
12	ASTM_CD	Char	9	The ASTM codes apply to only a few of the tests (e.g., cell counts, antibiotic sensitivities). These are the codes included in the appendices of HL7 and ASTM E1238-94.

#	Field Name	Type	Width	Description
13	IUPAC_CD	Char	8	The IUPAC code identifies the component, kind of property, and system. Note: Most of the IUPAC codes for chemistry assume the component is measured in substance concentration, e.g., moles, while most U.S. labs report in mass concentration. We have applied the IUPAC code for substance concentration to mass concentration, because IUPAC has no code for the mass concentration variant.
14	DT_LAST_CH	Char	8	Date last changed, in the format YYYYMMDD
15	CHNG_REAS	Char	254	Reason term was changed. If a term has been changed, the reason for the change is detailed here.
16	CHNG_TYPE	Char	3	Change Type Code. DEL = Delete; ADD = add, NAM = change to Analyte/Component (field #2); MAJ = change to name field other than #2 (#3 - #7); MIN = change to field other than name.
17	COMMENTS	Char	254	Free-text comments relating to the test result.
18	ANSWERLIST	Char	254	The list of answers for results that are reportable from a multiple choice list (e.g., the answers for the term DISPOSITION OF BLOOD PACK are GIVEN;PARTIALLY GIVEN;DISCARDED). This field provides examples, not required answer lists.
19	STATUS	Char	3	Deprecated or superseded status indicated by DEL in this field (otherwise blank). Used to mark terms as the database evolves. LOINC codes will not ever be re-used nor will they be removed from the database, they will instead be cross-referenced to superseding terms in Field 20.
20	MAP_TO	Char	7	Used when a field has been dropped from the active database (by entering "DEL" in the Status field) because it has been replaced by an updated term. In those cases, Map_To contains the LOINC code of the new term that should be used.
21	SCOPE	Char	254	Not currently used.
22	SNOMED_CD	Char	10	SNOMED Code (future versions). Not currently used.
23	VA_CD	Char	8	VA Code (future versions). Not currently used.
24	METPATH_CD	Char	10	Metpath Code. Not currently used.
25	HCFA_CODE	Char	12	HCFA code (future versions). Not currently used.

#	Field Name	Type	Width	Description
26	CDC_CODE	Char	6	Code from CDC Complexity file which maps laboratory tests to the instruments used to perform them. These codes are at the analyte level, not the test instrument level.
27	NORM_RANGE	Char	30	Normal Range - Example answers from real tests
28	EX_US_UNITS	Char	30	Example units used in the US.
29	IPCC_UNITS	Char	30	Example units used by IUPAC/IFCC (future)
30	GPI_CD	Char	11	GPI Code. For drugs, this field contains a map to the Medispan GPI codes, a hierarchical system of classifying pharmaceutical products.
31	GPI_CD_TOT	Char	254	GPI Code Total. For a few products, a simple one-to-one mapping with a GPI code was not possible. In these cases, all applicable GPI codes are contained in this field, separated by semicolons.
32	REFERENCE	Char	254	Contains references to medical literature, product announcements, or other written sources of information on the test or measurement described by the LOINC record.
33	EXACT_CMP_SY	Char	254	Exact core component synonym: This field contains an exact synonym for the "core component" of the LOINC component name. We have included the mixed case and "superscript" form of blood bank and HLA antigens (e.g., Lu[a]) here. As there is no ASCII representation for superscript letters, we use the hat (^) to signify superscripts in this field. (E.g., if the core component is represented as L LITTLE U LITTLE SUPER A in the LOINC component/analyte name field, it is represented in the Exact Core Synonym field as Lu^a.) In a future release we will add more exact synonyms for the core components.
34	MOLAR_MASS	Char	13	Molecular weights: This field contains the molecular weights of chemical moieties when they are provided to us. This release contains values kindly contributed by IUPAC.
35	IUPC_ANLT_CD	Char	13	IUPAC analyte code: This field contains the Chemical Abstract service number or the Enzyme Nomenclature number for the chemical components for chemicals and/or enzymes. These were also contributed by IUPAC.
36	ANSWERLIST2	Char	254	These two fields provide an overflow for ANSWERLIST values that exceed the 254 characters allowable in most 16-bit spreadsheet and database programs (such as Excel 5.0/95 and FoxPro 2.5)

#	Field Name	Type	Width	Description
37	ANSWERLIST3	Char	254	
38	CLASSTYPE	Int	2	1=Laboratory class; 2=Clinical class
39	FORMULA	Char	254	Regression equation details for many OB.US calculated terms.
40	MULTUM_CD	Char	6	Maps to Multum Inc.database of codes for drugs.
41	DEEDS_CD	Char	7	Data Elements for Emergency Department Systems Codes (CDC). This field contains the DEEDS code value which maps to the LOINC code in question.
42	CSCQ_FRNCH_NM	Char	255	French name for LOINC term. Supplied by Centre Suisse de Contr⊥le de Qualitϑ. This field contains extended characters and will not transfer correctly to 7-bit systems
43	SPECIES	Char	20	Codes detailing which non-human species the term applies to. If blank, "human" is assumed.
44	EXAMPL_ANSWERS	Char	50	For some tests and measurements, we have supplied examples of valid answers, such as "1:64", "negative @ 1:16", or "55". This differs from the ANSWERLIST field, which details possible choices for nominal scale terms.

Table 18: Classes				
Abbr	**Laboratory Term Classes**		**Abbr**	**Clinical Term Classes**
ABXBACT	Antibiotic susceptibility		BDYCRC	Body circumference
ALLERGY	Response to antigens		BDYHGT	Body height
BC	Cell counts (blood, CSF, pleuritic fluid)		BDYSURF	Body surface area
BLDBK	Blood bank		BDYTMP	Body temperature
CELLMARK	Cell surface models		BDYWGT	Body weight
CHAL	Challenge tests		BP	Blood pressure
CHALSKIN	Skin challenge tests		BP.CENT	Blood pressure – central
CHEM	Chemistry		BP.PSTN	Blood pressure – positional
COAG	Coagulation study		BP.TIMED	Blood pressure – timed
CYTO	Cytology		BP.VENOUS	Blood pressure – venous
DRUG	Drug levels		CLIN	Clinical NEC
DRUGDOSE	Drug dose (for transmitting doses for pharmacokinetics)		ED	Emergency department
FERT	Fertility		EKG	Electrocardiogram
HEM	Hematology (excluding coagulation & differential count)		EKG.IMP	Electrocardiogram impression
HLA	HLA tissue typing antigens		EKG.MEAS	Electrocardiogram measures
MICRO	Microbiology		EYE	Eye
PATH	Pathology		FUNCTION	Functional status (e.g. Glasgow)
SERO	Serology (antibodies and most antigens except blood bank and infectious agents)		H&P	History and physical
SURGPATH	Sugical pathology		HEMODYN	Hemodynamics
TOX	Toxicology		HRTRATE	Heart rate
UA	Urinalysis		IO	Input/Output
VET	Veterinary Medicine		NEONAT	Neonatal measures
			OB.US	Obstetric ultrasound
			OBGYN	Obstetrics/gynecology
			RESP	Respiration
			SKNFLD	Skinfold measurements
			US.URO	Urological ultrasound
			VOLUME	Volume (specimens)

Appendix B -- Calculating Mod 10 Check Digits

The algorithm for calculating a Mod 10 check digit is as follows:

Instructions	Example
	12345
(1) Take the odd digit positions counting from the right	531
(2) Multiply by 2	1062
(3) Take the even digits starting from the right	42
(4) Append these to the front of the results of (2)	421062
(5) Add the digits of (4) together	
(6) Find the next highest multiple of 10	4+2+1+0+6+2 = 15
(7) Subtract (5) from (6)	20
	20 - 15 = 5. Thus, 5 is the Mod 10 check digit for 12345.

Appendix C -- Procedure for Submitting Additions/Changes to the Database

Introduction

We receive two kinds of requests for additions:

(1) The first kind of request deals with (a) an entirely new kind of measurement, e.g., DNA sequencing or (b) the use of LOINC codes in manners that have not been agreed upon by the LOINC committee, e.g., the definition of terms to accommodate the organism 1, organism 2, etc., structures that are present in many laboratory databases.

(2) Other requests are variations on observations that are already in the database. E.g., we have a term for a particular test result with serum as the specimen (system) and a user requests an identical term for a specimen of gastric contents. Provided that the requestor followed the rules given below and the number of terms requested at a given time are modest, we will try to respond to these kinds of requests quickly.

We will only be able to respond quickly to such requests if the requestor provides us with clear information about the new terms, as detailed in the first part of Table 19, which defines the content that we need to determine whether a submitted code requires a new LOINC code assignment or not. Before sending a request, make sure that you have, at a minimum, provided information about items 1 through 7 (and 8 if applicable). It is also very important to us to know the units and (when possible) a sample value of the test/observation that is being requested.

We cannot guarantee a response for requests that do not include items 11 and 12. This information enables us to verify the property, precision, and method.

Please note that we tend to avoid the use of methods for chemistry tests. We will not routinely accept requests for method-specific chemistry tests. Only in very special circumstance will we distinguish among analytic methods in chemistry. We do distinguish microbiology, serology, and coagulation tests by method type. Even here, however, we do not distinguish every variation in methods. Look in the body of this guide for information about the kinds of distinctions we make.

When you find a test in the data base that you believe is wrong, please send us a letter or email calling attention to the concept and the reason it is wrong, e.g., we are not using the standard nomenclature, a typographical error has occurred, the name carries some internal contradiction - e.g., we have listed it as being done on serum when it is only valid when performed on plasma - or it is a duplicate of some other concept in the data base.

Note that our policy is to allow both method vague (no method) as well as method specific measures in serology (measures of AB and AG), but not in antibiotic susceptibility testing.

Please pay special attention to requests for submissions that include the system of serum or plasma alone. For most chemical analyses there is no important clinical difference between the values obtained from serum and those obtained from plasma, and we would like to represent them in the database as SER/PLAS to indicate our indifference to the distinction. Unfortunately, many requestors of new terms define their request in terms of the one that they happen to use (e.g., serum or plasma) without telling us that the measure can really be done on either serum or plasma, equally. Most such requests should be for SER/PLAS as the system (sample). If the measurement MUST be done either serum or plasma, please scientifically justify your request; otherwise you will greatly delay our response to your submission.

When you wish to submit tests or measures which are radically different from those we currently carry, please provide a full description of the test, its purpose, and procedure. (A Xerox copy of test kit vendors descriptive material or from a textbook describing the procedure and its purpose would be very helpful.) We often will require a committee discussion to decide how to represent new subject matter, so response times will be slower.

The requestors also need to supply some evidence that they are familiar with the database and that they are sure the term is not already represented in LOINC. The major work these requests generate is the effort to be sure the observation is not already in the database. We can perform this service if the requestors have done most of this work themselves. For this reason, we request that you identify the LOINC term that is closest to your request and to flag the difference between the requested test and the existing test. That is, when a new observation is only a variation on an old one, use an existing LOINC observation as the template;

change the part that is different in the new term and indicate that difference. Later in this appendix, we discuss how to make a submission as either a Microsoft Access database or an ASCII text file. If you use an Access file submission, you may use the S_COMMENT field (see Table 20a) to indicate the difference of the new term. If you are making the submission as an ASCII file, you should append three asterisks ("***") to the different term. Terms should be submitted in an acceptable LOINC database format (Access or dBase), Excel or Lotus spreadsheet, or tab delimited ASCII file. All submissions should include, at a minimum, the 7 or 8 required parts of the term as detailed in Table 19.

Please sort the input file by the your proposed LOINC name. We will maintain the order of the submitted file when we return with our proposed new or existing LOINC codes mapped to your submission. It makes it a lot easier to work with an alphabetically sorted file from the outset.

If you transmit an ASCII tab delimited file (see Section 4, Submission in ASCII File Format) please maintain the field order as outlined in Table 19 below, using whatever delimiter is appropriate to your file format to indicate blank fields. An example submission (which, because of space limitations, includes columns for only the first eight fields) appears below. Real submissions should have columns for all 14 attributes listed in Table 19. Additional details are provided in the section titled Access Database and Excel Submissions presented later in this appendix.

Table 19: Example submission

Row#	Your test ID	Analyte/Component	Property	Time	System	Prec	Method	Class	Related	Etc
1	G23	GLUCOSE^90M POST 50G LACTOSE PO	MCNC	T	UR***	ORD	TEST STRIP	CHAL		
2	C47	COPROPORPHYRIN 1 ISOMER***	MRAT	24H	UR	QN		CHEM		
3	I98	INDICAN	MRAT	24H	UR	QN		CHEM		
4	T51	THYROXINE.FREE	MCNC	PT	UR					

When we first get a file we run it through a filter program that looks for identical or close matches. Our first response to you will often be an email asking some clarifying questions. We will refer to your submissions by the row number of the submitted file (first concept is row 1, second is row 2, etc.). We would prefer to clear up the general intent of the file via an email dialogue before proposing LOINC codes for your submissions. Please respond to the email by inserting your answers below the questions in a response email.

We will return the output in a file with all of the fields you submitted plus a number of fields that we will add it as part of our internal review process. We will also add fields that identify the LOINC code and formal LOINC name when we are able to map your term to a LOINC concept. These will include an action code, explaining whether we mapped your term to a pre-existing LOINC code or made up a new one to accommodate it. (We also indicate in both cases whether we had to change your term to make it fit our rules -- please check these closely to be sure that we did not misunderstand your proposal). We also will point out internal contradictions in the naming, and show close matches (these help us decide whether your term is formatted correctly for the subject matter.)

Table 20a				Access Field Names for Submissions

Row #	Field Name	Data Type	Size (Bytes)	Description
1	S_ROW	LONG	4	Row number of this term in submitter's file. This submitted row number will be preserved even when outputs are sorted differently.
2	S_LOCAL_CD	TEXT	50	The submitter's local code used to identify the test/observation in the submitter's master file. This can be any string of up to 50 characters.
3	S_COMPO	TEXT	150	Submitter's Analytes/Component. Mandatory. (User Guide 2.2)
4	S_PROP	TEXT	10	Submitter's Kind of Property. Mandatory – but we can help if you provide enough details. (User Guide 23)
5	S_TIME	TEXT	10	Submitter's Time Aspect. Mandatory. (User Guide 2.4)
6	S_SYS	TEXT	35	Submitter's System/Sample Type. Mandatory. (User Guide 2.5)
7	S_SCALE	TEXT	30	Submitter's Type of Scale. Mandatory. (User Guide 2.6)
8	S_METH	TEXT	50	Submitter's Type of Method. If required. (User Guide 2.7)
9	S_REL_NAM	TEXT	250	Submitter's Related Names. Strongly recommended. Common names, acronyms or synonyms. (User Guide - Appendix A)
10	S_LOINC	TEXT	10	Submitter's LOINC number. Strongly recommended. This is the LOINC number that is similar, but not the same as, the submitter's test.
11	S_RESULTS	TEXT	50	Submitter's Example Results. Strongly recommended. As reported by your lab.
12	S_UNITS	TEXT	20	Submitter's Example Units. Strongly recommended. As reported by your lab.
13	S_ID	TEXT	50	If the submitter includes a reference code ID for each unique submission to LOINC, record that ID here, and this will be returned with questions or an assigned LOINC number on a returned file
14	S_COMMENT	TEXT	250	Comments from the submitter may wish to pass to RI when needed.
15	BLANK1	TEXT	50	Place holder. Do not use
16	BLANK2	TEXT	20	Place holder. Do not Use

Table 20b Content Added by Regenstrief (Fields left blank in submission)				
17	RI_REF	TEXT	50	Regenstrief Reference code. A unique reference code assigned by RI to the submitted concept. This code is produced by concatonating RIs abbreviation to the submitter, the date the file was received by RI, and the row # position of the concept in the submitted spread sheet/file
18	LOINC	TEXT	10	Assigned LOINC code for submitted concept. This may be a new code or a pre-existing code. Blank if questions still remain about the meaning of the concept.
19	RI_ACTION	TEXT	30	Regenstrief Action Code: ADD – term accepted and new code assigned DUP – submitted term already exists in LOINC databsae IDUP – submitter inadvertently submitted same term twice (internal Duplicate) INFO – more information needed from submitter HOLD – submission is area not currently being considered
20	RI_COMMENT	TEXT	250	RI's comments to submitter.
21	R_COMPO	TEXT	150	RI's revised version of submitter's analyted/component
22	R_PROP	TEXT	10	RI's revised version of submitter's kind of property
23	R_TIME	TEXT	10	RI's revised version of submitter's time aspect
24	R_SYS	TEXT	35	RI's revised version of submitter's system/sample type
25	R_SCALE	TEXT	30	RI's revised version of submitter's type of scale
26	R_METH	TEXT	50	RI's revised version of submitter's type of method
27	L_COMPO	TEXT	150	Formal LOINC name for analyte/component if LOINC number assigned
28	L_PROP	TEXT	10	Formal LOINC name for kind of property if LOINC number assigned
29	L_TIME	TEXT	10	Formal LOINC name for time aspect if LOINC number assigned
30	L_SYS	TEXT	35	Formal LOINC name for system/sample type if LOINC number assigned
31	L_SCALE	TEXT	30	Formal LOINC name for type of scale if LOINC number assigned
32	L_METH	TEXT	50	Formal LOINC name for type of method if LOINC number assigned
33	L_CLASS	TEXT	20	Formal LOINC name for class if LOINC number assigned
The following fields are used only for internal Regenstrief purposes and should not be of much interest to the submittor:				
34	STATUS	TEXT	20	Regenstrief's Status for submitted term
35	ID	TEXT	50	Regenstrief 's internal assigned ID for the submitter's file. (Internal path and file name information.)
36	COMMENT	TEXT	250	Regenstrief's automated comments about the submitted term. These identify internalcontraditions, automated equivalencing (e.g., serum to SER/plas).
37	UNIQ	TEXT	150	This lists any words in a concept that are new to the LOINC data base. These may indicate typo's, mis-statements of words or new words in the concepts.
38	DUPS	TEXT	150	These are lists of subsets or near matches for submitted terms. These are produced only to assist the submission review process and should not be given too much credence.
38	EDIT_CTL	TEXT	10	Regenstrief's Edit Control

Making a Submission

Tables 1a and 1b describe a submission that is in the form of a Microsoft Access database. If you send an Access data base you should use this template to be sure the field names are right. A blank Access database template named SUBMIT.MDB is included in the RELMA software package. You should be diligent in filling in the first 13 fields of the table for each term in your submission.

Along with the database file for your submission, you should also include a cover letter (or email) that contains the following information:

1. The name of the organization making the submission
2. A contact name and their telephone number
3. A contact FAX phone number
4. A contact email address

Including this information will help us to respond to your request in a more efficient manner.

Access Database and Excel Submissions

You may make a submission in the form of a Microsoft Access database or an Excel spreadsheet. Most of the actual processing of a submission ends up in the form of an Access database, so, when feasible, send the submission as an Access database file. If you wish to submit an Access database, the fields described in Table 20 of this appendix must be used as the field names in the database. You may also use the field names presented in Table 20 as column names in an Excel spreadsheet. We will assume, for purposes of illustration, that the submission is in the form of an Access database.

Note that the field names are stored in uppercase letters and must be spelled exactly as shown in Table 20. Once you have created an empty database with the fields specified in Table 20, you may enter your submission data. (A blank database template named SUBMIT.MDB is included in the RELMA software package.)

The data could then be entered into a row of the Access database with values similar to those above. Note that fields 15 through 39 in Table 20 are empty when first submitted to RI. You should, however, make every attempt to supply information for first 14 fields presented in Table 20. Other fields in the database (e.g. R_COMPO, R_PROP, L_COMPO, L_PROP, etc.) become populated by us during the evaluation process.

Using a previously shown example, a submission may appear as follows:

Corresponding Row In Table 1a	Field Name	Submitted Data
1	S_ROW	1
2	S_LOCAL_CD	G23
3	S_COMPO	GLUCOSE^90m POST 50g LACTOSE PO
4	S_PROP	MCNC
5	S_TIME	PT
6	S_SYS	UR
7	S_SCALE	ORD
8	S_METH	TEST STRIP
9	S_REL_NAME	(null)
10	S_LOINC	6762-9
11	S_RESULTS	(null)
12	S_UNITS	MG/DL
13	S_ID	(null)
14	S_COMMENT	(null)

Submission in ASCII File Format

Although we prefer that submission be in an Access database format, you may also send your submission data as an ASCII file, it must have the following format:

> S_ROW|S_LOCAL_CD|S_COMPO|S_PROP|S_TIME|S_SYS|S_SCALE|S_METH|
> S_REL_NAM|S_LOINC|S_RESULTS|S_UNITS|S_ID|S_COMMENT<CRLF>

Each field is separated from the other by a Tab character. That is, each vertical bar above would actually be a Tab character (i.e., an ASCII 9). Each line is terminated by a carriage-return/line-feed pair (i.e., the <CRLF> above). Therefore, each <CRLF>-terminated line in the ASCII file becomes a submission record. Note that the field lengths presented in Table 20 still apply to ASCII file submissions because we read the ASCII file data you submit into an Access database as described in Tables 20a and 20b.

Using the previous example, one line might appear as:

1|G23|GLUCOSE^90m POST 50g LACTOSE PO|MCNC|PT|UR|ORD|TEST STRIP|||6762-9||MG/DL|||

where the vertical bars represent the Tab character. Notice that two vertical bars appear between "TEST STRIP" and "6762-9". In this example, this means that the related names field is empty (i.e., a null field value). The example also shows that fields S_RESULTS, S_ID, and S_COMMENT are also empty. Without the empty field, the field information would get out of sync and it would appear that the related names for this submission was actually the closest LOINC number for the submission (i.e., "6762-9"). Therefore, the ordering of the fields and the use of the Tab character to delimit the fields is very important.

Printed Reports

Submissions ultimately end up being processed by various software programs at RI to help evaluate the submissions. One such program, named "Filter", is used to scan the information, looking for duplicates with existing LOINC tests, errors, and similar inconsistencies. The output of Filter can be printed, and RI may send you a copy of the Filter program output as part of our communication with you. The purpose of this section is to explain the information that is presented in the Filter report.

Table 21   Filter Reports
SUBMITTER: SMITH – FILE:TEST.MDB – DATE SUBMITTED:2/98 (14911 LOINC RECORDS)

Index	Comment	LOINC #	Component	Property	Time	System	Scale	Method
1	Hit 5 of 8 micromol/L	A123	5-HYDROXYINDOLEACETATE	SCNC	PT	UR	QN	
	ADD		5-[HYDROXYINDOLEACETATE]	SCNC***	PT	UR	QN	
			5-HYDROXYINDOLEACETATE	MCNC	PT	UR	QN	
			5-HYDROXYINDOLEACETATE/ CREATININE	MCRTO	PT	UR	QN	

At the beginning of Line 1 (Table 21) is the index number, which is actually the value stored in the REGEN_ROW field of the submitted database after being processed by the Filter program. Next is the comment: "Hit 5 of 8". Each submission record is "decomposed" by the filter program into words. For the submission with the local code name of "A123" (which you can see in Line 1), there were six words: "5", "HYDROXYINDOLEACETATE", "SCNC", "PT", "UR", and "QN". Notice that hyphens, as well as several other special characters, are temporarily "ignored" by Filter when the words are parsed. Therefore, Filter sees six words in the submission with a local code of A123.

Table 21 also shows "micromol/L" in Line 1, which is the unit of measure for the submission. (This is the S_UNITS field of the database.)

The first line of Table 21 continues with the remainder of the submission data. The Property of the submission is "SCNC" (stored in field S_PROP), then the Time field with the value "PT" (field S_TIME), System is "UR" (field S_SYS), Scale is "QN" (field

S_SCALE), and Method is null (field S_METH). Notice that Line 1 contains the original data as received from the submitter.

Line 2 is a blank line, used to separate the original submitter's data from the remaining data for the submission.

Line 3 is the revised submitter's data (i.e., R_COMPO, R_PROP, R_TIME, etc.). The data in this line represents the submitter's data, but perhaps revised by RI to more clearly fit the LOINC naming conventions. Often, the revisions represent correction of typographical errors and inconsistencies. **NOTE**: These revisions may change the intention of your submission. Therefore, it is very important that you review such revisions very carefully when we return the mapped codes to you.

Notice the three asterisks ("***") following SCNC in the Property field. The asterisks are used to mark the "word" where the revised item deviated from a similar test as stored in the LOINC database. So how is the database search done? Simply stated, Filter looks at each "word" in the submission (e.g., "5", "HYDROXYINDOLEACETATE", "SCNC", and selects one to use as the keyword in the query for searching the database. To speed up the search process, every word in the LOINC database is indexed, along with how many times that word appears in the database. In our example, Filter looks at the word count for each word (e.g., "5", "HYDROXYINDOLEACETATE", "SCNC", etc.) and selects the one with the lowest frequency count as the keyword. In this example, HYDROXYINDOLEACETATE has the lowest count, so it was used to return all LOINC records that contain this keyword. For example, the word "5" has 66 occurrences in the database but HYDROXYINDOLEACETATE has only 7 (at the present time). By contrast, PT has 13,887 instances. By using HYDROXYINDOLEACETATE as the keyword, Filter only has to return 7 records from the database search. (Keywords for searches are almost always found in the Component field.)

The Filter program is fairly complex and performs numerous probes on the submitted data. However, we can categorize the probes into two broad types of database search: 1) perfect match searches, and 2) *ad hoc* searches. A search for a perfect match means that the Filter program is looking to see if your submission already exists in the database. If Filter did find a perfect match, it would be marked as such in your submission file (A "DUP" entry in field RI_ACTION in Table 20b.)

An ad hoc search uses the "lowest-frequency keyword" approach described earlier to select a keyword in order to search the database more efficiently. The keyword used in the search is surrounded by brackets ("[", "]") in the printed report, as shown in Table 21.

Lines 4 and 5 show two existing LOINC records that come fairly close (5 out of 6 words) to matching the submission. The first LOINC term (1694-9) differs only in the Property field (which explains the three asterisks in Line 3). Line 5 is simply another near match. Filter may print up to a maximum of 10 near-match terms as part of an *ad hoc* search.

If there was a perfect match between the submission and an existing LOINC record, there would only be four lines of output for the term, and the "LOINC #" column would have the matching LOINC number displayed in the column.

The Filter program replicates the data in Tables 2a and 2b for each submitted term.

Conclusion

There may be a need to communicate with you about your submission. To simplify this communication, we may return your submission as an Access database with queries/comments about specific terms in the submission. You may edit the S_* fields returned to you, with the exception of the S_LOCAL_CD field, which should remain unchanged.

Appendix D -- LOINC Printed Report Description

Changes to standard report format: We have changed the content of the printable (WordPerfect and Word) LOINC reports in the following ways:

The ASTM Code, IUPAC Code, MetPath Code, and Comments columns are no longer displayed. They are still maintained in the database, they are just not printed on the word processing reports. Columns representing the Exact Core Component Synonym, Change Reason, IUPAC Analyte Code, and Molar Mass have been added to the report. (The Exact Core Component Synonym, IUPAC Analyte Code, and Molar Mass fields are new to LOINC with Release 1.0h -- see Section 4 for a description.) We stress that this is a change to the printed reports only; we have not and never will change the order of the fields in the database itself (in either the tab-delimited ASCII "LOINDBT1.TXT" or the dBase "LOINC.DBF" formats).

Table 22: Columns Appearing on Printed Reports
The order of the columns on the reports is: Status   Class   Loinc Number   Map To   Analyte/Component Name   Type of Property   Time Aspect   System/Specimen   Type of Scale   Method   Related Names   Exact Core Component Synonym   Date Last Changed   Reason for Change   Answer List   EUCLIDES Code   IUPAC Analyte Code   Molar Mass

Appendix E -- Examples for LOINC Property Matching

1. **Content (CNT).** Like concentration except that *volume* in the denominator is replaced by *mass*. By extension:

   CCNT   Catalytic Content, catalytic activity of a component per unit mass of a sample (system).
       1813-5|ALPHA GALACTOSIDASE:CCNC:PT PLAS   QN

   MCNT   Mass Content, mass of component per unit mass of a sample (system).
       9435-9|ISOPROPANOL:MCNT:PT:TISS:QN

   NCNT   Number Content, number of component entities per unit mass of a sample (system).
       Hypothetical: Number of organisms per gram of tissue.

        Note: All of the heavy metal measurements in hair, nails, and tissue should all be mass contents. Example:

          Should be : 8157-0|ARSENIC:MCNT:PT:NAIL:QN

2. **Fraction (FR)**. Fraction of component A in group of entities B, C, Y, N in system 1. By extension:

   CFR   Catalytic Fraction
       2536-1|LACTATE DEHYDROGENASE.FRACTION 1:CFR:PT:SER:QN

   NFR   Number Fraction
       10602-1|SPERMATOZOA.ABNORMAL HEAD/100:NFR:PT:SMN:QN
       764-1|NEUTROPHILS BAND FORM/100:NFR:PT:BLD:QN:MANUAL COUNT

   MFR   Mass Fraction
       2614-6|METHEMOGLOBIN:MFR:PT:BLD:QN

        Note: Hematocrit is a volume fraction.

        4545-0|HEMATOCRIT:VFR:PT:BLD:QN:SPUN

       Note: CK BB (also MB, MM) is a catalytic fraction.

      Current Bad: 9642-0|CREATINE KINASE.BB/CREATINE KINASE.TOTAL   :PCT:PT:SER:QN

3. **Ratio (RTO)**. Ratio of component A to component B in system 1. By extension:

   CRTO   Catalytic Concentration Ratio
       2325-9|GAMMA GLUTAMYL TRANSFERASE/ASPARTATE AMINO   TRANSFERASE
         :CCRTO:PT:SER:QN

   SCRTO   Substance Concentration Ratio
       2958-7:SODIUM/POTASSIUM:SCRTO:PT:SWT:QN

   MCRTO   Mass Concentration Ratio
       2768-0|PHENYLALANINE/TYROSINE:MCRTO:PT:SER:QN

       Note: CSF/SERUM Protein calculation is not a ratio, because the measured components are not in the same system. It should be a relative mass concentration (RLMCNC), e.g.:
       2858-9|PROTEIN CSF/PROTEIN SERUM:RLMCNC:PT:CSF+SER:QN

4. **Relative (RL)**. Relative amount of component A in system 1 compared to system 0. By extension:

    RLCCNC   Relative Catalytic Concentration
    RLMCNC   Relative Mass Concentration
    RLSCNC   Relative Substance Concentration

  RL should be used anywhere an actual measurement is divided by a measurement on a normal or control. It should also be used when a quotient is created by dividing a measured substance in SERUM by the same substance measured in CSF, URINE, etc.

    RLCCNC   Relative Catalytic Concentration

       6302-4|COAGULATION TISSUE FACTOR INDUCED.NORMAL/ACTUAL:RLCCNC:PT: PPP^PATIENT:QN

  RLM Relative mass

   3278-9|KININOGEN.HIGH MOLECULAR WEIGHT.ACTUAL/NORMAL|RLM|PT:PPP:QN

    RLMCNC   Relative Mass Concentration (as noted previously)

   2858-9|PROTEIN CSF/PROTEIN SERUM:RLMCNC:PT:CSF+SER:QN

    RLSCNC   Relative Substance Concentration

   3190-6|COAGULATION FACTOR IX AG ACTUAL/ NORMAL :RLSCNC:PT:QN

5. **CMPLX**. Other divisions of one measurement by another that are not covered by the above rules should be classed as having Complex (CMPLX) properties, and the exact formula for deriving the quantity should be explicitly stated.

6. **ARBITRARY**. Arbitrary concentration of items. If we are **not** measuring the activity of an enzyme then the units of measure and properties are:

Possible Values	Property	Precision
Units, International Units, IU	ARB	QN
Units/ml, IU/ml, etc.	ACNC	QN
Units/gm, IU/gm, etc.	ACNT	QN
Unit/min, IU/24hr, etc.	ARAT	QN
Unitless (Patient/Control)	AFR	QN

  When measuring presence/absence or ordering measures of a component, ACNC is also the correct property.

  If we **are** measuring the activity of an enzyme then the units of measure and properties are:

Possible Values	Property	Precision
Units, International Units, IU	CRB	QN
IU/ml, Units/ml, etc.	CCNC	QN
IU/gm, Units/gm, etc.	CCNT	QN
IU/24hr, Unit/min, etc.	CRAT	QN
Unitless (Patient/Control)	CFR	QN

7. If the property is TITR then the precision is always QN.
   For:
   Any X AB
   Any X AG

Possible Values	Property	Precision
<1:2, 1:4, 1:8...	TITR	QN

8. For:
   Any X AB
   Any X AG

Possible Values	Property	Precision
Neg, Indeterminate, Pos	ACNC	ORD
1+, 2+, 3+, ...	ACNC	ORD
<1:2, 1:4, 1:8...	TITR	QN
Neg, 1:4, 1:8, ...	ACNC/TITR	ORDQN

9. For any intensive evaluation whose value comes from a finite set of unranked (independent) coded items the property will be PRID (TYPE?) and precision NOM. For extensive measures whose value comes from a finite set of unranked coded items, the property will be the extensive property, and the precision will be NOM.

Intensive Properties	Possible Values (coded)	Property	Precision
Organism Identified	E. coli, S. aureus, etc.	PRID	NOM
ABO Group	A, B, AB, O	PRID	NOM
Surgery (Dis. Summary)	Cholecystectomy, Appendectomy	PRID	NOM

Extensive Properties	Possible Values (coded)	Property	Precision
Urine Color	Amber, straw, etc.	COLOR	NOM
Urine Turbidity	Hazy, cloudy, opaque	TURBIDITY	NOM

10. For any intensive evaluation whose value comes from a finite set of unranked free text items (or a paragraph) the property will be PRID, FIND, or ATTRIBUTE, and precision NAR to indicate that the result is free text narrative. For extensive measures whose value comes from a finite set of unranked text items (or a paragraph), the property will be the extensive property, and the precision will be NAR.

Intensive Properties	Possible Values (text)	Property	Precision
Organism Identified	E. coli, S. aureus, etc.	PRID	NAR
ABO Group	A, B, AB, o	PRID	NAR
Surgery (Dis. Summary)	Cholecystectomy, Appendectomy	PRID	NAR

Extensive Properties	Possible Values (text)	Property	Precision
Urine Color	Amber, straw, etc.	COLOR	NAR
Urine Turbidity	Hazy, cloudy, opaque	TURBIDITY	NAR

11. IMP is used to represent the property when the evaluation is a mental abstraction based on one a collection of measurements and or data. For example, if several measurements are made relative to immunoglobin levels in SERUM and CSF in a myasthenia gravis panel, and if by examining all of the evidence a pathologist decided that this pattern of findings represented active disease (which could be represented as a coded value), the result of the pathologist thought process would be represented as:

	Possible Values (text)	Property	Precision
Myasthenia Evaluation	No disease, chronic disease	IMP	NOM

If the pathologist evaluation was free text or a paragraph of information, the representation would be:

Myasthenia Evaluation   No disease, chronic disease   IMP   NAR

12.   Methods are only used to distinguish things that are identical in the other five LOINC fields but may differ because the sensitivity or specificity is different for the given methods.

13.   Need to be careful in distinguishing end point detection method from property. For example, if sodium is measured using an ion specific electrode, the property is not a voltage difference. The voltage difference is just a method for indirectly measuring the sodium concentration. Concentration is the real property. Likewise, many antigens and antibodies are now measured using optical density as the detection method. However, the property we are really measuring is an arbitrary concentration (ACNC), not the optical density. If it is a ratio of optical densities (as with Gliadin AB, Parvovirus B19 AB, etc.) that are compared (patient value divided by a standard control), then the property should be ACRTO (arbitrary concentration ratio).

14.   ml/min/1.73sqM (Milliliters per min per 1.73 square meters BSA): Similar to the immediately preceeding item. This result has the same property as if it had units of ml/min/sqM. The property of this measurement should be called "areic volume rate". The hierarchy of units should be RateUnits->AereicVolumeRateUnits->ml/min/sqM. A sibling to ml/min/sqM should be ml/min/1.73sqM.