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Standard Specification for Representing Clinical Laboratory Procedure and Analyte Names[1]

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1. Scope

1.1 This specification covers the construction of elected laboratory procedure and analyte names, because data concerning clinical laboratory tests must identify these procedures in a common fashion if such data are to be transferable between databases or to be recognized in lookups or searches. It details the representations of procedure and analyte names as they are used in the clinical laboratory and in either the patient care record or the messages that exchange requests for those procedures and analytes and return results to the requestor for insertion into the record. This specification details the form of the elected standard procedure name and resulting analytes in records and messages. It was written to unify several existing conventions that have been published for the identification of laboratory procedures or other billable or cost management items. It is intended to produce an explicit identifier not only of the procedure but also of each of the constituent results for each unique analyte. It is applicable to those situations that refer to the names of either the procedures or the analytes resulting from clinical laboratory testing. These situations may include the following: Computer-based Patient Record Systems (CPR), Clinical Laboratory Information Management Systems (CLIMS), billing systems, cost identification and management systems, clinical decision support systems, epidemiologic registries and databases, and clinical research information management systems. The mnemonics of that name and the codes to be used as unique identifiers for the names of either the procedures or resulting analytes are given as examples in a nonnormative appendix.

2. Referenced Documents

2.1 *ASTM Standards:*

E 1238 Specification for Transferring Clinical Observations Between Independent Computer Systems[2]

E 1284 Guide for Nosologic Standards and Guides for Construction of New Biomedical Nomenclature[2]

2.2 *Cen Standards:*

CEN EN 12264 Medical Informatics—Categorical Structures of Systems of Concepts—Model for Representation of Semantics, 1995

3. Terminology

3.1 *Definitions of Terms Specific to This Standard:*

3.1.1 *analyte name*—the name of a single item or species identified or quantified by a laboratory procedure-denoted component in the IUPAC/IFCC **(1-6)**.[3]

3.1.2 *multiple analyte test*—a single laboratory procedure that results in a series of measurements, each relating to a separate identifiable entity. Separation and spectral techniques typically produce results of this type.

3.1.3 *procedure battery*—the generic clinical term for an aggregate of laboratory procedures requested by a single name and consisting of the names of both single procedures or panels/profiles.

3.1.4 *procedure name*—the name of a laboratory analytical procedure that leads to the identification or quantification, or both, of one or more analytes.

3.1.5 *procedure panel/profile*—an aggregate of clinical laboratory procedures requested by a single name, the constituent procedures of which are single procedures.

3.1.6 *qualitative method precision*— a procedure that results only in an observable quantity, not a measurable property.

3.1.7 *quantitative method precision*—a procedure resulting in a measureable quantity that is governed by the chemical measurement process defined in Ref **(7)** and containing a measure of uncertainty **(8)**.

3.1.8 *screen/semiquantitative method precision*—a laboratory procedure resulting in a measurable property that is categorized into an ordinal or nominal value without a measure of uncertainty **(8)**.

3.1.9 *single analyte procedure*—a single laboratory procedure that results in one measurement that is characteristic of a single entity.

4. Significance and Use

4.1 *General*:

4.1.1 The identification of procedure names used in the clinical laboratory has traditionally relied on multiple sources, each of which was created for a specific purpose. CPT-4 **(9)** is

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[2] *Annual Book of ASTM Standards*, Vol 14.01.

[3] The boldface numbers in parentheses refer to the list of references at the end of this standard.

currently used for fee-for-service payment and is being considered for prospective payment through an agreement between the American Medical Association (AMA) and the Health Care Financing Administration (HCFA). SNOMED terminology **(10)** was developed for pathology reporting. The CAP Workload reporting terminology **(11)** was devised for laboratory management. The International Classification of Procedures **(12)** was produced for statistical purposes. A replacement for this document is being piloted based on previous work **(13)** and will be referred to as ICD-10 Procedure Coding System. CEN TC 251 WG 2 has developed terminology documents for laboratory procedures **(14, 15)**. When applied to the recording into the care record of specific results from testing, these prior schemes in the United States have all had one common major deficiency: they were oriented toward identifying the general but not the specific process and not the specific results. This arrangement, although not able to keep up with the rapidly changing number of new procedures, was adequate when dealing with single analyte procedures, but many procedures, and several commonly used ones, determined and reported multiple analytes. Three common examples of this are: the "CBC," or complete blood count, the differential white blood cell count, and the urine sediment microscopic count. Each of these procedures may have a variable number of specifically identifiable analytes/species. Other procedures include separation methods, such as chromatographic separations of amino acids, in particular. It is well known that each result is a separate and important measurement but that the emphasis of current naming systems is on the test method. Common representation conventions have not yet been agreed upon for specifically identifying the analytes, although the European EUCLIDES Foundation developed an analyte catalog.

4.1.2 This specification unifies the naming rules used in current separate terminologies and then adds to the unified list additional defined terms and representations for each analyte when these are different from the procedure name. It uses the ideas stated in ISO general terminology standards as applied to health care in CEN EN 12264. It also includes conventions used by the IUPAC/IFCC Commission/Committee on Quantities and Units in Clinical Chemistry **(16)** and the EUCLIDES project of the European Standardization effort **(17)**. A unique coding convention, which can be crossreferenced to the existing coding conventions, for uniquely identifying each analyte can be specified from the nomenclature so determined and the accompanying lexicon of terms. This unique coding convention can then be used whenever specific measurements are reported for a particular specimen from an individual patient. The coding convention is stated so that it, or specific variants of it, can be specified for aggregating and storing results into, or communicating laboratory procedure results from, transportable patient care records. It is based on the general principles set down in CEN EN 12264 and Ref **(18)**. Because computer-based records are longitudinal over the lifetime of the patient and over the geographic locations where care may be delivered, the naming and coding conventions must be adhered to within the specifications, if the recipient of the patient's record is to clearly, quickly, and unequivocally identify the laboratory data recorded therein. The use of this convention places certain constraints on system implementors and laboratory professionals to maintain the convention, during the growth of laboratory science, in an upward compatible way. That is, new entries to the lexicon must always be added in such a way that does not invalidate prior entries. New knowledge may require extensions and additions but not deletions or modifications that will change the meaning of prior entries.

4.1.3 The development of a classification and coding system for valid procedure names is being conducted by several mandating agencies. The principles for linking the naming conventions to these schemes is given in Appendix X1, which is nonnormative at this time.

4.2 *Structure of the Terms for Procedures and Analytes*:

4.2.1 *Terms for Procedure Names*—Each procedure shall have a full formal name based on the nomenclature principles of IUB/IUPAC **(16, 19, 20)** for chemical and biological substances, or on the International Non-Proprietary Names convention for drug products as mandated by USAN **(14)** and a structured formal representation of that name. Each procedure should also have a common name or short name. The first part of the formal structured name is the primary analyte measured. The name may have a species modifier separated from the analyte name by a "." character. This analyte name may be modified by additional subattributes separated from the primary analyte by one or more "," characters (ASCII 44). These subattributes are challenge, adjustment, and person, in that order. This name and additional modifiers shall be sequential: first, a procedure name, or one that invokes several independent procedure names, shall be termed a "battery," and this shall mean that the names included may be single procedure names or the names of either panels/profiles or other batteries. An example is an admitting battery. There may be just a list of single procedures that is given the category of panel/profile, but that circumstance is not required for the use of the term "battery." Battery/profile/panel names shall begin with a "*" (ASCII 42) character to uniquely visually identify the procedure name aggregate. As a procedure name, the battery name does not itself contain the constituent procedures of the battery. This list of names is an associated attribute of the name in the same way that the various codes are associated attributes (see 4.3).

4.2.1.1 The challenge subattribute has the following form:< time delay> POST <challenge> <route>. The value sets for these sub-subattributes are given in Table 1. The adjustment subattribute is a phrase such as "Adj to pH 7.4," again set off by commas. The person subattribute has the following values: CONT = control, PAT = patient, DON = donor, BPU = blood product unit, and FET = fetus. For example, GLUCOSE, 30M POST 100 GM GLUCOSE PO:MCNC: PT:SER:QN:.

4.2.1.2 The formal procedure name shall also have levels of specificity beyond just the basic procedure name. In the following order, the additional major attributes of the procedure name shall uniquely identify the property observed or measured, timing of the specimen, source of the specimen, degree of precision (qualitative, semiquantitative, quantitative), and methodology or instrumentation, or both, for that procedure, when required. The property observed or measured

(14, 15) shall be the second attribute, separated from the procedure/analyte name by a ":" (ASCII 58). The timing of the specimen is the third attribute, which shall also always appear. The source of the specimen shall always appear as the fourth attribute of the name separated from the second by a ":" character. The degree of precision shall be the fifth attribute separated from the fourth by a ":" and followed by a ":" and shall also always appear. These higher levels of specificity shall be organized as hierarchical extensions of the basic term in that order of priority. The method attribute is optional but, if absent, shall contain NS (meaning "not specified") and shall be the sixth attribute of the name. The list of attribute abbreviations used in components of the formal structured form of the name are shown in Table 1. The source attribute may be broken into five subclasses, which are combined independently to form the full source attribute. The five subclasses which appear in that order are: specimen type, specimen origin, collection method, collection device, and pathologic condition. The first (specimen type) subattribute always appears. These subattributes of the source apply in the priority order noted above and are separated by the delimiting ASCII character 44 ",". Trailing delimiters shall be dropped if all of the remaining fields are empty; subattributes need not appear. Examples of the construction of procedure names are given in Appendix X1.

TABLE 1 Test Analyte Term Attribute and Subattribute Abbreviations[A]

	A. Specimen Type
SER	serum (SZ)
UR	urine (UZ)
PLAS	plasma (PZ)
STL	stool (LZ)
AMN	amniotic fluid (FA)
CSF	cerebral spinal fluid (CZ)
BLD	whole blood, NOS (BZ)
BLDA	blood arterial (BA)
BLDV	venous blood (BV)
BLDC	blood capillary (BC)
CBLD	cord blood (BC)
UMB	umbilical blood (BU)
MBLD	menstrual blood (BM)
SEM	seminal fluid (GF)
SPRM	spermatozoa (GM)
SMN	semen (GN)
HAIR	hair (TH)
BONE	bone (BN)
MEC	meconium (FU)
MILK	breast milk (FM)
VOM	vomitus (VZ)
NAIL	nail (TN)
SNV	synovial fluid (FS)
RBC	erythrocytes (RZ)
FIB	fibroblasts (TB)
BIFL	fluid bile
FLU	body fluid, unsp (FZ)
COL	colostrum (FT)
WBC	leucocytes (WZ)
MAC	macrophages (WM)
MAR	marrow (BM)
EOS	eosinophils (WE)
BPH	basophils (WB)
PMN	polymorphonuclear neutrophils (WN)
LYM	lymphocytes (WL)
THRB	thrombocyte (platelet) (WT)
TEAR	tears (FR)
BRTH	breath (BT)
PUS	pus (UP)
CALC	calculus (TC)
SAL	saliva (AL)
SKN	skin (TK)
SPT	sputum, NOS (TS)
GAST	gastric fluid (FG)
LIQ	liquid (LQ)
BDY	whole body (BY)
USUB	unknown substance
WAT	water (ZW)
PRC	packed red cells (RP)
TISS	tissue, NOS (TI)
DUFL	duodenal fluid (FD)
PRT	fluid, peritoneal (ascites) (FC)
PRL	fluid pleural (FB)
WNDE	wound exudate (FE)
WNDD	wound drainage (FI)
SWT	sweat (SW)
CVM	cervical mucous (GM)
CVX	cervix (GR)
EARW	earwax
CNJT	conjunctiva
ORH	other
PAFL	pancreatic fluid
SWAB	swab
TUBE	tube, NOS
TUNK	type unknown
TUNS	type unspecified
ELCT	electrode (ZE)
BPU	blood product unit
DIAF	dialysis fluid
EHG	exhaled gas
IHG	inhaled gas
ENDC	endocardium
ENDM	endometrium
MLK	milk
PPP	platelet-poor plasma
PRP	platelet-rich plasma
URNS	urine sediment
UMED	unknown medicine
PAT	patient
XXX	specified at test time
	B. Specimen Origin
PLC	placenta (PC)
ABS	abscess
BRO	bronchus
EAR	ear
ENDM	endometrium
GEN	genital, NOS
SKM	skeletal muscle
PER	peritoneum
NOS	nose
THRT	throat
GENL	genital, lochia
GENV	genital, vagina
CDM	cardiac muscle
TLGI	tissue, large intestine
TSMI	tissue, small intestine
	C. Collection Method
ASP	aspirate
URC	urine clean catch
SPTC	sputum coughed
SPTT	sputum tracheal aspirate
CGH	coughed
WASH	washing
BRSH	brushing
TCNT	thoracentesis
PCNT	paracentesis
CUR	tissue, curettage
RT	route of medication
	D. Collection Device
CTP	catheter tip

TABLE 1 *Continued*

URT	urine catheter
DRN	drain
LN	line
LNA	line arterial
LNV	line venous
WICK	wick
BBL	blood bag
FLT	filter
IT	intubation tube
CNL	cannula
PLB	plasma bag
TAP	gummed tape
	E. Pathologic Condition
CYST	cyst
FIST	fistula
LAM	lamella
BURN	burn tissue
WND	wound, NOS
WNDA	wound abscess
ULC	tissue, ulcer
	F. Specimen Timing
PT	point specimen
TIMED	individually timed specimen
12H	12 h specimen
24H	24 h specimen
	G. Property
Code	Property Name
	Subclass: Measurement
ABS	absorbance
ASB	amount of substance
AREA	area
CACT	catalytic activity
CCNC	catalytic concentration
CCNT	catalytic content
CFR	catalytic fraction
CRTO	catalytic ratio
DEN	density
LEN	length
MASS	mass
MCNC	mass concentration
MCRTO	mass concentration ratio
NUM	number
NCNC	number concentration
NCNT	number content
NFR	number fraction
NRTO	number ratio
OSMOLL	osmolality
PRES	pressure (partial)
RDEN	relative density
SCNC	substance concentration
SCRTO	substance concentration ratio
SCNT	substance content
SCNRAT	substance content rate
SFR	substance fraction
SRAT	substance rate
SRTO	substance ratio
TEMP	temperature
TIME	time
TITR	times diluted (titer)
UCNCI	unit concentration, international
URTOI	unit ratio, international
VEL	velocity
VISC	viscosity
VOL	volume
VFR	volume fraction
VRAT	volume rate
	Subclass: Property
SUSC	antibiotic sensitivity
APP	appearance
ASPECT	aspect
CLAS	class
COLOR	color
CONS	consistency

TABLE 1 *Continued*

ELAS	elasticity
LIQ	liquifaction
MORPH	morphology
MOTIL	motility
SHAPE	shape
SMELL	smell
SUSC	susceptability
TASTE	taste
TYPE	type
ACNC	unit concentration, arbitrary
VCNT	volume content
ACACT	arbitrary catalytic activity
ACNC	arbitrary concentration
ACNT	arbitrary content
AENTSUB	arbitrary entic amount of substance
AENTNUM	arbitrary entic number
ANCNC	arbitrary entic number concentration
ARAT	arbitrary rate
AVRAT Areic	volume rate
AMRAT Areic	mass rate
ASRAT Areic	substance rate
CCRTO	catalytic activity ratio
CRAT	catalytic activity rate
CTP	concentration time product
CONS	consistency
DIA	diameter
ENTSUB	entic amount of substance
ENTCNT	entic content
ENTLEN	entic length
ENTNUM	entic number
ENTVOL	entic volume
FREQ	frequency
HALFLF	halflife
HT	height
LINC	length increment
MFR	mass fraction
MINC	mass increment
MRAT	mass rate
MSRTO	mass: amount of substance ratio
MOLL	molality
PH	pH
PPRES	partial pressure
RCRLTM	reciprocal relative time
RLSRTO	relative substance ratio
RLTM	relative time
SATFR	saturation fraction
SCNCIN	substance concentration increment
TEMPDF	temperature difference
THRACNC	threshold arbitrary concentration
THRMCNC	threshold mass concentration
THRSCNC	threshold substance concentration
TIMDF	time difference
VELRTO	velocity ratio
CLRN	clearness
COAG	coagulation
CMPO	composition
DMAT	distribution of material
PRID	presence/identity
SIZE	size
SMELL	smell
	H. Level of Precision to Scale
QN (N)	
SQ (S)	
QL (L)	
	I. Method
Extension Abbreviation	Full Name
AB AGG, BACT-AHG	agglutination, bacterial, antihuman globulin
AC AGGL, C-PART	agglutination, coated particle
AL AGGL, LATEX	agglutination, latex
AG AGGL	agglutination, NOS
AH AGGL, SHEEP	agglutination, sheep cells
BS BACT-SENS	bacterial-sensitivity
BA BIOASSAY	bioassay
BL LCTX	bioassay, lymphocytotoxicity

TABLE 1 *Continued*

CU CALC	calculation
CS CALORIM, DSC	calorimetry, differential scanning
CT CALORIM, DTA	calorimetry, differential thermal analysis
CM CALORIM	calorimetry, NOS
CD CHEMILUM	chemiluminescence, NOS
CA CHROMAT, ADSORP	chromatography, adsorption
CY CHROMAT, AFFINITY	chromatography, affinity
GC CHROMAT, GAS	chromatography, gas-liquid
CC CHROMAT, GAS, CAPIL	chromatography, gas-liquid, capillary
GM GC/MS	chromatography, gas-liquid, mass-spectrometry
CG CHROMAT, GEL FILTR	chromatography, liquid, gel-permeation
HP CHROMAT, HI PRESS LIQ	chromatography, liquid, high-performance
CH CHROMAT, ION EXCH	chromatography, liquid, ion-exchange
CI CHROMAT, LIQ	chromatography, liquid, NOS
CO CHROMAT, OTL	chromatography, liquid, open-tubular
CP CHROMAT, PARTITION	chromatography, liquid, partition
CR CHROMAT, REV PHASE	chromatography, liquid, reverse-phase
CN CHROMAT	chromatography, NOS
PC CHROMAT, PAPER	chromatography, paper
TL CHROMAT, THIN LAYER	chromatography, thin-layer
TH CHROMAT, HPTLC	chromatography, thin-layer, high-performance
CL COLORIMETRY	colorimetry
CB COMP PROT BNDG	competitive-protein-binding
CF COMP-FIX	complement-fixation
VC VISUAL COUNT	count, visual
VM VISUAL, MICROSC	count, visual, microscope
FA CULT, AEROBIC	culture, aerobic
FN CULT, ANAEROBIC	culture, anaerobic
FM CULT, ENRICH	culture, enrichment
FO CULT, ORG-SPEC	culture, organism-specific
FC FLOW CYTOMETRY	cytometry, flow
DP PCR	DNA-hybridization, PCR
DH DNA-HYBRID	DNA-hybridization, RFLP
DI DOUB-ISOTOPE	double isotope
DF DRY FILM	dry-film
IM INSTR, AMPER	electrochemical, amperometric
EV INSTR, ASV	electrochemical, anodic-stripping-voltammetry
EC INSTR, CSV	electrochemical, cathodic-stripping-voltammetry
IU INSTR, CONDUCT	electrochemical, conductimetric
IC INSTR, COULOMETR	electrochemical, coulometric
IE INSTR, ISE	electrochemical, ion-selective-electrode
OX OXIMETRY	electrochemical, ion-selective-electrode, oxygen
EH INSTR, PH-STAT	electrochemical, pH-stat
IP INSTR, POLAROGR	electrochemical, polarography
IN INSTR, POTENTIOM	electrochemical, potentiometric
HR ELECTROPH, DISC	electrophoresis, acrylamide, discontinuous
EP ELECTROPH, ACRYL	electrophoresis, acrylamide-gel
EG ELECTROPH, AGAR	electrophoresis, agarose gel
EL ELECTROPH, CAP	electrophoresis, capillary
EA ELECTROPH, CELLULAC	electrophoresis, cellulose acetate
EO ELECTROPH, COUNTER IMM	electrophoresis, counter-immuno
CE ELECTROPH, CROSS	electrophoresis, cross-immuno
EM ELECTROPH, IMMUNO	electrophoresis, immuno
EX ELECTROPH, IMM-FIX	electrophoresis, immunofixation
EF ELECTROPH, ISO ELC FOC	electrophoresis, isoelectric-focusing
ET ELECTROPH, ISOTACHY	electrophoresis, isotachyphoresis
EN ELECTROPH	electrophoresis, NOS
ER ELECTROPH, PAPER	electrophoresis, paper
EB ELECTROPH, STARCH GR	electrophoresis, starch-block
ES ELECTROPH, STARCH GEL	electrophoresis, starch-gel
FT FLOCCULATION	flocculation, NOS
FQ FLUORESCENCE QUENCH	fluorescence-quench
FL FLUOR	fluorimetry
HA HEMAGGL	hemagglutination
HS HEMAGGL, PASS	hemagglutination, passive
HI HEMAGGL-INHIB	hemagglutination-inhibition
IY IMAG-ANAL	image-analysis
IL IMM-ASS, CHEMIL	immunoassay, chemiluminescence

TABLE 1 *Continued*

EI EIA	immunoassay, enzymatic, NOS
IF IMM-ASS, FLUOR-TR	immunoassay, fluorescence, time-resolved
EJ IMM-ASS, HM, ENZ	immunoassay, homogeneous, enzymatic
FP IMM-ASS, HM, FLUOR-P	immunoassay, homogeneous, fluorescence-polarization
IH IMM-ASS, HM, FLUOR	immunoassay, homogeneous, fluorescence
ID IMMUN DIFF	immunoassay, immunodiffusion, double
RD RADIAL DIFF	immunoassay, immunodiffusion, radial
IB IMM-INH	immunoassay, inhibition
II IMM-ASS, INH	immunoassay, inhomogeneous, enzymatic, NOS
IJ IMM-ASS, INH, DOUB-AB	immunoassay, inhomogeneous, double-antibody
IO IMM-ASS, INH, ENZ, SA	immunoassay, inhomogeneous, enzymatic, single AB (COMP)
IQ IMM-ASS, INH, ENZ, DA	immunoassay, inhomogeneous, enzymatic, double AB (NON-C)
FI IMM-ASS, INH, FLUOR-P	immunoassay, inhomogeneous, fluorescence-polarization
IG IMM-ASS, INH, FLUOR	immunoassay, inhomogeneous, fluorescence
IK IMM-ASS, INH, SING-AB	immunoassay, inhomogeneous, single-antibody
IA IMM-ASS	immunoassay, NOS
PP IMM-ASS, PRECIPTN	immunoassay, precipitin
RB RIA-DA	immunoassay, radioisotopic, double-antibody
RI RIA	immunoassay, radioisotopic, NOS
RS RIA-SA	immunoassay, radioisotopic, single-antibody
IS IMM-ASS, SPF	immunoassay, solid-phase-fluoro
IT IMM-ASS, TURBID	immunoassay, turbidometric
MA MANOMETRY	manometry
MD MICROSC, DARK FLD	microscopy, dark-field
ME MICROSC, ELECTR	microscopy, electron
MF MICROSC, FLUOR	microscopy, fluorescence
MN MICROSC	microscopy, NOS
MH MICROSC, PHASE	microscopy, phase-contrast
MP MICROSC, POLARIZ	microscopy, polarizing
ML MICROSC, SEM	microscopy, scanning-electron
MT MICROSC, STEREO	microscopy, stereo
MC MICROSC, VIS	microscopy, visible
NE NEPHELOMETRY	nephelometry
NU NEUT	neutralization
FD FREEZ PT DEP	osmometry, freezing-point-depression
OS OSMOMETRY	osmometry, NOS
VP VAPOR PRESS	osmometry, vapor-pressure-depression
PB LIQ-SCINT	particle-counting, beta-liquid-scintillation
PL CHEMILUMIN	particle-counting, chemiluminescent
PG GAMMA-SCINT	particle-counting, gamma-scintillation
PM GEIGER-MUELLER	particle-counting, Geiger-Mueller
PN PART-COUNT	particle-counting, NOS
PH PHOTOGR	photography
PE PPT	precipitation/flocculation
PY PYNCNOMETRY	pyncnometry
RT RADAUTO	radioautography
RA R-RECEPT-ASSAY	radioreceptor
RL REFLECTOMETRY	reflectometry
RF REFRACTOMETRY	refractometry
SG SPEC-GRAV	specific-gravity
SF SPECTROFLUOR	spectrofluorimetry
SE ESR-SPEC	spectrometry, electron-spin-resonance
SM EMISS-SPEC, FLAME	spectrometry, emission, flame
SI ICP-SPEC	spectrometry, emission, inductively-coupled plasma
SP EMISS-SPEC, SPARK	spectrometry, emission, spark
FR FREE RAD ASSAY TECH	spectrometry, free-radical
MS MASS-SPEC	spectrometry, mass
SN NMR-SPEC	spectrometry, nuclear-magnetic-resonance
AS AA-SPEC	spectrophotometry, atomic-absorption
IR IR-SPEC	spectrophotometry, infrared
US UV-SPEC	spectrophotometry, ultraviolet
VS V-SPEC	spectrophotometry, visible
ST SPOT TEST	spot-test
SA STAIN	stain, NOS
TS TEST STRIP	test-strip
TC TITRATION, COMPLEX	titrimetry, complexometric
TI TITRATION	titrimetry, NOS
TP TITRATION, POTENIOM	titrimetry, potentiometric
TT TITRATION, SPECT	titrimetry, spectrophotometric
TB TURBIDOMETRY	turbimetry

TABLE 1 *Continued*

UA UTRACENTRIF, ANAL	ultracentrifugation, analytical
UD UTRACENTRIF, DEN-GRAD	ultracentrifugation, density-gradient
UC ULTRACENTRIF	ultracentrifugation, NOS
VE VISCOMETRY	viscometry
VI VISUAL	visual
XD XRAY-DIFF	X ray-diffraction
J. Analyte Subattributes	
Time delay:	
BS	baseline
PEAK	peak concentration
TR	trough concentration
1–10, 15, 25M	minutes
1–8H	hours
1–7D	days
1–4W	weeks
1–3MO	months
Challenge:	
CLFST	calorie fast
EXCZ	exercise
FLDFST	fluid fast
<substance name>	name of challenge substance
Route:	
AP	apply externally
B	buccal
DT	dental
GTT	gastronomy tube
GU	GU irrigant
IH	inhalation
IA	intra-arterial
IC	intracardiac
ID	intradermal
IM	intramuscular
IN	intranasal
IO	intraocular
IP	intraperitoneal
IS	intrasynovial
IT	intrathecal
IV	intravenous
NS	nasal
NG	nasogastric
OP	opthalmic
PO	oral
OT	otic
PR	rectal
SC	subcutaneous
SL	sublingual
TP	topical
TD	transdermal
TL	translingual
UR	urethral
VG	vaginal

[A] Parentheses indicate extensions that may be used in mnemonics and codes (see Appendix X1).

4.2.1.3 *Multiple Analyte Procedures*—Certain single procedure names, such as the chromatographic analysis of amino acids or the electrophoresis of serum proteins, also produce multiple measurements of analytes. These procedure names are not batteries and shall not be identified as such. The analyte names resulting from each single analyte procedure, however, shall be identified by the procedure name. Multiple analyte procedures shall identify the analytes, as in 4.2.2, by prepending the analyte identifier to the procedure name in the procedure name segment noted below, separated by the " | " (ASCII 124) delimiter character. The full current list of formal procedure names appears in Appendix X2; it is nonnormative.

4.2.2 *Terms for Analyte Names*—Each procedure/analyte name, and any appropriate extensions noted in 4.2.1 for a single analyte procedure name, shall stand for that analyte. The full analyte name resulting from a battery shall be represented by optionally appending to the specific analyte name either the battery or the procedure name, separated from it by a " | " (ASCII 124) character. In a procedure that involves measurement of multiple analytes, each specific analyte name may be modified by adding a subterm to it that is separated from the prior subterm by means of a delimiter character (specified to be the ASCII 44, "," character). Each specific analyte name shall conform to the rules of the IUB/IUPAC for naming chemical or biologic substances **(12)** or to USAN Council Rules for naming medicinal drug species **(21)**. The approved list of extension abbreviations for analytes and permitted methods or instrumentation appears in Table 1, while the full catalog of procedure name terms appears in Appendix X2. An example of the formation of analyte names in a single procedure name result is "Albumin | Albumin:MCNC:PT:Ser:QN:V-Spec" and "CO2,Tot | CO2,Tot:SCNC:PT:Ser:QN:"; a battery name result is "Sodium | *Electrolytes:Ser:QN:"; an example of a multiple analyte procedure analyte name is "Phenylalanine | Amino acids:SCNC:PT:Ser:QN:Chrom." The segment of an analyte name following the " | " is optional in condensed reports, but the full name is recommended for clarity.

4.3 *Attributes Associated with a Procedure or Analyte Name*:

4.3.1 The elected standard name of a clinical laboratory procedure has other attributes associated with that name that are identified and maintained in tables such as "procedure directories." These attributes allow the recognition of synonyms or local variants of the name as well as mnemonics or short versions of the name for reporting and a variety of codes and coding systems. There are also lists of constituent procedure names for batteries/panels/profiles and of resulting analytes for multiple analyte procedures. The structure of these associated attributes is given in Fig. 1. They are nonnormative but are presented here to illustrate how such familiar attributes are tied to the elected standard form of the name.

4.3.2 The semantic address code is described in Guide E 1284 and Ref **(18)** and is used to classify the procedure name term by one or more classification pathways that relate to different perspectives in the use of the term. Procedures are generally placed mentally into a single category, but some are placed into more than one. Table 2 gives the categories identified for clinical laboratory procedures. They are used to group procedures into more homogeneous sub-lists for practical use. A name, an abbreviation, and a single letter code is given for each of these categories, which may be used in coding system construction. Each represents a pathway to the same terminal node containing the term.

5. Table of Test and Analyte Names and Codes

5.1 Appendix X2 lists the names and common codes of all

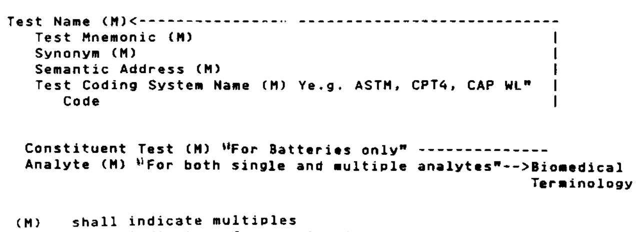

FIG. 1 Attributes Associated with Test Names

TABLE 2 Analyte Classes

Name	Class Abbreviation	Class Single Letter Code
Chemistry/Toxicology		
Amino acid/nitrogen metabolism	AA	A
Nucleic acid/nucleotide metabolism	NA	N
Carbohydrate metabolism	CH	C
Oxidative metabolism and tissue gasses	OX	O
Electrolytes/homeostasis/acid-base	EL	L
Endocrine	EN	D
Enzymes	EZ	Z
Excretory/transport function	EX	E
Ligand receptors	RE	R
Lipid metabolites	LI	I
Membrane/cell adhesion	ME	M
Mineral metabolism	MI	B
Trace metals	TR	T
Vitamins/cofactors	VI	V
Therapeutic drugs	TD	H
Toxic agents	TX	X
Physiologic indices	PH	Y
Plasma proteins	PP	P
Functional tests	FU	F
Hematology		
Cell counts	CT	G
RBC/heme metabolism	RB	J
Leucocytes	WB	K
Thrombocytes	PT	Q
Thrombosis and hemostasis	TH	S
Blood and plasma volume	VL	U
Complement	CO	W
Bone marrow	BM	1
Spleen function	SL	2
Special function	SF	3
Immunology/Serology		
Tumor markers	TU	4
Antibodies	AB	5
Antigens	AG	6
Microbiology		
Microbiologic	MC	7
Virologic	VR	8
Parasitologic	PA	9
Cytologic/Anatomic		
Cytologic/cells	CY	c
Urine cells	UA	u
Anatomic pathology	AN	a
Imaging/Radiologic/Nuclear Medicine		
Image: NMR	IN	h
Image: PET	IP	p
Image: radiologic	IR	r
Image: ultrasound	IE	s
Image: visual	IV	v
Other		
Electromyograms	EY	m

laboratory tests cataloged as of the release date of this specification. It is not part of the specification and is for information purposes only. The up-to-date list is maintained by the University of Indiana and can be obtained from that organization.

NOTE 1—This compilation is part of a National Library of Medicine/Agency for Health Care Policy and Research contract to the Regenstrief Institute, University of Indiana, Purdue University, Indianapolis announced September 1994 and is part of an evolving collection. The excerpt in Appendix X2 is part of the contribution from the University of Washington to that compilation and, because of the evolutionary character of the overall collection, is illustrative rather than exhaustive.

6. Keywords

6.1 analyte codes; analyte names; laboratory procedure names; procedure codes

APPENDIXES

(Nonmandatory Information)

X1. EXAMPLES

X1.1 *Test Name Mnemonics*—Each test name may also have been assigned one or more unique 1−7 letter mnemonics that, in addition to assigned codes, may also stand for that name in reports or other documents. A mnemonic, like a code, is an associated attribute to the name. Moreover, the mnemonic, which is usually used locally for brief references to this specific procedure name, specimen source, and level of precision, is separate from it. The final character in a mnemonic may be a single letter representation of the specimen type or null. The first characters represent analyte, method, and precision properties and may include the analyte class characters given in Table 2. See X1.3 for examples of mnemonics.

X1.2 *Structure of the Codes for Procedures and Analytes*—Codes are sequences of characters that are information dense and are designated to uniquely represent defined terms; they are surrogates for terms and identify those terms. As noted in Guide E 1284, codes may or may not be interpretable directly. This characteristic differentiates them from mnemonics, which are designed to be maximally dense but visually understandable. Codes are most often designed around a systematic that does allow information to be gained from visually reading the code, but codes need not be designed for easy visual understanding and may be randomly assigned characters. There already exist several coding schemes for clinical laboratory procedure names that can be crossreferenced to the terms described in 4.2 and that are listed in Appendix X2. As noted above, these include CPT-4, CAP Workload, SNOMED, ICP, CMIT **(9–12, 22)** , EUCLIDES **(17)** , and IFCC/IUPAC **(20)**. All are numeric to some degree, although SNOMED uses the initial letter “P” in the code and has hierarchical implications in the succeeding digits. Other coding schemes also use a hierarchical structure. The other codes are fully numeric and contain a variable degree of systematics in the digits of the code, primarily by assigning ranges of digits to various functional areas in a variety of ways. Some use decimal digit places as extensions for classification purposes.

X1.2.1 *Test Codes*— This example will use the following procedure coding convention: the basic code shall consist of twelve alphanumeric characters, in several subsegments that will identify either single analyte tests or the name of a battery or multiple result procedure. The portion of the name to be coded includes the analyte, specimen source, precision, and, optionally, method attribute. The property attribute (second) and specimen timing attribute (third) are incorporated into the analyte segment of the code as they are clearly associated. Their combination is always unique. Consistent with Ref **(13)**, the first character of the universal code for laboratory procedures contains an“ L.” The second character is the primary analyte class character shown in Table 2. The third and fourth characters contain the unique sequential test/analyte identifier within the analyte class. The fifth and sixth characters identify the specimen source according to Table 1. The seventh character is the precision. The remaining characters identify the basic technique or protocol **(15)**, method, equipment, and reagent, consistent with Table 1 and the EUCLIDES axes **(17)**. The method/instrumentation segment (Table 1) of the code shall use upper case alphabetic characters. As noted in Fig. 1, the logical data structure for a laboratory procedure term record includes an unspecified number of coding systems and code values denoted by registered coding systems, including those noted in 6.6.3 of Specification E 1238. A EUCLIDES single axis identifier can also be constructed using the single axis codes listed in Ref **(17)** concatenated sequentially as analyte, specimen, and basic method, which could be included in this list.

X1.2.2 *Analyte Codes*— The code extension used to identify analytes shall precede the basic procedure name code, be alphanumeric, and be separated from the subsequent procedure identifier by a “.” character (ASCII 46) as a delimiter; this“ .” is compatible with the convention used in Specification E 1238. This complete code shall be considered, for sorting purposes, as a string of ASCII characters. Since batteries consist of a limited number of constituent procedures, although each constituent procedure of the battery may contain hierarchies of batteries and procedures and each individual procedure may contain multiple analytes, the total number of reportable analytes for either a battery or a multiple analyte procedure is unlikely to be larger than approximately 50 for any single procedure or battery identifier. Therefore, the analyte code extension is presently defined to be five characters to be consistent with the EUCLIDES convention, and this should identify any number of analytes that may be associated with a procedure identifier. This collating sequence will ensure that, in addition to grouping analytes together, generic and specified procedure codes may also be grouped together in the sorting process by sorting on any substring following the “.” delimiter. Using the code string specified in this specification, the analytes from a specific procedure may also be grouped within that procedure, if desired. Likewise, if desired, the procedure identifier segment may be ignored during sorting in order to group all common analyte data together; it must, however, be present in the code to identify specific analyte results that relate to particular clinical orders containing unique procedure identifiers. The analyte names to which the code extension applies must be considered to be elected terms included in a biomedical terminology defined by Guide E 1284 and EUCLIDES **(17)**. The coding scheme described in this specification can exist in parallel with those already existing systems noted in X1.2, and it has the prime purpose of uniquely identifying, as a name surrogate, individual procedures and their resulting analytes and of grouping these terms for clinical use.

X1.2.2.1 *Example 1*—Phenylalanine determined from chromatographic analysis of plasma might be coded as “03980.LA12PZNCH000” Procedure MNEMONIC:

AAPHEPL," assuming that 03980 is the EUCLIDES code for phenylalanine and "LA12PZN" is the code segment for quantitative plasma amino acid analysis (the first" A" is the amino acid class of analytes from Table 2, while the next two characters are for amino acids followed by specimen and precision codes from Table 1) and assuming that the "CH" method extension is taken from Table 1.

X1.2.2.2 *Example 2*—The code for serum sodium measured as part of an electrolyte panel on whole blood by ion-specific electrodes might appear as "04720.LL23BZNIE Battery MNEMONIC: PHELS; Test MNEMONIC: NAIP, as opposed to NAAP using atomic absorption spectrometry, for example."

NOTE X1.1—In these coding examples, the specific character strings for names, mnemonics, and codes are examples only; the agreed upon consensus values have yet to be established.

X1.3 *Further Examples of Names, Mnemonics, and Codes:*

X1.3.1 *Names*:

CALCIUM,IONIZED:SCNC:PT:SER:QN:INSTR,POTENT
OCCULT BLD::PT:STL:QUAL:VISUAL
AMINO ACIDS:MCNC:PT:PLAS:QN:CHROMAT,ION EXCH
BILIRUBIN,DIRECT:MCNC:PT:SER:QN:V-SPEC

Source Attributes:
SODIUM:SCNC:PT:SER:QN:
SODIUM:SCNC:PT:BLD,,LNA:QN:

X1.3.2 *Test Mnemonics*:

UAM URINANALYSIS::PT:UR:QN:MICROSCOP,VIS

X1.3.3 *Test Codes*:

LG29BZNFC	COMPLETE BLOOD COUNT::PT:BLD:QN:
LF01UZNMC	URINANALYSIS::PT:UR:QN:MICROSC,VIS

X2. TABLE OF TEST AND ANALYTE NAMES AND CODES

X2.1 Fig. X2.1 shows the table of test and analyte names and codes.

	ANALYTE CLASS: CHEM:AMINO ACID/NITROGEN METABOLITE
1684-0	3-METHOXY-4-HYDROXYPHENYLGLYCOL:MCNC:PT:UR:QN:
1692-3	5-HYDROXYINDOLEACETATE:MCNC:PT:CSF:QN:
1693-1	5-HYDROXYINDOLEACETATE:MCNC:PT:SER:QN:
1695-6	5-HYDROXYINDOLEACETIC ACID:MCNC:PT:UR:QN:
1789-7	ALPHA AMINO-N-BUTYRATE:MCNC:PT:SER:QN:
1792-1	ALPHA AMINOADIPATE:MCNC:PT:PLAS:QN:
1793-9	ALPHA AMINOADIPATE:MCNC:PT:UR:QN:
1817-6	ALPHA KETOGLUTARATE:MCNC:PT:SER:QN:
1839-0	AMMONIA:SCNC:PT:BLD:QN:
1840-8	AMMONIA:SCNC:PT:CSF:QN:
1841-6	AMMONIA:SCNC:PT:SER:QN:
1842-4	AMMONIA:SCNC:PT:UR:QN:
1896-0	ARGINOSUCCINATE:MCNC:PT:SER:QN:
1936-4	BETA AMINOISOBUTYRATE:MCNC:PT:UR:QN:
2046-1	CARNITINE:MCNC:PT:SER:QN:
2055-2	CATECHOLAMINES.TOTAL:MCNC:PT:BLD:QN:
2058-6	CATECHOLAMINES.TOTAL:MRAT:24H:UR:QN:
2148-5	CREATINE:MCNC:PT:SER:QN:
2149-3	CREATINE:MCNC:PT:UR:QN:
2150-1	CREATINE:MRAT:24H:UR:QN:
2159-2	CREATININE:MCNC:PT:AMN:QN:
2161-8	CREATININE:MCNC:PT:UR:QN:
2162-6	CREATININE:MRAT:24H:UR:QN:
2163-4	CREATININE RENAL CLEARANCE:VRAT:PT:12H:UR:QN:
2164-2	CREATININE RENAL CLEARANCE:VRAT:24H:UR:QN:
2175-8	CYSTINE:MCNC:PT:BLD:SQ:
2178-2	CYSTINE:MCNC:PT:UR:QN:
2179-0	CYSTINE:MRAT:24H:UR:QN:
2198-0	DELTA-AMINOLEVULINATE:MCNC:PT:PLAS:QN:
2199-8	DELTA-AMINOLEVULINATE:MCNC:PT:SER:QN:
2218-6	DOPAMINE:MRAT:24H:UR:QN:
2219-4	DOPAMINE BETA-MONOOXYGENASE:CCNC:PT:SER:QN:
2318-4	GAMMA AMINOBUTYRATE:MCNC:PT:PLAS:QN:
2319-2	GAMMA AMINOBUTYRATE:MCNC:PT:UR:QN:
2370-5	GLUTAMINE:MCNC:PT:CSF:QN:
2378-8	GLUTATHIONE REDUCTASE:CCNC:PT:SER:QN:
2383-8	GLUTATHIONE.TOTAL:MCNC:PT:SER:QN:
2415-8	HISTAMINE:MCNC:PT:BLD:QN:
2416-6	HISTAMINE:MCNC:PT:SER:QN:
2417-4	HISTAMINE:MCNC:PT:UR:QN:
2418-2	HISTIDINE:MCNC:PT:BLD:SQ:
2419-0	HISTIDINE:MCNC:PT:BLD:QN:
2420-8	HISTIDINE:MCNC:PT:SER:QN:
2422-4	HISTIDINE:MCNC:PT:UR:SQ:
2424-0	HISTIDINE:MRAT:TIMED:UR:QN:
2432-3	HOMOGENTISATE:MCNC:PT:UR:QL:
2433-1	HOMOGENTISATE:MCNC:PT:UR:QN:
2435-6	HOMOVANILLIC ACID:MCNC:PT:SER:QN:
2446-3	HYDROXYPROLINE:MCNC:PT:PLAS:QN:
2447-1	HYDROXYPROLINE EXCRETION:MRAT:PT:UR:QN:
2450-5	HYDROXYPROLINE.FREE:MCNC:PT:UR:QN:
2451-3	HYDROXYPROLINE.TOT:MCNC:PT:UR:QN:
2475-2	INDICAN:MCNC:PT:UR:QN:
2476-0	INDOLAMINE:MCNC:PT:SER:QN:
2477-8	INDOLE:MCNC:PT:SER:QN:
2515-5	KYNURENATE:MCNC:PT:UR:QN:
2606-2	MELANIN:MCNC:PT:UR:SQ:
2659-1	NITROGEN.TOTAL:MRAT:24H:STL:QN:

FIG. X2.1 Table of Test and Analyte Names and Codes