Properties and Units in the Clinical Laboratory Sciences. Part XVIII. Properties and Units in Clinical Molecular Biology (IUPAC Technical Report)

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Basic research in biology and medicine and innovations in laboratory methodology have greatly increased the range of properties available to medical practitioners to help them in diagnosis, treatment, and prevention of disease. The increase in variety of properties examined is now such that the individual physician has insight into or understanding of only a limited number of properties offered to him from the various clinical laboratory specialties.

In the laboratory, local terms (jargon) may be well understood among colleagues, but they are not appropriate for communication with the outside world. Likewise, a laboratory and its local community of users, such as hospital or community physicians, may use a “local dialect” of the language of clinical laboratory sciences that is well understood by all concerned, but when the communication possibilities are wider, even transnational, risks of serious misunderstanding arise. It is, therefore, essential to promote clear, unambiguous, meaningful, and fully informative communication.

Coherence of statements made within and between medical specialties and uniformity in structure of presentation is an objective to be actively pursued. This will facilitate the transfer of information across sociolinguistic barriers. The purpose of this document is to apply the IUPAC–IFCC (International Federation of Clinical Chemistry and Laboratory Medicine) recommended syntax structures for request and report, providing formats and names of properties observed in the domain of medical molecular biology, and to facilitate unequivocal written or electronic communication between health care professionals.

For identification of genes, the “approved names” given in the HUGO [Human Genome Nomenclature Database <www.gene.ucl.ac.uk/nomenclature>], in the form of symbols, have been used except for symbols of mitochondrial genes. (Variations in mitochondrial genes and chromosomes are not dealt with in this technical report.) The use of symbols rather than names is in contrast to previous reports for other medical domains where names have been applied systematically. This is because the names of genes are often very extensive and of limited value to the nonspecialist. Admittedly, the symbols also are of limited direct informative value, but they are gaining increasing general application and hence meaningful connotation.

One of the main points of this paper is the recognition that any report of a variation of a nucleic acid sequence should include the identity of the sequence referred to. For this purpose, reference is given to “Nomenclature for the description of sequence variation” elaborated by Prof. Stylianos Antonarakis and Dr. Johan T. den Dunnen [7 March 2001; <http://archive.uwcm.ac.uk/uwcm/mg/docs//mut_nom.html>].

The list of properties shown in this document comprises the list of symbols for components as given in the HUGO as of 24 September 2003. This list, which is an integral part of this technical report, can be accessed at <www.iupac.org/publications/pac/2004/7609/7609x1799.html>.

Since the list of properties contains more than 16 000 entries, it is not suitable for printing on paper. The online version contains links to databases that allow the reader to obtain information about the selected genes. Frequently updated versions of the listing can be obtained at <http://dior.imt.liu.se/cnpu>, the official C-NPU site, also from <www.labinfo.dk/English/download_uk.asp> the listing can be downloaded as an Excel file or HTML file.

www.iupac.org/publications/pac/2004/7609/7609x1799.html

Compilation of k_0 and Related Data for NAA in the Form of Electronic Database (IUPAC Technical Report)

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This report describes the principles underlying a comprehensive electronic database that contains data essential for calculation of analytical results from neutron-activation analysis (NAA). The database is available through IUPAC. The method used is a comparator method called the k_0 method, where k_0 is a dimensionless factor that is experimentally measured with high