A technician preparing to run microbial genomes on the Roche 454 sequencing platform at the Advanced Technology Research Facility (ATRF), Frederick National Laboratory for Cancer Research, National Cancer Institute.

Advanced methods for assessment of risks of false decisions in analytical chemistry (testing) laboratories—basic concepts and associated terms

There are three main documents by ISO and IEC for risk management: ISO 31000:2018 "Risk management—Guidelines", IEC 31010:2019 "Risk management—Risk assessment techniques", and ISO 31073:2022 "Risk management—Vocabulary". These documents provide a common approach (based on the risk assessment) for the management of any type of risk and are not industry- or sector- specific. They can be customized to any organization, and are applicable to any activity, including decision-making. However, the authors of the documents (ISO/TC 262) emphasize that in practice the concepts and terminology need to be adapted to the field or discipline of application, to avoid misinterpretation, misrepresentation, or misuse.

During the past decade several IUPAC projects have been dedicated to risk assessment in an analytical laboratory:

1. A position paper of the IUPAC project team (project 2014-027-1-500) on the risks of false decisions originated by human errors (2013), https://doi.org/10.1007/s00769-012-0934-y, has reached about 16000 readers (ResearchGate, 25 July 2024). The IUPAC/CITAC Guide on assessment of the risks caused by human errors (2016), https://doi.org/10.1515/ci-2016-0520, was implemented recently even in such unexpected fields as medicine (2023), https://doi.org/10.21037/jlpm-23-7, and military equipment testing (2024), https://doi.org/10.37701/dndivsovt.20.2024.15.

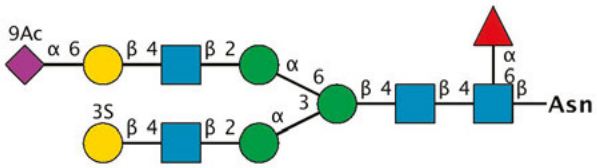
2. The topic of risks of false decisions in conformity assessment due to measurement uncertainty was initially addressed in the IUPAC/CITAC Guide on assessment of the risks of out-of-specification test results of a single component content (2012), https://doi.org/10.1351/PAC-REP-11-10-04. It was further developed in the IUPAC/CITAC Guide for multicomponent objects, when test results may be correlated (2020), https://doi.org/10.1515/pac-2019-0906; and in the IUPAC/CITAC Guide for multicomponent objects under a mass balance constraint (2023), https://doi.org/10.1515/pac-2022-0801.

In the current project a harmonization of basic concepts and associated terms applied in advanced methods for assessment of the risks is offered. This harmonization will contribute to quality assurance wherever measurements and tests are made in analytical chemistry (testing) laboratories, in industry, trade, environmental analysis, or another field. The project will also contribute to the IUPAC Mission "providing a common language for chemistry".

For more information and comment, contact Task Group Chair Ilya Kuselman <ilya.kuselman@gmail.com> | https://iupac.org/project/2024-012-2-500/

IUPAC HELM Glycans Extension

HELM (Hierarchical Editing Language for Macromolecules) is a machine-readable linear notation for representing biopolymers, including peptides,



Neu5Ac(a6 -U "9Ac")Gal(b4)GlcNAc(b2)Man(a6)
[Gal(b4 -U "3S")GlcNAc(b2)Man(a3)]Man(b4)
GlcNAc(b4)[Fuc(a6)]GlcNAc(b)Asn(-CHAR)

Example of structure generated using DrawGlycan-SNFG shown with the IUPAC string used to generate it; from <http://www.virtualglycome.org/DrawGlycan/>

antibodies, other oligonucleotides and therapeutic proteins. HELM has been developed and supported by the Pistoia Alliance since 2013 through an active user community and member organizations. As of 2021, HELM is a mature digital motif with demonstrated efficacy and applicability in informatics and structure representation. The HELM notation is now jointly stewarded by IUPAC and the Pistoia Alliance.

The scope of HELM monomers presently includes only amino acids and nucleic acids. However, carbohydrates are branching biopolymers and are difficult to represent using a linear notation. Thus, rules are needed to ensure that they are represented uniquely.

The introduction of monosaccharides as monomers to HELM notation would provide a standardized representation of glycoconjugates, including glycoproteins and glycolipids in addition to glycosides. Such molecules can be used to represent substrates for glycosyltransferase enzymes, for example, as can be seen in the Gene Ontology, Reactome, and other pathway databases.

The initial set of monomers identified by the Pistoia Alliance is based on the well-established convention for the pictorial display of structures: Symbol Nomenclature For Glycans (SNFG), recommended for submission to major journal and other publications. The SNFG system was originally released in 2015, building on earlier symbolic notation in coordination with the IUPAC-IUBMB Joint Commission on Biochemical Nomenclature (JCBN) and other community resources [1]. The approach to represent glycans in HELM outlined by the Pistoia Alliance describes the use of SNFG for nomenclature and display.

The project will work through several objectives, including:

- Update HELM notation to include appropriate methodology to properly represent glycan moieties
- Establish a set of commonly used glycan monomers (e.g., found in public databases)
- Establish a validation data set to ensure appropriate implementation of the IUPAC HELM glycan extensions
- Represent glycan-containing structures using the newly established HELM glycan extensions
- Work with the stakeholder communities to adopt HELM glycan extensions

Addition of glycan monomers by HELM would provide critical support for machine readable large molecule representation and extend the utility of the HELM line notation. Furthermore, this effort would be able to better inform the IUPAC InChI large molecule initiative.

References

1. Symbol Nomenclature for Graphical Representation of Glycans, *Glycobiology* 25: 1323-1324, 2015. https://doi.org/10.1093/glycob/cwv091

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Molecular Machine Terminology

Artificial molecular machines (AMMs) are molecular-scale "devices" that, despite disagreements on how best to define them, dissipate energy and convert inputs to outputs in general, often in service of some prescribed function. The field of research on AMMs is reaching unprecedented levels of complexity with regard to the diversity of AMMs reported in the literature. As yet, there appears to be no consensus on the exact meaning of "molecular machine" and many associated words such as "molecular motor" and "molecular pump."

The objective of the project is therefore to identify, review, and summarize the terminology that is used in the literature to discuss artificial molecular machines, including terms such as artificial molecular machine, molecular switch, molecular motor, molecular pump, and numerous others (pulleys, gates, transporters, walkers, muscles, drills, *etc*). There may be a need to consolidate and rectify terminological discrepancies in the literature associated with these frequently-used words because it leads to frequent confusion and unproductive debate among researchers in the field (see, for example, https://cen.acs.org/materials/Chemists-debate-fuel-molecular-machines/101/i5 and https://doi.org/10.1038/s41565-022-01247-5).