Resource Summary Report

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HUPO Proteomics Standards Initiative

RRID:SCR_003158
Type: Tool

Proper Citation

HUPO Proteomics Standards Initiative (RRID:SCR_003158)

Resource Information

URL: http://www.psidev.info/

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Description: Initiative to define community standards for data representation in proteomics to facilitate data comparison, exchange and verification. The main organizational unit is the work group, with a Gel Electrophoresis (GEL) work group, a Mass Spectrometry (MS) work group, a Molecular Interactions (MI) work group, a Protein Modifications (MOD) work group, a Proteomics Informatics (PI) work group, and a Sample Processing (SP) work group. The Gel Electrophoresis (GEL) work group aims to develop reporting requirements that supplement the Minimum Information About a Proteomics Experiment (MIAPE) parent document, describing the minimum information that should be reported about gel-based experimental techniques used in proteomics. The group will also develop data formats for capturing MIAPE-compliant data about gel electrophoresis and informatics performed on gel images. The Mass Spectrometry Standards Working Group defines community data formats and controlled vocabulary terms facilitating data exchange and archiving in the field of proteomics mass spectrometry. A past achievement is the mzData standard, which captures mass spectrometry output data. mzData's aim is to unite the large number of current formats (pkl's, dta's, mgf's, ...) into a single format. mzData has been released but is now deprecated in favor of mzML. The Molecular Interactions workgroup is concentrating on improving the annotation and representation of molecular interaction data wherever it is published, be this in journal articles, authors web-sites or public domain databases; and improving the accessibility of molecular interaction data to the user community. By using a common standard data can be downloaded from multiple sources and easily combined using a single parser. The protein modification workgroup focuses on developing a consensus nomenclature and provide an ontology reconciling in a hierarchical representation the complementary descriptions of residue modifications. The protein modification ontology (PSI-MOD) is available in OBO format or in OBO.xml. A spreadsheet containing the mapping of the descriptive labels used in various databases and search engines, the consensus list of proposed short name for protein modifications established by collaborative effort of mass spectrometry community, and the proposed rules and recommendations for this nomenclature are available. These

short names are included in the ontology as synonyms of the corresponding terms. The Proteomics Informatics Standards Group (PSI-PI) goals are to provide a set of minimal reporting requirements which augment the MIAPE reporting guidelines with respect to analysis of data derived from proteomics experiments; to provide vendor-neutral and standard formats for representing results of analyzing and processing experimental data; to foster adoption of the format by highlighting efforts made by vendors and individuals that utilize the format in their products. The remit of the Sample Processing Working Group is to produce reporting guidelines, data exchange formats and controlled vocabulary covering all separation techniques not considered to be "classical" one- or two-dimensional gel electrophoresis (cf. the Gel WG home page), along with other kinds of sample handling and processing (for example, "tagging" proteins or peptides, splitting, combining and storing samples). Where possible we seek to develop our products in collaboration with all proteomics stakeholders and, where relevant, developers from other standards communities, most notably metabolomics. * Minimum reporting requirements: The evolving Minimum Information About a Proteomics Experiment (MIAPE) documents offer guidelines on how to adequately report a proteomics experiment. It is expected that these documents will be published, and that the requirements within will be enforced by journals, compliant repositories and funders (cf. MIAME). * XML formats for data exchange: Derived from the FuGE general object model, the formats developed by this workgroup are designed to function both as standalone files and as part of a "parent" FuGE-ML document. These formats will facilitate data exchange between researchers, and submission to repositories or journals. * Controlled vocabularies (CVs) and ontology: Lists of clearly defined terms are crucial for the construction of unambiguously worded data files. In addition to providing supporting CVs for the individual data capture formats as part of the integrated PSI CV, the Sample Processing WG will contribute terms to the Functional Genomics Ontology (FuGO).

Abbreviations: HUPO PSI

Synonyms: The HUPO Proteomics Standards Initiative

Resource Type: controlled vocabulary, data or information resource, knowledge environment, meeting resource, narrative resource, ontology, standard specification, training resource

Keywords: proteomics, work group, gel electrophoresis, mass spectrometry, molecular interaction, protein modification, proteomics informatics, sample processing, controlled vocabulary, miape, transcriptome, metabolome, proteome, metadata, mass spectrometry informatics, community standards, annotation system, protein-protein interaction, protein, data format, annotation, minimal reporting requirement, nomenclature, reporting guideline, data exchange format, ontology development, rdf development, FASEB list

Availability: Free, Freely available

Resource Name: HUPO Proteomics Standards Initiative

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Alternate IDs: nif-0000-00568, OMICS_01781

Record Creation Time: 20220129T080217+0000

Record Last Update: 20260912T195552+0000

Ratings and Alerts

No rating or validation information has been found for HUPO Proteomics Standards Initiative.

No alerts have been found for HUPO Proteomics Standards Initiative.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 46 mentions in open access literature.

Listed below are recent publications. The full list is available at PRECISE-TBI .

Orchard SE, et al. (2025) What Have Data Standards Ever Done for Us? Molecular & cellular proteomics : MCP, 24(6), 100933.

Garrard C, et al. (2025) Fostering and sustaining collaborative innovation: Insights from ELIXIR Europe's life science Communities. F1000Research, 14.

Kopczynski D, et al. (2024) The lipidomics reporting checklist a framework for transparency of lipidomic experiments and repurposing resource data. Journal of lipid research, 65(9), 100621.

Deutsch EW, et al. (2023) The ProteomeXchange consortium at 10 years: 2023 update. Nucleic acids research, 51(D1), D1539.

Deutsch EW, et al. (2023) Proteomics Standards Initiative at Twenty Years: Current Activities and Future Work. Journal of proteome research, 22(2), 287.

García-Rojas NS, et al. (2022) Build, Share and Remix: 3D Printing for Speeding Up the Innovation Cycles in Ambient Ionisation Mass Spectrometry (AIMS). Metabolites, 12(2).

Kwon YW, et al. (2021) Application of Proteomics in Cancer: Recent Trends and Approaches for Biomarkers Discovery. Frontiers in medicine, 8, 747333.

Berman HM, et al. (2019) Federating Structural Models and Data: Outcomes from A Workshop on Archiving Integrative Structures. Structure (London, England : 1993), 27(12), 1745.

Iacobucci C, et al. (2019) First Community-Wide, Comparative Cross-Linking Mass Spectrometry Study. Analytical chemistry, 91(11), 6953.

Rojas-Macias MA, et al. (2019) Towards a standardized bioinformatics infrastructure for N- and O-glycomics. Nature communications, 10(1), 3275.

Menschaert G, et al. (2018) The proBAM and proBed standard formats: enabling a seamless integration of genomics and proteomics data. Genome biology, 19(1), 12.

van Rijswijk M, et al. (2017) The future of metabolomics in ELIXIR. F1000Research, 6.

Vizcaíno JA, et al. (2017) The mzIdentML Data Standard Version 1.2, Supporting Advances in Proteome Informatics. Molecular & cellular proteomics : MCP, 16(7), 1275.

Vaudel M, et al. (2016) Exploring the potential of public proteomics data. Proteomics, 16(2), 214.

Cvijovic M, et al. (2016) Strategies for structuring interdisciplinary education in Systems Biology: an European perspective. NPJ systems biology and applications, 2, 16011.

Ortea I, et al. (2016) Review on proteomics for food authentication. Journal of proteomics, 147, 212.

Deutsch EW, et al. (2015) Development of data representation standards by the human proteome organization proteomics standards initiative. Journal of the American Medical Informatics Association : JAMIA, 22(3), 495.

Jorrín Novo JV, et al. (2015) Scientific standards and MIAPEs in plant proteomics research and publications. Frontiers in plant science, 6, 473.

Lapatas V, et al. (2015) Data integration in biological research: an overview. Journal of biological research (Thessalonike, Greece), 22(1), 9.

Hur J, et al. (2015) Development and application of an interaction network ontology for literature mining of vaccine-associated gene-gene interactions. Journal of biomedical semantics, 6, 2.