



UvA-DARE (Digital Academic Repository)

The EuPA Standardization Initiative

Canals, F. ; Elortza, F. ; Paradelo, A. ; Corthals, G.; Camenzuli, M.; Muñoz, A. ; Schiltz , O. ; Gonzalez de Peredo, A.; Sickman, A.; Borchers , C. ; Corrales, F.J.

DOI

[10.1016/j.euprot.2016.03.007](https://doi.org/10.1016/j.euprot.2016.03.007)

Publication date

2016

Document Version

Final published version

Published in

EuPA Open Proteomics

License

CC BY-NC-ND

[Link to publication](#)

Citation for published version (APA):

Canals, F., Elortza, F., Paradelo, A., Corthals, G., Camenzuli, M., Muñoz, A., Schiltz , O., Gonzalez de Peredo, A., Sickman, A., Borchers , C., & Corrales, F. J. (2016). The EuPA Standardization Initiative. *EuPA Open Proteomics*, 11, 31-32.
<https://doi.org/10.1016/j.euprot.2016.03.007>

General rights

It is not permitted to download or to forward/distribute the text or part of it without the consent of the author(s) and/or copyright holder(s), other than for strictly personal, individual use, unless the work is under an open content license (like Creative Commons).

Disclaimer/Complaints regulations

If you believe that digital publication of certain material infringes any of your rights or (privacy) interests, please let the Library know, stating your reasons. In case of a legitimate complaint, the Library will make the material inaccessible and/or remove it from the website. Please Ask the Library: <https://uba.uva.nl/en/contact>, or a letter to: Library of the University of Amsterdam, Secretariat, Singel 425, 1012 WP Amsterdam, The Netherlands. You will be contacted as soon as possible.

UvA-DARE is a service provided by the library of the University of Amsterdam (<https://dare.uva.nl>)

Available online at www.sciencedirect.com

journal homepage: <http://www.elsevier.com/locate/euprot>

The EuPA Standardization Initiative

Mass spectrometry has experienced huge advances in the last decade increasing the coverage, accuracy and capacity of protein/peptide measurements in complex biological samples. The ability to massively identify and quantify proteins places proteomics as one of the most valuable analytical resources to such measurements, leading to a better understanding of sophisticated cellular processes at the functional level. To increase accuracy and enable inter- and intra-laboratory experimental comparisons, reliability, robustness and reproducibility must be possible and embedded in the technology. To this end, it is critical to define quality control procedures and standardized protocols for the whole proteomics workflow, from sample collection and preparation to data collection and computational analysis and finally data exchange.

The EuPA Standardization initiative (Figure 1) is of utmost importance since standardization of proteomics workflows will promote the consolidation of a common space, integrating proteomic strengths across Europe, based on the easy exchange of information generated according to normalized protocols based on standardized data formats. Besides improving the efficiency within the proteomics environment, standardization is crucial to increase the impact and relevance of proteomics in other scientific disciplines. It is important to note that the translation of analytical results into relevant biological knowledge and practical applications is often hampered by the lack of standardized protocols that emerge, therefore, as an urgent need.

The overall aim of this initiative is the organization of multi-laboratory studies to:

- Evaluate protocols, protocol variants, workflows and data processing procedures to assess reproducibility, robustness and technical limits. Optimization of existing protocols. Interaction with potential industrial partners; the collaboration with SIGMA has been remarkable in previous standardization initiatives and their participation has been already agreed. (Other efforts to strengthen our initiatives are welcome).
- Deliver protocols of common proteomics procedures under standardized conditions. Definition of standard operation procedures (SOPs), limit of detection (LOD), limit of quantification (LOQ). Ensure open access and communication with existing and ongoing HUPO-PSI. Easy exchange of technology and results across laboratories.
- Facilitate the implementation of standardized protocols in current and emergent facilities with limited experience and scope. Methods for self-performance evaluation.

Milestones

- Annual strategic discussions to define the study.
- Reference sample preparation.
- Call for participants via EuPA network.
- Sample distribution.
- Analysis of the results.
- Meeting for presentation and discussion of the results.
- Creation of a repository of standardized protocols publicly accessible from the EuPA web page.

Deliverables

- Study proposal. Description, guidelines and recommendations. Publication on the EuPA web page [www.eupa.org].
- Intermediate report and congress submission.
- Publication of the results and main conclusions.
- Standardized protocol posted on the EuPA web page.

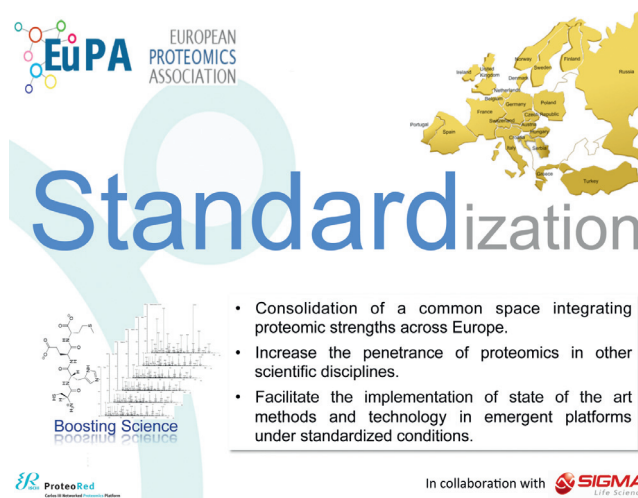


Figure 1. Launching of the EuPA Standardization Initiative.

Communicated by:

- F. Canals [fcanals@vhio.net] (Vall d'Hebron Oncology Institute. ProteoRed, Spain)
 F. Elortza [felortza@cicbiogune.es] (CIC bioGUNE. ProteoRed, Spain)
 A. Paradela [Alberto.Paradela@cnb.csic.es] (National Biotechnology Center. ProteoRed, Spain)
 G. Corthals [G.L.Corthals@uva.nl] & Michelle Camenzuli

[M.Camenzuli@uva.nl] (Van't Hoff Institute for Molecular Sciences, University of Amsterdam, The Netherlands)
A. Muñoz [Amalia.MUNOZ-PINEIRO@ec.europa.eu] (Institute for Reference Materials and References (JRC-IRMM), Belgium)
O. Schiltz [Odile.Schiltz@ipbs.fr] & Anne Gonzalez de Peredo [Anne.Gonzalez-de-Peredo@ipbs.fr] (IPBS, CNRS, ProFI, France)

A Sickman [albert.sickmann@isas.de] & C. Borchers [Christoph@proteincentre.com], Leibniz Institut für Analytische Wissenschaften, Germany
Fernando J. Corrales [fjcorrales@unav.es] (CIMA, University of Navarra, ProteoRed, Spain)