DESCRIPTION

*Journal of Proteomics* is aimed at protein scientists and analytical chemists in the field of proteomics, biomarker discovery, protein analytics, plant proteomics, microbial and animal proteomics, human studies, tissue imaging by mass spectrometry, non-conventional and non-model organism proteomics, and protein bioinformatics. The journal welcomes papers in new and upcoming areas such as metabolomics, genomics, systems biology, toxicogenomics, pharmacoproteomics.

*Journal of Proteomics* unifies both fundamental scientists and clinicians, and includes translational research. Suggestions for reviews, webinars and thematic issues are welcome. All manuscripts are strictly peer reviewed and conform the highest ethical standards. *Journal of Proteomics* is an official journal of the European Proteomics Association (EuPA) and also publishes official EuPA reports and participates in the International Proteomics Tutorial Programme with HUPO and other partners.

**Benefits to authors**

We also provide many author benefits, such as free PDFs, a liberal copyright policy, special discounts on Elsevier publications and much more. Please click here for more information on our author services.

Please see our Guide for Authors for information on article submission. If you require any further information or help, please visit our Support Center.

Should you have an idea for a thematic issue, please complete the thematic issue proposal form and send it to the Editorial Office (Ms. Carly Middendorp, c.middendorp@elsevier.com). The guidelines to prepare a proposal for the journal can be found here.

AUDIENCE

Academic and industrial researchers in the fields of proteomics, analytical chemistry, biochemistry, biology, medicine, bioinformatics, protein science, biotechnology and applied physics.

IMPACT FACTOR

2017: 3.722 © Clarivate Analytics Journal Citation Reports 2018
ABSTRACTING AND INDEXING

BIOSIS
Chemical Abstracts
Current Contents/Life Sciences
EMBASE
EMBiology
Elsevier BIOBASE
INSPEC Information Services
MEDLINE®
Pascal et Francis (INST-CNRS)
Reference Update
Science Citation Index
Scopus

EDITORIAL BOARD

Editor in Chief:
Juan Calvete, Instituto de Biomedicina de Valencia, C.S.I.C., Valencia, Spain

Executive Editors:
Animal Proteomics:
Ingrid Miller, University of Veterinary Medicine Vienna, Vienna, Austria

Bioinformatics in Proteomics:
Christoph Borchers, University of Victoria, Victoria, British Columbia, Canada

Computational Mass Spectrometry:
Paulo Carvalho, Instituto de Biofísica Carlos Chagas Filho-UFRJ, Curitiba/PR, Brazil

Food Sciences and Nutrition:
Paola Roncada, Università degli Studi di Milano, Milan, Italy

Multomics, Membrane Proteins and Lipid-protein Assemblies
Andrej Shevchenko, Max Planck Institute of Molecular Cell Biology and Genetics (MPI-CBG), Dresden, Germany

Proteomics for Biotechnological Applications:
Gabriel Padrón, Centro de Ingeniería Genética y Biotecnología, La Habana, Cuba

Proteomics in Cell Biology:
Jean-Jacques Diaz, Centre Léon Bérard, Lyon, France
Alessandra Nita-Lazar, National Institutes of Health (NIH), Bethesda, Maryland, USA

Proteomics in Plant Systems:
Jesús Jorrín-Novo, Universidad de Cordoba, Córdoba, Spain

Proteomics in Protein Science:
Hisashi Hirano, Yokohama City University, Yokohama, Japan

Proteomics of Body Fluids and Proteomic Technologies:
Manfred Raida, National University of Singapore, Singapore, Singapore

Protein Mass Spectrometry:
Ole Norregaard Jensen, University of Southern Denmark, Odense, Denmark

Translational Proteomics:
Steve Pennington, University College Dublin, Belfield, Ireland

Associate Editor Tutorials
Andrea Scaloni, Napoli, Italy

Associate Editor Webinars
Andrea Scaloni, Napoli, Italy
Editorial Board:

Ganesh Agrawal, Sanepa, Indrayani, Kathmandu, Nepal
Christian Ahrens, Waedenswil, Switzerland
Günter Allmaier, Vienna, Austria
Francisco Amado, Aveiro, Portugal
Per Andrén, Uppsala, Sweden
Jean Armengaud, Bagnols-sur-Cèze, France
Ghulam Ashraf, Jeddah, Saudi Arabia
Angela Bachi, Milan, Italy
Amos Baircho, Geneva, Switzerland
Carlos Batthyány, Montevideo, Uruguay
Marc Baumann, Helsinki, Finland
Emoke Bendixen, Tjele, Denmark
Ruth Birner-Grünberger, Graz, Austria
Hans-Peter Braun, Hannover, Germany
Odile Burlet-Schiltz, Toulouse, France
Giovanni Candiano, Genova, Italy
Sebastien Carpentier, Leuven, Belgium
Daniela Cecconi, Verona, Italy
Niranjan Chakraborty, New Delhi, India
Julia Chamot-Rooke, Paris cedex 15, France
Sixue Chen, Gainesville, Florida, USA
Maxey Chung, Singapore, Singapore
Thomas Conrad, Pittsburgh, Pennsylvania, USA
Fernando Corrales, Pamplona, Spain
Garry Corthals, Turku, Finland
Gilberto Domont, Cidade Universitária, Rio de Janeiro, Brazil
Jorg Durner, Neuherberg, Germany
Felix Elortza, Derio, Spain
Christine Finnie, Kogens Lyngby, Denmark
Jay Fox, Charlottesville, Virginia, USA
Ángel Garcia, Santiago de Compostela, Spain
Concha Gil, Madrid, Spain
Bjorn Gjertsen, Bergen, Norway
Luis Javier González, La Habana, Cuba
Harsha Gowda, Bangalore, India
Paul Hensbergen, Leiden, Netherlands
Connie R. Jimenez, Amsterdam, Netherlands
Setsuko Komatsu, Tsukuba, Ibaraki, Japan
Simone Lemeer, Utrecht, Netherlands
Niels Lion, Epalinges, Switzerland
Andrea Sabine Llera, Buenos Aires, Argentina
Bruno Lomonte, San José, Costa Rica
Martina Marchetti-Deschmann, Vienna, Austria
Katrin Marcus, Bochum, Germany
Liam A. McDonnell, Leiden, Netherlands
Helmut Meyer, Bochum, Germany
Harvey Millar, Crawley, Western Australia, Australia
Gloria Molero, Madrid, Spain
Silvia Moreno, Buenos Aires, Argentina
Javier Muñoz, Madrid, Spain
Jarliath E Nally, Ames, Iowa, USA
George Panayotou, Varkiza, Greece
Deborah Penque, Lisbon, Portugal
Ángel Pérez Díz, Vigo, Spain
Yasset Perez-Riverol, Hinxton, Cambridge, UK
Daniel Petras, La Jolla, California, USA
Paola Picotti, Zürich, Switzerland
Andrew Pitt, Birmingham, England, UK
Randeep Rakwal, Tsukuba, Ibaraki, Japan
Xavier Robin, Genève, Switzerland
Manuel Rodriguez-Ortega, Madrid, Spain
Jean-Charles Sanchez, Geneva, Switzerland
Manuel Sánchez del Pino, Burjassot (Valencia), Spain
Marek Sebela, Olomouc, Czech Republic
Miguel Angel Sentandreu, Paterna (Valencia), Spain
Yogeshwer Shukla, Lucknow, India
Hanno Steen, Boston, Massachusetts, USA
Yohsuke Taira, Nagasaki, Japan
Takeshi Tomonaga, Ibaraki, Osaka, Japan
George Tsangaris, Athens, Greece
Marius Ueffing, Tübingen, Germany
Henning Urlaub, Göttingen, Germany
Luis Valledor, Vienna, Austria
Juan Antonio Vizcaíno, Hinxton, Cambridge, UK
Antonia Vlahou, Athens, Greece
Stefanie Wienkoop, Vienna, Austria
Li-Rong Yu, Jefferson, Arkansas, USA
Bo-xiong Zhong, Hangzhou, China
Lello Zolla, Viterbo, Italy
GUIDE FOR AUTHORS

Journal of Proteomics is an official journal of the European Proteomics Association (EuPA) and is aimed at both European and international protein scientists and analytical chemists in the field of proteomics, biomarker discovery, protein analytics, plant proteomics, microbial and animal proteomics, human studies, tissue imaging by mass spectrometry, non-conventional and non-model organism proteomics, and protein bioinformatics. The journal welcomes papers in new and upcoming areas such as metabolomics, genomics, systems biology, toxicogenomics, pharmacoproteomics. Journal of Proteomics unifies both fundamental scientists and clinicians, and includes translational research. Suggestions for reviews, webinars and thematic issues are welcome. All manuscripts are strictly peer reviewed and conform the highest ethical standards. Journal of Proteomics also publishes official EuPA reports and participates in the International Proteomics Tutorial Programme with HUPO and other partners.

Types of paper
The following types of paper are published:

Original Articles: Original articles are the normal medium of publication. Although there is no fixed length, articles should be as concise as possible, while providing sufficient information for the work to be repeated and for the claims of the authors to be judged by the readers. Authors are encouraged to use proteomics data in the context of interdisciplinary projects to elaborate appropriate biological hypotheses, and use these hypotheses to validate the proteomics data through hypothesis-driven experiments and/or elaborate on future research to check the proposed biological model/mechanism.

Mandatory requirements for reporting of clinical biomarker studies:

1) A clinical biomarker is only relevant in specific contexts of use per disease, it must have a potential to improve the current state of the art (either being of added value, or based on its sole performance), and its application must be linked to a clear change in patient management. As such, the specific proposed context of use of the presented biomarker must be clearly provided and the expected practical consequence of the biomarker application should be discussed.
2) A biomarker can only be assessed in an independent (ideally blinded) test set, containing sufficient samples to demonstrate significant value and justify relevant claims regarding biomarker use. Assessment of performance in a discovery set is inappropriate.
3) This initial independent validation and performance assessment has to be performed in samples that reflect the typical clinical situation depending on the targeted context of use.
4) Authors submitting clinical biomarker studies should address the above points in the cover letter, so that the Editor can assess and evaluate if the submitted manuscript fulfils the requirements for publication in Journal of Proteomics.

Reviews: These are contributed by scientists who are leading specialists in their field of expertise, normally at the invitation of the Editors. Authors wishing to contribute a review paper are advised first to contact one of the responsible Editors (listed in the issues of Journal of Proteomics to avoid overlap with Reviews already commissioned.)

Technical reports: Technical reports should present brief descriptions of novel apparatus, a new experimental or computational method, test or procedure, or an improvement or noteworthy modification of an already existing technique or platform used in the proteomic workflow. Technical reports should show a realistic application of the methodology described. Theoretical papers dealing with mechanistic aspects of proteomic techniques will also be considered. A technical report should be a short (no more than two pages when published) description written in a continuous style with no more than two figures and one table.

Tutorials: The International Proteomics Tutorial Programme, initiated by the education committees of the Human Proteome Organisation (HUPO) and the European Proteomics Association (EuPA) is aimed at Masters/PhD level students who are starting out their research and who would benefit from a solid grounding in the techniques used in modern protein-based research. The tutorial program will cover core techniques and basics as an introduction to scientists new to the field. Authors are generally invited to contribute a Tutorial. For suggestions, prospective authors of high standing may contact the Journal's Tutorial editor Peter James.
News & Views: News & Views point out the author(s) vision of the character and importance of a new direction in proteome research. They are not intended to be accounts or analyses of an individual's personal research. Although News & Views will usually be invited, they can be submitted without invitation. Author(s) are encouraged to suggest experts in the field who can act as reviewers.

Letters to the Editor: Letters to the Editor are intended to stimulate discussion and debate in areas of general concern and controversy in proteomics, and generally reflect the personal opinions of the author(s). They should be written in a continuous style and should normally not exceed two printed pages and contain no more than one figure or table.

BEFORE YOU BEGIN

Ethics in publishing
Please see our information pages on Ethics in publishing and Ethical guidelines for journal publication.

Studies in humans and animals
If the work involves the use of human subjects, the author should ensure that the work described has been carried out in accordance with The Code of Ethics of the World Medical Association (Declaration of Helsinki) for experiments involving humans. The manuscript should be in line with the Recommendations for the Conduct, Reporting, Editing and Publication of Scholarly Work in Medical Journals and aim for the inclusion of representative human populations (sex, age and ethnicity) as per those recommendations. The terms sex and gender should be used correctly.

Authors should include a statement in the manuscript that informed consent was obtained for experimentation with human subjects. The privacy rights of human subjects must always be observed.

All animal experiments should comply with the ARRIVE guidelines and should be carried out in accordance with the U.K. Animals (Scientific Procedures) Act, 1986 and associated guidelines, EU Directive 2010/63/EU for animal experiments, or the National Institutes of Health guide for the care and use of Laboratory animals (NIH Publications No. 8023, revised 1978) and the authors should clearly indicate in the manuscript that such guidelines have been followed. The sex of animals must be indicated, and where appropriate, the influence (or association) of sex on the results of the study.

Conflict of interest
* Journal of Proteomics follows the ICMJE recommendations regarding conflict of interest disclosures (COI forms are mandatory for all co-authors of the manuscript). All authors are required to report the following information with each submission: (1) All third-party financial support for the work in the submitted manuscript. (2) All financial relationships with any entities that could be viewed as relevant to the general area of the submitted manuscript. (3) All sources of revenue with relevance to the submitted work who made payments to you, or to your institution on your behalf, in the 36 months prior to submission. (4) Any other interactions with the sponsor of outside of the submitted work should also be reported. (5) Any relevant patents or copyrights (planned, pending, or issued). (6) Any other relationships or affiliations that may be perceived by readers to have influenced, or give the appearance of potentially influencing, what you wrote in the submitted work. As a general guideline, it is usually better to disclose a relationship than not. This information will be acknowledged at publication in a Transparency Document link directly in the article. Additional information on the ICMJE recommendations can be found at: http://www.icmje.org/. The form for conflict of interest disclosure can be downloaded here: http://www.icmje.org/doi.pdf (if this link does not display properly in your browser, please right-click the link and select "Save Target As..." or "Save Link as..." from the pop-up menu).

Submission declaration and verification
Submission of an article implies that the work described has not been published previously (except in the form of an abstract, a published lecture or academic thesis, see 'Multiple, redundant or concurrent publication' for more information), that it is not under consideration for publication elsewhere, that its publication is approved by all authors and tacitly or explicitly by the responsible authorities where the work was carried out, and that, if accepted, it will not be published elsewhere in the same form, in English or in any other language, including electronically without the written consent of the copyright-holder. To verify originality, your article may be checked by the originality detection service Crossref Similarity Check.
Use of inclusive language
Inclusive language acknowledges diversity, conveys respect to all people, is sensitive to differences, and promotes equal opportunities. Articles should make no assumptions about the beliefs or commitments of any reader, should contain nothing which might imply that one individual is superior to another on the grounds of race, sex, culture or any other characteristic, and should use inclusive language throughout. Authors should ensure that writing is free from bias, for instance by using 'he or she', 'his/her' instead of 'he' or 'his', and by making use of job titles that are free of stereotyping (e.g. 'chairperson' instead of 'chairman' and 'flight attendant' instead of 'stewardess').

Author contributions
For transparency, we encourage authors to submit an author statement file outlining their individual contributions to the paper using the relevant CRediT roles: Conceptualization; Data curation; Formal analysis; Funding acquisition; Investigation; Methodology; Project administration; Resources; Software; Supervision; Validation; Visualization; Roles/Writing - original draft; Writing - review & editing. Authorship statements should be formatted with the names of authors first and CRediT role(s) following. More details and an example

Authorship
All authors should have made substantial contributions to all of the following: (1) the conception and design of the study, or acquisition of data, or analysis and interpretation of data, (2) drafting the article or revising it critically for important intellectual content, (3) final approval of the version to be submitted.

Changes to authorship
Authors are expected to consider carefully the list and order of authors before submitting their manuscript and provide the definitive list of authors at the time of the original submission. Any addition, deletion or rearrangement of author names in the authorship list should be made only before the manuscript has been accepted and only if approved by the journal Editor. To request such a change, the Editor must receive the following from the corresponding author: (a) the reason for the change in author list and (b) written confirmation (e-mail, letter) from all authors that they agree with the addition, removal or rearrangement. In the case of addition or removal of authors, this includes confirmation from the author being added or removed.

Copyright
Upon acceptance of an article, authors will be asked to complete a 'Journal Publishing Agreement' (see more information on this). An e-mail will be sent to the corresponding author confirming receipt of the manuscript together with a 'Journal Publishing Agreement' form or a link to the online version of this agreement.

Subscribers may reproduce tables of contents or prepare lists of articles including abstracts for internal circulation within their institutions. Permission of the Publisher is required for resale or distribution outside the institution and for all other derivative works, including compilations and translations. If excerpts from other copyrighted works are included, the author(s) must obtain written permission from the copyright owners and credit the source(s) in the article. Elsevier has preprinted forms for use by authors in these cases.

For gold open access articles: Upon acceptance of an article, authors will be asked to complete an 'Exclusive License Agreement' (more information). Permitted third party reuse of gold open access articles is determined by the author's choice of user license.

Author rights
As an author you (or your employer or institution) have certain rights to reuse your work. More information.

Elsevier supports responsible sharing
Find out how you can share your research published in Elsevier journals.
Role of the funding source
You are requested to identify who provided financial support for the conduct of the research and/or preparation of the article and to briefly describe the role of the sponsor(s), if any, in study design; in the collection, analysis and interpretation of data; in the writing of the report; and in the decision to submit the article for publication. If the funding source(s) had no such involvement then this should be stated.

Funding body agreements and policies
Elsevier has established a number of agreements with funding bodies which allow authors to comply with their funder's open access policies. Some funding bodies will reimburse the author for the gold open access publication fee. Details of existing agreements are available online.

Open access
This journal offers authors a choice in publishing their research:

Subscription
• Articles are made available to subscribers as well as developing countries and patient groups through our universal access programs.
• No open access publication fee payable by authors.
• The Author is entitled to post the accepted manuscript in their institution's repository and make this public after an embargo period (known as green Open Access). The published journal article cannot be shared publicly, for example on ResearchGate or Academia.edu, to ensure the sustainability of peer-reviewed research in journal publications. The embargo period for this journal can be found below.

Gold open access
• Articles are freely available to both subscribers and the wider public with permitted reuse.
• A gold open access publication fee is payable by authors or on their behalf, e.g. by their research funder or institution.

Regardless of how you choose to publish your article, the journal will apply the same peer review criteria and acceptance standards.

For gold open access articles, permitted third party (re)use is defined by the following Creative Commons user licenses:

Creative Commons Attribution (CC BY)
Lets others distribute and copy the article, create extracts, abstracts, and other revised versions, adaptations or derivative works of or from an article (such as a translation), include in a collective work (such as an anthology), text or data mine the article, even for commercial purposes, as long as they credit the author(s), do not represent the author as endorsing their adaptation of the article, and do not modify the article in such a way as to damage the author's honor or reputation.

Creative Commons Attribution-NonCommercial-NoDerivs (CC BY-NC-ND)
For non-commercial purposes, lets others distribute and copy the article, and to include in a collective work (such as an anthology), as long as they credit the author(s) and provided they do not alter or modify the article.

The gold open access publication fee for this journal is USD 3550, excluding taxes. Learn more about Elsevier's pricing policy: https://www.elsevier.com/openaccesspricing.

Green open access
Authors can share their research in a variety of different ways and Elsevier has a number of green open access options available. We recommend authors see our open access page for further information. Authors can also self-archive their manuscripts immediately and enable public access from their institution's repository after an embargo period. This is the version that has been accepted for publication and which typically includes author-incorporated changes suggested during submission, peer review and in editor-author communications. Embargo period: For subscription articles, an appropriate amount of time is needed for journals to deliver value to subscribing customers before an article becomes freely available to the public. This is the embargo period and it begins from the date the article is formally published online in its final and fully citable form. Find out more.

This journal has an embargo period of 12 months.
Language (usage and editing services)
Please write your text in good English (American or British usage is accepted, but not a mixture of these). Authors who feel their English language manuscript may require editing to eliminate possible grammatical or spelling errors and to conform to correct scientific English may wish to use the English Language Editing service available from Elsevier's WebShop.

Submission
Our online submission system guides you stepwise through the process of entering your article details and uploading your files. The system converts your article files to a single PDF file used in the peer-review process. Editable files (e.g., Word, LaTeX) are required to typeset your article for final publication. All correspondence, including notification of the Editor's decision and requests for revision, is sent by e-mail.

Referees
Please provide the names and addresses of 4 - 5 suitable potential reviewers. If there are compelling reasons for excluding some individuals as potential reviewers, these can be mentioned. However, choice of reviewers is at the Editors' discretion.

PREPARATION

Peer review
This journal operates a double blind review process. All contributions will be initially assessed by the editor for suitability for the journal. Papers deemed suitable are then typically sent to a minimum of two independent expert reviewers to assess the scientific quality of the paper. The Editor is responsible for the final decision regarding acceptance or rejection of articles. The Editor's decision is final. More information on types of peer review.

Double-blind review
This journal uses double-blind review, which means the identities of the authors are concealed from the reviewers, and vice versa. More information is available on our website. To facilitate this, please include the following separately:

Title page (with author details): This should include the title, authors' names, affiliations, acknowledgements and any Declaration of Interest statement, and a complete address for the corresponding author including an e-mail address.

Blinded manuscript (no author details): The main body of the paper (including the references, figures, tables and any acknowledgements) should not include any identifying information, such as the authors' names or affiliations.

Use of word processing software
It is important that the file be saved in the native format of the word processor used. The text should be in single-column format. Keep the layout of the text as simple as possible. Most formatting codes will be removed and replaced on processing the article. In particular, do not use the word processor's options to justify text or to hyphenate words. However, do use bold face, italics, subscripts, superscripts etc. When preparing tables, if you are using a table grid, use only one grid for each individual table and not a grid for each row. If no grid is used, use tabs, not spaces, to align columns. The electronic text should be prepared in a way very similar to that of conventional manuscripts (see also the Guide to Publishing with Elsevier). Note that source files of figures, tables and text graphics will be required whether or not you embed your figures in the text. See also the section on Electronic artwork.

To avoid unnecessary errors you are strongly advised to use the 'spell-check' and 'grammar-check' functions of your word processor.

To assist in the reviewing of your paper, please add line numbering to your manuscript file

Article Structure
Original articles are usually divided into the sections Introduction, Materials and methods, Results, Discussion and Conclusions:

Abstract
The Abstract should describe in a single paragraph the findings of the study, and should be comprehensible to readers before they have read the paper. Non-standard abbreviations and reference citations should be avoided.
Significance

Starting January 2013, manuscripts submitted to Journal of Proteomics must include a paragraph entitled "Significance" detailing the biological relevance of the reported research or technological innovation. Authors shortly but realistically state how the paper impacts its field of research (please consult Calvete JJ (2012) Updating JPROT's publication standards for large-scale proteomic studies: towards hypothesis-driven interpretation of predictive biological models. J Proteomics 76, 1-2).

Introduction
This is a short section in which the authors should state the reasons for performing the work, with brief reference to relevant previous work.

Material and methods
Provide sufficient detail to allow the work to be reproduced. Methods already published should be indicated by a reference: only relevant modifications should be described.

Results
Results should be clear and concise.

Discussions
This should explore the significance of the results of the work, not repeat them. A combined Results and Discussion section is often appropriate. Avoid extensive citations and discussion of published literature.

Conclusions
The main conclusions of the study may be presented in a short Conclusions section, which may stand alone or form a subsection of a Discussion or Results and Discussion section.

Technical reports, News & Views, Letters to the Editor: These types of papers are not divided into sections after the summary, except for the reference list. The first paragraph serves as an introduction; acknowledgments are added as a final paragraph before the reference list.

Tutorials are a combination of article and slides. Specific instructions are provided upon invitation. Authors are encouraged to submit Author Vitae at first submission. Please include in the manuscript a short (maximum 100 words) biography of each author, along with a passport-type photograph accompanying the other figures.

Experimental design data analysis for 2-D PAGE and MS-based experiments:
The experimental design must be provided and must include details of the number of biological and analytical replicates. Only one biological/analytical replicate will not be acceptable. In clinical studies, it is highly desirable that a power analysis predicting the appropriate sample size for subsequent statistical analysis of the data is carried out.

For expression analysis studies, summary statistics (mean, standard deviation) must be provided and results of statistical analysis must be shown. Reporting fold differences alone is not acceptable. For comparative proteomics multivariate analysis of the variance should be used (Please consult: Valledor, L., Jorrin, JV (2010). Back to the basics: Maximizing the information obtained by quantitative two dimensional gel electrophoresis analyses by an appropriate experimental design and statistical analyses. J. Proteomics 74, 1-18).

Proper terminology should be used. "Protein species" or "Gene product" are preferred terms when referring to "isoforms" and "allelic variants", respectively, (please consult Jungblut et al. The speciation of the proteome. Chemistry Central Journal 2008; 2: 16, and Schlüter et al. Finding one's way in proteomics: a protein species nomenclature. Chemistry Central Journal 2009; 3: 11). Terms, such as "differences in protein expression" and "induction/repression" should be avoided, since this terminology relates to gene regulation, and quantitative proteomics deals with the measure of differential abundances of spots (2DE) or peptide ions (LC-MS/MS).
Authors must report the following: methods of data normalization, transformation, missing value handling, the statistical tests used, the degrees of freedom and the statistical package or program used. Where biologically important differences in protein (gene) expression are reported, confirmatory data (e.g. from Western blot, RT-PCR analysis, etc.) are desirable. For biomarker discovery/validation studies, the sensitivity and specificity of the biomarker(s) should be provided wherever possible. It is desirable that receiver operator characteristic (ROC) curves and areas under the curves are given. The method(s) used to generate the mass spectrometry data must be described. The name and version of the program used for database searching, the values of critical search parameters (e.g. the mass over charge (m/z) and the charge (z) of the precursor ion, fragment mass tolerance, cleavage rules used, allowance for number of missed cleavages and modifications) and the name and version of the database(s) searched must be provided. For each protein identified, measures of certainty (e.g. pvalues) must be provided. For MS/MS, the number of peptides used to identify a protein must be given as well as the sequence and charge state of each peptide. If new software or bioinformatic tool are employed or described, these should be made available (free or shareware) at least for reviewing purposes.

Identification of proteins based solely on mass fingerprinting will be considered only if the sequence of the genome of the organism under study is known. For peptide mass fingerprinting, the number of peptides that match the sequence, the number of unmatched peaks, and the total percent of sequence coverage must be stated.

Identification of proteins from organisms with unknown genome sequence will be accepted only if MS/MS-derived peptide sequence data have been used for database searching or BLAST analysis. The score for the highest ranked hit to an homologous, orthologous, or paralogous protein should be indicated.

For experiments with large MS/MS data sets, estimates of the false positive rates are required (e.g. through searching randomized or reversed sequence databases). This information should be provided as supporting information. Where post-translational modifications are reported, the methods used to discover the modification must be described. The modification should be mapped to amino acid(s) by fragmentation analysis, but reported as ambiguous if mapping to a single amino acid is not possible. For isobaric modifications, evidence for assigning a specific modification must be provided and the spectra included as supporting information. Where protein sequence isoforms are reported, the peptide sequence that matches the unique amino acid sequence of a particular isoform must be provided. Fragmentation analysis of the appropriate peptides should be described.

Graphical abstract
A graphical abstract is mandatory for this journal. It should summarize the contents of the article in a concise, pictorial form designed to capture the attention of a wide readership online. Authors must provide images that clearly represent the work described in the article. Graphical abstracts should be submitted as a separate file in the online submission system. Image size: please provide an image with a minimum of 531 \times 1328 pixels (h \times w) or proportionally more. The image should be readable at a size of 5 \times 13 cm using a regular screen resolution of 96 dpi. Preferred file types: TIFF, EPS, PDF or MS Office files. You can view Example Graphical Abstracts on our information site. Authors can make use of Elsevier’s Illustration Services to ensure the best presentation of their images also in accordance with all technical requirements.

Highlights
Highlights are mandatory for this journal. They consist of a short collection of bullet points that convey the core findings of the article and should be submitted in a separate editable file in the online submission system. Please use ‘Highlights’ in the file name and include 3 to 5 bullet points (maximum 85 characters, including spaces, per bullet point). You can view example Highlights on our information site.

Formatting of funding sources
List funding sources in this standard way to facilitate compliance to funder’s requirements:

Funding: This work was supported by the National Institutes of Health [grant numbers xxxx, yyyy]; the Bill & Melinda Gates Foundation, Seattle, WA [grant number zzzz]; and the United States Institutes of Peace [grant number aaaa].
It is not necessary to include detailed descriptions on the program or type of grants and awards. When funding is from a block grant or other resources available to a university, college, or other research institution, submit the name of the institute or organization that provided the funding.

If no funding has been provided for the research, please include the following sentence:

This research did not receive any specific grant from funding agencies in the public, commercial, or not-for-profit sectors.

**Artwork**

**Electronic artwork**

**General points**

- Make sure you use uniform lettering and sizing of your original artwork.
- Save text in illustrations as "graphics" or enclose the font.
- Only use the following fonts in your illustrations: Arial, Courier, Times, Symbol.
- Number the illustrations according to their sequence in the text.
- Use a logical naming convention for your artwork files.
- Provide captions to illustrations separately.
- Produce images near to the desired size of the printed version.
- Submit each figure as a separate file.

A detailed guide on electronic artwork is available on our website: https://www.elsevier.com/artworkinstructions

**You are urged to visit this site; some excerpts from the detailed information are given here.**

**Formats**

Regardless of the application used, when your electronic artwork is finalised, please "save as" or convert the images to one of the following formats (note the resolution requirements for line drawings, halftones, and line/halftone combinations given below):

- EPS: Vector drawings. Embed the font or save the text as "graphics".
- TIFF: color or grayscale photographs (halftones): always use a minimum of 300 dpi.
- TIFF: Bitmapped line drawings: use a minimum of 1000 dpi.
- TIFF: Combinations bitmapped line/halftone (color or grayscale): a minimum of 500 dpi is required.
- DOC, XLS or PPT: If your electronic artwork is created in any of these Microsoft Office applications please supply "as is".

**Please do not:**

- Supply embedded graphics in your wordprocessor (spreadsheet, presentation) document;
- Supply files that are optimised for screen use (like GIF, BMP, PICT, WPG); the resolution is too low;
- Supply files that are too low in resolution;
- Submit graphics that are disproportionately large for the content.

**Figure captions**

Ensure that each illustration has a caption. Supply captions separately, not attached to the figure. A caption should comprise a brief title (not on the figure itself) and a description of the illustration. Keep text in the illustrations themselves to a minimum but explain all symbols and abbreviations used.

**Color artwork**

Please make sure that artwork files are in an acceptable format (TIFF (or JPEG), EPS (or PDF) or MS Office files) and with the correct resolution. If, together with your accepted article, you submit usable color figures then Elsevier will ensure, at no additional charge, that these figures will appear in color online (e.g., ScienceDirect and other sites) in addition to color reproduction in print. Further information on the preparation of electronic artwork.

**Tables**

Please submit tables as editable text and not as images. Tables can be placed either next to the relevant text in the article, or on separate page(s) at the end. Number tables consecutively in accordance with their appearance in the text and place any table notes below the table body. Be sparing in the use of tables and ensure that the data presented in them do not duplicate results described elsewhere in the article. Please avoid using vertical rules and shading in table cells.

**References**
**Citation in Text**

The numerical system of references should be used. References in the text should be cited by numbers in square brackets in the order of their citation.

References are listed together in their order of appearance in a separate section at the end of the text under the heading References. All references should be numbered consecutively. References to journals should contain initials and names of all authors, article title, abbreviation of the name of the journal according to the List of Serial Title World Abbreviations (International Series Data System, 20, rue Bachaumont, 75002 Paris, France. ISBN 2-904938-02-8), year of publication, volume number, and page numbers. References to books should also include the title (of series and volumes), initials and names of the editor(s), the publisher and place of publication.

Examples:

Reference to a journal publication:


Reference to a book:


Reference to a chapter in an edited book or book series:


Reference to a paper as "in press" implies that it has been accepted for publication. Evidence (e.g., a photocopy of the note of acceptance from the journal concerned) should accompany the submitted typescript. Papers that are "in press" should be included as a number in the text. Other papers submitted before or simultaneously with the paper in question should be included as a number in the text and in the References section, stating the name of the journal. Copies of papers that are submitted elsewhere should be provided for inspection by the Editors. Omission of this information will delay publication and may lead to redating of a submitted manuscript. Papers presented at scientific meetings that are not available in published form should not be cited as references in the References section.

Unpublished results should not be listed in the References section. In the text they are mentioned as follows: "(Tervoort MV and Glimcher J, unpublished data)". When unpublished results are cited, the data should be provided for the Editors' information when essential for proper evaluation, or if requested.

A personal communication should be mentioned in the text as follows: "(Tervoort MV, personal communication)". Authors should not make unauthorized use of personal communications. Personal communications are not to be included in the Reference section.

**Data references**

This journal encourages you to cite underlying or relevant datasets in your manuscript by citing them in your text and including a data reference in your Reference List. Data references should include the following elements: author name(s), dataset title, data repository, version (where available), year, and global persistent identifier. Add [dataset] immediately before the reference so we can properly identify it as a data reference. The [dataset] identifier will not appear in your published article.

**Reference management software**

Most Elsevier journals have their reference template available in many of the most popular reference management software products. These include all products that support Citation Style Language styles, such as Mendeley. Using citation plug-ins from these products, authors only need to select the appropriate journal template when preparing their article, after which citations and bibliographies will be automatically formatted in the journal's style. If no template is yet available for this journal, please follow the format of the sample references and citations as shown in this Guide. If you use reference management software, please ensure that you remove all field codes before submitting the electronic manuscript. More information on how to remove field codes from different reference management software.
Users of Mendeley Desktop can easily install the reference style for this journal by clicking the following link:
http://open.mendeley.com/use-citation-style/journal-of-proteomics

When preparing your manuscript, you will then be able to select this style using the Mendeley plug-ins for Microsoft Word or LibreOffice.

**Reference style**

**Text:** Indicate references by number(s) in square brackets in line with the text. The actual authors can be referred to, but the reference number(s) must always be given.

Example: '..... as demonstrated [3,6]. Barnaby and Jones [8] obtained a different result ....'

**List:** Number the references (numbers in square brackets) in the list in the order in which they appear in the text.

**Examples:**

Reference to a journal publication:

Reference to a journal publication with an article number:

Reference to a book:

Reference to a chapter in an edited book:

Reference to a website:

Reference to a dataset:

**Video**

Elsevier accepts video material and animation sequences to support and enhance your scientific research. Authors who have video or animation files that they wish to submit with their article are strongly encouraged to include links to these within the body of the article. This can be done in the same way as a figure or table by referring to the video or animation content and noting in the body text where it should be placed. All submitted files should be properly labeled so that they directly relate to the video file's content. In order to ensure that your video or animation material is directly usable, please provide the file in one of our recommended file formats with a preferred maximum size of 150 MB per file, 1 GB in total. Video and animation files supplied will be published online in the electronic version of your article in Elsevier Web products, including ScienceDirect. Please supply 'stills' with your files: you can choose any frame from the video or animation or make a separate image. These will be used instead of standard icons and will personalize the link to your video data. For more detailed instructions please visit our video instruction pages. Note: since video and animation cannot be embedded in the print version of the journal, please provide text for both the electronic and the print version for the portions of the article that refer to this content.

**Data visualization**

Include interactive data visualizations in your publication and let your readers interact and engage more closely with your research. Follow the instructions here to find out about available data visualization options and how to include them with your article.

**Supplementary material**

Supplementary material such as applications, images and sound clips, can be published with your article to enhance it. Submitted supplementary items are published exactly as they are received (Excel or PowerPoint files will appear as such online). Please submit your material together with the article and supply a concise, descriptive caption for each supplementary file. If you wish to make changes to supplementary material during any stage of the process, please make sure to provide an updated file. Do not make any corrections on a previous version. Please switch off the 'Track Changes' option in Microsoft Office files as these will be published in the updated version.
**Research data**

This journal requires and enables you to share data that supports your research publication where appropriate, and enables you to interlink the data with your published articles. Research data refers to the results of observations or experimentation that validate research findings. To facilitate reproducibility and data reuse, this journal also encourages you to share your software, code, models, algorithms, protocols, methods and other useful materials related to the project.

Below are a number of ways in which you can associate data with your article or make a statement about the availability of your data when submitting your manuscript. When sharing data in one of these ways, you are expected to cite the data in your manuscript and reference list. Please refer to the "References" section for more information about data citation. For more information on depositing, sharing and using research data and other relevant research materials, visit the research data page.

**Data linking**

If you have made your research data available in a data repository, you can link your article directly to the dataset. Elsevier collaborates with a number of repositories to link articles on ScienceDirect with relevant repositories, giving readers access to underlying data that gives them a better understanding of the research described.

There are different ways to link your datasets to your article. When available, you can directly link your dataset to your article by providing the relevant information in the submission system. For more information, visit the database linking page.

For supported data repositories a repository banner will automatically appear next to your published article on ScienceDirect.

In addition, you can link to relevant data or entities through identifiers within the text of your manuscript, using the following format: Database: xxxx (e.g., TAIR: AT1G01020; CCDC: 734053; PDB: 1XFN).

**Mendeley Data**

This journal supports Mendeley Data, enabling you to deposit any research data (including raw and processed data, video, code, software, algorithms, protocols, and methods) associated with your manuscript in a free-to-use, open access repository. During the submission process, after uploading your manuscript, you will have the opportunity to upload your relevant datasets directly to Mendeley Data. The datasets will be listed and directly accessible to readers next to your published article online.

For more information, visit the Mendeley Data for journals page.

**Data in Brief**

You have the option of converting any or all parts of your supplementary or additional raw data into one or multiple data articles, a new kind of article that houses and describes your data. Data articles ensure that your data is actively reviewed, curated, formatted, indexed, given a DOI and publicly available to all upon publication. You are encouraged to submit your article for Data in Brief as an additional item directly alongside the revised version of your manuscript. If your research article is accepted, your data article will automatically be transferred over to Data in Brief where it will be editorially reviewed and published in the open access data journal, Data in Brief. Please note an open access fee of 500 USD is payable for publication in Data in Brief. Full details can be found on the Data in Brief website. Please use this template to write your Data in Brief.

**MethodsX**

You have the option of converting relevant protocols and methods into one or multiple MethodsX articles, a new kind of article that describes the details of customized research methods. Many researchers spend a significant amount of time on developing methods to fit their specific needs or setting, but often without getting credit for this part of their work. MethodsX, an open access journal, now publishes this information in order to make it searchable, peer reviewed, citable and reproducible. Authors are encouraged to submit their MethodsX article as an additional item directly alongside the revised version of their manuscript. If your research article is accepted, your methods article will automatically be transferred over to MethodsX where it will be editorially reviewed. Please note an open access fee is payable for publication in MethodsX. Full details can be found on the MethodsX website. Please use this template to prepare your MethodsX article.
**Data statement**
To foster transparency, we require you to state the availability of your data in your submission if your data is unavailable to access or unsuitable to post. This may also be a requirement of your funding body or institution. You will have the opportunity to provide a data statement during the submission process. The statement will appear with your published article on ScienceDirect. For more information, visit the Data Statement page.

**Submission checklist**
The following list will be useful during the final checking of an article prior to sending it to the journal for review. Please consult this Guide for Authors for further details of any item.

**Ensure that the following items are present:**
One author has been designated as the corresponding author with contact details:

- E-mail address
- Full postal address
- Phone numbers

All necessary files have been uploaded, and contain:
- Keywords
- Graphical Abstract
- Highlights
- bulleted "Significance" paragraph after the Abstract
- All figure captions
- All tables (including title, description, footnotes)

Further considerations:
- Manuscript has been 'spell-checked' and 'grammar-checked'
- References are in the correct format for this journal
- All references mentioned in the Reference list are cited in the text, and vice versa
- Permission has been obtained for use of copyrighted material from other sources (including the Web)

For any further information please visit our customer support site at http://support.elsevier.com.

Line numbers have been added to your manuscript file
Does the information on mass spectrometry data meet the Guidelines of the journal? (JPROT encourages authors to read the MIAPE-MS document available addressing [http://www.psidev.info/sites/default/files/MIAPE_MS_2.98.pdf](http://www.psidev.info/sites/default/files/MIAPE_MS_2.98.pdf)). Does your paper cite databank accession codes? (J. Proteomics encourages authors to adopt the linking scheme to link out from ScienceDirect to CRAN, the Comprehensive R Archive Network ([http://cran.r-project.org/](http://cran.r-project.org/)). More info about this kind of linking is available at [https://www.elsevier.com/databaselinking](https://www.elsevier.com/databaselinking).

If you are submitting a revised version of a manuscript, and to facilitate peer-reviewing, changes introduced in the revised version of the manuscript should be highlighted.

**AFTER ACCEPTANCE**

**Online proof correction**
Corresponding authors will receive an e-mail with a link to our online proofing system, allowing annotation and correction of proofs online. The environment is similar to MS Word: in addition to editing text, you can also comment on figures/tables and answer questions from the Copy Editor. Web-based proofing provides a faster and less error-prone process by allowing you to directly type your corrections, eliminating the potential introduction of errors.

If preferred, you can still choose to annotate and upload your edits on the PDF version. All instructions for proofing will be given in the e-mail we send to authors, including alternative methods to the online version and PDF.

We will do everything possible to get your article published quickly and accurately. Please use this proof only for checking the typesetting, editing, completeness and correctness of the text, tables and figures. Significant changes to the article as accepted for publication will only be considered at this stage with permission from the Editor. It is important to ensure that all corrections are sent back to us in one communication. Please check carefully before replying, as inclusion of any subsequent corrections cannot be guaranteed. Proofreading is solely your responsibility.

**Offprints**
The corresponding author will, at no cost, receive a customized Share Link providing 50 days free access to the final published version of the article on ScienceDirect. The Share Link can be used for sharing the article via any communication channel, including email and social media. Corresponding authors who have published their article gold open access do not receive a Share Link as their final published version of the article is available open access on ScienceDirect and can be shared through the article DOI link.
**Appendix**

Standard abbreviations allowed to be used without explanation or definition in all articles published in the *Journal of Proteomics*.

<table>
<thead>
<tr>
<th>Abbreviation</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>A</td>
<td>absorbance</td>
</tr>
<tr>
<td>ACES</td>
<td>2-[(2-amino-2-oxoethyl)amino] ethanesulphonic acid</td>
</tr>
<tr>
<td>ACN</td>
<td>acetonitrile</td>
</tr>
<tr>
<td>A/D</td>
<td>analog to digital converter</td>
</tr>
<tr>
<td>AEBSF</td>
<td>4-(2-aminoethyl)benzenesulphonyl fluoride</td>
</tr>
<tr>
<td>amu</td>
<td>atomic mass unit</td>
</tr>
<tr>
<td>ANOVA</td>
<td>analysis of variance</td>
</tr>
<tr>
<td>API</td>
<td>atmospheric pressure ionization</td>
</tr>
<tr>
<td>AUC</td>
<td>area under curve</td>
</tr>
<tr>
<td>Bis N,N'-methylenebisacrylamide</td>
<td></td>
</tr>
<tr>
<td>bp</td>
<td>base pairs</td>
</tr>
<tr>
<td>BSA</td>
<td>bovine serum albumin</td>
</tr>
<tr>
<td>%C</td>
<td>cross-linking agent (g/100 mL)/%T</td>
</tr>
<tr>
<td>CAPS</td>
<td>3-(cyclohexylamino)-1-propanesulphonic acid</td>
</tr>
<tr>
<td>CBB</td>
<td>Coomassie Brilliant Blue</td>
</tr>
<tr>
<td>CCD</td>
<td>charge-coupled device</td>
</tr>
<tr>
<td>CD</td>
<td>circular dicroism</td>
</tr>
<tr>
<td>CE</td>
<td>capillary electrophoresis</td>
</tr>
<tr>
<td>CEC</td>
<td>capillary electrochromatography</td>
</tr>
<tr>
<td>CFE</td>
<td>continuous flow electrophoresis</td>
</tr>
<tr>
<td>CHAPS</td>
<td>3-[(3-cholamidopropyl)dimethylammonio]-1-propanesulphonate</td>
</tr>
<tr>
<td>CHCA</td>
<td>α-cyano-4-hydroxycinnamic acid</td>
</tr>
<tr>
<td>CHES</td>
<td>2-((N-cyclohexylamino)ethanesulphonic acid</td>
</tr>
<tr>
<td>CID</td>
<td>collision-induced dissociation</td>
</tr>
<tr>
<td>CIEF</td>
<td>capillary isoelectric focusing</td>
</tr>
<tr>
<td>CMC</td>
<td>critical micelle concentration</td>
</tr>
<tr>
<td>Con A</td>
<td>Concanavalin A</td>
</tr>
<tr>
<td>CNS</td>
<td>central nervous system</td>
</tr>
<tr>
<td>cpm</td>
<td>counts per minute</td>
</tr>
<tr>
<td>CTAB</td>
<td>ethyltrimethylammonium bromide</td>
</tr>
<tr>
<td>CV</td>
<td>coefficient of variation</td>
</tr>
<tr>
<td>CZE</td>
<td>capillary zone electrophoresis</td>
</tr>
<tr>
<td>1-D</td>
<td>one-dimensional</td>
</tr>
<tr>
<td>2-D</td>
<td>two-dimensional</td>
</tr>
<tr>
<td>Da</td>
<td>dalton (molecular mass)</td>
</tr>
<tr>
<td>2-DE</td>
<td>two-dimensional electrophoresis</td>
</tr>
<tr>
<td>DIGE</td>
<td>fluorescence difference gel electrophoresis</td>
</tr>
<tr>
<td>DGGE</td>
<td>denaturing gradient gel electrophoresis</td>
</tr>
<tr>
<td>DMEM</td>
<td>Dulbecco’s modified Eagle medium</td>
</tr>
<tr>
<td>DMF</td>
<td>N,N-dimethylformamide</td>
</tr>
<tr>
<td>DMSO</td>
<td>dimethyl sulphoxide</td>
</tr>
<tr>
<td>DOC</td>
<td>sodium deoxycholate</td>
</tr>
<tr>
<td>dsDNA</td>
<td>double-stranded DNA</td>
</tr>
<tr>
<td>DTE</td>
<td>dithioerithiol</td>
</tr>
<tr>
<td>DTT</td>
<td>dithiothreitol</td>
</tr>
<tr>
<td>ECL</td>
<td>enhanced chemiluminescence</td>
</tr>
<tr>
<td>EDTA</td>
<td>ethylenediaminetetraacetic acid</td>
</tr>
<tr>
<td>EEO</td>
<td>electroendosmosis</td>
</tr>
<tr>
<td>EGTA</td>
<td>ethylene glycol-bis(β-aminoethyl)-N,N,N',N'-tetraacetic acid</td>
</tr>
<tr>
<td>EKC</td>
<td>electrokinetic chromatography</td>
</tr>
<tr>
<td>ELISA</td>
<td>enzyme-linked immunosorbent assay</td>
</tr>
<tr>
<td>EMSA</td>
<td>electrophoretic mobility shift assay</td>
</tr>
<tr>
<td>EOF</td>
<td>electroosmotic flow</td>
</tr>
<tr>
<td>ER</td>
<td>endoplasmic reticulum</td>
</tr>
<tr>
<td>ESI</td>
<td>electrospray ionization</td>
</tr>
<tr>
<td>EST</td>
<td>expressed sequence tag</td>
</tr>
</tbody>
</table>
EUPA European Proteome Association
FAB fast atom bombardment
FACS fluorescence activated cell sorting
FBS fetal bovine serum
FCS fetal calf serum
FIGE field inversion gel electrophoresis
FITC fluorescein isothiocyanate
FT Fourier transform
FT-ICR Fourier transform-ion cyclotron resonance
GC gas chromatography
GIF graphic interchange format
GRAVY grand average hydrophobicity
GSH glutathione
GST glutathione-S-transferase
HE hematoxylin and eosin
HEPES N-(2-hydroxyethyl)piperazine-2'-(2-ethanesulphonic acid)
HPCE high-performance capillary electrophoresis
HPLC high-performance liquid chromatography
HRP horseradish peroxidase
HSA human serum albumin
HSP heat shock protein
HTML hypertext mark-up language
HUPO Human Proteome Organisation
HVR hypervariable region
ICAT isotop-coded affinity tag
ICR ion cyclotron resonance
id inside diameter
IEF isoelectric focusing
Ig immunoglobulin
IMAC immobilized metal affinity capture
IPG immobilized pH gradient
IT ion trap
iTRAQ isobaric tag for relative and absolute quantitation
kbp kilobase pairs
kDa kilodalton (molecular mass)
LC liquid chromatography
LED light-emitting diode
LOD limit of detection
LOQ limit of quantitation
mAb monoclonal antibody
MALDI-MS matrix-assisted laser-desorption ionization-mass spectrometry
Mb megabase
MEKC micellar electrokinetic capillary chromatography
MES 2-(N-morpholino)ethanesulphonic acid
MHC major histocompatibility complex
MOPS 3-(N-morpholino)propanesulphonic acid
M_r relative molecular mass (dimensionless)
MS mass spectrometry
MS/MS tandem mass spectrometry
MTT 3-(4,5-dimethylthiazol-2-yl)-2,5-diphenyltetrazolium bromide
m/z mass-to-charge ratio
NC nitrocellulose NEPHGE nonequilibrium pH gradient electrophoresis
NMR nuclear magnetic resonance
NP-40 Nonidet P-40
od outside diameter
OD optical density
OFAGE orthogonal field alternation gel electrophoresis
ORF open reading frame
PAGE polyacrylamide gel electrophoresis
PBS phosphate-buffered saline
PCR polymerase chain reaction
PDMS polydimethylsiloxane
PED pulsed electrochemical detection PEG polyethylene glycol
PFGE pulsed-field gel electrophoresis
PU plaque-forming units
pI isoelectric point
PMF peptide mass fingerprinting
PMS phenazine methosulphate
PMSF phenylmethylsulphonyl fluoride
PMT photomultiplier tube
PSD post-source decay
PTFE polytetrafluoroethylene
PTH phenylthiohydantoin
PTM post-translational modification
PVA polyvinyl alcohol
PVDF polyvinylidene difluoride
PVP polyvinylpyrrolidone
Q-TOF quadrupole time-of-flight
RACE rapid amplification of cDNA ends
RFLE restriction fragment length polymorphism
RIA radioimmunoassay
ROS reactive oxygen species
RP reversed phase
rpm revolutions per minute
RSD relative standard deviation
RT-PCR reverse transcriptase-PCR
SAGE serial analysis of gene expression
SD standard deviation
SDS sodium dodecyl sulphate
SEC size-exclusion chromatography
SELDI surface-enhanced laser desorption/ionization
SEM standard error of the mean
SIM selected ion monitoring
S/N signal-to-noise ratio
SPE solid-phase extraction
SPR surface plasmon resonants
SSCP single-strand conformation polymorphism
ssDNA single-stranded DNA
SSP sample spot number
STR short tandem repeat
%T total gel concentration (acrylamide plus cross-linking agent; g/100 mL)
TBS Tris-buffered saline
TCA trichloroacetic acid
TEMED N,N',N',N''-tetramethylethylenediamine
TFA trifluoroacetic acid
THF tetrahydrofuran
TIC total ion current
TLC thin-layer chromatography
TNF tumour necrosis factor
TOF time of flight
Tris tris(hydroxymethyl)aminomethane
TRITC tetramethylrhodamine isothiocyanate
URL uniform resource locator
UTR untranslated region
UV ultraviolet
Vh volt × hours
z ion charge
AUTHOR INQUIRIES
Visit the Elsevier Support Center to find the answers you need. Here you will find everything from Frequently Asked Questions to ways to get in touch. You can also check the status of your submitted article or find out when your accepted article will be published.

© Copyright 2018 Elsevier | https://www.elsevier.com