Last update: January 2015

Overview

Instructions and Forms

To ensure fast publication we kindly ask you to follow our **Instructions to Authors** when preparing your manuscript. Please return **both Agreement forms** as soon as your manuscript has been accepted:

Instructions to Authors (html)
Instructions to Authors (pdf)
Color and Page Charge Agreement (pdf)

Language Assistance

Should authors who are not native English speakers have problems writing their papers, assistance is available with style, grammar and vocabulary. Improvement of the English can maximize the accuracy of the submission and help to communicate clearly and concisely the contents to the readers, editors and reviewers of Proteomics Clinical Applications.

Please note: Wiley provides a new professional language and manuscript editing service.

English Language Editing
Translation Service
Manuscript Formatting
Figure Preparation

For detailed information and instructions please go to:
http://wileyeditingservices.com/en/

Japanese authors can also find a list of local English improvement services at
www.wiley.co.jp/journals/editcontribute.html.

Style of References

The Proteomics Clinical Applications reference style is included in EndNote as well as other referencing programs. Authors may choose the program they are most comfortable with. However they must ensure that all information needed is included in the ted manuscript.

Further details and reference examples can be found in the Instructions to Authors.

Conflict of Interest Statement

All authors must declare financial/commercial conflicts of interest. Even if there are none, this should be stated in a separate paragraph following on from the acknowledgements section. This is a mandatory requirement for all articles.

Online Submission of Manuscripts

Proteomics Clinical Applications offers a web-based manuscript submission and peer review system. Using this system is obligatory; conventional submission of manuscripts is not accepted.

If you have any questions concerning the online submission, do not hesitate to contact Editorial Support at proteomics@wiley.com.

Charges

Page Charge
Research articles up to 7 printed pages, review articles up to 15 printed pages, and rapid communications, technical briefs, dataset briefs and reports up to 4 pages, are free of charge. For each additional page beyond these limits, the corresponding author will be charged 196 EUR +VAT.
To calculate the number of printed pages your manuscript will have, count the number of text pages, tables and figures and divide the total by three. This will give you a rough estimate.
No page charge will be levied for viewpoint articles and standardisation & guidelines articles.

Color Charge
We do ask our authors to contribute towards the extra costs incurred for the reproduction of color in print.
The prices (excl. VAT) are listed below.

1 color figure	500.00 Euro
2 color figures	832.00 Euro
3 color figures	1248.00 Euro
4 color figures	1664.00 Euro

For 5 and more color figures please contact our Production Department for an individual offer at: idolecki@wiley.com

Reprint Permissions

Please note that if you are submitting material which has already been published elsewhere, you must also send to the Editorial Office permission in writing that this material may be reprinted in Proteomics Clinical Applications.
You can use the Copyright Permission Request Form (pdf) for this purpose.

If you want to request permission to use material published by Wiley you can use our Online Permission Request From.

Wiley-Blackwell policy regarding the NIH mandate

Wiley-Blackwell will support our authors by posting the accepted version of articles by NIH grant-holders to PubMed Central upon acceptance by the journal. The accepted version is the version that incorporates all amendment made during peer review, but prior to the publisher's copy-editing and typesetting. This accepted version will be made publicly available 12 months after publication. The NIH mandate applies to all articles based on research that has been wholly or partially funded by the NIH and that are accepted for publication on or after April 7, 2008.

The NIH has also announced a Request For Information (RFI) process, and we encourage our journal editors and society partners to participate in this. During this process, Wiley-Blackwell will also consult directly with authors, editors and society partners to determine how we as their publisher may best support them going forward.

Wiley-Blackwell also offers a OnlineOpen service. Upon payment of the OnlineOpen fee, we will deposit the published version of the article into PubMed Central, with public availability in PubMed Central and on the journal's website immediately upon publication.

OnlineOpen

Proteomics Clinical Applications offers an OnlineOpen service for all authors. OnlineOpen is available to authors of primary research articles who wish to make their article available to non-subscribers on publication, or whose funding agency requires grantees to archive the final version of their article. With OnlineOpen, the author, the author's funding agency, or the author's institution pays a fee to ensure that the article is made available to non-subscribers upon publication via Wiley Online Library, as well as deposited in the funding agency's preferred archive. For the full list of terms and conditions, see OnlineOpen Terms.

Any authors wishing to send their paper OnlineOpen will be required to complete the payment form available from our website at: https://authorservices.wiley.com/bauthor/onlineopen_order.asp

Prior to acceptance there is no requirement to inform an Editorial Office that you intend to publish your paper OnlineOpen if you do not wish to. All OnlineOpen articles are treated in the same way as any other article. They go through the journal's standard peer-review process and will be accepted or rejected based on their own merit.

Visit Wiley-Blackwell Author Services
A wealth of information for journal authors is now available at http://authorservices.wiley.com.

- Browse journals by subject
- Set up your favorite journals to provide quick links to online submission websites, author guidelines, and more
- Review editorial policies on issues such as ethics, retraction of articles, and more
- Get help for authors whose native language is not English
- View author benefits and rights
- Learn where to order reprints and how to request permission to use copyrighted material
- Claim your 25% author discount on books
- And more…

Instructions to Authors (html)

Instructions to authors

for Proteomics Clinical Applications
January 2015

Authors are requested to follow these Instructions carefully and completely. Manuscripts not prepared accordingly may be rejected without review. These instructions represent the minimal requirements in order to ensure that any reviewer and reader can evaluate a manuscript critically. Further relevant points may also be found in published guidelines of good practice, for example the STARD (http://stard-statement.org/) and REMARK (http://www.cancerdiagnosis.nci.nih.gov/assessment/progress/remark.htm) guidelines which cover critical elements of the design and reporting of biomarker studies.

1 Aims and scope

Proteomics Clinical Applications is a premier source of information in the field of applying proteomics to the study of human disease and translational research to the clinic. The journal publishes papers in all relevant areas including basic proteomic research designed to further understand the molecular mechanisms underlying dysfunction in human disease including both cell line and animal models, the results of proteomic studies dedicated to the discovery and validation of disease biomarkers, the use of proteomics for the discovery of novel drug targets, the application of proteomics in the drug development pipeline and the use of proteomics as a component of clinical trials.

Proteomics Clinical Applications is published in 12 issues per year, including regular issues as well as topical issues.

2 Terms of publication

2.1 Copyright policy and Open Access

If your paper is accepted, the author identified as the formal corresponding author will receive an email prompting them to login into Author Services, where via the Wiley Author Licensing Service (WALS) they will be able to complete the license

agreement on behalf of all authors on the paper. Preparation of accepted manuscripts for publication will not proceed until a completed license agreement is returned.

For authors signing the copyright transfer agreement
If the OnlineOpen option is not selected the corresponding author will be presented with the copyright transfer agreement (CTA) to sign. The terms and conditions of the CTA can be previewed in the samples associated with the Copyright FAQs below:

For authors choosing OnlineOpen

If the OnlineOpen option is selected the corresponding author will have a choice of the following Creative Commons License Open Access Agreements (OAA):

- Creative Commons Attribution License OAA
- Creative Commons Attribution Non-Commercial License OAA
- Creative Commons Attribution Non-Commercial -NoDerivs License OAA

To preview the terms and conditions of these open access agreements please visit the Copyright FAQs hosted on Wiley Author Services http://authorservices.wiley.com/bauthor/faqs_copyright.asp and visit http://www.wileyopenaccess.com/details/content/12f25db4c87/Copyright--License.html If you select the OnlineOpen option and your research is funded by The Wellcome Trust and members of the Research Councils UK (RCUK) you will be given the opportunity to publish your article under a CC-BY license supporting you in complying with Wellcome Trust and Research Councils UK requirements. For more information on this policy and the journal's compliant self-archiving policy please visit: http://www.wiley.com/go/funderstatement. Other funding agencies currently supporting OnlineOpen:

- Imperial College London
- FWF Austrian Science Fund
- Telethon Italy
- University of Nottingham
- UKPMC funders: http://ukpmc.ac.uk/funders/

NIH Public Access Mandate
To be fully compliant with NIH requirements, Proteomics Clinical Applications and Wiley-Blackwell will upload all required files to PubMedCentral. Authors do not need to upload any files. For further information, please visit http://authorservices.wiley.com/bauthor/NIH_policy.asp

2.2 Cover letter

Manuscripts must be accompanied by a cover letter from the corresponding author. By submitting this letter, the corresponding author accepts responsibility for all statements contained therein. Clear and concise statements on all the following points should be included:

- The list of the coauthors includes all appropriate persons, and all persons listed have contributed in some way to the design, implementation and/or analysis, interpretation and reporting of the study. Provision of clinical samples with no other input does not constitute justification for inclusion as an author.
- All coauthors have seen a draft copy of the manuscript and agree with its publication.
- The work has not been published elsewhere, either completely, in part, or in any other form (with the exception of a meeting abstract), and the manuscript is not currently being considered by another journal.
- The manuscript does/does not contain experiments using animals. The permission of the national or local authorities (giving the permission or the accreditation number of the laboratory and of the investigator) should be stated if animal experiments are included. Permission statements should also be included in the text of the manuscript. If no such rules or permissions have been implicated in the particular country, this must be stated in the cover letter.
- The manuscript does/does not contain human studies. If such studies are included, it should be stated that local Ethical Committee approval was received for the studies and that the informed consent of all participating subjects was obtained. Permission statements relating to this should also be included in the text of the manuscript.
- All funding for the studies in the manuscript, together with the names of the principal funding recipients, must be listed in the Acknowledgements.

- Any financial/commercial conflicts of interests have been disclosed. Such conflicts should be detailed in the cover letter and stated in the manuscript after the Acknowledgements.

2.3 General

All scientific contributions are assessed initially by one of the Editors and/or the Editor-in-Chief. Manuscripts failing to reach the required priority rating, failing to comply with the Instructions to Authors or not fitting within the scope of the journal are not considered further and are returned to authors without detailed comments. It should be noted that rebuttals that challenge rejections based on priority and/or scope alone will rarely be successful, since such a decision is necessarily a matter of opinion.

All manuscripts meeting the requirements will be peer-reviewed on the criteria of originality, quality, and scientific impact. On acceptance, papers may be subjected to editorial changes. Responsibility for the factual accuracy of a paper rests entirely with the authors.

All instances of publishing misconduct, including, but not limited to, plagiarism, data fabrication, image/data manipulation to falsify/enhance results, etc. will result in rejection/retraction of the manuscript.

This journal endorses the COPE (Committee on Publication Ethics) Code of Conduct and Guidelines and will pursue cases of suspected research and publication misconduct. In such cases, the journal will follow the processes set out by COPE. For more information about COPE please visit the COPE website at http://www.publicationethics.org.The journal also participates in the new CrossRef service (http://www.crossref.org/crosscheckindex.html), a plagiarism screening tool that allows the comparison of authored work against the content in the internet database of published work to highlight matching or similar text sections. Please be aware that all manuscripts prior to acceptance will be subject to testing using the CrossCheck software.

Once the corresponding author has received the scientific acceptance of his/her contribution, he/she must scan and return by email to the editorial office (proteomics@wiley.com) the attached color and page charge agreement, even if he/she does not wish to have any figures printed in color as this agreement also covers any page charges that might accrue (for details go to: http://onlinelibrary.wiley.com/journal/10.1002/(ISSN)1862-8354/homepage/ForAuthors.html#charg).

Please note that when submitting material (figure or data) which has already been published elsewhere, permission must be provided in writing that this material may be reprinted in **Proteomics Clinical Applications**.

After all necessary files have been received by the Editorial Office, the final acceptance letter will be sent and the manuscript will be forwarded to production. The corresponding author will then receive an email from Wiley's Author Services system which will ask them to log in and will present them with the appropriate license (copyright transfer) for completion. For a rapid online publication of the accepted article it is essential that the license (copyright transfer) agreement will be completed and returned as soon as possible.

All color figures will appear in color online free of charge even if they are not selected to be printed in color in the hardcopy print version of the journal.

Our Early View online publication is updated weekly and enables papers to be available online and citable before going into print. The respective DOI (Digital Object Identifier) can be found online.

3 Online manuscript submission

Submission to **Proteomics Clinical Applications** is via a web-based manuscript submission and peer review system. According to the current configuration of the system the corresponding author who submits the paper must also sign the License Agreement (on behalf of all the authors).

Together the authors must decide who should be listed as the Corresponding Author in the manuscript itself.

3.1 General remarks

Manuscripts must be written in English and be grammatically and linguistically correct. Either American or English spelling is acceptable. Authors who are not native English speakers should seek assistance with style, grammar and vocabulary if necessary. This may help to communicate clearly and concisely the contents to the readers, editors and reviewers of **Proteomics Clinical Applications**.

Please note: Wiley provides a new professional language and manuscript editing service.

English language editing
Translation service

Manuscript formatting
Figure preparation

For detailed information, costs and instructions please go to: http://wileyeditingservices.com/en/

To submit your manuscript online, please proceed as follows:

- Prepare your manuscript and illustrations in the appropriate format, according to the instructions given below.
- If you have not already done so, create an account for yourself in the system at the submission site http://mc.manuscriptcentral.com/clinical by clicking on the "Create Account" button.
- The online system will guide you through the submission process. Online help is available at all times during the process. You are also able to exit/re-enter at any stage before finally "submitting" your work.
- To support and expedite the review process, you should indicate as a “preferred reviewer” two candidates from the journal’s Editors and Members of the Editorial Board whose fields of expertise are closest to the topic of your contribution. For information on the Editors and Members and their respective fields, go to Section 4 of the manuscript submission process. You may suggest potential reviewers, preferably from outside your own country. Additionally, you may mention non-preferred reviewers.

All submissions are strictly confidential. To monitor the progress of your manuscript throughout the review process, you can log in periodically and check your Author Center. If you have any questions concerning the online submission program, do not hesitate to contact Editorial Support at proteomics@wiley.com.

3.2 Manuscript requirements

Please follow the instructions in Sections 6 and 7 when preparing the electronic version of the manuscript and ensure that data are given in the correct order and style for the journal.

- Main text (including front material) as well as figure legends and tables (in this order) should be given in one file, preferably saved in .doc(x) or .rtf format. Data should be typed without hyphenation except for compound words.
- Do not use the space bar to make indents; where required, use the TAB key. If working in Microsoft Word, please create special characters using Insert/Symbol.
- Figures should be in TIFF, EPS, PPT or the original format. See Section 6.2 for details.

All submissions will be converted to PDF format during the upload process. The system automatically generates one PDF file, which contains all parts of the manuscript, apart from any supporting information. It is important that you check the final PDF created before approving it.

3.3 Revised manuscripts

When submitting a revised manuscript, the authors must respond to the reviewers' comments using the "Respond to these comments" field on page 1 of the manuscript submission site. They should indicate in detail the changes that they have made and why. Also, they should indicate which of the suggested changes, if any, they have elected not to make and their reasons. A clean (non-highlighted) version of the revised manuscript should be uploaded as the main document file. In addition, a second version of the manuscript must be uploaded as a "Supplementary file for review" indicating the changes made in the manuscript itself, either by using the track change mode in Word or by changing the script colour of the revised sections. Upon acceptance of the manuscript, the final uploaded version with all changes accepted will be taken as the basis for copyediting and the subsequent production process.

4 Types of contributions

Seven types of scientific contributions are considered for publication:

(i) **Research articles** describing complete investigations. Unsolicited research articles should be concise and should not exceed 5000 words in length (including references as well as figure and table legends) and contain no more than five display elements (figures and tables). Manuscripts must not have been published previously, except in the form of a preliminary communication. Research articles should be divided into sections as specified in Section 7.3 below.

(ii)**Review articles** are normally invited by the Editor-in-Chief. Authors wishing to submit a review article should send a brief outline of its contents to Prof. Dunn (eic.proteomics1@ucd.ie) before the manuscript is drafted. Reviews should not exceed

8500 words (including references as well as figure and table legends) and contain no more than eight display elements (figures and tables). The articles should be divided into sections that are appropriate to the topic.

(iii) **Technical briefs** describing the development of a novel method or an improvement or noteworthy modification of an already existing technique or platform used in proteomic analysis. These manuscripts should bear the words "Technical Brief" immediately above the title on the first page. They should not be subdivided into titled sections but written in a continuous style. Technical briefs should not exceed 2500 words (including references as well as figure and table legends) and contain no more than three display elements (figures and tables).

(iv) **Dataset briefs** describing novel proteomic data sets of specific types of samples, such as organisms, tissues, cells, microbes, viruses and organelles. These data sets can be generated with any proteomic platform including two-dimensional gels, mass spectrometry or protein arrays. An important criterion is that the data set contains a significant number of identified proteins that will benefit further research on that particular sample type. Biological replicates are needed and their number must be detailed in the text. Purely descriptive manuscripts (e.g. cataloguing the proteome of a single sample type) will only be considered as Dataset briefs. The manuscripts should bear the words "Dataset Brief" immediately above the title on the first page. They should not be subdivided into titled sections but written in a continuous style. Data set briefs should not exceed 2500 words (including references as well as figure and table legends) and contain no more than three display elements (figures and tables). Authors are encouraged to submit supporting information, such as annotated two-dimensional gel images and tables of protein identifications, which will only appear online. Deposition of supporting data in a public and global open access database is mandatory (see Section 5.5). Examples of such suitable global, open access databases are the ProteomeXchange consortium (http://www.proteomexchange.org) (including receiving repositories PRIDE and PASSEL) or World-2DPAGE (http://world-2dpage.expasy.org/repository/).

(v) **Viewpoint articles** are intended to stimulate discussion and debate in areas of general concern and controversy in Proteomics Clinical Applications, and generally reflect the personal opinions of the author(s). These manuscripts should bear the word "Viewpoint" immediately above the title on the first page. The format of Viewpoint articles is a continuous style without formal headings but where it helps to provide structure to the article, for example moving between arguments and points, the use of subheadings or questions in an italicized font can be used. Viewpoint articles should normally not exceed 3500 words (including references as well as figure and table legends) and contain no more than three display elements (figures and tables). Potential authors considering contributing a viewpoint article to the journal should contact the Editor-in-Chief by e-mail (eic.proteomics1@ucd.ie) to discuss their proposal prior to submission. In order to provide a forum for debate of the issues raised in the viewpoint articles, correspondence concerning these articles will be published in a special area on the journal's homepage (http://onlinelibrary.wiley.com/journal/10.1002/(ISSN)1862-8354/homepage/viewpoint_forum.htm).

(vii) **Standardisation & Guidelines articles** describing recommendations or best practices on all aspects of proteomics, from experiment planning to data availability. Manuscripts of this type are normally invited by the Editor-in-Chief. Authors wishing to submit a Standardization & Guidelines article should send a brief outline of its contents to Prof. Dunn (eic.proteomics1@ucd.ie) before the manuscript is drafted. Standardization & Guidelines articles should be as concise as possible and should not exceed 5000 words in length (including references as well as figure and table legends) and contain no more than 5 display elements (figures and tables). Manuscripts must not have been published previously, though previous publicly accessible discussion documents are acceptable. The articles may be divided into sections that are appropriate to the topic.

5 Experimental design, description, and validation

5.1 Aims of the study

- The study aims should be clearly stated in the Abstract (the main conclusions should also appear in the Abstract) and at the end of the Introduction.
- For clinical studies the study aims should also be accompanied by a clear indication of the clinical relevance and in the context of a brief description of the study design and type, e.g. whether pilot, discovery or validation/qualification, etc.

5.2 Experimental design

- A clear and full description of the study design should be presented at the beginning of the Materials and methods section. For clinical studies this should include, whether prospectively or retrospectively, a clear definition of all clinical endpoints examined and a list of all variables examined/included in the data analysis.
- The experimental design must be provided and must include details of the number of biological replicates. Only one biological replicate is not acceptable, even for cell line-based studies.

- For clinical studies, the relationship between the patient group(s)/samples used in the different parts of the study should be clear, e.g. biomarker discovery phase versus validation/qualification phases. Independent cohorts are required for the different stages in biomarker studies. The validity of the proteomics findings must be confirmed through independent and complementary validation experiments (except dataset briefs).
- The rationale/statistical justification for the numbers of samples used should be provided, for example, if selected on the basis of detecting a specific effect size, the significance level, power and effect size should be stated. For further guidance on best practice in statistical reporting please see the article series published by the Physiological Society and the British Pharmacological Society at http://jp.physoc.org/cgi/collection/stats_reporting.
- For clinical studies a statement regarding appropriate Ethical Committee approval must be included and that the informed consent of all participating subjects was obtained.
- If the manuscript describes experiments using animals, the approval of the national or local authorities (giving the approval or the accreditation number of the laboratory and of the investigator) should be stated. If no such rules or permission are stipulated in the particular country, this must also be mentioned in the paper. The ARRIVE guidelines which are hosted on the NC3Rs website at http://www.nc3rs.org.uk/ARRIVEpdfshould be followed.

5.3 Patient groups and clinical samples (where relevant)

- The method of recruitment should be described together with any inclusion and selection/exclusion criteria (e.g. prospective or retrospective, attendance at specific clinic, etc.). The time period over which recruitment and sample collection took place, together with follow-up periods where relevant for outcome studies, should be provided for each clinical group. Consideration should be given to the most appropriate control group for the specific study aims; for example, whether healthy controls or other disease groups should be used and whether they are representative of the intended eventual use of a potential biomarker.
- For each group, the clinical condition and any categorisation based on disease severity (e.g. stage, grade or clinical scoring system) or subtype (e.g. histological or etiological) should be clearly described. Demographic and clinical summary details (preferably in a table) should be provided for each group, including any control subjects, together with any additional relevant lifestyle factors such as diet or smoking history.
- Where relevant, any specific procedures used for sample timing, e.g. morning fasted blood sample or first-void urine, should be described. Similarly details of any therapies or a statement that patients were previously untreated at the time of sampling should be provided.
- The sources of the different samples should be indicated, for example single center or multiple centers– in the latter case it should be clear whether samples from the different clinical groups/subgroups were provided by different centers and over what time periods.
- Full details of sample processing should be given. A statement should be provided as to whether these conditions were the same for all samples and any differences between groups must be described. For fluids this should include method and volume of collection, tube types and any additives, processing times and temperatures, centrifugation conditions and storage conditions (storage duration, temperature and any freeze-thaw cycles). For tissues, this should include method of collection, block sizes, processing times and conditions including delay to fixation/freezing, type of fixation and details of any histological review.

5.4 Sample analysis

- The proteomic methods used to analyze the samples should be described with a level of stringency and detail to allow repetition by other scientists, including manipuulation of samples prior to analysis. Provision of information relating to gel electrophoresis, mass spectrometry and other techniques in accordance with the more detailed “Minimum Information About a Proteomics Experiment” recommendations (http://www.psidev.info/MIAPE/) is strongly encouraged. If their work is MIAPE-compliant, authors should state this explicitly in the Materials and methods.
- The design of the analysis process should be described, for example, technical and biological replicate number, method and type of randomization, technical controls used, time span of sample analysis and whether this was undertaken with the operator blinded to sample status.
- Relevant details of key technical aspects of the analytical processes such as inter- and intra-experimental variation, normalization, sensitivity and specificity (with regard to the analyte), lower and upper limits of detection, should be provided as appropriate to the technology being used. Any experimental quality control processes should be described, such as use of statistical QC analysis procedures or inclusion of positive and negative controls, for example. Similarly, for reagents such as antibodies, details of the characterization in terms of specificity should be provided or a citation provided. Application notes (when available) may also be cited.

- For label and label-free methods the authors should include technical controls and state the number of technical replicates and also false positive rates.
- For any algorithmic pattern or recognition-based profiling approaches where the protein/peptide identities of the key determinants are not known, analysis must be reproducible and replicated on an independent test set. The pattern must also be shown to be stable and reproducible over time.

5.5 Protein identification and characterization

- Authors should adhere to the Paris guidelines (http://www.mcponline.org/misc/ParisReport_Final.dtl).
- The method(s) used to generate the mass spectrometry data must be described, including the methods used to create peak lists from raw MS or MS/MS data.
- The name and version of the program(s) used for database searching, the values of critical search parameters (e.g. parent ion and fragment mass tolerance, cleavage rules used, allowance for number of missed cleavages) and the name and version of the database(s) searched must be provided.
- For each protein identified, measures of certainty (e.g. *p*-values) 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. For peptide mass fingerprinting, the number of peptides that match the sequence and the total percent of sequence coverage must be quoted. If extensive, the above information should be collected as supporting information, which is available online.
- For experiments using multiple reaction monitoring to measure the amount of protein in a sample, a list of all transitions must be provided. The estimated LOD and LOQ should be provided for targeted proteins.
- Identifications based on at least two significant peptides are encouraged. However, if single peptides are used, an interpreted MS spectrum for each of these peptides must be supplied as supporting information.
- Protein name clustering should be used to reduce protein name redundancy.
- 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 or other stable chemical labeling 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 must be described.
- If a proteomics experiment reports a protein that is an enzyme, then relevant data to describe the enzyme should follow the standards for reporting enzymology data (STRENDA). For details see the Beilstein Institut/STRENDA website at http://www.beilstein-institut.de/en/projekte/strenda/guidelines/.

5.6 Data analysis

- Full details of any software, bioinformatic tools or image capture processes used for data processing or analysis should be provided. Where a manuscript describes an academic database or software, it must be freely accessible for review, either through a web interface, or for download and local installation of a functional test version. Deposition of supporting data in a public and global open access database is strongly recommended and mandatory for dataset briefs. Where an author states that a dataset is being made available as an integral part of a submitted manuscript, this must be within a public and global open access database and not solely a private or institute website (although that can occur simultaneously), to ensure permanent availability of the dataset. Examples of such suitable global, open access databases are the ProteomeXchange consortium (http://www.proteomexchange.org) (including receiving repositories PRIDE and PASSEL) or World-2DPAGE (http://world-2dpage.expasy.org/repository/).
- The specific hypotheses being tested should be clearly described. Any statistical tests should be fully described with relevant summary statistics, *p*-values and confidence intervals being given and consideration given to corrections for multiple testing as appropriate. Authors are strongly advised to consult with a professional statistician and bioinformatician to aid in experimental design, analysis and appropriate result reporting.
- 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. 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 validated immunoassays) are desirable.
- For biomarker discovery/validation studies, scatter plots of data, sensitivity and specificity values with confidence intervals and results of receiver operating characteristic curve analysis should be given, as a minimum. The number of patients and the variables included at each stage of the analysis must be clearly described and reasons and support for

dropout/exclusion provided. If a marker is already routinely used as a "gold standard" for that disease and clinical scenario, comparison with the performance of that marker should be included.

- Any manipulation of data such as data normalization, transformation or handling of missing values should be clearly described. Similarly, variables included in any multiple regression analysis should be indicated.
- Factors considered and included in the analyses as potentially confounding should be listed.
- Selection of specific technical cut-offs for quantitative or qualitative analyses (e.g. proteins differing by >2-fold) and statistical thresholds for evaluation of biomarker utility should be justified. Where reference ranges are used, details of the reference population and how the range was derived should be provided.

5.7 Data validation

- In comparative or shotgun-like discovery studies, confirmatory data (e.g. from validated immunoassays, immunohistochemistry, alternative MS-based methods, Western blotting, etc.) are required using independent replication sets for at least a subset of proteins.
- Where models are generated based on a training set, validation results from an independent test set or some form of bootstrapping/cross-validation should also be included.
- Where the output of the study is a model generated without knowledge of protein/peptide identity, for example, mass spectra or gel patterns/algorithms, the reproducibility and hence utility of the findings should be demonstrated over a prolonged time period using that experimental platform.

5.8 Data interpretation

- In the Discussion, the results must be interpreted and discussed in the context of the defined aims and purpose of the study and other relevant published literature.
- Any possible limitations of the study must be described and discussed and insight should be provided into the future implications of the findings.

6 Manuscript lengths, figures and page/figure charges

6.1 Manuscript length and page charges

Articles should conform to the following length restrictions:

- Research articles - seven printed pages (~5000 words and no more than five display elements)
- Review articles - 15 printed pages (~8500 words and no more than eight display elements)
- Technical briefs - four printed pages (~2500 words and no more than three display elements)
- Dataset briefs - four printed pages (~2500 words and no more than three display elements)
- Viewpoint articles - six printed pages (~3500 words and no more than three display elements)
- Standardisation & Guidelines articles - seven printed pages (~5000 words and no more than five display elements)

Please note that page charges (see the journal's For Authors page) will be levied for all contributions exceeding these numbers of printed pages. Also note that the length of an article depends greatly on the type of figures and tables provided. There are no page charges levied for Viewpoint articles.

Note: These charges also apply to invited articles.

6.2 Figures

Please prepare your figures according to the following guidelines:

- Each figure should be given in a separate file and must have the following resolution at their final published size:

Type	Resolution

Graphs	800-1200 DPI
Photos	400-800 DPI
Color (only RGB)	300-400 DPI

-
- Monochrome art (black on white) should be in ‘bitmap’ mode (also called 1-bit). Grayscale art should be in ‘grayscale’ mode, a palette of colors that has 256 shades ranging from white to black (also called 8-bit). Colour art should be in RGB mode. RGB stands for Red, Green and Blue – these are the colors that are displayed by computer monitors. For details please go to http://authorservices.wiley.com/electronicartworkguidelines.pdf
- Use the zoom function to check the resolution of the figures: if an image viewed at 400% on screen is blurry (pixellated), then the image will not reproduce well in print. An image viewed at 100% on screen may look fine but will not necessarily reproduce well as the screen resolution is much lower (72-96 dpi) than that of a printing press.
- Crop, or scale, figures to the size intended for publication; no enlargement or reduction should be necessary. Otherwise figures should be submitted in a format that can be reduced to a width of 50-80mm or 120-170mm, with symbols and labels to a height of 2.0mm (after reduction) and a minimum line weight of 0.3 pt for black lines.
- Photographic images often produce large files. Most software has an option to use LZW compression and this will produce smaller files, especially when the image contains large areas of single color or repeating textures and patterns.
- In electropherograms presented horizontally, the anode should be on the left while in vertical presentations the anode should be at the bottom. Two-dimensional presentations, e.g. with isoelectric focusing and sodium dodecyl sulfate electrophoresis in the two dimensions, are thus presented consistently with the standard coordinate system.
- Figures should be numbered consecutively with Arabic numerals in the order of their appearance.
- Each figure is to be accompanied by a legend that should be self-explanatory. The legends should not appear under the figures but be included after the references.

By supplying high-quality electronic artwork, delays in production can be reduced as follow-up requests for improvement are no longer necessary.

6.3 Color charges

While all color figures submitted will appear in color online free of charge, authors will be charged for additional costs incurred for the reproduction of color in print if they select that option (see Section 2).

7 Manuscript format

Manuscripts must be typewritten with double spacing throughout (including references, legends, etc.).

7.1 Title page

The first page of all manuscripts should contain only the following:

(i) Title of the paper - standard abbreviations may be used in the title.
(ii) Full names (including first name) of the authors and the name of the institute. If the publication originates from several institutes the affiliations of all authors should be clearly stated by using superscript numbers after the name and before the institute.
(iii) Name (and title) and full postal address of the author to whom all correspondence (including galley proofs) is to be sent. Email, address and fax number must be included to expedite communication.
(iv) A list of abbreviations used in the paper excluding standard abbreviations (see list of "Standard Abbreviations", Section 10).
(v) Keywords (max. five, in alphabetical order).
(vi) Total number of words (including references as well as figure and table legends).

7.2 Statement of clinical relevance

On the page immediately after the title page, a statement describing the potential clinical significance of the study in terms of clinical need, goals and how the study moves the field forward should be provided (max. 200 words). This does not apply to review and viewpoint articles.

7.3 Abstract

The third page of the manuscript should contain the abstract only. For research articles, rapid communications, technical briefs and dataset briefs, it should be structured as follows:

Purpose
Experimental design
Results
Conclusions and clinical relevance The abstract should not exceed 200 words. Non-standard abbreviations must be written in full when first used and the abstract should not contain any references.

7.4 Sections in research articles

Research articles should be divided into the following sections and include the information required in the guidelines in Section 5:

"1 Introduction" containing a description of the problem under investigation and a brief survey of the existing literature on the subject before ending with a brief summary of the aims of the study in the context of the study design.

"2 Materials and methods" providing an outline of the experimental design of the study. The main methodological steps should be described and, where possible, references to previously published methods provided. Special materials and equipment, and the manufacturer's name and location should also be indicated. The section should be understandable as a standalone text. Any further experimental details can be placed in supporting information.

"3 Results"

"4 Discussion"

"5 References"

Sections 3 and 4 may be combined and should then be followed by a short section entitled "Concluding remarks". Subdivisions of sections should be indicated by numbered subheadings.

7.5 References

References should be numbered sequentially in the order in which they are cited in the text. The numbers should be set in brackets thus [2, 18]. References are to be collected in numerical order at the end of the manuscript under the heading "References"; they should also be typed with double spacing throughout. Papers with multiple authors should be limited to listing five authors. Where there are more than five authors, the first four should be listed, followed by et al. Please include the title of the manuscript in full followed by a full stop. Journal names should be abbreviated according to the practice of PubMed. The abbreviated title and the volume number should be in italics. Please note the following examples.

Journals:
[1] Hu, J., Qian, J., Borisov, O., Pan, S. et al., Optimized proteomic analysis of a mouse model of cerebellar dysfunction using aminespecific isobaric tags. *Proteomics* 2006, *6*, 4321-4334.
[2] Vosseller, K., Proteomics of Alzheimer's disease: Unveiling protein dysregulation in complex neuronal systems. *Proteomics Clin. Appl.* 2007, *1*, 1351-1361.

Other serial publications such as "Advances in Protein Chemistry" should be cited in the same manner as journals.

Books:
[3] Elves, M. W., *The Lymphocytes*, Lloyd-Luke Ltd., London 1972.

Chapter in a book:
[4] Müller, E., Greaves, M. F., in: Mäkelä, O., Cross, A., Kosunen, T. U. (Eds.), *Cell Interactions and Receptor Antibodies in Immune Responses*, Academic Press, New York 1971, pp. 101-125.

Allusions to "unpublished observations", papers "to be published" or "submitted for publication" and the like should be part of the text, in parentheses. Material "in press" should be entered under references along with the DOI, if available. Posters and abstracts in meetings books must not be cited unless they are generally accessible. Responsibility for the accuracy of bibliographic references rests entirely with the author.

Please note that website addresses must not be included as a reference, but should be inserted in parentheses in the text directly after the data to which they refer.

Authors should provide complete references in as accessible a way as possible, using software that they are most comfortable using.

7.6 Acknowledgements

Acknowledgements as well as information regarding funding sources should be provided on a separate page at the end of the text (before "References").

7.7 Conflict of interest statement

All authors must declare financial/commercial conflicts of interest. Even if there are none, this should be stated as "The authors have declared no conflict of interest" on a separate line following the acknowledgements section. This is a mandatory requirement for all articles.

7.8 Tables

Tables with suitable captions at the top and numbered with Arabic numerals should be collected at the end of the text on separate pages for each table. Column headings should be kept as brief as possible and indicate units. Footnotes to tables should be indicated with a), b), c), etc. and typed on the same page as the table.

7.9 Supporting information

For details on what can be included in the supporting information, go to Author Services at http://authorservices.wiley.com/bauthor/suppinfo.asp. For example, extensive tables should be published online as supporting information. This material will not be typeset so authors should prepare this in the final form. Also for this reason there will be no galley proofs of this material. Supporting information will be made freely available on the web (similar to the table of contents and the article abstracts). Authors are permitted to place this material on their homepages when they are setting up a link to the full-text version of the article in Wiley Online Library.

Further, other files may be submitted as supporting information (e.g. animations, video sequences). All supporting information will also undergo review and should therefore be submitted electronically along with the main body of the article. The Editor-in-Chief reserves the right to make any final decisions about suitability of material for publication as supporting information or within the main article.

Protein identification results, expression data and mass spectrometry peak lists should also be submitted as supporting information, and may be identical to data deposited in a public database. Note that all data must be in processed, not raw, form. Authors are encouraged to deposit their data in public, open access databases, formatted according to conventions of the relevant communities prior to manuscript submission (this is mandatory for dataset briefs, see Sections 4(v) and 5.5), and database accession numbers provided in the manuscript. In particular, novel protein sequences should be deposited in UniProt (http://www.uniprot.org), molecular interactions in an IMEx partner database (http://www.imexconsortium.org), and protein identification data in the ProteomeXchange Consortium (http://www.proteomexchange.org) (including receiving repositories PRIDE and PASSEL) or World-2DPAGE (http://www.world-2expasy.org/repository/). Where an author states that a dataset is being made available as an integral part of the supporting data, this must be within a public and global open access database and not solely a private or institute website (although that can occur simultaneously), to ensure permanent availability of the dataset.

7.10 Image manipulation

Manipulation of images is unacceptable. All figures must accurately reflect the original data. Information should not be enhanced, eliminated, added, obscured or moved. In cases where manipulation is unavoidable, this should be clearly detailed in the Figure legend. All instruments, software and processes used to obtain the images must be fully detailed in the manuscript either in the Figure legends or the Materials and methods. Acceptable image manipulation includes uniformly adjusting the contrast of an entire image and any control images, ensuring that all original data, including the background, remains visible and that no new features are introduced. Cropping of gels, or re-positioning of lanes/fields, is permitted providing that all alterations are clearly indicated by the use of dividing lines in the image itself, vital data are not removed, an explanation of the alterations is included in the Figure legend and images of full blots or gels that the figures are derived from are supplied in the supporting information. Unacceptable manipulation includes, but is not limited to, the enhancement of one feature/ band over others, removal of background noise/bands, *etc*. Authors must be able to produce all data in their raw format upon editorial request.

7.11 Structural formulae

Structural formulae should be drawn in the manuscript in the position where they belong. They must be numbered in consecutive order with the other figures.

7.12 Equations

Mathematical and chemical equations are to be written in the manuscript at the place in which they belong and should be marked by Arabic numerals in parentheses in the right margin in the order of their appearance.

7.13 Abbreviations

Abbreviations are hindrances to a reader working in a field other than that of the author, and to abstractors. Therefore, their

use should be restricted to a minimum and introduced only when repeatedly used. Section 9 at the end of these instructions contains the list of standard abbreviations that may be used without definition anywhere in the paper, including in the title and keywords. Nonstandard abbreviations must be written in full when first used and included in the list of abbreviations of the manuscript. Abbreviations used only in a table or a figure may be defined in the legend. If nonstandard abbreviations are used in the Abstract they should be defined in the Abstract, in the list of abbreviations of the manuscript as well as when first used in the body of the paper. .

7.14 Sharing of materials

With manuscript submission to **Proteomics Clinical Applications**, all authors agree that all described materials and reagents that are not commercially available (antibodies, cell lines, constructs, etc., but not clinical samples) and associated protocols are to be freely available to academic researchers in a timely manner upon request.

8 Proofs and reprints

Before publication authors will be sent a link to access their proofs via e-mail together with instructions and a reprint order form. The proofs should be carefully corrected following the instructions. In particular, authors should answer any editing queries. Please return proof corrections as instructed.

Note: Authors will be charged for extensive alterations of their article.

The reprint order form, which includes the prices, should be filled out and returned by email to the Editorial Office proteomics@wiley.com

9 Standard abbreviations

The abbreviations as listed below may be used without definition in the articles published in **Proteomics Clinical Applications**.

A	absorbance
ACES	2-[(2-amino-2-oxoethyl)amino] ethanesulfonic acid
ACN	acetonitrile
amu	atomic mass unit
ANOVA	analysis of variance
APCI	atmospheric pressure chemical ionization
API	atmospheric pressure ionization
AUC	area under curve
BCIP	5-bromo-4-chloro-3-indolyl phosphate
Bis	*N,N*-methylenebisacrylamide
bp	base pairs
BSA	bovine serum albumin
%C	cross-linking agent (g/100 mL)/%T
CAPS	3-(cyclohexylamino)-1-propanesulfonic acid
CBB	Coomassie Brilliant Blue
CCD	charge-coupled device
CE	capillary electrophoresis
CEC	capillary electrochromatography
CFE	continuous flow electrophoresis
CHAPS	3-[(3-cholamidopropyl)dimethylamonio]-1-propanesulfonate
CHCA	a-cyano-4-hydroxycinnamic acid
CHES	2-(*N*-cyclohexylamino)ethane sulfonic acid
CID	collision-induced dissociation
CIEF	capillary isoelectric focusing

CMC	critical micelle concentration
Con A	Concanavalin A
CNS	central nervous system
cpm	counts per minute
CTAB	cetyltrimethylammonium bromide
CTL	cytotoxic T lymphocyte
CV	coefficient of variation
CZE	capillary zone electrophoresis
1D	one-dimensional
2D	two-dimensional
Da	dalton (molecular mass)
DAPI	4',6-diamidino-2-phenylindole
2DE	two-dimensional gel electrophoresis
DIGE	fluorescence difference gel electrophoresis
DGGE	denaturing gradient gel electrophoresis
DHB	dihydroxybenzoic acid
DMEM	Dulbecco's modified Eagle medium
DMF	*N,N*-dimethylformamide
DMSO	dimethyl sulfoxide
DTT	dithiothreitol
ECD	electron capture dissociation
ECL	enhanced chemiluminescence
EDTA	ethylenediaminetetraacetic acid
EEO	electroendosmosis
EGTA	ethylene glycol-*bis*(ß-aminoethylether)-*N,N,N′,N′*-tetraacetic acid
EKC	electrokinetic chromatography
ELISA	enzyme-linked immunosorbent assay
EOF	electroosmotic flow
ER	endoplasmic reticulum
ESI	electrospray ionization
EST	expressed sequence tag
eV	electron volt
FAB	fast atomic bombardment
FBS	fetal bovine serum
FCS	fetal calf serum
FDR	false discovery rate
FACS	fluorescence-activated cell sorting
FITC	fluorescein isothiocyanate
FRET	fluorescence resonance energy transfer
FT-ICR	Fourier transform-ion cyclotron resonance
GC	gas chromatography
GIF	graphic interchange format
GO	Gene Ontology

GRAVY	grand average of hydrophobicity
GSH	glutathione
GST	glutathione-S-transferase
H&E	hematoxylin and eosin
HEPES	*N*-(2-hydroxyethyl)piperazine-2'-(2-ethanesulfonic 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
ICAT	isotope-coded affinity tag
ICP	inductively coupled plasma
ICR	ion cyclotron resonance
id	inside diameter
IEF	isoelectric focusing
Ig	immunoglobulin
IMAC	immobilized metal affinity chromatography
IP	immunoprecipitation
IPG	immobilized pH gradient
IPI	international protein index
IPTG	isopropyl-b-D-thiogalactopyranoside
IRB	institutional review board
ITMS	ion trap mass spectrometry
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
MACS	magnetic-activated cell separation
MALDI-MS	matrix-assisted laser desorption/ionization-mass spectrometry
Mbp	megabase pairs
MES	2-(*N*-morpholino)ethanesulfonic acid
MHC	major histocompatibility complex
MOPS	3-(*N*-morpholino)propanesulfonic acid
M_r	relative molecular mass (dimensionless)
MRM	multiple-reaction monitoring
MS	mass spectrometry
MS/MS	tandem mass spectrometry

MudPIT	multidimensional protein identification technology
m/z	mass-to-charge ratio
NBT	nitroblue tetrazolium
NEPHGE	nonequilibrium pH gradient electrophoresis
NIH	National Institutes of Health
NMR	nuclear magnetic resonance
NP-40	Nonidet P-40
od	outside diameter
OD	optical density
ORF	open reading frame
PAGE	polyacrylamide gel electrophoresis
PBMC	peripheral blood mononuclear cell
PBS	phosphate-buffered saline
PCA	principal components analysis
PCR	polymerase chain reaction
PEG	polyethylene glycol
PFU	plaque-forming units
p*I*	isoelectric point
PMF	peptide mass fingerprinting
PMSF	phenylmethylsulfonyl fluoride
PMT	photomultiplier tube
PRIDE	PRoteomics IDEntifications database
PRM	parallel reaction monitoring
PSD	post-source decay
PTFE	polytetrafluoroethylene
PTM	post-translational modification
PVA	polyvinyl alcohol
PVDF	polyvinylidene difluoride
PVP	polyvinylpyrrolidone
Q-TOF	quadrupole time-of-flight
RNA-Seq	next generation RNA sequencing
RIA	radioimmunoassay
ROC	receiver operating characteristic
ROS	reactive oxygen species
RP	reversed phase
rpm	revolutions per minute
RT-PCR	reverse transcriptase-PCR
SCX	strong cation exchange
SD	standard deviation
SDS	sodium dodecyl sulfate
SEC	size-exclusion chromatography
SELDI	surface-enhanced laser desorption/ionization
SEM	standard error of the mean

SILAC	stable isotope labelling with amino acids in cell culture
SIM	selected ion monitoring
S/N	signal-to-noise ratio
SPE	solid-phase extraction
SPR	surface plasmon resonance
SSCP	single-strand conformation polymorphism
ssDNA	single-stranded DNA
SRM	selected-reaction monitoring
%T	total gel concentration (acrylamide plus cross-linking agent; g/100mL)
TBS	Tris-buffered saline
TEMED	*N,N,N′,N′*-tetramethylethylenediamine
TFA	trifluoroacetic acid
THF	tetrahydrofuran
TIC	total ion current
TLC	thin-layer chromatography
TOF	time of flight
Tris	tris(hydroxymethyl)aminomethane
URL	uniform resource locator