

Editorial and Author Guidelines for Publication in PROTEOMICS

These guidelines outline issues that authors must follow when submitting a paper for publication in **PROTEOMICS**. Failure to follow these guidelines may be grounds for an Editorial decision to reject a manuscript without review. Authors are also requested to take note of the different types of manuscripts that are suitable for **PROTEOMICS** as detailed in the 'Instructions to Authors'.

Experimental design and 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. 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 immunoassays) 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.

Protein identification and characterization

- The method(s) used to generate the mass spectrometry data must be described, as should the methods used to create peak lists from raw MS or MS/MS data.
- The name and version of the program 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 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.

Bioinformatics

- Where a manuscript describes an academic database or software, it must be either freely accessible *via* the Internet, or downloadable and the access options must be provided. This also applies to commercial software or databases.

Supporting information

- Supporting information is encouraged. This includes protein identification results, expression data, and mass spectrometry peak lists. Note that all data must be in processed, not raw, form. This material will not be published in the journal but will be available online at the **PROTEOMICS** website (www.proteomics-journal.com).

INSTRUCTIONS TO AUTHORS

Revised December 2007

Authors are requested to follow these Instructions and the Editorial and Author Guidelines carefully. Manuscripts not prepared accordingly will not be accepted.

- 1 Aims and scope
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- 7 Funding information
- 8 Standard abbreviations

1 Aims and scope

PROTEOMICS is the premier international source for information on all aspects of applications and technologies in proteomics. Its mission is to integrate the various areas of this rapidly developing field which is having a major impact on all areas of the life sciences and industry. We welcome papers describing novel applications of proteomics. Topics include whole proteome analysis of any organism, expression profiling, disease studies, pharmaceutical, agricultural and biotechnological applications, and analysis of cellular systems, organelles and protein

complexes. Technological topics covered include new or improved separation techniques, methods of protein identification and characterization including the analysis of post-translational modifications, transcriptomics and bioinformatics. **PROTEOMICS** publishes articles in English. Manuscripts must be grammatically and linguistically correct, and authors less familiar with English usage are advised to seek the help of English-speaking colleagues. Either American or English spelling is acceptable. **PROTEOMICS** is published in 24 issues *per* year, including regular issues as well as topical issues.

2 General terms of publication

The author vouches that the work has not been published elsewhere, either completely, in part, or in any other form and that the manuscript has not been submitted to another journal. The submitting author (listed under "Correspondence") accepts the responsibility of including as coauthors all appropriate persons. The submitting author certifies that all coauthors have seen a draft copy of the manuscript and agree with its publication.

Upon acceptance of the manuscript the author is required to fill in the "Copyright Transfer Agreement" and the "Color and Page charge Agreement" forms (please see the journal homepage for current charges), sign them and submit them along with hardcopies of the illustrations of the paper to:

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These mandatory forms can be found directly on the homepage of the journal at <http://www.proteomics-journal.com> under the link "For Authors". 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**. Authors are expected to carry any costs arising from permissions.

All scientific contributions will be peer-reviewed on the criteria of originality and quality. Authors may suggest up to five potential referees (please provide their e-mail addresses) as well as individuals whom they wish to be excluded from the review process. On acceptance, papers may be subjected to editorial changes. A revised paper will retain its original date of receipt only if it is resubmitted to the Editors within two months after revision was requested. Responsibility for the factual accuracy of a paper rests entirely with the author.

Our **Early View** online publication is updated weekly and enables papers to be available online and citable before going into print.

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.

3 Online submission of manuscripts

PROTEOMICS offers a web-based manuscript submission and peer-review system. This service guarantees fast and safe submission of manuscripts and rapid assessment. Using this system is obligatory; conventional submission of manuscripts is no longer accepted.

3.1 General remarks

To submit your manuscript online, please proceed as follows:

- Prepare your manuscript and illustrations in the appropriate format, according to the instructions given below (see Sections 4 to 8). Please also make sure that your paper conforms with the scientific and style instructions of **PROTEOMICS** as given herein. You can also find a link to these instructions on the homepage of the journal at <http://www.proteomics-journal.com> under the link "For Authors". Links for English language assistance are also provided here.
- If you have not already done so, create an account for yourself in the system at the submission site <http://mc.manuscriptcentral.com/proteomics/> by clicking on the "Create Account" button.
- Let the system 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. All submissions are strictly confidential. To monitor the progress of your manuscript throughout the review process, just login 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-vch.de.

3.2 Electronic manuscripts

Please follow the instructions in Section 5 "Organization of manuscripts" 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 (incl. front material) as well as figure legends and tables (in this order) should be given in one file, preferably saved in .doc or .rtf format (Word 2003 or older, not .docx).
- Data should be typed unjustified, without hyphenation except for compound words. Use carriage returns only to end headings and paragraphs; spacing will be introduced by the typesetter.
- Do not use the space bar to make indents; where these are required use the TAB key.
- If working in Word for Windows, please create special characters through **Insert/Symbol**.
- Figures should preferably be in TIFF, EPS, PPT or the original format. Each figure should be given in a separate file and should have the following resolution:

Type	Resolution
Graphs	800 – 1200 DPI
Photos	400 – 800 DPI
Color (only CMYK)	300 – 400 DPI

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. It is not necessary to submit the graphics with high resolution at this stage.

3.3 Revised manuscripts

In revised manuscripts the areas containing the major required changes should be marked and the script color changed. The file(s) with the changes visible on screen should be submitted to the online procedure.

Upon acceptance of the manuscript the final uploaded version will be taken as the basis for copy editing 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 not exceed 6500 words in total; this includes references, figure legends and tables. Papers of up to 7 printed pages will be published free of charge; for papers exceeding that length a **page charge** (see the journal homepage) will be levied. Please note that the length of an article depends greatly on the type of figures and tables provided. Manuscripts must not have been published previously, except in the form of a preliminary communication.
- (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.
- (iii) Rapid communications describing results that are brief, timely and/or of such importance that rapid publication is warranted. These manuscripts should bear the words "Rapid Communication" immediately above the title on the first page. They should not be subdivided into titled sections but should be written in a continuous style. Rapid communications should normally not exceed four printed pages and contain no more than two figures and one table.
- (iv) Technical briefs describe 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. A technical brief is a short (no more than two pages when published) description written in a continuous style with no more than two figures and one table.

- (v) Dataset briefs describe novel proteomic datasets of specific types of samples, such as organisms, tissues, organelles, and cells. These datasets can be generated with any proteomic platform including two-dimensional gels, mass spectrometry or protein arrays. An important criterion is that the dataset contains a significant number of identified proteins that will benefit further research on that particular sample type. 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 should be written in a continuous style. Dataset briefs should normally not exceed two printed pages and contain no more than two figures and one table in the published text, but authors are encouraged to submit supporting information, such as annotated two-dimensional gel images and tables of protein identifications, that will only appear online.
- (vi) Viewpoint articles 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). These manuscripts should bear the word “Viewpoint” immediately above the title on the first page. They should not be subdivided into titled sections but should be written in a continuous style. Viewpoint articles should normally not exceed two printed pages and contain no more than one figure. Potential authors considering contributing a viewpoint article to the journal should in the first instance contact the Editor-in-Chief by e-mail (eic.proteomics1@ucd.ie) to discuss their proposal. In order to provide a forum for debate of the issues raised in the viewpoint articles, correspondence concerning these articles will be published for a special area on the journal's homepage (<http://viewpoint.proteomics-journal.com>).
- (vii) Reports on meetings, workshops, and other events of relevance to the field of proteomics are invited. These manuscripts should bear the word “Report” immediately above the title on the first page. They should not be subdivided into titled sections but should be written in a continuous style. Report articles should normally not exceed two printed pages and may contain a single figure to illustrate the meeting. Potential authors considering contributing a report article to the journal should in the first instance contact the Editor-in-Chief by e-mail (eic.proteomics1@ucd.ie) to discuss their proposal.

5 Organization of manuscripts

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

5.1 Contents of first page of manuscript

The first page of the manuscript should contain only the following:

- 1) Title of the paper containing only the keywords pertaining to the subject matter. Standard abbreviations may be used in the title.
- 2) 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.
- 3) Name (and title) and full postal address of the author to whom all correspondence (including galley proofs) is to be sent. E-mail address and fax number must be included to speed up communication.
- 4) A list of abbreviations used in the paper excluding standard abbreviations (see list of “Standard Abbreviations”, Section 8).
- 5) Keywords (max. 5, in alphabetical order).

5.2 Abstract

The second and (if necessary) third page of the manuscript should contain the abstract only. This must be self-explanatory and intelligible without reference to the text. It should not exceed 200 words for research and review articles. Abstracts for rapid communications, technical and dataset briefs, viewpoint articles, and reports should not

exceed 80 words. Abbreviations, but not standard abbreviations, must be written in full when first used. Any references cited must be given in full.

5.3 Division into sections

Manuscripts should be divided into the following sections:

- “1 Introduction”: containing a description of the problem under investigation and a brief survey of the existing literature on the subject.
- “2 Materials and methods”: for special materials and equipment, the manufacturer's name and, if possible, the location should be provided.
- “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.

5.4 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 amine-specific 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] Möller, 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 (Digital Object Identifier), 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 the text directly after the data to which they refer.

A link to the latest End Note style sheet can be found on the homepage www.proteomics-journal.com under the link For Authors.

5.5 Acknowledgements

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

5.6 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.

5.7 Tables

Tables with suitable captions at the top and numbered with Arabic numerals should be collected at the end of the text on separate sheets (one page *per* 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.

5.8 Supporting information

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 InterScience.

Further, other files may be submitted as supporting information (*e.g.* animations, video sequences). All supporting information will also undergo the peer-review process. Thus, this material has to be submitted electronically along with the main body of the article. It is in the hands of the Editor-in-Chief to decide which part of the manuscript will be published as supporting information.

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. Data should be deposited in public, open access databases, formatted according to conventions of the relevant communities prior to manuscript submission, and database accession numbers provided in the manuscript. In particular, novel protein sequences should be deposited in UniProt (www.uniprot.org); molecular interactions in an IMEx partner database (imex.sf.net); and protein identification data in PRIDE (www.ebi.ac.uk/pride), World-2DPAGE (www.expasy.org/world-2dpag/), or a comparable database.

5.9 Figures and legends

Diagrams and photographs should be submitted as separate files. Upon acceptance of the paper hardcopies of fine quality suitable for reproduction should be sent to the Editorial Office (address see Section 2). Figures should be numbered consecutively with Arabic numerals in the order of their appearance. Figures should be submitted in a format which can be reduced to a width of 50–80 mm or 120–170 mm, and symbols and labels to a height of 2.0 mm (after reduction). 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 two dimensions, are thus presented consistently with the standard coordinate system. Each figure is to be accompanied by a legend which should be self-explanatory. The legends should not appear under the figures but be collected and typewritten with double spacing following the references.

Color figures can be reproduced: however authors will be charged for additional costs incurred for the reproduction of color (see Section 2).

5.10 Image manipulation

Manipulation of images is strongly discouraged and 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 and an explanation of the alterations is included in the Figure legend. 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.

5.11 Biographic material

Corresponding authors of review and viewpoint articles are invited to submit a portrait photograph of themselves and a short biographical text (no more than 80 words) which will appear at the very end of the article.

5.12 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.

5.13 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.

5.14 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. Abbreviations should be introduced only when repeatedly used. Abbreviations used only in a table or a figure may be defined in the legend. Standard abbreviations may be used in the title and keywords. 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.

Section 8 at the end of these instructions contains the list of standard abbreviations which may be used without definition in the articles published in **PROTEOMICS**.

5.15 Ethics

If the manuscript describes 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 no such rules or permission are stipulated in the particular country, this must also be mentioned in the paper. In the case of human studies, it should be stated that local ethical committee approval has been received and that the informed consent of all participating subjects was obtained. These statements must be confirmed in the cover letter.

5.16 Sharing of materials

All materials and reagents that are not commercially available (antibodies, cell lines, constructs *etc.*) and associated protocols detailed in manuscripts published in **PROTEOMICS** are to be freely available to academic researchers in a timely manner upon request. The authors agree to this condition by submitting a manuscript to **PROTEOMICS**.

6 Proofs and reprints

Before publication authors will receive page proofs *via* e-mail in PDF low resolution file format, together with instructions and a reprint order form, also as PDF files. The page proofs and the reprint order form should be printed out. The proofs should be carefully corrected following the instructions. In particular, authors should answer any

editing queries. The reprint order form should be filled out (even if additional reprints are not required), and both should be returned, preferably by fax, to the address given in Section 2.

Authors will be charged for extensive alterations of their article. Reprints can be ordered at prices shown on the reprint order form. Upon publication the submitting author (listed under "Correspondence") will receive a complimentary copy of the issue containing the article.

7 Funding information

7.1 NIH Authors

On behalf of our authors who are also NIH grantees, Wiley will deposit in PMC at the same time that the article is published in our journal the peer-reviewed version of the author's manuscript. Wiley will stipulate that the manuscript may be available for "public access" in PMC 12 months after the date of publication.

By assuming this responsibility, Wiley will ensure that authors are in compliance with the NIH request, as well as make certain the appropriate version of the manuscript is deposited.

When an NIH grant is mentioned in the Acknowledgments, Wiley will assume that the author wants the manuscript deposited into PMC, unless the author states otherwise. The author can communicate this via email, or a note in the manuscript. The version of the manuscript that Wiley sends to PMC will be the accepted version.

Because Wiley is taking the responsibility for sending the manuscripts to PMC, in order to ensure an orderly process, authors should not deposit Wiley articles to PMC themselves. Authors should not make corrections to their Wiley-deposited manuscripts in PMC.

Wiley reserves the right to change or rescind this policy.

For further information, please see the NIH Policy on Public Access, located at <http://publicaccess.nih.gov/>

7.2 Funded access

Wiley is now offering a funded access service for authors of journal articles whose funding agency requires deposit of an article in an archive. Interested authors should go to http://www3.interscience.wiley.com/authorresources/funded_access.html for further information.

8 Standard abbreviations

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

A	absorbance	FCS	fetal calf serum	OD	optical density
ACES	2-[(2-amino-2-oxoethyl)amino]ethanesulfonic acid	FIGE	field inversion gel electrophoresis	OFAGE	orthogonal field alternation gel electrophoresis
ACN	acetonitrile	FITC	fluorescein isothiocyanate	ORF	open reading frame
A/D	analog to digital converter	FT-ICR	Fourier transform-ion cyclotron resonance	PAGE	polyacrylamide gel electrophoresis
amu	atomic mass unit	GC	gas chromatography	PBS	phosphate-buffered saline
ANOVA	analysis of variance	GIF	graphic interchange format	PCA	principal components analysis
API	atmospheric pressure ionization	GRAVY	grand average of hydrophobicity	PCR	polymerase chain reaction
AUC	area under curve	GSH	glutathione	PDMS	polydimethylsiloxane
BCIP	5-bromo-4-chloro-3-indolyl phosphate	GST	glutathione-S-transferase	PED	pulsed electrochemical detection
Bis	<i>N,N'</i> -methylenebisacrylamide	HE	hematoxylin and eosin	PEG	polyethylene glycol
bp	base pairs	HEPES	<i>N</i> -(2-hydroxyethyl)piperazine-2'-(2-ethanesulfonic acid)	PFGE	pulsed-field gel electrophoresis
BSA	bovine serum albumin	HPCE	high-performance capillary electrophoresis	PFU	plaque-forming units
%C	cross-linking agent (g/100 mL)/%T	HPLC	high-performance liquid chromatography	pI	isoelectric point
CAPS	3-(cyclohexylamino)-1-propanesulfonic acid	HRP	horseradish peroxidase	PMF	peptide mass fingerprinting
CBB	Coomassie Brilliant Blue	HSA	human serum albumin	PMS	phenazine methosulfate
CCD	charge-coupled device	HSP	heat shock protein	PMSF	phenylmethylsulfonyl fluoride
CE	capillary electrophoresis	HTML	hypertext mark-up language	PMT	photomultiplier tube
CEC	capillary electrochromatography	HUPO	Human Proteome Organisation	PSD	post-source decay
CFE	continuous flow electrophoresis	HVR	hypervariable region	PTFE	polytetrafluoroethylene
CHAPS	3-[(3-cholamidopropyl)dimethylammonio]-1-propanesulfonate	ICAT	isotope-coded affinity tag	PTH	phenylthiohydantoin
CHCA	α -cyano-4-hydroxycinnamic acid	ICR	ion cyclotron resonance	PTM	post-translational modification
CHES	2-(<i>N</i> -cyclohexylamino)ethanesulfonic acid	id	inside diameter	PVA	polyvinyl alcohol
CID	collision-induced dissociation	IEF	isoelectric focusing	PVDF	polyvinylidene difluoride
CIEF	capillary isoelectric focusing	Ig	immunoglobulin	PVP	polyvinylpyrrolidone
CMC	critical micelle concentration	IMAC	immobilized metal affinity capture	RFLP	restriction fragment length polymorphism
Con A	Concanavalin A	IPG	immobilized pH gradient	RIA	radioimmunoassay
CNS	central nervous system	IPTG	isopropyl- β -D-thiogalactopyranoside	ROS	reactive oxygen species
cpm	counts <i>per</i> minute	IT	ion trap	RP	reversed phase
CTAB	cetyltrimethylammonium bromide	iTRAQ	isobaric tag for relative and absolute quantitation	rpm	revolutions <i>per</i> minute
CV	coefficient of variation	kbp	kilobase pairs	RSD	relative standard deviation
CZE	capillary zone electrophoresis	kDa	kilodalton (molecular mass)	RT-PCR	reverse transcriptase-PCR
1-D	one-dimensional	LC	liquid chromatography	SAGE	serial analysis of gene expression
2-D	two-dimensional	LED	light-emitting diode	SD	standard deviation
Da	dalton (molecular mass)	LOD	limit of detection	SDS	sodium dodecyl sulfate
2-DE	two-dimensional gel electrophoresis	LOQ	limit of quantitation	SEC	size-exclusion chromatography
DIGE	fluorescence difference gel electrophoresis	mAb	monoclonal antibody	SELDI	surface-enhanced laser desorption/ionization
DGGE	denaturing gradient gel electrophoresis	MALDI-MS	matrix-assisted laser desorption/ionization-mass spectrometry	SEM	standard error of the mean
DMEM	Dulbecco's modified Eagle medium	Mbp	megabase pairs	SIM	selected ion monitoring
DMF	<i>N,N</i> -dimethylformamide	MEKC	micellar electrokinetic capillary chromatography	S/N	signal-to-noise ratio
DMSO	dimethyl sulfoxide	MES	2-(<i>N</i> -morpholino)ethanesulfonic acid	SPE	solid-phase extraction
DOC	sodium deoxycholate	MHC	major histocompatibility complex	SPR	surface plasmon resonance
dsDNA	double-stranded DNA	MOPS	3-(<i>N</i> -morpholino)propanesulfonic acid	SSCP	single-strand conformation polymorphism
DTT	dithiothreitol	<i>M_r</i>	relative molecular mass (dimensionless)	ssDNA	single-stranded DNA
ECL	enhanced chemiluminescence	MS	mass spectrometry	SSP	sample spot number
EDTA	ethylenediaminetetraacetic acid	MS/MS	tandem mass spectrometry	STR	short tandem repeat
EEO	electroendosmosis	<i>m/z</i>	mass-to-charge ratio	%T	total gel concentration (acrylamide plus cross-linking agent; g/100 mL)
EGTA	ethylene glycol-bis(β -aminoethyl-ether)- <i>N,N,N',N'</i> -tetraacetic acid	NBT	nitroblue tetrazolium	TBS	Tris-buffered saline
EKC	electrokinetic chromatography	NC	nitrocellulose	TCA	trichloroacetic acid
ELISA	enzyme-linked immunosorbent assay	NEPHGE	nonequilibrium pH gradient electrophoresis	TEMED	<i>N,N,N',N'</i> -tetramethylethylenediamine
EOF	electroosmotic flow	NMR	nuclear magnetic resonance	TFA	trifluoroacetic acid
ER	endoplasmic reticulum	NP-40	Nonidet P-40	THF	tetrahydrofuran
ESI	electrospray ionization	od	outside diameter	TIC	total ion current
EST	expressed sequence tag			TLC	thin-layer chromatography
FAB	fast atomic bombardment			TOF	time of flight
FBS	fetal bovine serum			Tris	tris(hydroxymethyl)aminomethane
				URL	uniform resource locator
				Vh	volt \times hours