JOURNAL OF PROTEOMICS
An official journal of the European Proteomics Association (EuPA)

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DESCRIPTION

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

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

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

**Types of paper**

The following types of paper are published:

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Mandatory requirements for reporting of clinical biomarker studies:

1) A clinical biomarker is only relevant in specific contexts of use per disease, it must have a potential to improve the current state of the art (either being of added value, or based on its sole performance), and its application must be linked to a clear change in patient management. As such, the specific proposed context of use of the presented biomarker must be clearly provided and the expected practical consequence of the biomarker application should be discussed.

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3) This initial independent validation and performance assessment has to be performed in samples that reflect the typical clinical situation depending on the targeted context of use.

4) Authors submitting clinical biomarker studies should address the above points in the cover letter, so that the Editor can assess and evaluate if the submitted manuscript fulfils the requirements for publication in Journal of Proteomics.

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

*Tutorials*: The International Proteomics Tutorial Programme, initiated by the education committees of the Human Proteome Organisation (HUPO) and the European Proteomics Association (EuPA) is aimed at Masters/PhD level students who are starting out their research and who would benefit from a solid grounding in the techniques used in modern protein-based research. The tutorial program will cover core techniques and basics as an introduction to scientists new to the field. Authors are generally invited to contribute a Tutorial. For suggestions, prospective authors of high standing may contact the Journal's Tutorial editor Peter James.
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Original articles are usually divided into the sections Introduction, Materials and methods, Results, Discussion and Conclusions:

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

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Starting January 2013, manuscripts submitted to Journal of Proteomics must include a paragraph entitled "Significance" detailing the biological relevance of the reported research or technological innovation. Authors should not realistically state how the paper impacts its field of research (please consult Calvete JJ (2012) Updating JPROT’s publication standards for large-scale proteomic studies: towards hypothesis-driven interpretation of predictive biological models. J Proteomics 76, 1-2).

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The main conclusions of the study may be presented in a short Conclusions section, which may stand alone or form a subsection of a Discussion or Results and Discussion section.
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The experimental design must be provided and must include details of the number of biological and analytical replicates. Only one biological/analytical replicate will not be acceptable. In clinical studies, it is highly desirable that a power analysis predicting the appropriate sample size for subsequent statistical analysis of the data is carried out.

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

Proper terminology should be used. "Protein species" or "Gene product" are preferred terms when referring to "isoforms" and "allelic variants", respectively, (please consult Jungblut et al. The speciation of the proteome. Chemistry Central Journal 2008; 2: 16, and Schlüter et al. Finding one's way in proteomics: a protein species nomenclature. Chemistry Central Journal 2009; 3: 11). Terms, such as "differences in protein expression" and "induction/repression" should be avoided, since this terminology relates to gene regulation, and quantitative proteomics deals with the measure of differential abundances of spots (2DE) or peptide ions (LC-MS/MS).

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**Appendix**

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

- A absorbance
- ACES 2-[(2-amino-2-oxoethyl)amino]ethanesulphonic acid
- ACN acetonitrile
- A/D analog to digital converter
- AEBSF 4-(2-aminoethyl)benzenesulphonyl fluoride
- amu atomic mass unit
- ANOVA analysis of variance
- API atmospheric pressure ionization
- AUC area under curve
- Bis N,N'-methylenebisacrylamide
- bp base pairs
- BSA bovine serum albumin
- %C cross-linking agent (g/100 mL)/%T
- CAPS 3-(cyclohexylamino)-1-propanesulphonic acid
- CBB Coomassie Brilliant Blue
- CCD charge-coupled device
- CD circular dicroism
- CEC capillary electrophoresis
- CEC capillary electrophoresography
- CFE continuous flow electrophoresis
- CHAPS 3-[(3-cholamidopropyl)dimethylammonio]-1-propanesulphonate
- CHCA a-cyano-4-hydroxycinnamic acid
- CHES 2-(N-cyclohexylamino)ethanesulphonic 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 ethyltrimethylammonium bromide
- CV coefficient of variation
- CZE capillary zone electrophoresis
1-D one-dimensional
2-D two-dimensional
Da dalton (molecular mass)
2-DE two-dimensional electrophoresis
DIGE fluorescence difference gel electrophoresis
DGGE denaturing gradient gel electrophoresis
DMEM Dulbecco's modified Eagle medium
DMF N,N-dimethylformamide
DMSO dimethyl sulphoxide
DOC sodium deoxycholate
dsDNA double-stranded DNA
DTE dithioerithriol
DTT dithiothreitol
ECL enhanced chemiluminescence
EDTA ethylenediaminetetraacetic acid
EEO electroendosmosis
EGTA ethylene glycol-bis(β-aminoethylether)-N,N,N',N'-tetraacetic acid
EKC electrokinetic chromatography
ELISA enzyme-linked immunosorbent assay
EMSA electrophoretic mobility shift assay
EOF electroosmotic flow
ER endoplasmic reticulum
ESI electrospray ionization
EST expressed sequence tag
EUPA European Proteome Association
FAB fast atom bombardment
FACS fluorescence activated cell sorting
FBS fetal bovine serum
FCS fetal calf serum
FIGE field inversion gel electrophoresis
FITC fluorescein isothiocyanate
FT Fourier transform
FT-ICR Fourier transform-ion cyclotron resonance
GC gas chromatography
GIF graphic interchange format
GRAVY grand average hydrophobicity
GSH glutathione
GST glutathione-S-transferase
HE hematoxylin and eosin
HEPES N-(2-hydroxyethyl)piperazine-2'-(2-ethanesulphonic acid)
HPCE high-performance capillary electrophoresis
HPLC high-performance liquid chromatography
HRP horseradish peroxidase
HSA human serum albumin
HSP heat shock protein
HTML hypertext mark-up language
HUPO Human Proteome Organisation
HVR hypervariable region
ICAT isotop-coded affinity tag
ICR ion cyclotron resonance
id inside diameter
IEF isoelectric focusing
Ig immunoglobulin
IMAC immobilized metal affinity capture
IPG immobilized pH gradient
IT ion trap
iTRAQ isobaric tag for relative and absolute quantitation
kbp kilobase pairs
kDa kilodalton (molecular mass)
LC liquid chromatography
SSCP single-strand conformation polymorphism
ssDNA single-stranded DNA
SSP sample spot number
STR short tandem repeat
%T total gel concentration (acrylamide plus cross-linking agent; g/100 mL)
TBS Tris-buffered saline
TCA trichloroacetic acid
TEMED $N,N',N''$-tetramethylethylenediamine
TFA trifluoroacetic acid
THF tetrahydrofuran
TIC total ion current
TLC thin-layer chromatography
TNF tumour necrosis factor
TOF time of flight
Tris tris(hydroxymethyl)aminomethane
TRITC tetramethylrhodamine isothiocyanate
URL uniform resource locator
UTR untranslated region
UV ultraviolet
Vh volt × hours
z ion charge

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