



# JOURNAL OF PROTEOMICS

An official journal of the [European Proteomics Association \(EuPA\)](#)

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ISSN: 1874-3919

### 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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- 2) A biomarker can only be assessed in an independent (ideally blinded) test set, containing sufficient samples to demonstrate significant value and justify relevant claims regarding biomarker use. Assessment of performance in a discovery set is inappropriate.
- 3) This initial independent validation and performance assessment has to be performed in samples that reflect the typical clinical situation depending on the targeted context of use.
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### Article Structure

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

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### Significance

Starting January 2013, manuscripts submitted to Journal of Proteomics must include a paragraph entitled "Significance" detailing the biological relevance of the reported research or technological innovation. Authors shortly but realistically state how the paper impacts its field of research (please

consult Calvete JJ (2012) **Updating JPROT's publication standards for large-scale proteomic studies: towards hypothesis-driven interpretation of predictive biological models.** J Proteomics 76, 1-2).

### *Introduction*

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

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

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### *Experimental design data analysis for 2-D PAGE and MS-based experiments:*

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

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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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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.

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[1] Resing KA, Ahn NG. Proteomics strategies for protein identification. *FEBS Letters* 2005;579:885-9.

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[2] Rehm H. *Protein Biochemistry and Proteomics*. San Diego: Academic Press/Elsevier Inc; 2006.

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[3] Morgan JW, Hettick JM, Russell DH. Peptide sequencing by MALDI 193-nm photodissociation TOF MS. In: Burlingame AL, editor. *Methods in Enzymology*, vol 402: Biological Mass Spectrometry. San Diego: Academic Press/Elsevier Inc; 2005, p.186-209.

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[1] J. van der Geer, J.A.J. Hanraads, R.A. Lupton, The art of writing a scientific article, *J. Sci. Commun.* 163 (2010) 51–59. <https://doi.org/10.1016/j.Sc.2010.00372>.

Reference to a journal publication with an article number:

[2] Van der Geer, J., Hanraads, J.A.J., Lupton, R.A., 2018. The art of writing a scientific article. *Heliyon.* 19, e00205. <https://doi.org/10.1016/j.heliyon.2018.e00205>.

Reference to a book:

[3] W. Strunk Jr., E.B. White, *The Elements of Style*, fourth ed., Longman, New York, 2000.

Reference to a chapter in an edited book:

[4] G.R. Mettam, L.B. Adams, How to prepare an electronic version of your article, in: B.S. Jones, R.Z. Smith (Eds.), *Introduction to the Electronic Age*, E-Publishing Inc., New York, 2009, pp. 281–304.

Reference to a website:

[5] Cancer Research UK, Cancer statistics reports for the UK. <http://www.cancerresearchuk.org/aboutcancer/statistics/cancerstatsreport/>, 2003 (accessed 13 March 2003).

Reference to a dataset:

[dataset] [6] M. Oguro, S. Imahiro, S. Saito, T. Nakashizuka, Mortality data for Japanese oak wilt disease and surrounding forest compositions, *Mendeley Data*, v1, 2015. <https://doi.org/10.17632/xwj98nb39r.1>.

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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 dichroism  
CE capillary electrophoresis  
CEC capillary electrochromatography  
CFE continuous flow electrophoresis  
CHAPS 3-[(3-cholamidopropyl)dimethylammonio]-1-propanesulphonate  
CHCA  $\alpha$ -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 etyltrimethylammonium 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( $\beta$ -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  
LED light-emitting diode  
LOD limit of detection  
LOQ limit of quantitation  
mAb monoclonal antibody  
MALDI-MS matrix-assisted laser-desorption ionization-mass spectrometry  
Mbp megabase  
  
MEKC micellar electrokinetic capillary chromatography  
MES 2-(*N*-morpholino)ethanesulphonic acid  
MHC major histocompatibility complex  
MOPS 3-(*N*-morpholino)propanesulphonic acid  
 $M_r$  relative molecular mass (dimensionless)  
MS mass spectrometry  
MS/MS tandem mass spectrometry  
MTT 3-(4,5-dimethylthiazol-2-yl)-2,5-diphenyltetrazolium bromide  
*m/z* mass-to-charge ratio  
NC nitrocellulose NEPHGE nonequilibrium pH gradient electrophoresis  
NMR nuclear magnetic resonance  
NP-40 Nonidet P-40  
od outside diameter  
OD optical density  
OFAGE orthogonal field alternation gel electrophoresis  
ORF open reading frame  
PAGE polyacrylamide gel electrophoresis  
PBS phosphate-buffered saline  
PCR polymerase chain reaction  
PDMS polydimethylsiloxane  
PED pulsed electrochemical detection PEG polyethylene glycol  
PFGE pulsed-field gel electrophoresis  
PFU plaque-forming units  
pI isoelectric point  
PMF peptide mass fingerprinting  
PMS phenazine methosulphate

PMSF phenylmethylsulphonyl fluoride  
PMT photomultiplier tube  
PSD post-source decay  
PTFE polytetrafluoroethylene  
PTH phenylthiohydantoin  
PTM post-translational modification  
PVA polyvinyl alcohol  
PVDF polyvinylidene difluoride  
PVP polyvinylpyrrolidone  
Q-TOF quadrupole time-of-flight  
RACE rapid amplification of cDNA ends  
RFLP restriction fragment length polymorphism  
RIA radioimmunoassay  
ROS reactive oxygen species  
RP reversed phase  
rpm revolutions *per* minute  
RSD relative standard deviation  
RT-PCR reverse transcriptase-PCR  
SAGE serial analysis of gene expression  
SD standard deviation  
SDS sodium dodecyl sulphate  
SEC size-exclusion chromatography  
SELDI surface-enhanced laser desorption/ionization  
SEM standard error of the mean  
SIM selected ion monitoring  
S/N signal-to-noise ratio  
SPE solid-phase extraction  
SPR surface plasmon resonants  
SSCP single-strand conformation polymorphism  
ssDNA single-stranded DNA  
SSP sample spot number  
STR short tandem repeat  
%T total gel concentration (acrylamide plus cross-linking agent; g/100 mL)  
TBS Tris-buffered saline  
TCA trichloroacetic acid  
TEMED *N,N,N',N'*-tetramethylethylenediamine  
TFA trifluoroacetic acid  
THF tetrahydrofuran  
TIC total ion current  
TLC thin-layer chromatography  
TNF tumour necrosis factor  
TOF time of flight  
Tris tris(hydroxymethyl)aminomethane  
TRITC tetramethylrhodamine isothiocyanate  
URL uniform resource locator  
UTR untranslated region  
UV ultraviolet  
Vh volt ×hours  
z ion charge

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