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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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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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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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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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Results

Results should be clear and concise.

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Conclusions

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

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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.

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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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Reference to a journal publication:
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Reference to a book:
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## Appendix

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

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