TRANSLATIONAL PROTEOMICS

AUTHOR INFORMATION PACK

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DESCRIPTION

Translational Proteomics covers all areas of **human proteomics** using multi-disciplinary approaches to untangle **complex disease processes**. Emphasis is placed on linking basic sciences to clinical research (from patient to bench to bedside). It focuses on the rapid dissemination of novel discoveries. Topics included but not limited to are:

Translational Systems Biology and **Integrative Bioinformatics Clinical Proteomics** and **Personalized medicine Comparative proteomics** and **drug development Medical bioinformatics** and **biostatistics Biomarkers Food** and **Health**

Translational Proteomics is intended to academic, industrial and clinical researchers, physicians, pharmaceutical scientists, biochemists, clinical chemists, disease molecular biologists in the fields of applied human proteomics. Examples of diseases include oncology, neurology, immunity, cardiovascular disease, infectious diseases and any internal medicine disorder.

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GUIDE FOR AUTHORS

Your Paper Your Way
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INTRODUCTION

Translational Proteomics covers all areas of human proteomics using multi-disciplinary approaches to untangle complex disease processes. Emphasis is placed on linking basic sciences to clinical research (from patient to bench to bedside). It focuses on the rapid dissemination of novel discoveries. Topics included but not limited to are:

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Types of paper

The following types of paper are published:

Original Articles: Original articles are the normal medium of publication. **Proteomics discovery should not be only verified on a small cohort of patients, but most importantly must be validated on a few hundreds of patients with deep statistical analysis.** Although there is no fixed length, articles should be as concise as possible, while providing sufficient information for the work to be repeated and for the claims of the authors to be judged by the readers.

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.

Reviews: These are contributed by scientists who are leading specialists in their disease field of expertise, normally at the invitation of the Editors. Authors wishing to contribute a review paper are advised first to contact the Editor in Chief (to avoid overlap with Reviews already commissioned).

News & Views: News & Views point out the author(s) vision of the character and importance of a new direction in traslational proteomics research. They are not intended to be accounts or analyses of an individual's personal research. Although News & Views will usually be invited, they can be submitted without invitation. Author(s) are encouraged to suggest experts in the field who can act as reviewers.

Letters to the Editor: Letters to the Editor are intended to stimulate discussion and debate in areas of general concern and controversy in translational proteomics, and generally reflect the personal opinions of the author(s). They should be written in a continuous style and should normally not exceed two printed pages and contain no more than one figure or table.

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Material and methods
Provide sufficient detail to allow the work to be reproduced. Methods already published should be indicated by a reference: only relevant modifications should be described.

Results
Results should be clear and concise.

Discussion
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.

Conclusions
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.

News & Views and *Letters to the Editor* are not divided into sections after the summary, except for the reference list. The first paragraph serves as an introduction; acknowledgements are added as a final paragraph before the reference list.

Experimental design data analysis for clinical and proteomics-based experiments:
The experimental design must be provided and must include details of the number of biological and analytical replicates and qualitative and quantitative measurement reproducibility. In clinical studies, it is mandatory to provide the STARD checklist and flow diagram for reporting of studies of diagnostic accuracy, the CONSORT checklist for randomized trials, the REMARK checklist for prognostic studies and any appropriate reporting guidelines.

For expression analysis studies, the appropriate Minimum Information for Biological and Biomedical Investigation (MIBBI) checklist(s) should be provided (MIAPE, MIAME, MIAPAR, MIARE, MIASPPE, MIMIx, MIGen, MINI, MIQE, MINSEQE, MIQAS, MIxS, BioDBCore, . . .).

Authors must report the following: methods of data normalization, transformation, missing value handling, the statistical tests used, the degrees of freedom, justification of outliers removal and the statistical package or program used. Where biologically important differences in omics expression are reported, orthogonal confirmatory data are mandatory. The method(s) used to generate the mass spectrometry data must be described. The name and version of the program used for database searching, the values of critical search parameters (e.g. the mass over charge (m/z) and the charge (z) of the precursor ion, fragment mass tolerance, cleavage rules used, allowance for number of missed cleavages, fixed and variable modifications) and the name and version of the database(s) searched must be provided with number of protein entries in the database. The number of unique peptides used to identify a protein must be given as well as the sequence and charge state of each peptide. For each protein identified, measures of certainty (e.g. FDR, p-values), the sequence coverage and the accession number must be provided. The score value for accepting single MS/MS spectra should be provided. How redundancy and isoforms are handled must be provided.

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In addition to the above mentioned checklist, *Translational Proteomics* also requires its own checklist for identification and quantification of peptides and/or proteins by Mass Spectrometry (download word file here here)

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

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

Reference to a chapter in an edited book or book series:
[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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A absorbance
ACES 2-[(2-amino-2-oxoethyl)amino] ethanesulphonic acid
CAN 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
CE capillary electrophoresis
CEC capillary electrochromatography
CFE continuous flow electrophoresis
CHAPS 3-[(3-cholamidopropyl)dimethylamonio]-1-propanesulphonate
CHCA ?-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(?-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
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
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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