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Article Title

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Research Topic

ABSTRACT

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Keywords: Text Text Text Text Text Text Text Text

1 INTRODUCTION

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2 MATERIAL & METHODS

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For Original Research Articles, Clinical Trial Articles, and Technology Reports the following sections are mandatory:

Table 1. Resolution Requirements for the figures

Image Type	Description	Format	Color Mode	Resolution
Line Art	An image composed of lines and text, which does not contain tonal or shaded areas.	TIFF, EPS, JPEG	RGB, Bitmap	900 - 1200 dpi
Halftone	A continuous tone photograph, which contains no text.	TIFF, EPS, JPEG	RGB, Grayscale	300 dpi
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This is a footnote

- Introduction: Succinct, with no subheadings.
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Please note that the Material and Methods section can be placed in any of the following ways: before Results, before Discussion or after Discussion.

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4 DISCUSSION

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Authors should provide relevant information relating to how the peptide/protein matches were undertaken, including methods used to process and analyze data, false discovery rates (FDR) for large-scale studies and threshold or cut-off rates for peptide and protein matches. Further information could include software used, mass spectrometer type, sequence database and version, number of sequences in database, processing methods, mass tolerances used for matching, variable/fixed modifications, allowable missed cleavages, etc.

Authors should provide as supplementary material information used to identify proteins and/or peptides. This should include information such as accession numbers, observed mass (m/z), charge, delta mass, matched mass, peptide/protein scores, peptide modification, miscleavages, peptide sequence, match rank, matched species (for cross species matching), number of peptide matches, ambiguous protein/peptide matches should be indicated, etc. For quantitative proteomics analyses authors should provide information to justify the statistical significance including biological replicates, statistical methods, estimates of uncertainty and the methods used for calculating error.

For peptide matches with biologically relevant post-translational modifications (PTM) and for any protein match that has occurred using a single mass spectrum, authors should include this information as raw data, annotated spectra or submit data to an online repository (recommended option). Authors are encouraged to submit raw or matched data and 2-DE images to public proteomics repositories. Submission codes and/or links to data should be provided within the manuscript.

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The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

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SUPPLEMENTAL DATA

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