

# Bioinformatics strategies for the comprehensive characterization of antigen processing and presentation



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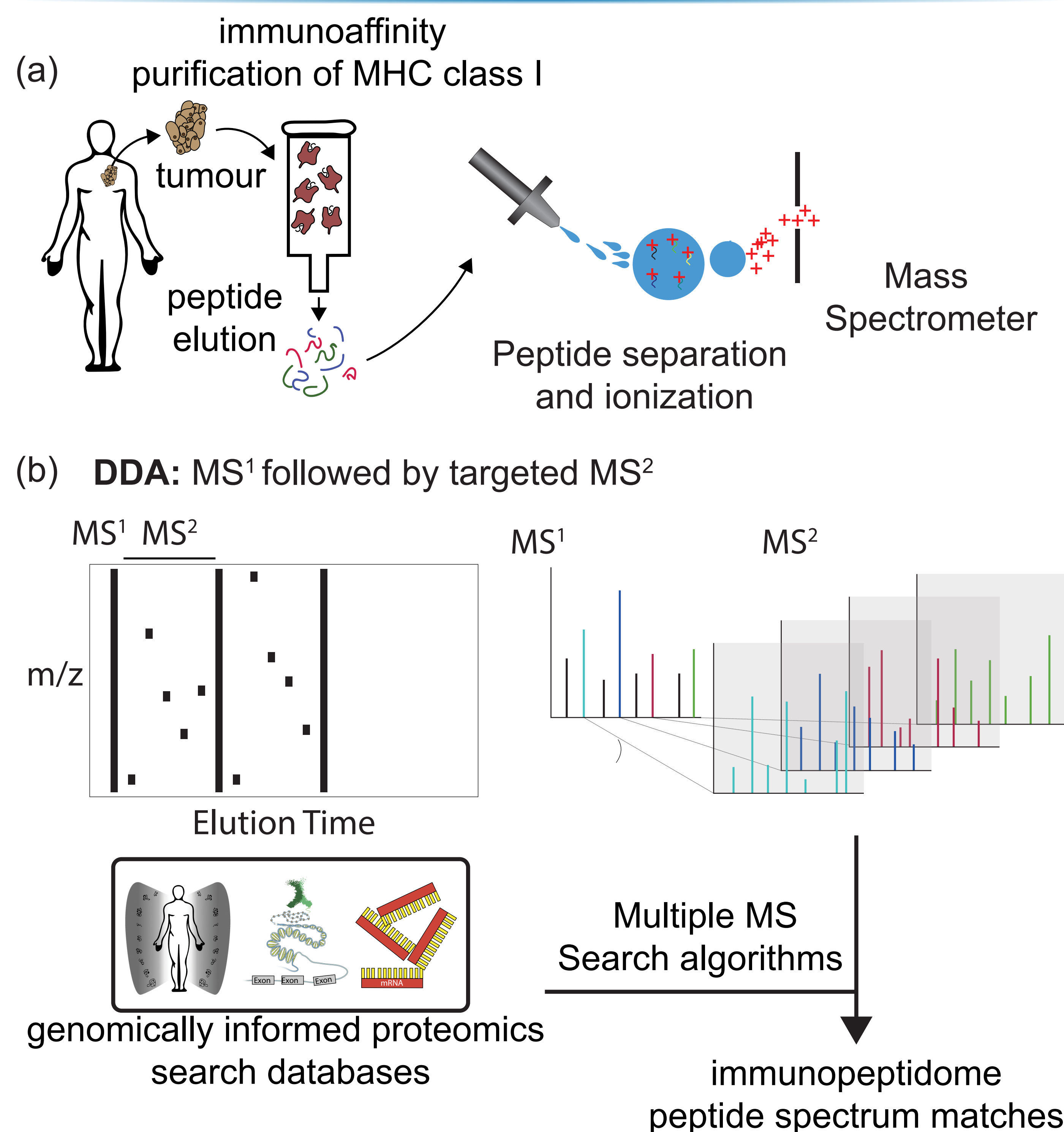
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## Introduction:

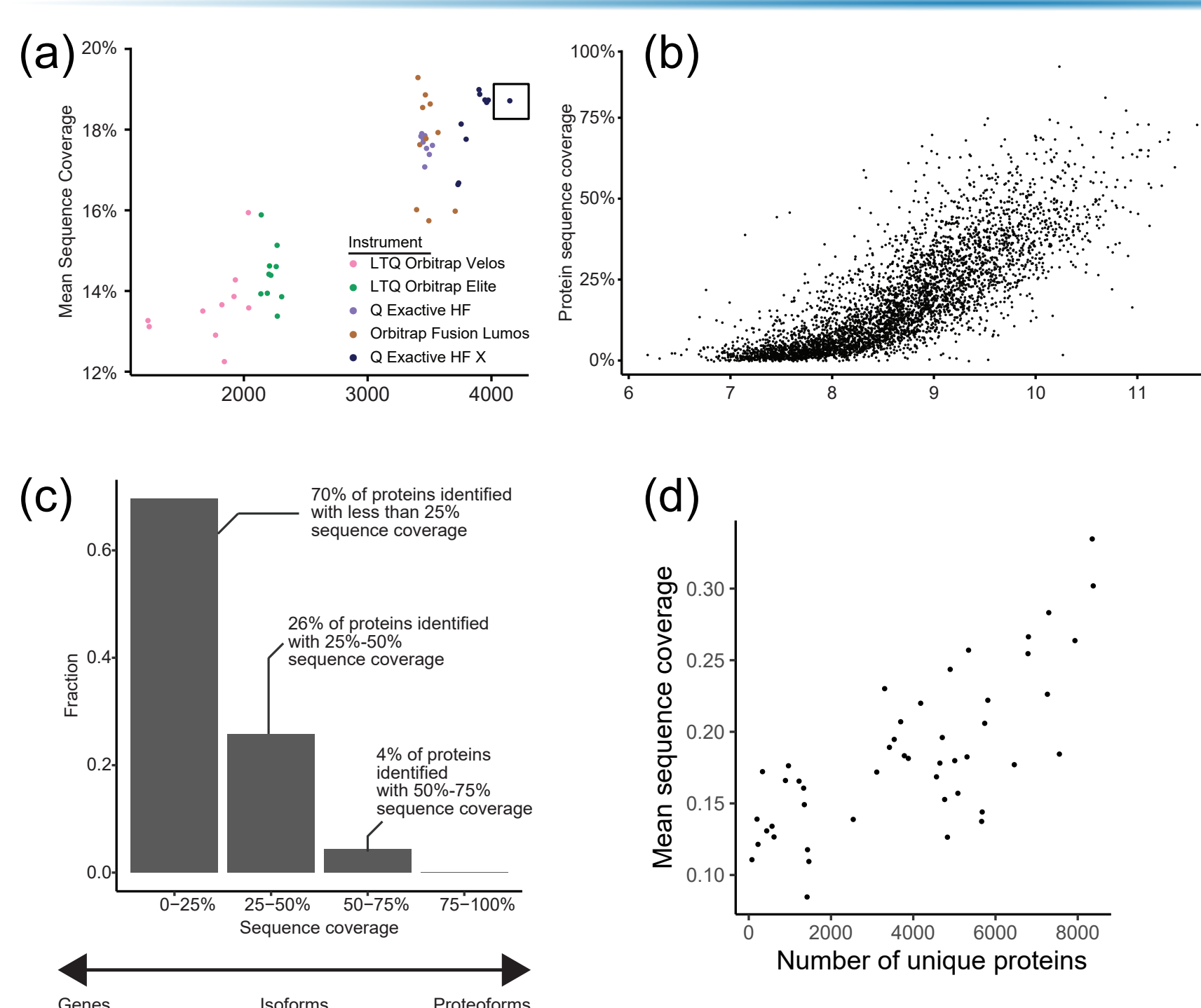
The bioinformatics group at the International Center for Cancer Vaccine Science (ICCVS) is engaged in a few key activities related to neoantigen discovery, the biology of antigen processing, and the development of new immunotherapies.

## Pipelines for immunopeptidome characterization



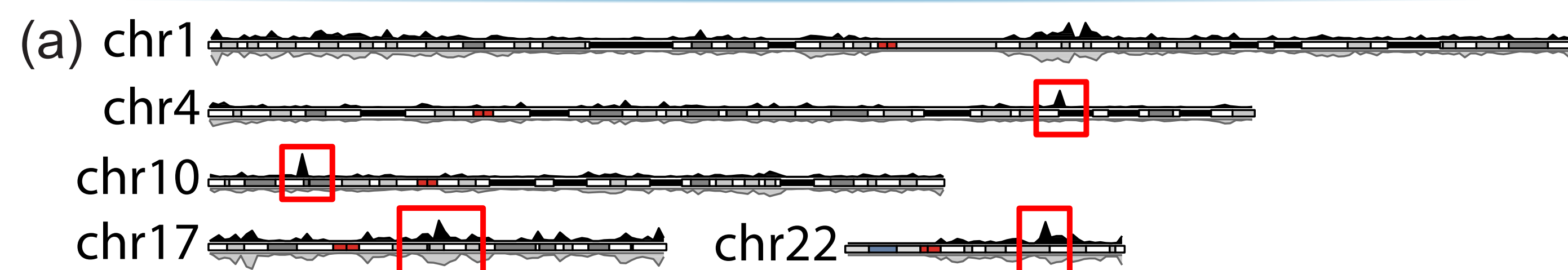
**Figure 1: Immunopeptidomics pipeline.** We have developed computational pipelines for the proteogenomic interrogation of immunopeptidomics datasets. (a) immunopeptidomes are typically characterized by immunoaffinity purification followed by tandem mass-spectrometry. (b) patient specific genomics and transcriptomics data along with publicly available mutation data can be used to identify variants within immuno-peptidomics datasets.

## Translating emerging proteomics technologies

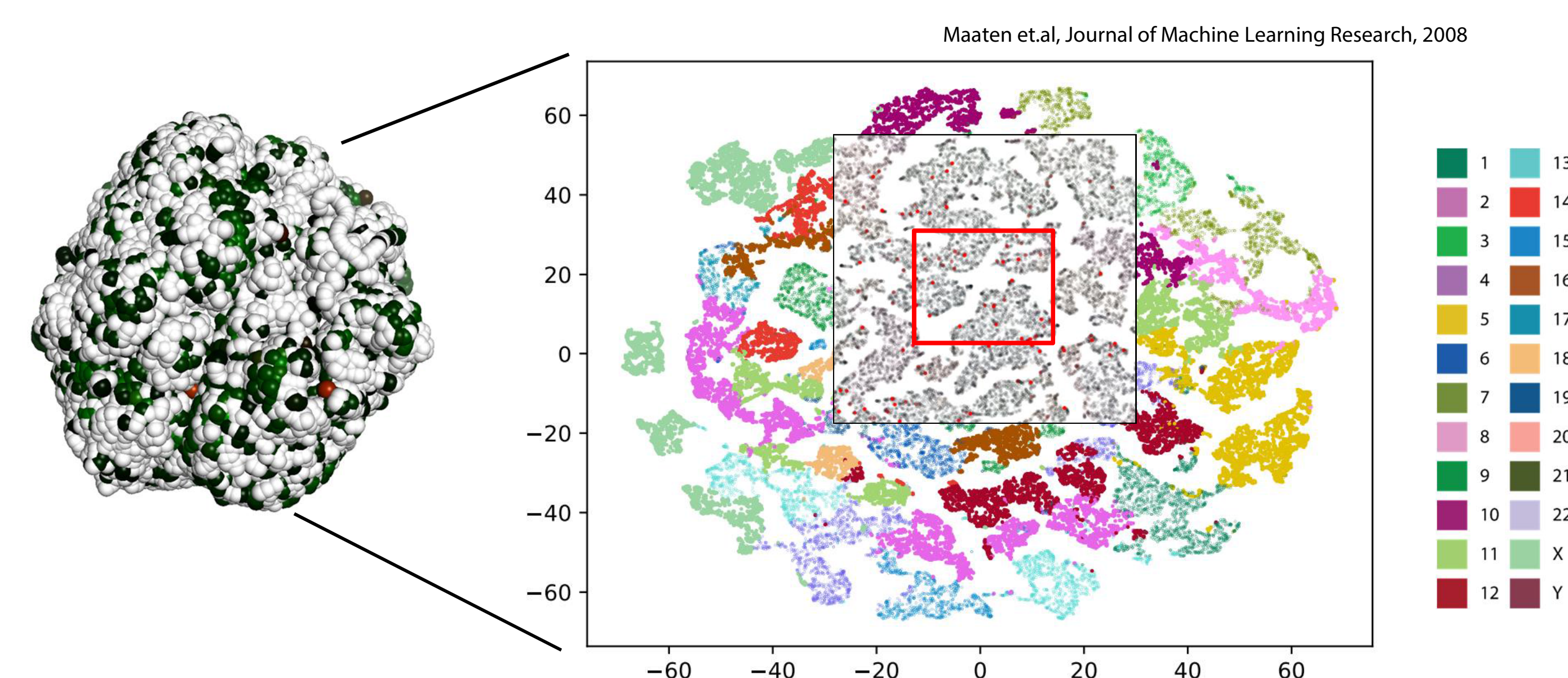


**Figure 2: The need for new technologies.** Understanding sequence coverage in global proteomics. (a) Average sequence coverage of proteins identified in HeLa cell lysate acquired from a single injection into different mass spectrometers. (b) Focus on the highlighted sample in (a). More abundant proteins tend to be covered by more peptides. (c) Distribution of proteins in (b). (d) The single best run from 47 publications present in proteomicsDB.

## Applied clinical proteogenomics

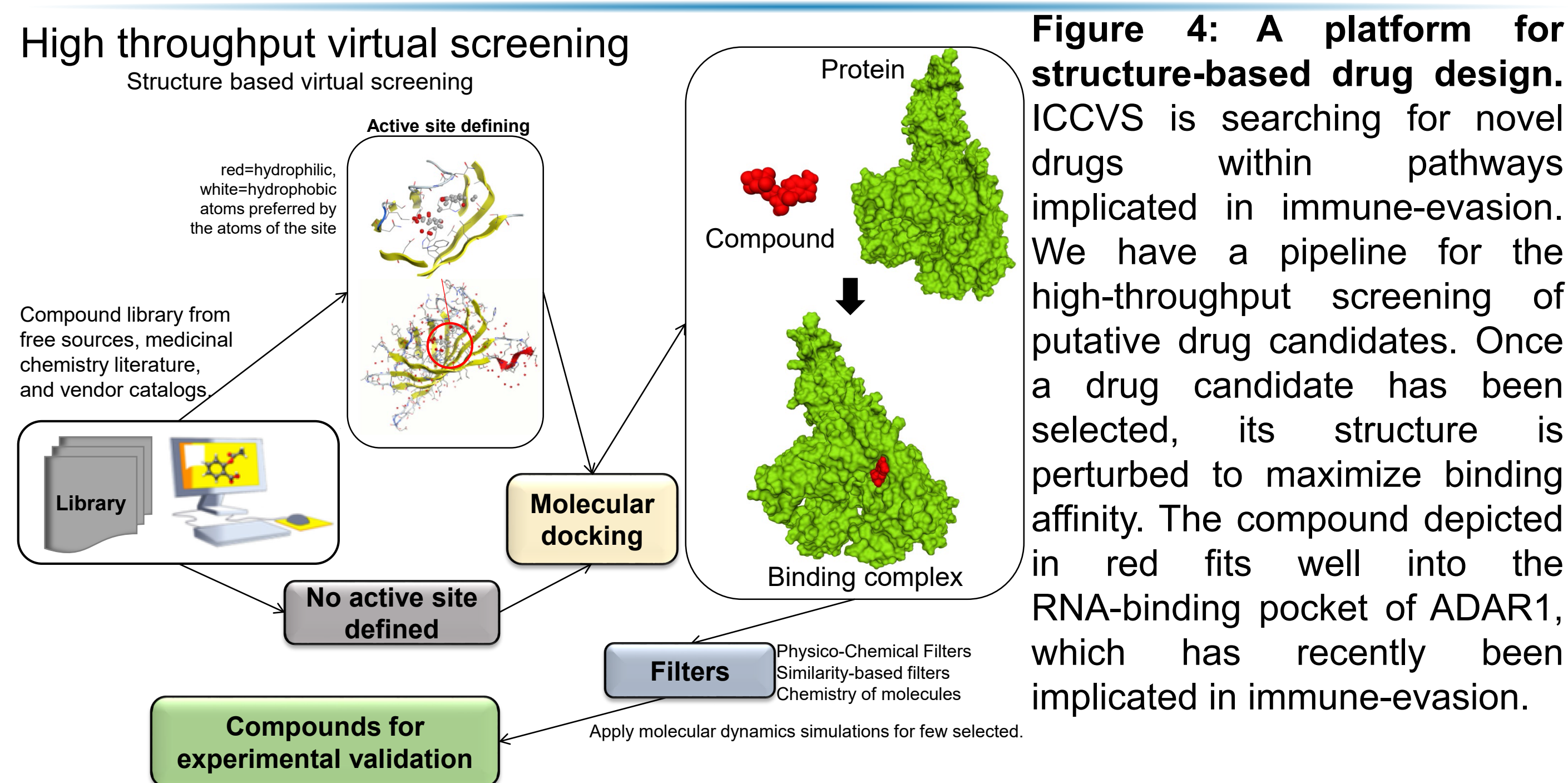


## Nuclear hotspots of antigen-presentation



**Figure 3: Clinical application.** (a) Proof of concept in 25 melanoma tumours of the existence of hotspots of antigen presentation within chromosomes and between chromosomes. (b) RNA-to-protein abundances in a single oesophageal cancer patient, highlighted points are proteins with identified mutations at the protein level. The RHS figure shows the fragment ion evidence for a single mutation.

## Structure-based drug design for immunotherapy



## Acknowledgements

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