

# Bioinformatics HUB: Proteogenomics Special interest topic

9.50am on Wed morning

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LED BY STEPHAN MICHALIK, ANDY JONES, YVES VANDENBROUCK

# Special interest topic on Proteogenomics

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- What is good enough evidence when it comes to “novel peptides” i.e. peptide evidence supporting new genes, new splice sites, changes to current gene models
  - HPP guidelines for human annotations: [https://hupo.org/resources/Documents/HPP/HPPDataGuidelines\\_2.1.0.pdf](https://hupo.org/resources/Documents/HPP/HPPDataGuidelines_2.1.0.pdf)
  - should these adopted for other species’ proteogenomics for novel peptides and for regular peptides, or are they too stringent? community guidelines on
- Best practice in proteogenomics:
  - in database design (using gene finders; RNA sequencing data)
  - In strategy, search tools and statistical methods
- Promoting use of proBed and proBAM standards for genome visualisation