Juan Antonio Vizcaino presents this webinar on PRIDE and ProteomeXchange. PRIDE is a resource that stores mass spectrometry-based protein expression data (including e.g. mass spectra, peptide and protein identifications, among other data types) derived from user submissions.

Some knowledge of proteomics is required to get the most out of this webinar.

This webinar took place on 25th November 2015.

NB: These videos works best using Google Chrome and when viewed in full screen.

Learning objectives:

- Discuss what PRIDE is and why it is important
- Evaluate some of the PRIDE tools

Your feedback

Please tell us what you thought about this webinar. Your feedback is invaluable and helps us to improve our courses and thus enhance your learning experience.

Contributors

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Juan is the Group Coordinator of EMBL-EBI's PRIDE resource for mass spectrometry proteomics data, and he has authored more than 65 papers. He joined the PRIDE team as a postdoc in 2006 and has been involved in numerous projects that span research, development of tools, and training and support for PRIDE users. Since 2011, he has been managing the ProteomeXchange consortium of proteomics resources. He has a background in the life sciences, with a PhD in Molecular Biology from the University of Salamanca, Spain, a Masters in Microbiology and undergraduate degrees in Pharmacy and in Biochemistry.

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