

Proteomics I & II

For discussion:

A draft map of the human proteome. Nature 509,575–581 (29 May 2014)

<http://www.nature.com/nature/journal/v509/n7502/full/nature13302.html>

Mass-spectrometry-based draft of the human proteome Nature 509, 582–587 (29 May 2014)

<http://www.nature.com/nature/journal/v509/n7502/full/nature13319.html>

Further reading I:

Initial sequencing and analysis of the human genome. Nature 409, 860-921 (15 February 2001) |

<http://www.nature.com/nature/journal/v409/n6822/full/409860a0.html>

Further reading II:

Krogan NJ, et al. Global landscape of protein complexes in the yeast *Saccharomyces cerevisiae*. Nature. 440:637 (2006)

Jesper V. Olsen, et al. Global, In Vivo, and Site-Specific Phosphorylation Dynamics in Signaling Networks. Cell 127: 635–648 (2006)

Hanno Steen and Matthias Mann. THE ABC'S (AND XYZ'S) OF PEPTIDE SEQUENCING. Nature Reviews Molecular and Cellular Biology 2004

de Godoy LM et al. Comprehensive mass-spectrometry-based proteome quantification of haploid versus diploid yeast. Nature. 455:1251 (2008)

Behrends C, et al. Network organization of the human autophagy system. Nature. 466:68 (2010)

Gstaiger M , Applying mass spectrometry-based proteomics to genetics, genomics and network biology. Nat Rev Genet. 10:617 (2009)

Vermeulen M, et al. Quantitative interaction proteomics and genome-wide profiling of epigenetic histone marks and their readers. Cell 142:967 (2010)