A complete mass-spectrometric map of the yeast proteome applied to quantitative trait analysis

ID 1609847
Author(s) Picotti, Paola; Clément-Ziza, Mathieu; Lam, Henry; Campbell, David S; Schmidt, Alexander; Deutsch, Eric W; Röst, Hannes; Sun, Zhi; Rinner, Oliver; Reiter, Lukas; Shen, Qin; Michaelson, Jacob J; Frei, Andreas; Alberti, Simon; Kusebauch, Ulrike; Wollscheid, Bernd; Moritz, Robert L; Beyer, Andreas; Aebersold, Ruedi
Author(s) at UniBasel Schmidt, Alexander ;
Year 2013
Title A complete mass-spectrometric map of the yeast proteome applied to quantitative trait analysis
Journal Nature
Volume 494
Number 7436
Pages / **Article-Number** 266-70
Experience from different fields of life sciences suggests that accessible, complete reference maps of the components of the system under study are highly beneficial research tools. Examples of such maps include libraries of the spectroscopic properties of molecules, or databases of drug structures in analytical or forensic chemistry. Such maps, and methods to navigate them, constitute reliable assays to probe any sample for the presence and amount of molecules contained in the map. So far, attempts to generate such maps for any proteome have failed to reach complete proteome coverage. Here we use a strategy based on high-throughput peptide synthesis and mass spectrometry to generate an almost complete reference map (97% of the genome-predicted proteins) of the Saccharomyces cerevisiae proteome. We generated two versions of this mass-spectrometric map, one supporting discovery-driven (shotgun) and the other supporting hypothesis-driven (targeted) proteomic measurements. Together, the two versions of the map constitute a complete set of proteomic assays to support most studies performed with contemporary proteomic technologies. To show the utility of the maps, we applied them to a protein quantitative trait locus (QTL) analysis, which requires precise measurement of the same set of peptides over a large number of samples. Protein measurements over 78 S. cerevisiae strains revealed a complex relationship between independent genetic loci, influencing the levels of related proteins. Our results suggest that selective pressure favours the acquisition of sets of polymorphisms that adapt protein levels but also maintain the stoichiometry of functionally related pathway members.

Publisher Macmillan
ISSN/ISBN 0028-0836
edoc-URL http://edoc.unibas.ch/dok/A6094005
Full Text on edoc No;
Digital Object Identifier DOI 10.1038/nature11835
PubMed ID http://www.ncbi.nlm.nih.gov/pubmed/23334424
ISI-Number WOS:000315137700046
Document type (ISI) Journal Article