Introduction
We present a stand-alone, platform-independent application for 2D-gel-based proteomics data management. Our software intends to bridge the gap between physical sample preparation and post-hoc analysis with software, such as Delta2D (Decodon GmbH, Greifswald), and mass-spectral analysis of gel-spots, i.e. with matrix-assisted laser-desorption-ionization (MALDI) for peptide and protein identification.

Project Creation and Browsing

Figure 1: Project creation with data import from Delta2D projects.

Figure 2: Overview of an open project (top-left), with an open gel view and selected spot (right) and highlighted picked spot location on a 96-well microtiter plate (bottom-left).

Figure 3: Gel viewer zoom in with spot selection, customized label colors and opened context menu for gel spots.

Figure 4: Detailed view of selected gel spot with editable properties.

Microtiter Plate Definition
The user can then define 96-well microtiter plates in order to associate physical spot locations on a gel with the physically picked spot within a well of the plate.

Figure 5: (a) Details of the project tree explorer displaying gel groups, individual gels, a MALDI target plate and 96-well microtiter plates, along with spot group information. (b) View of a 96-well microtiter plate.

MALDI Target Plate Definition

Figure 6: Program overview with Project Explorer (top-left), 96-well microtiter plates (bottom-left), 384 well MALDI target plate (bottom) and linked gel view (center). The gels are both centered on a spot from the same spot group. The corresponding wells belonging to the picked spot in the left gel are highlighted on the plates.

Figure 7: View on a MS identification of a MALDI target spot. Multiple identification results (i.e. from different methods) can be selected.

Spot Browsing and Identification

Figure 8: View on a MS identification of a MALDI target spot. Multiple identification results (i.e. from different methods) can be selected.

Results and Outlook
The software is based on the NetBeans Rich Client Platform, which enforces a high level of modularity and leads to easy extensibility of core functionality through additional plugins. It will be available under the GNU LGPL v3 OpenSource license.

Future work will integrate Proteus with our Metabolomics software Maui (http://maltcms.sf.net) and machine learning algorithms for combined time course data analysis.

Poster copy available at: http://www.cebitec.uni-bielefeld.de/~hoffmann