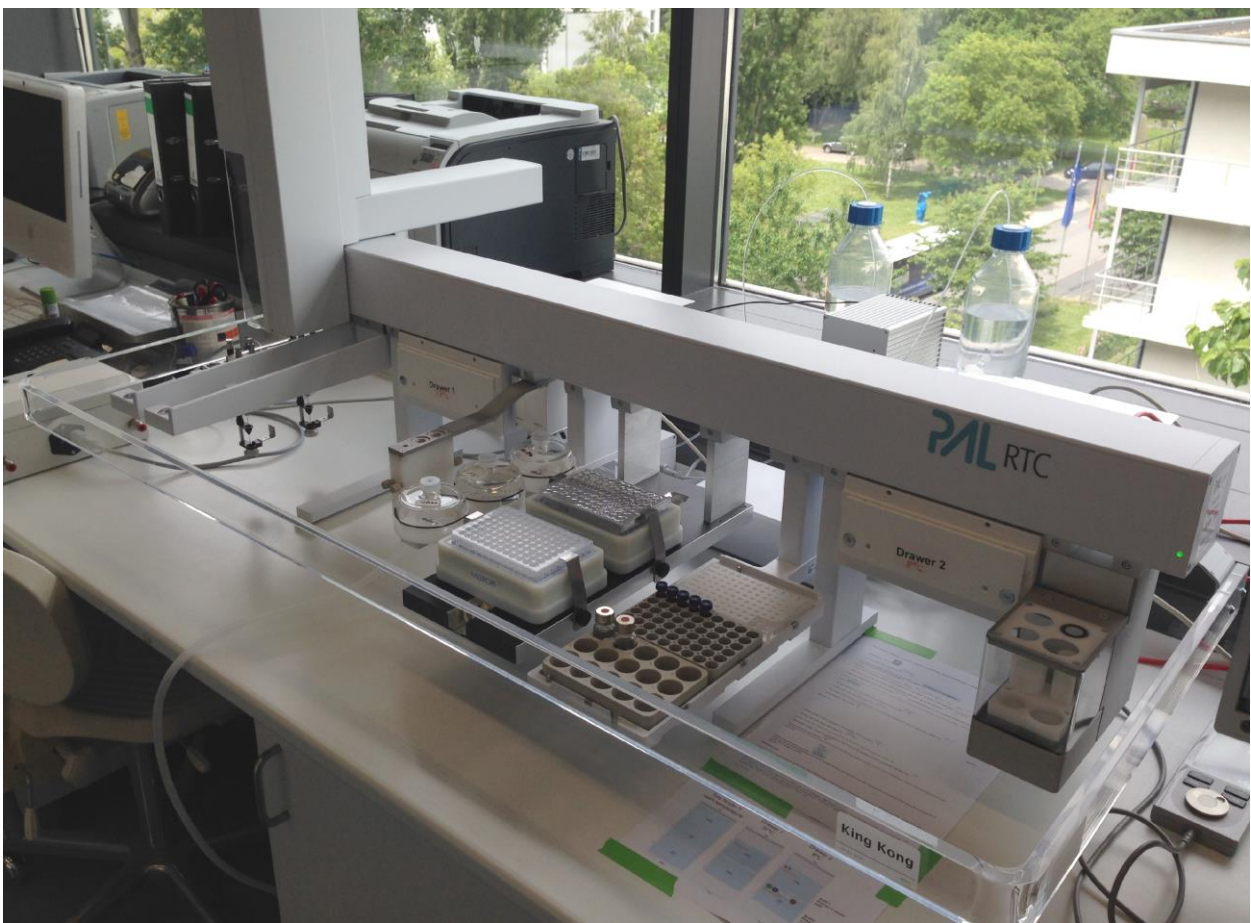




**Axel Semrau®**

# **CHRONECT** *Proteomics* Workstation



**Product Information**

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## Introduction

The mass-spectrometric identification and quantification requires a prior splitting of the proteins into peptides. This splitting, also known as protein digestion, uses enzymes like the protease trypsin or the endopeptidase Lys-C.

The analysis by mass spectrometric methods can be processed using proteins within the solution or proteins which have been isolated by SDS gel electrophoresis. Sample preparation is divided into several steps. The first step after denaturation and washing of the sample is a reduction and subsequent alkylation of the sulfhydryl group in the proteins. Therefore, the reagents TCEP and CAA are used. This is followed by the actual enzymatic digestion and extraction of the newly emerged peptides, which then will be analyzed mass-spectrometrically

For the generation of robust proteomics data, a reproducible procedure is required. Therefore, the usage of automated sample preparation robots is highly recommended.

The Max-Delbrück-Centrum for molecular medicine within the Helmholtz Community in cooperation with Axel Semrau® developed a standard method for the automated protein digestion and transmitted it to the PAL RTC sample robotics.

CHRONOS is used for the efficient yet simple control of the system. It is a software for time-optimized usage of the robotic system and thereby enables a higher sample throughput.

## Automation process

### Protein digestion within the solution (In-solution digest)

- provide protein sample in sample buffer
- add TCEP for reduction reaction / 30 min
- alkylate by CAA / 20 min
- add Lys-C hinzufügen für first digestion / 3 h
- dilute sample with buffer
- add trypsin for second digestion / 10h
- quench digestion by adding TFA

The CHRONECT Workstation Proteomics includes a special tray with a connection to a vacuum pump enabling the digestion of the proteins directly within the electrophoresis gel.

### Protein digestion within the electrophoresis gel (In-gel digest)

- provide gel piece in the tray with the vacuum station
- wash gel intensively
- add TCEP for reduction reaction / 30 min
- alkylate by CAA / 20 min
- add trypsin for digestion / 10 h
- quench digestion by adding TFA

### System components

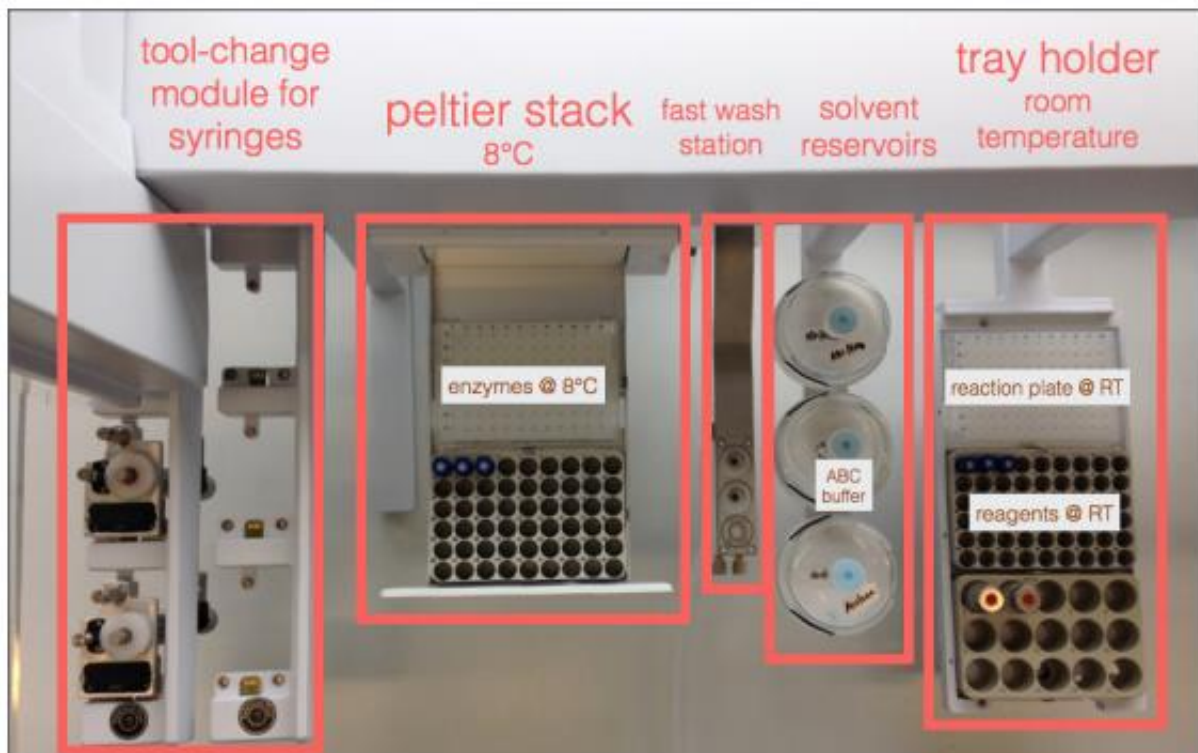
Automation is performed based on the reliable Pal samplers and the software platform CHRONOS. The application system consists of the following components:

- RTC PAL
- Vacuum tray for In-gel digest with a vacuum pump
- CHRONOS Software with pre-installed methods
- Data system for controlling
- SOP generated by the Max-Delbrück-Centrum for molecular medicine
- Accessories and consumables
- Briefing, commissioning, training and support

### Advantages of automation

The CHRONECT Workstation Proteomics features the following benefits:

- high sample throughput
- high degree of automation
- flexible, easy to customize
- based on the know-how of a major proteomics research institute
- ideal for laboratories with medium sample throughput
- no risk of contamination
- excellent reproducibility
- investment safety



**Figure 1:** Overview of the system components.

The application solutions of Axel Semrau® will be preinstalled and tested at the application laboratory and delivered completely operational to the user. This ensures the quickest possible commence of the routine measurement operation.

**The CHRONECT Workstation Proteomics is a development of the Max-Delbrück-Centrum for molecular medicine and Axel Semrau®**

Subject to technical changes

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