

# Urinary Proteomics as a Tool for Discrimination of the Positive Surgical Margin Status after Radical Prostatectomy

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## Introduction

Prostate cancer (PCa) is one of the most frequent malignant diseases of older men. Even with the sophisticated pre-operative staging techniques, an average of 28% of those undergoing radical prostatectomy are found to have positive surgical margins (PSM). Our objective was to determine changes in urinary proteomes of subjects with PSM and negative surgical margins (NSM) after radical prostatectomy using 2D-PAGE and MALDI-TOF.

## Materials/methods

Urine samples from patients suffering from PCa (15 PSM and 15 NSM) were obtained from University Hospital in Motol, Department of Urology, Prague (approval reference EK-377/13). Proteins were isolated using acetone precipitation and separated on 2D-PAGE. After staining using Coomassie Brilliant Blue spots of urinary proteins were excised, in-gel digested and analyzed using MALDI-TOF MS.

### **Results and conclusions**

Following 2D-PAGE and staining, the most prominent spots were picked up for the MS analysis. Some proteins were presented as a horizontal row of multiple spots (with small changes in pI and molecular weight), likely caused by variable posttranslational modifications. It was revealed that majority of proteins (19 overlapping proteins) can be identified in both groups. From all identified proteins, 3 unique proteins have been determined in PSM group. All of them (cyclin-dependent kinase 6, L-lactate dehydrogenase C chain and retinol-binding protein) were determined in more than one case (27 - 67% abundance), which points at their possible connection with presence of residual tumorous tissue. These proteins were previously described in any aspect of PCa. The significance of these findings is represented by molecular changes leading to alterations in biochemical pathways, hopefully related to the presence of residual tumor after surgical treatment failure.

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