

Proteins reveal new mechanisms in prostate cancer

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A study by the University of Tampere in Finland used protein profiling to find new prostate cancer mechanisms that are not shown by aberrations at the genomic level. Several new potential biomarkers of prostate cancer were also found.

Genes that affect prostate cancer evolution have been studied for a long time. However, changes in the protein levels are not well known.

The Center for Prostate Cancer Research and the Center for Proteomics and Personalized Medicine at the University of Tampere cooperated to profile the [protein expression](#) of prostate cancer by using mass spectrometry for the first time. The researchers compared protein expression to genomic and messenger RNAs in the same samples.

The result was that the changes in gene copy numbers and DNA methylation largely explain messenger RNA expression, but not the changes on the protein level. The association between messenger RNA expression and [protein levels](#) was also weak. The study thus uncovered such mechanisms of [prostate cancer](#) that are not indicated by the alterations at the genomic level.

"In particular, changes in the citric acid cycle emerged in our analyzes," Adjunct Professor Leena Latonen says. "The results enable exploring the significance of these changes."

In addition to the disease mechanisms, protein profiling revealed several

potential new biomarkers.

According to Professor Tapio Visakorpi, biomarkers able to recognize the aggressive forms of [prostate cancer](#) would be especially useful. That is one of the aspects on which the researchers will focus next. The research was published in *Nature Communications*.

More information: *Nature Communications* (2018). [DOI: 10.1038/s41467-018-03573-6](https://doi.org/10.1038/s41467-018-03573-6)

Provided by University of Tampere

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