Report from active participation in 10th Siena Meeting entitled "From genome to proteome" 20 Years of Proteomics, August 31st – September 4th, 2014, Siena, Italy – Malgorzata Bajor

The 10th Siena Meeting "From genome to proteome" was held in Siena biannually since 1994 when, at the first one, the idea of the Proteome was first introduced to a large audience by Marc Wilkins. As a consequence this year it was a celebration of the 20th birthday of the Proteome concept. Therefore, the 10th Siena Meeting was a special edition, with the presence of the most representative invited speakers in the field of Proteomics. The Siena Meeting is recognized as one of the most important proteomics conference and is extremely well attended by scientists from all over the world. During this conference I had an opportunity to hear state-of-the-art lectures and key historical and breakthrough discoveries authored by leading researchers, in and around the area of Proteomics, whose contributions have left significant and lasting marks in the field. Moreover, the goal of this meeting was to provide a platform for sharing newest results in broad range of proteomics. I had a pleasure to present our data during MAIN SESSION 2 – Towards Clinical Applications. Professor Denis Hochstrasser from the University of Geneva, Switzerland was moderating this session.

Title of the poster: **An antibody-based proteomic approach for identification of PRDX1 as a biomarker in estrogen receptor positive breast cancer**

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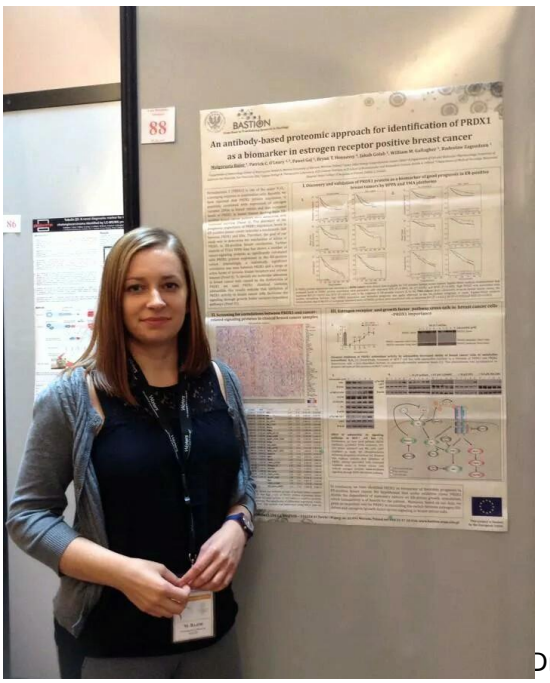

Dr Bajor at the poster during poster session

Recent advances in genomics and gene expression-profiling approaches have enriched our understanding of the heterogeneity of breast cancer. However, it is known that large genomic analyses not always can be translate into protein expression and/or function. Thus, an urgent need exists to define the functional proteomes in parallel to genomic and transcriptional studies for prediction of novel biomarkers in breast cancer.

Peroxideroxin 1 (PRDX1) is one of the major H_2O_2 - scavenging enzymes in mammalian cells. Recently, we have reported that PRDX1 protein expression is positively correlated with expression of estrogen receptor (ER)α in breast cancer, and that increased levels of PRDX1 in tumor tissues derived from ER-positive breast cancer patients were associated with improved survival. The discovery of the prognostic importance of PRDX1 expression levels in ER-positive breast cancer indicates a mechanistic link between PRDX1 and ERα. Therefore, the goal of our study was to determine the mechanism of action of PRDX1 in ER-positive breast carcinomas. Further analysis of TCGA RPPA data has shown a number of cancer-signaling proteins as significantly correlated with PRDX1 protein expression in the ER-positive cohort. Interestingly, a statistically significant correlation was seen between PRDX1 and a range of active forms of tyrosine kinase receptors and cellular kinases. To identify the molecular alteration in breast cancer cells caused by the dysfunction of PRDX1 we used PRDX1 chemical inhibitor, adenanthin. Our results indicate that inhibition of PRDX1 activity in breast cancer cells facilitates the signaling through growth factor receptor-dependent pathways.

Our new studies suggest an important role for PRDX1 in controlling the switch between estrogen/ER-driven and oncogene/growth factor-driven signaling in breast cancer cells. The elucidation of the PRDX1 function in breast cancer may help provide various opportunities for pharmacological intervention, especially in the context of recent observations connecting the oxidative stress and resistance to endocrine therapy.