

# Identification of immunogenic markers in pancreatic and ovarian cancer by seromics

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## Abstract

Protein arrays offer a miniaturized platform that can be used to determine specific reactivity of serum or plasma samples against very large sets of antigens, a process that can be referred to as seromics. We first validated the technology in comparison to ELISA-based assays using sera with previously determined specificity to antigens present on microarrays. We also defined a set of stringent normalization and calculation strategies tailored to the challenges posed by the use of serum for antigen detection: high variability between individuals in reactivity and serum composition, large range of titers expected to individual antigens with variable frequency, etc.

A set of 60 sera from pancreatic patients and 52 sera from ovarian cancer patients were selected according to disease status (localized vs. metastatic) and outcome (long-term vs. short-term survival), and compared to a set of 53 sera from age-matched healthy donors. Data were analyzed according to algorithms dedicated to this type of analyses.

We describe here the results of these analyses, which yielded a series of antigens capable of eliciting immune responses with higher frequency and specificity in the sera of cancer patients in comparison to normal subjects. We compare the frequency of these immunogenic antigens in pancreatic vs. ovarian cancer, define shared targets, and their relationship to clinical status. Together, these data highlight the potential for the discovery of new immunogenic targets in cancer with immunotherapeutic potential for vaccine development, but also for the definition of biomarker signatures able to diagnose cancer status, with possible predictive value. We finally applied these discoveries to determine their use as predictive tools during response to immunotherapeutic intervention, such as the manipulation of immunomodulatory pathways during CTLA-4 blockade.

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