

 PROSTATE CANCER

Biomarkers from liquid biopsy

Researchers have identified liquid-biopsy signatures indicative of extracapsular prostate cancer, demonstrating that computationally guided proteomics can be used to discover biomarkers from samples obtained in a noninvasive manner.

Kim and colleagues combined quantitative targeted proteomics with computational biology to discover robust proteomic signatures for prostate cancer. Initially, 133 proteins were identified in expressed prostatic secretions in urine from men with prostate cancer. These proteins were validated in samples from 74 men, which resulted in 34 proteins demonstrating potential for classifying patients based on disease status.



Optimized assays for absolute quantification were generated and these 34 proteins were quantified in an independent cohort of 207 men, of which 31 showed strong reproducibility. The two most abundant peptides represented *KLK3* (also known as *PSA*) and the detector response was so strong that it was removed from further analysis.

Univariate analysis showed that 27 of the remaining 33 peptides were more abundant in samples from patients with cancer than normal control samples. However, no individual peptide could stratify patients by risk.

A signature generated using peptides as features to distinguish patients found that the six top-ranked features mapped to five genes and discriminated cancer patients better than *PSA*.

These data indicate that computationally guided proteomics can be used to discover biomarkers present in samples collected in a noninvasive manner and can be used to stratify patients.

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 34 proteins demonstrating potential for classifying patients 

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