We draw attention to a commentary published in this issue of JASN by Knepper regarding studies undertaken in search of new biomarkers using urinary proteomics. Many of us who review or read these studies want important information to grace our journal pages. Proteomic technology today, even as it rapidly evolves, is capable of clever measurement and presentation, but harnessing this technology to better understand clinical or experimental disease is where true progress lies. By and large, we are not there yet. Reasonable people acknowledge this concern is more of an observation than a complaint about a discipline in its adolescence.

Identification of protein/fragment signatures in urine needs context and credible evidence of improving on what is already known. A useful experimental design should test protein signatures for relevance to pathophysiology and specificity for certain diseases. We cannot get to this level without everyone making an effort to raise the bar.

As editors of your journal, like any well-regarded journal, we are always torn between publishing new preliminary data of potential interest versus a more penetrating story that truly advances the ball. We hope Knepper’s insightful discussion now, and what will come from new work by our community of investigators, forges greater expectations for future studies: Expectations for replication in parallel populations accompanying the initial identification of a signature, disease specificity controls where appropriate, and additional biochemical or immunologic confirmation where available. When contemplating a more advanced validation study, the design should develop along the lines of a comparative clinical trial against other markers, other diseases, or various treatments with appropriate attention to sensitivity and specificity of the results.

JASN editors going forward will expect future manuscripts using urinary proteomics to contain the above enhancements. If we all promote a rigorous scientific body of work, then we can be optimistic that urinary proteomics will provide a powerful tool by which we can identify new markers, understand their use, and better care for our patients.

DISCLOSURES
None.

REFERENCES