From the Editor

Universal Standards and Practices

The Editors, *BioTechniques*

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In 2008, the Human Proteome Organisation (HUPO) generated a white paper describing for the first time the scope, mission, and direction of a potential human proteome project. Projected to take more than 10 years and cost more than \$1 billion dollars, the goal would be to better understand the functions and interactions among the more than 21,000 human proteins. Much of the initial effort as described in that white paper would go toward improving existing technology in proteomics and developing new approaches to studying protein interactions.

Ironically, one of the core needs in the burgeoning field of proteomics lies in one of the most commonly used biochemical tools: the antibody or affinity reagent. More than 300,000 antibodies are now available to researchers, directed not only at an impressive array of human proteins, but at modified forms of those proteins, as well. But quantity is one thing. Quality—that is, whether or not a particular antibody will work for a given assay or method—is another issue entirely. Generating antibodies or affinity reagents such as protein scaffolds is a time-consuming process, but so too is the validation of those reagents, which requires testing with assays such as Western blotting, immunohistochemistry, and immunofluorescence. When it comes to affinity reagents, validation is a step that is desperately lacking. It is this problem that lies at the heart of a review article from David Rimm's lab at Yale University in this issue of *BioTechniques* (page 197). While critical to interpreting an experiment, antibody validation is ad hoc now: there are no steadfast rules or requirements for proper antibody validation, whether the affinity reagent is intended for use in a basic research project or as part of a clinical assay kit. This means it is up to each researcher to obtain the necessary validation information prior to performing an assay. This is done either by researching previous literature on a particular antibody, or by in-lab experimental validation prior to use. One may wonder if such time-consuming steps are truly the best use of a scientist's time.

A better option could be the establishment of a universal set of validation guidelines and tests for antibodies prior to distribution to researchers. Indeed, many commercial antibody suppliers already provide some level of validation for their antibodies with certain assays. But these are not standardized or customizable to particular

experimental conditions, so the onus still falls on end-users. While additional validation steps will be more time-consuming and costly at the outset for developers, increased confidence in purchased affinity reagents—without the need for extensive in-house validation—will both speed up and enhance researchers' efforts at the bench. In time, more biologists could turn to affinity reagents for their studies, which would more than make up for these initial investments.

This all leads back to the HUPO initiative. One goal for the project is the generation of renewable affinity reagents to all 21,000 human proteins. While this in itself is an admirable goal, what makes this effort all the more important for biochemists is the level of testing that each generated reagent will undergo; validation will be performed with multiple assays for each antibody using a standardized pipeline, giving researchers a level of confidence in their antibody that might even eliminate the need to perform additional validation studies prior to use. Although a Human Proteome Project is still being discussed and debated, the idea of more thorough antibody validation is picking up steam within the proteomics community. The review in this issue describes the validation approach being taken in the Rimm lab, which could serve as a guide to others in the community performing immunohistochemistry on tissue blocks. Other efforts—such as the Protein Atlas in Sweden and a recent study in *Molecular and Cellular Proteomics* from the ProteomeBinders consortium recommending a virtual affinity reagent database—are generating well-validated affinity reagents along with comprehensive datasets for distribution.

Similar to the Human Genome Project, the financial cost of any Human Proteome Project will be large. But also similar is how the tools, technological advancements, and information derived from such an effort will save money and time for future generations of scientists and enable new insights into human biology and disease. As always, post your thoughts and comments at our Molecular Biology Forums under “To the Editor” (<http://molecularbiology.forums.biotechniques.com>) or send an email directly to the editors (bioeditor@biotechniques.com).

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