Both groups identified peptides resulting from the translation of several hundred RNA molecules that had been thought to be non-coding. The importance of this observation is unclear, but the authors suggest that some of these gene products might be functional whereas others might represent biological noise. An exciting speculation is that the latter might represent the leading edge of evolution—products of random gene expression that, if functional, could be selected for and eventually evolve to become canonical transcripts. Kim *et al.*[3] created and searched several custom sequence databases to identify new coding regions of the genome derived from pseudogenes and alternative open reading frames, of which they found many examples. By closely examining protein terminal sequences, both groups also validated thousands of protein translation start and stop sites. These examples clearly illustrate the potential contribution of proteomics data toward the validation and refinement of genome annotation.

Wilhelm *et al.*[4] describe ProteomicsDB, a powerful new web-based resource for mining the human proteome. It is structured similarly to the BioGPS gene expression resource[8] in that, for any human protein, one can quickly determine expression patterns across any sample in the database using multiple quantitation methods. A user can also view the protein's proteotypic peptides, examine annotated plots of all identified spectra and determine the experiments from which the peptides were found. In this respect, ProteomicsDB offers similar features as the PeptideAtlas project[9] but is specific for human proteins. Many other exciting analytical tools are available or are in development within ProteomicsDB, such as an interface for designing highly selective targeted mass spectrometry assays that minimize interference from other peptides in the database. Moreover, ProteomicsDB is constructed as a community data repository, built to accommodate the enormous amount of new data that will become available in the coming years.

These two projects demonstrate the incredible potential of mass spectrometry to interrogate the human proteome using large-scale experiments (**Fig. 1**). When examined in the context of genetic diversity, disease states and environmental perturbations, the proteome might have profound implications for human health. For example, on the basis of spatial protein expression profiles, we may be able to predict which organs are most susceptible to a particular protein-coding mutation or to side effects from targeted therapeutics.

The draft assembly of a quantitative catalog of nearly all human proteins and their abundance throughout the body is an impressive accomplishment. Nonetheless, the dynamic and information-rich molecular architecture of the proteome leaves much to be explored. We anticipate that this resource will fuel scientific insight and provide a robust platform for future endeavors in human proteomics research.

COMPETING FINANCIAL INTERESTS
The authors declare no competing financial interests.

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