What can you do with two omes that you can't do with one?

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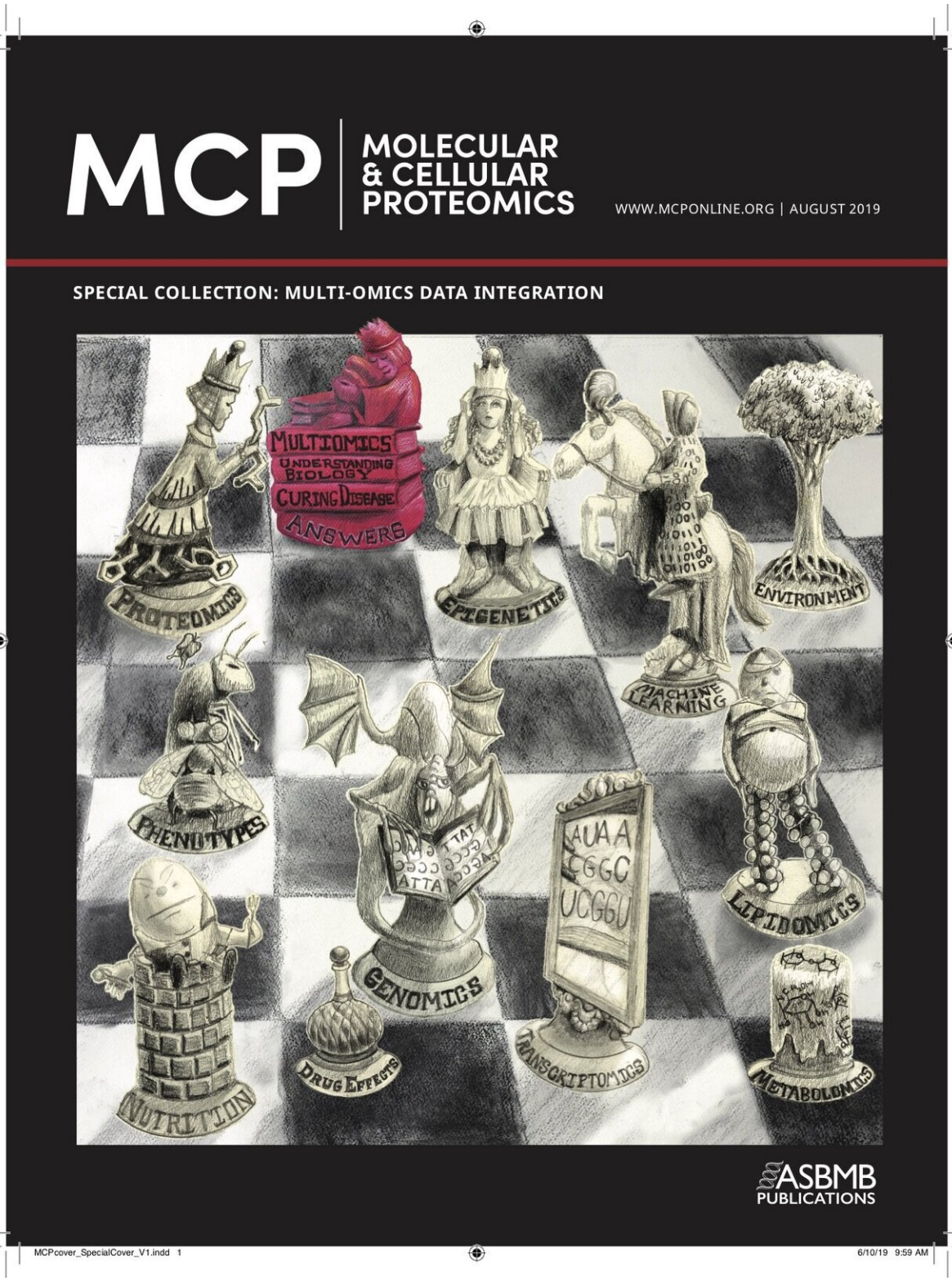

As analytical tools improve, researchers are combining proteomic, genomic, transcriptomic and other omic data to better understand biological systems. The

current issue of *Molecular and Cellular Proteomics* focuses on multiomics tools and research results. Credit: Molecular & Cellular Proteomics

What can you learn from two omes that you can't tell from one? You might determine how different bacterial strains in a water sample contribute specific functions to its overall microbiome. You might find that duplication of a section of a chromosome in cancer cells has wide-reaching effects on important proteins—or that it has a smaller effect than expected. First, though, you need to find a way to wrangle gigabytes of data saved in numerous, perhaps incompatible formats.

As high-throughput analytical tools improve, allowing researchers to collect more and more data, the challenge becomes how to interpret it all. When transcriptomic, genomic, metabolomic and proteomic analyses are layered together, parsing out a signal can be a monumental task. The field needs new analytical strategies, and new user-friendly software, to condense RNA counts, genotypes, and mass spectra showing proteins, post-translational modifications, complex carbohydrates and metabolites into coherent, interpretable results.

Researchers surfing this multiomics wave report a plethora of new tools and approaches this month in a special issue of the journal *Molecular & Cellular Proteomics* devoted to integrating multiple omics. The issue, edited by Bernhard Kuster of the Technical University of Munich and Bing Zhang of the Baylor College of Medicine, includes sixteen articles that explore ways to combine data from two or more omes at a time.

More information: Weiping Ma et al, Integrative proteo-genomic analysis to construct CNA-protein regulatory map in breast and ovarian tumors, *Molecular & Cellular Proteomics* (2019). DOI: 10.1074/mcp.RA118.001229