About the Cover

The image shows a protein network in the tumor tissue of a Filipino patient with non-small cell lung cancer (NSCLC). Through quantitative proteomic analysis, 1855 out of 4518 identified proteins were found to be aberrantly expressed relative to the adjacent normal tissue, with 860 upregulated and downregulated proteins having at least a four-fold change. The key proteins possibly involved are MUC1 in angiogenesis promotion and apoptosis prevention, STAT1 and STAT3 in cell proliferation, HIF in cell growth and tumor metabolic adaptation, and EIF2 in continuous translation of oncogenic proteins. Proteomic profiling of a larger group of Filipino NSCLC patients could provide the information for potential biomarker and drug discovery, which could lead to early diagnosis and better treatment monitoring needed for lowering the incidence and mortality rate of NSCLC in the Philippines. To learn more, go to pages 1611–1625.