Semin Oncol. 2003 Apr;30(2):156-60.

Proteomic analyses in Waldenstrom's macroglobulinemia and other plasma cell dyscrasias.

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The proteomic analysis of tumor cells emerges as a key complement to gene expression profiling, primarily because regulation of protein expression (at the translational and post-translational levels) can buffer the magnitude of changes occurring at the gene transcription level, in order to fine tune cellular functions. Herein we describe the concept of proteomic analysis of the signaling state of tumor cells, as well as its application in the study of signaling pathways in plasma cell dyscrasias, such as Waldenstrom's macroglobulinemia (WM) and multiple myeloma (MM). Comparative studies of WM versus MM cells at baseline and in the setting of drug treatment reveals proteomic profiles of the signaling state with significant overlap (that could reflect a putative B-cell lineage-related proteomic signature), but also distinct differences, possibly associated with differential features in the biologic behavior and drug sensitivity of these diseases. These proteomic studies pave the way for a more comprehensive insight into the molecular basis of WM versus other B-cell malignancies.