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The central goal of proteomics is to characterize the role that each protein plays in a given cell type. The field of location proteomics is the branch of proteomics that describes the location pattern of individual proteins and their relationships. The determination of the location of a protein within cells is critical in understanding the role and the function of that protein. Various methods have been used in the classification and clustering of proteins, with the aim to automate the process of protein recognition. Already, there has been success in the use of numerical features derived from fluorescent microscope images in classification and clustering of proteins. This work furthers research in location proteomics through the use of optical flow analysis of image sequences. Optical flow for sequences of two-dimensional fluorescent microscope images is computed, and numerical features including divergence, curl and speed are computed. Further work involves the use of these features in protein classification. (Received September 27, 2005)