

5th Annual Joint Bioinformatics Workshop

July 19, 2005
2229 Seamans Center
University of Iowa

by

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To the proteome and beyond: A new approach to retinal development

ABSTRACT

The developing vertebrate retina is a well characterized structure that has been widely used as a model to study nervous system development. The retina contains 5 basic cell types that originate from a common retinal progenitor cell. These five cell types are generated in a characteristic yet overlapping order that is conserved across vertebrate species. The adoption of cell fate is dependent upon both expression of appropriate receptors and transcription factors by the progenitors as well as expression of appropriate secreted factors, cell-surface molecules and extra-cellular matrix molecules by earlier born retinal neurons. In order to begin to better understand the coordination of such complex developmental events, we have characterized the proteome of the developing mouse retina from embryonic day 13 to postnatal day 5. Analysis using self organizing mapping and adaptive resonance theory was used to cluster protein spots into groups based on dynamic changes in their levels of expression. In addition to clusters of proteins that generally increased or decreased, several clusters had peak expression levels that temporally correlated with the peak genesis of specific retinal cell types. These results represent the first efforts to use proteomics to investigate retinal development, and are the basis for future biological and computational efforts to understand the coordination of multiple cell-specific events required for proper function of this vital organ.