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by

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Development of Neural Stem Cell Ontology Trees

ABSTRACT

Protein expression in pluripotent retinal cells is central to understanding retinal development patterns. Using two-dimensional protein gel electrophoresis to obtain data from IGF-differentiated neurospheres, proteins potentially important in retinal development were identified and the amount of expression quantified. Using this protein expression data, novel database software was created and existing software was utilized to visualize the relationships of this protein data on gene ontology trees in three major categories: molecular function, cellular component, and biological process. These gene ontology trees will facilitate visualization of protein interactions and expression in developing retinal/brain cells. Comparisons of these stem cell populations will help determine the efficacy of using brain progenitor cells as a treatment for complex retinal diseases such as macular degeneration.