

## **Transcriptome and Proteome Analyses of Human, Monkey and Mouse Embryonic Stem Cells During Embryoid Body-Based Differentiation**

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We have applied proteomics and transcriptomics approaches to investigate the molecular mechanisms that control embryonic stem cell (ESC) self-renewal and differentiation. We analyzed total, nuclear and membrane proteomes of differentiated and undifferentiated human, mouse and monkey embryonic stem cells. The transcriptome of proliferating and differentiating human ESCs has also been analyzed using a microarray approach. Comparative analyses across species and organelles revealed several proteins and mechanisms emerged as key participants in stem cells proliferation and differentiation. Microarray and Real-Time analyses of ESCs also resulted in identification of several new mechanisms. The results of transcriptome and proteome data will be compared and the methods to maximize the benefit of the integration of transcriptome and proteome data will be discussed.

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