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Metabolic State as a Regulator of Transcriptional Dynamics in Human Embryonic Stem Cell Differentiation

Human embryonic stem cell (hESC) fate decisions require tight coordination between cellular metabolic states and transcriptional programs, yet the mechanisms that integrate these layers remain incompletely understood. In this work, we investigate how global metabolic and redox states act as regulatory inputs that couple the cellular bioenergetic environment to transcriptional control during differentiation.

By integrating single-cell transcriptomics (scRNA-seq), proteomics, and directed differentiation protocols, together with organoid-based models, we identify metabolic pathways and gene regulatory networks that are coordinately engaged during the transition from pluripotency toward neural and adipogenic lineages. Our organoid approaches provide a platform to explore how metabolic regulation influences tissue organization and functional maturation during development.

Overall, our work establishes a mechanistic framework linking cellular metabolism to gene regulation in hESC differentiation, offering new perspectives on how bioenergetic signals guide human tissue formation.