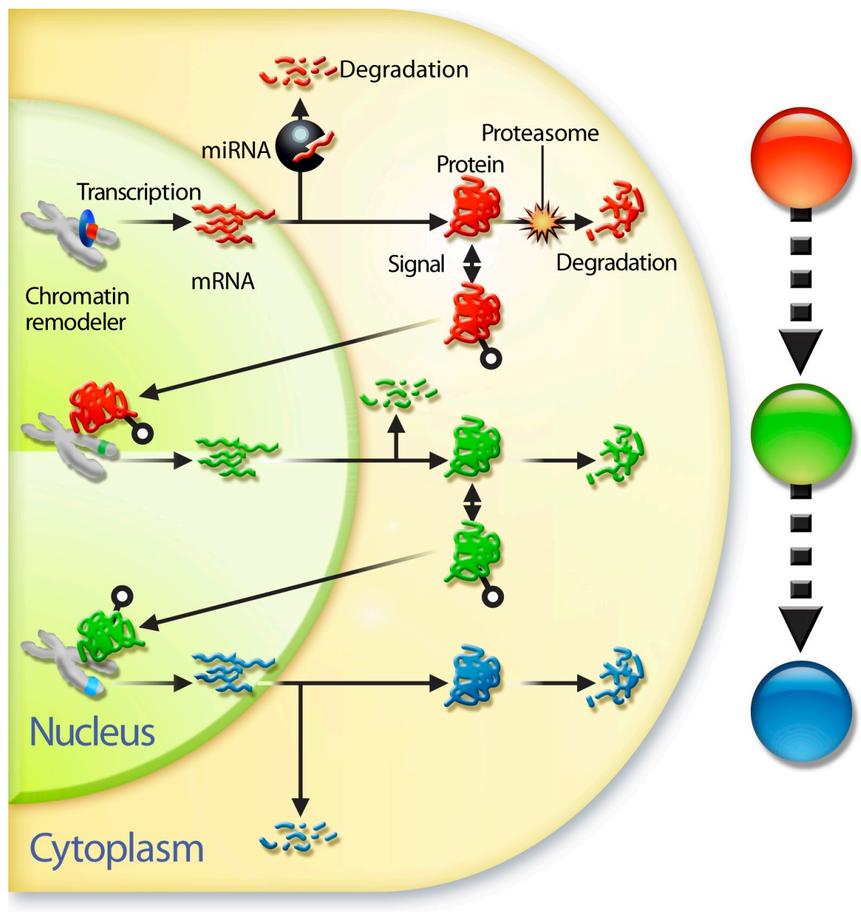
# Rising Star




*Regulated stages of gene expression (left). Network representation of the transcriptional regulatory cascade (right).*

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Interested in understanding how transcription regulators and epigenetic modifications control gene expression programs during cellular development and differentiation. Showed that a distinctive SWI/SNF-like ATP-dependent chromatin remodeling complex, esBAF, is an essential component of the core pluripotency transcriptional network in mouse ES cells. Recently showed that a link between regulatory network architecture and transcription factor dynamics may explain differential cell-fate outcome among members of a clonal cell population, e.g., fractional survival/death of cancer cells upon drug treatment. Currently focused on characterizing regulatory elements and epigenomes in stem cells, T cells and cancer cells.

Received the NIEHS Early Career Award in 2009.

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