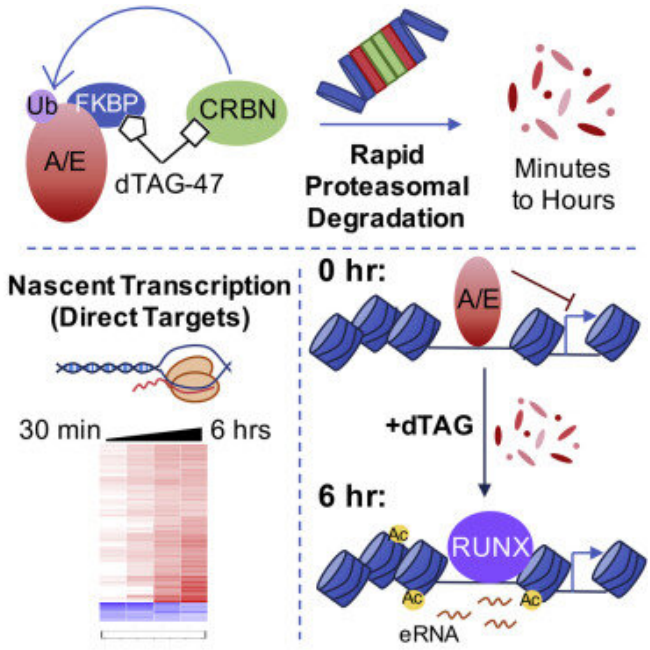
Gene network for leukemia factor

5 February 2021, by Leigh MacMillan



Graphical abstract. *Molecular Cell* (2020). DOI: 10.1016/j.molcel.2020.12.005

Transcription factors—proteins that regulate gene expression—play critical roles in cell fate decisions and are frequent targets of mutation in a variety of human cancers. Understanding how transcription factors contribute to disease requires the identification of their direct gene targets, but traditional methods are time-consuming and make it difficult to distinguish direct from secondary changes.

Kristy Stengel, Ph.D., Scott Hiebert, Ph.D., and colleagues have now devised a chemical genetic approach that speeds transcription factor analysis from days to minutes.

Reporting in *Molecular Cell*, the researchers applied the new approach to analysis of the fusion protein AML1-ETO, the most frequent chromosomal translocation in acute myeloid leukemia. They defined a small core network of about 60 direct AML1-ETO-regulated genes, including mediators of myeloid differentiation and cell fate decisions.

Their findings demonstrated that AML1-ETO repression of this small network impairs myeloid differentiation, and the mechanistic insights point to novel therapeutic strategies.

More information: Kristy R. Stengel et al. Definition of a small core transcriptional circuit regulated by AML1-ETO, *Molecular Cell* (2020). DOI: 10.1016/j.molcel.2020.12.005

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