

# Molecular Cell

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and J.W. Conaway 637

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- Destabilization of Binding to Cofactors  
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- The Transition between Transcriptional  
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SNIP1 Is a Candidate Modifier of the Transcriptional Activity of c-Myc on E Box-Dependent Target Genes

M. Fujii, L.A. Lyakh, C.P. Bracken, J. Fukuoka, M. Hayakawa, T. Tsukiyama, S.J. Soll, M. Harris, S. Rocha, K.C. Roche, S.-i. Tominaga, J. Jen, N.D. Perkins, R.J. Lechleider, and A.B. Roberts

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## Technique

Receptor-Selective Coactivators as Tools to Define the Biology of Specific Receptor-Coactivator Pairs

S. Gaillard, L.L. Grasfeder, C.L. Haeffele, E.K. Lobenhofer, T.-M. Chu, R. Wolfinger, D. Kazmin, T.R. Koves, D.M. Muoio, C.-y. Chang, and D.P. McDonnell

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## Erratum

The Mechanisms of PML-Nuclear Body Formation

T.H. Shen, H.-K. Lin, P.P. Scaglioni, T.M. Yung, and P.P. Pandolfi

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## Announcements Positions Available

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Sen1 functions in termination of transcription by RNA polymerase II (Pol II), but the spectrum of genes that requires this factor is unknown. In this issue of *Molecular Cell*, Steinmetz et al. (pp. 735–746) map sites of Sen1-dependent termination by comparing Pol II occupancy across the entire yeast genome in wild-type and *sen1* mutant strains. The trace on the cover shows wild-type (blue) and *sen1* mutant (green) Pol II occupancy for a 50 kb segment of chromosome 12. The analysis reveals Sen1-dependent termination on many noncoding RNA genes and some short protein-coding genes. In addition, Sen1-dependent attenuation (upstream termination) was found to regulate several protein-coding genes. Unexpectedly, Sen1 appears to influence the efficiency of silencing at some loci. (Artwork by H. Adam Steinberg; molecular graphics rendered with PyMol: <http://www.pymol.org>.)