

BIOGRAPHICAL SKETCH

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NAME Jef D. Boeke	POSITION TITLE Professor		
eRA COMMONS USER NAME jboeke1			
EDUCATION/TRAINING <i>(Begin with baccalaureate or other initial professional education, such as nursing, and include postdoctoral training.)</i>			
INSTITUTION AND LOCATION	DEGREE <i>(if applicable)</i>	YEAR(s)	FIELD OF STUDY
Bowdoin College, Brunswick, ME (summa cum laude)	A.B.	1976	Biochemistry
McGill University, Montreal, QUE		1974-1975	
Rockefeller University, New York	Ph.D.	1982	Molecular Biology

A. Positions and Honors.Research and Professional Experience

2002-present Founding Director, High Throughput Biology Center, The Johns Hopkins University
 1995-present Professor, Department of Molecular Biology and Genetics, The Johns Hopkins University School of Medicine (MB&G/JHU/SOM), Baltimore, MD
 1990-1995 Associate Professor, (MB&G/JHU/SOM), Baltimore, MD
 1986-1990 Assistant Professor, (MB&G/JHU/SOM), Baltimore, MD
 1982-1985 Postdoctoral Fellow, The Whitehead Institute/Massachusetts Institute of Technology

Academic Awards, Honors, Fellowships and Scholarships

James Bowdoin Scholar each semester at Bowdoin (total 6), 1972-1976; Macomber Prize in Biology and George Wood MacArthur Prize, Highest Departmental Honors in Biochemistry and Phi Beta Kappa Bowdoin College, 1976; Thomas J. Watson Fellowship, 1976-1977 Project title: "Plant collection in the high Andes"; Rockefeller Univ. Fellowship, 1977-1978; William DeWitt Wallace Fellowship, 1978-1982 at Rockefeller; Helen Hay Whitney Fellowship, 1982-1985; Searle Scholar, 1986-1989; Mellon Foundation Award, 1986; American Cancer Society Faculty Research Award, 1990-1995; Annual Hoffman-LaRoche Lecture, New York Yeast Club, 1992; Honorary Degree of D.Sc., honoris causa, Bowdoin College, May 1998; Ira Herskowitz Award, Genetics Society of America, 2004

Professional Activities

1983-present Member, Genetics Society of America
 1984-present Member, American Society for Microbiology
 1986-present Member, American Association for the Advancement of Science
 1986-present Ad hoc member of NIH and ACS study sections, reviewer for NSF and other foundations
 1989-2000 Editorial Board, Molecular and Cellular Biology
 1997-2001 American Cancer Society grant review panel, regular member; 2000, Vice Chair; 2001, Chair
 1997-present Chair, Retroelement Study Group on Taxonomy of Viruses

B. Selected peer-reviewed publications (total of 202).

Boeke, J.D., Devine, S.E. (1998) Yeast retrotransposons: finding a nice quiet neighborhood. Cell 93: 1087-1089.
 Cost, G. C., Boeke, J. D. (1998). Targeting of human retrotransposon integration is directed by the specificity of the L1 endonuclease for regions of unusual DNA structure. Biochemistry 37, 18081-18093.
 Boeke, J. D., Pickeral, O. K. (1999). Retroshuffling the genomic deck. Nature 398, 108-111.
 Winzeler, E. A., Shoemaker, D. D., Astromoff, A., Liang, H., et al. (1999). Functional characterization of the S. cerevisiae genome by gene deletion and parallel analysis. Science, 285: 901-906.
 Smith, J.S., Boeke, J.D. (2001) Is S phase important for transcriptional silencing? Science; 291: 608-9.

- Ooi, S.-L., Shoemaker, D., Boeke, J. D. (2001). A genome-wide DNA microarray based genetic screen for components of the nonhomologous end-joining pathway in *S. cerevisiae*. *Science*. 294: 2552-2556.
- Wei, W., Gilbert, N., Ooi, S. L., Lawler, J. F., Ostertag, E. M., Kazazian, H. H., Boeke, J. D., Moran, J. V. (2001). Human L1 retrotransposition: cis-preference vs. trans-complementation. *Mol. Cell. Biol.* 21: 1429-1439.
- Lawler, J. F. J., Merkulov, G. V., Boeke, J. D. (2002). A nucleocapsid functionality within the amino terminus of the Ty1 protease that is distinct and separable from proteolytic activity. *J. Virol.* 76: 346-354.
- Bachman, N., Biery, M., Boeke, J. D., Craig, N. L. (2002). Tn7-mediated mutagenesis of *Saccharomyces cerevisiae* DNA in vitro. *Meth. Enzymol.* 350: 230-247.
- Sandmeier, J. J., Celic, I., Boeke, J. D., Smith, J. S. (2002). Telomeric and rDNA silencing in *Saccharomyces cerevisiae* depend on a nuclear NAD⁺ salvage pathway. *Genetics* 160, 877-889.
- Bolton, E. C., Mildvan, A. S., Boeke, J. D. (2002). Inhibition of reverse transcription in vivo by elevated manganese ion concentration. *Mol. Cell* 9: 879-889.
- Lawler, J. F. J., Dull, A., Haeusser, D. P., Boeke, J. D., Keeney, J. B. (2002). Reduced Ty1 transposition at high temperature is due to a decrease in protease activity. *J. Virol.* 76: 4233-4240.
- Symer, D. E., Connelly, C., Szak, S. T., Caputo, E. M., Cost, G. J., Parmigiani, G., Boeke, J. D. (2002). Human L1 retrotransposition is associated with genetic instability in vivo. *Cell* 110: 327-338.
- Giaever, G., Chu, A. M., Ni, L., Connelly, C., et al. (2002). Functional profiling of the *Saccharomyces cerevisiae* genome. *Nature* 418: 387-91.
- Cost, G. C., Feng, Q., Jacquier, A., Boeke, J. D. (2002). Human L1 element retrotransposition in vitro. *EMBO J.* 21: 5899-5910.
- Park, J., Cosgrove, M., Youngman, E., Wolberger, C., Boeke, J. D. (2002). A core nucleosome surface critical for transcriptional silencing. *Nature Genet.* 32, 273-9.
- Avalos, J. L., Celic, I., Muhammad, S., Cosgrove, M. S., Boeke, J. D., Wolberger, C. (2002). Structure of a Sir2 enzyme bound to an acetylated p53 peptide. *Mol. Cell* 10: 523-535.
- Onyango, P., Celic, I., McCaffery, J. M., J.D., B., Feinberg, A. P. (2002). SIRT3, a human SIR2 homologue, is an NAD-dependent deacetylase localized to mitochondria. *Proc. Natl. Acad. Sci. USA* 99: 13653-13658.
- Bolton, E. C., Boeke, J. D. (2003). Interactions between tRNA genes, flanking genes and Ty elements: a genomic point of view. *Genome Res.* 13: 254-263.
- Starai, V. J., Celic, I., Cole, R. N., Boeke, J. D., Escalante-Semerena, J. C. (2002). Sir2-dependent activation of acetyl-coenzyme A synthetase by deacetylation of an active site lysine residue. *Science* 298:2390-2392.
- Boeke, J.D. (2003). The unusual phylogenetic distribution of retrotransposons: a hypothesis. *Genome Res.* 13:1975-1983.
- Ooi, S.L., Shoemaker, D.D., Boeke, J.D. (2003) DNA helicase interaction network defined using a synthetic lethality analyzed by microarray. *Nat. Genet.* 35:277-286.
- Avalos, J.L., J.D. Boeke, C. Wolberger. 2004. Structural basis for the mechanism and regulation of Sir2 enzymes. *Mol. Cell* 13: 639-648.
- Han, J.S., Szak, S.T., Boeke, J.D. (2004) transcriptional disruption by the L1 retrotransposon and implications for mammalian transcriptomes, *Nature* 429:268-274.
- Han, J.S., Boeke, J.D. (2004) A highly active synthetic mammalian retrotransposon, *Nature* 429:314-318.
- Bachman, N. Eby, Y., Boeke, J.D. (2004) Local definition of Ty1 target preference by Long Terminal Repeats and clustered tRNA genes. *Genome Res.* 14:1232-1247.
- Boeke, J.D. (2004) Evolution: A is for adaption. *Nature* 431:408-409.
- Cosgrove, M.S., Boeke, J.D., Wolberger, C. (2004) Regulated nucleosome mobility and the histone code. *Nature Struct. Mol. Biol.* 11:1037-1043.
- Bolton, E.C., Coombes, C.E., Eby, Y., Cardell, M., Boeke, J.D. (2005) Identification and characterization of critical cis-acting sequences within the yeast Ty1 element. *RNA* 11:308-322.
- Coombes, C.E., Boeke, J.D. (2005) An evaluation of detection methods for large lariat RNAs. *RNA* 11:323-331.
- Pan, X., Yuan, D.S., Xiang, D., Wang, X., Sookhai-Mahadeo, S., Bader, J.S., Hieter, P., Spencer, F., Boeke, J.D. (2004) A robust toolkit for wiring genome-wide genetic networks in yeast, *Mol. Cell.* 16:487-496.
- Han, J.S., Boeke, J.D. (2005) LINE-1 retrotransposons: modulators of quantity and quality of mammalian gene expression? *Bioessays* In press.
- Pan, X., Ye, P., Wang, X., Bader, J.S., Boeke, J.D. (2005) DNA integration network in the yeast *Saccharomyces cerevisiae*. (submitted)

C. Research Support.Ongoing Research Support

5PO1 CA16519-30 (Boeke, J.D.)

05/01/00 - 03/31/06 (no cost extension)

NIH, NCI

Program on Molecular Biology of Viral Tumorigenesis

Project #6 (Boeke, J.D.): Endogenous Retroelements

The major goals of this project are: 1) To define the L1 retrotransposition mechanism; 2) To identify and characterize sequence signals in L1 element RNA; 3) To investigate the regulation of L1 retrotransposition; and 4) to mine genome databases for information on L1 biology.

RO1 HG02432-03 (Boeke, J.D.)

02/06/02-11/30/05 (no cost extension)

NIH

Yeast Genetic Interaction Map

The Major goals of this project are: 1) To construct a complete set of yeast gene disruptions bearing a marker compatible with *kanMX*; 2) To identify all null allele synthetic lethality interactions in the yeast genome; 3) To create a database of synthetic lethality interactions; 4) To create a resource of double mutant pools accessible to the research community; and 5) To develop high-throughput methods to assess genetic interactions of essential genes.

5 R01 GM36481-19 (Boeke, J.D.)

07/1/03 - 06/30/07

NIH, National Institute of General Medical Sciences

Transposition Mechanisms

The major goals of this project are: 1) Molecular definition of the Ty1 reverse transcription pathway; 2) Definition and characterization of the pathway leading to targeted integration of Ty1 upstream of pol III-transcribed genes; and 3) Characterization of the host response to retrotransposition.

RO1 GM62385-03 (Boeke, J.D.)

06/1/01 - 05/31/06 (no cost extension)

NIH, National Institute of General Medical Sciences

Transcriptional Silencing Mechanisms

The major goals of this project are: 1) Determine the function of *S. cerevisiae* SIR2 protein family members; 2) Determine the structures of silencing proteins; 3) Determine the histone requirements for transcriptional silencing; 4) Identification of important cis-elements required for rDNA silencing.

1U54RR020839-01 (Boeke, J.D.)

09/30/04 – 07/31/09

NIH/TCNP

Networks and Pathways of Lysine Modification

The pathways regulating the interplay between diverse modifications on lysines will be studied. This proposal combines genetic and computational approaches for decrypting redundant activities of multi-gene, multi-substrate families, with a new and innovative proteomics technology, protein microarrays, and a new affinity ligand technology for identifying novel acetyltransferases. These newer approaches will be complemented in this Technology Center for Networks and Pathways by a heavy emphasis on the development and application of innovative mass spectrometry technologies, including sensitive technologies for quantifying dynamics of lysine modification in cells.

1 R41 GM074543-01A1 – Phase I STTR (Ziman, M.)

*09/27/04 – 03/26/05

NIH

Phenotyping All Genes of S. Cerevisiae

The overall goal of this project is to provide, for the first time, a genome-wide annotation of gene function by *phenotypic* assay of all known genes. Phase I is designed to lower the overall cost and increase the speed of the testing. Phase II will produce the bulk of the testing and the bioinformatic organization of the data.

* This will run 1/1/05 through 6/30/05 on a no-cost extension.