Rando Curriculum Vitae

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Personal details

Name: Oliver Rando
Date of birth: 05/17/1974
Nationality: USA
Marital status: married
Address: Oliver Rando
Dept. of BMP
UMass medical school
364 Plantation St., LRB Rm 903
Worcester, MA 01605-4321
Phone#:508-856-8879
Email: Oliver.Rando@umassmed.edu

Experience

Professor, Department of Biochemistry and Molecular Pharmacology, University of Massachusetts Medical School, Worcester, MA, May 2014 – present
Associate Professor, Department of Biochemistry and Molecular Pharmacology, University of Massachusetts Medical School, Worcester, MA, November 2010 – May 2014
Assistant Professor, Department of Biochemistry and Molecular Pharmacology, University of Massachusetts Medical School, Worcester, MA, January 2007 – November 2010
Bauer Genome Fellow, Harvard University, Cambridge, MA, February 2002 – December 2006
Graduate research with Dr. Gerald Crabtree, Stanford University, Stanford, CA, September 1995 – June 2002

Education

2/02-1/07: Genome Fellow at the Bauer Center for Genomic Research, Harvard University. Ran a small laboratory investigating chromatin structure and function.
9/95-6/02: MD, PhD studies at Stanford University, Stanford, CA, under the supervision of Dr. Gerald R. Crabtree. Investigated the function of actin and actin-related proteins in chromatin remodeling, and carried out genomic studies on T cell activation.
9/91-6/95: BA studies at Harvard University, Cambridge, MA. Graduated magna cum laude with highest honors in biochemistry. Thesis project was under the supervision of Dr. Tom Maniatis, on the proteolytic processing of the NF-κB p50 subunit from the p105 precursor.

Honors/Awards

Henderson Prize for outstanding thesis in Biochemical Sciences, Harvard University, 1995

Burroughs Wellcome Career Award in the Biomedical Sciences, 2006
NIH Director's Pioneer Award, 2014
Fellow of the American Academy of Microbiology, 2015
National Finalist, Blavatnik Awards for Young Scientists, 2016

Professional Memberships

2006-present: American Society for Cell Biology
2015-present: Genetics Society of America

Research Support

Current Funding:

1 DP1 ES025458-01 (Rando) 9/16/2014 – 7/31/2019 6.12 calendar
NIH/NIEHS $500,000/yr
tRNA fragments as transgenerational information carriers
The goal of this study is to explore the role of small RNAs in paternal effect paradigms.
Role: PI

1 R01 GM100164-01A1 (Multi-PI) 4/1/2014 – 3/31/2019 0.48 calendar
NIH $54,000/yr
Breaking Nucleosomal Symmetry
The major goal of this proposal is to develop genetic methods to interrogate the function of asymmetrically-modified nucleosomes in vivo.
Role: Co-PI

1 R01 HD080224-01A1 (Rando) 4/14/2014 – 2/28/2019 1.8 calendar
NIH $329,000/yr
Dietary Effects on the Sperm Genome
The major goals of this proposal are to carry out cytosine methylation and chromatin profiling of sperm isolated from male mice on various diets, and to characterize "epivariation" among control animals.
Role: PI

Completed Funding:

A systems approach to epigenetic decisions in yeast
Principal Investigator: Paulsson, Johan
Agency: Human Frontiers Science Program
Funding Number: RGY86/2005
Project Period: 6/1/2005 – 5/30/2008
Aims: Screen for epigenetically-regulated genes in yeast.

Pleiotropic Effects of Chromatin Regulators in Evolution
Principal Investigator: Rando, Oliver
Agency: Worcester Foundation for Biomedical Research
Project Period: 8/1/2008 – 7/31/2009
Aims: Swap chromatin regulators between related yeast strains.

Technology center for networks and pathways of lysine modification
Principal Investigator: Boeke, Jef
Agency: National Institutes of Health
Funding Number: U54 RR-020839
Project Period: 8/1/2007 – 7/31/2010
Aims: Study variation in histone lysine modifications during the cell cycle

Transgenerational effects of diet in mammals
Principal Investigator: Rando, Oliver J
Agency: National Institutes of Health
Funding Number: 1R01GM025723
Project Period: 9/1/2009 – 8/31/2013
Aims: Screen mice for transgenerational effects of paternal diets

Transgenerational effects of nicotine
Principal Investigator: Rando, Oliver J (MPI)
Agency: National Institutes of Health
Funding Number: 1R01DA033664
Project Period: 4/1/2012 – 3/31/2017
Aims: Investigate the effects of paternal nicotine exposure on offspring phenotype

Role of tRNA Fragments in Paternal Dietary Effects on Offspring Metabolism
Principal Investigator: Rando, Oliver J (PI)
Agency: March of DImes
Funding Number: FY13-1268
Project Period: 6/1/2014 – 5/31/2017
Aims: Investigate the role of diet in regulation of tRNA fragments in murine sperm

Chromatin dynamics in yeast
Principal Investigator: Rando, Oliver J
Agency: National Institutes of Health
Funding Number: 1R01GM079205
Project Period: 3/8/2008 – 2/28/2017
Aims: Investigate the mechanisms of genome-wide histone dynamics in yeast

Invited Seminars (2007-present)

2007:
NYU Department of biology
2nd NIGMS Workshop on Human Embryonic Stem Cell Research
2007 Cold Spring Harbor Meeting on Systems Biology
Penn State Summer Symposium on Molecular Biology
2007 FASEB Summer Research Conference: Chromatin and Transcription
2007 Gordon Research Conference: Chromosome Dynamics

Transregio 5 Symposium, Munich, Germany
2007 ORFeome
ICGEB Meeting and EURASNET Symposium, Bariloche, Argentina

2008:
Albert Einstein medical school
Netherlands Cancer Institute
Princeton University
Wadsworth Institute
Chromatin and Transcriptional regulation, Weizmann Institute, Israel
Hebrew University of Jerusalem
2008 Gordon Research Conference: Chromatin Structure and Function
LRI Symposium on Chromosome Biology, London Research Institute
2008 FASEB Summer Research Conference: Transcriptional Regulation During Cell Growth, Differentiation, and Development

2009:
Johns Hopkins Medical School, HiT Center
Sloan Kettering Memorial Cancer Center
Harvard Medical School, Department of BCMP
Duke University, Department of Biochemistry
NIEHS
Friedrich Miescher Institute, Basel, Switzerland
Institute Curie, Paris, France
University of Pennsylvania, Department of Biology
2009 Cold Spring Harbor: Mechanisms of Eukaryotic Transcription
2009 SKMB Gene Regulation workshop, Lausanne, Switzerland

2010:
University of Colorado, Department of MCDB
Rutgers University, Department of MBB, and BioMaPS Institute
University of California Berkeley (STUDENT INVITE)
University of California Santa Cruz, Department of MCB
ENS Lyon, Lyon, France
Max Planck Institute of Biochemistry, Munich, Germany (STUDENT INVITE)
2010 CSHL Meeting on Systems Biology
2010 International Conference on Intelligent Systems for Molecular Biology
2010 FASEB: Yeast Chromosome Structure, Replication, and Segregation
Columbia Medical School, Department of Biochemistry and Biophysics
UMass Medical School, Department of MGM

2011:
MIT, Department of Biology
University of Toronto Department of Molecular Genetics
Institut de Recherches Cliniques de Montreal (IRCM)
Northwestern University Physical Sciences-Oncology Center

2011 Gordon Research Conference: Chromosome Dynamics
2011 Gordon Research Conference: Mammalian Gametogenesis
Wellcome Trust: Epigenomics of Common Disease
University of Dundee
Tittisee Conference on Genomic Regulation
Cell Symposium : Epigenetics and Transgenerational Inheritance

2012:
2012 Keystone Conference: Epigenomics
2012 Salem State Darwin Days Festival
University of Massachusetts Medical School, Department of Cell Biology
University of Texas, Austin
2012 American Society for Andrology annual meeting
Stanford University, Frontiers in Genetics
UCSF, Biomedical Sciences
Karolinska Institutet, Symposium on Molecular and Physiological Aspects of Diabetes Mellitus
University of Pennsylvania, CRRWH

2013:
IMBA/IMBL, Vienna, Austria – (STUDENT INVITE)
Dana Farber, Harvard Medical School, Seminars in Oncology
Wesleyan University, Department of Molecular Biology
University of Massachusetts Medical School, Program in Molecular Medicine
UCSD, CMM/LICR
MPI, Freiburg
EMBL Chromatin and Epigenetics meeting
College de France, Epigenetic Mechanisms and Genetic Disease
Labex DEEP retreat, Institute Curie
LBNL, Berkeley (POSTDOC INVITE)
2013 Gordon Research Conference: Fertilization and Activation of Development
Jackson Laboratory short course on medical and experimental mammalian genetics
Karolinska Institutet, DBRM Summer School
Novo Nordisk conference, Genomics in Metabolism

2014:
Fred Hutchinson Cancer Research center
University of Washington, Department of Genome Sciences
Harvard University, Cell Dynamics Seminar Series
Keystone Symposium: Epigenetic Programming and Inheritance
EMBO Conference: Gene Transcription in Yeast
2014 Gordon Research Conference: Post-transcriptional gene regulation
Chromatin and Epigenetics: From Omics to Single Cells 2014
PPTOX IV: Environmental Stressors in Disease and Implications for Human Health

2015:
Jackson labs, Bar Harbor ME
BU medical center
University of Missouri, LSSP – keynote speaker
UNC Chapel Hill
Karolinska Institutet, Nobel Minisymposium on Epigenetics in health and disease
Abcam conference: Non-Coding RNA: New Mechanisms and Approaches
Wellcome Trust Waddington Symposium, Edinburgh Scotland
2015 Gordon Research Conference: Developmental Biology
2015 Gordon Research Conference: Molecular Mechanisms in Evolution
2015 Gordon Research Seminar: Mechanisms of Mitotic and Meiotic Epigenetic Inheritance – keynote speaker
Company of Biologists workshop on Transgenerational Epigenetic Inheritance, UK
UMass Bioinformatics Core
University of Nebraska Biotechnology / Life Sciences Seminar Series

2016:
Joslin Diabetes Center, Harvard Medical School
Epigenomics2016, Puerto Rico
SFB Chromatin Dynamics Symposium, Munich
Institute for Advanced Study, Princeton
Frontiers in Developmental Biology, Stanford
University of Oregon, Institute of Molecular Biology
Dartmouth College (STUDENT INVITE)
UMass medical school/UMass Amherst BMP retreat, keynote speaker
2016 CSHL Meeting on Germ Cells
Wellcome Trust: Epigenomics of Common Disease – keynote speaker
University of Cambridge, Epigenetics Club speaker

2017:
University of Utah, Department of Biology
Huntsman Cancer Institute
NYU Department of Biology
Columbia Medical School Department of Biochemistry
North American Testis Workshop – benchmark speaker
NCI RNA Biology Symposium
CSHL 82nd Symposium: Chromosome Segregation & Structure
UMass medical school, Neuroscience retreat
2017 Gordon Research Conference: Mechanisms of Toxicology – keynote speaker
Boston Children's Hospital, Newborn Medicine Grand Rounds
Helmholtz Centrum distinguished speaker seminar series, Munich
EMBL conference: The nucleosome, from atoms to genomes
RNA Society of Sweden meeting – keynote speaker

Cornell University Biomedical Sciences seminar series
IRB Barcelona BioMed Conference on “Multidimensional Genomics: The 3D/4D organization of chromatin”
American Diabetes Association research Symposium – Epigenetics and Epigenomics: Implications for Diabetes and Obesity

2018:
Keystone Symposium: Gene Regulation in Development and Disease

Teaching

Frontiers in Reproduction, Marine Biological Laboratories:

Yearly lecture on epigenetics. 2010 – 2013.

Graduate school courses, UMass Med School:

2-5 lectures per year, including:

Core Course:	Yeast genetics I-II	2 hrs
Advanced Topics in Bioinformatics	Gene expression/location analysis	2 hrs
Advanced Topics in Gene expression	Chromatin dynamics	2 hrs
Cancer Biology and Medicine	Intro to epigenetics	2 hrs
Development and Stem Cells	Transgenerational epigenetics	2 hrs

2-3 (average) Discussion Sections per year, from the following:

Core Course:	Nucleic Acids	2 hrs
	Cell cycle	2 hrs
	Transcription	2 hrs
	Chromatin	2 hrs
	Systems Biology	2 hrs

1 Discussion Section per year

MD/PHD “RAPS”:	Epigenomics	2 hrs

Graduate school course design:

Advanced Topics in Bioinformatics

TRAC and Thesis Committees:

Naveen Kommajosyula (Rhind)
Jessica LopesdaRosa (Kaufman)
Fan Zhang (Theurkauf)
Kristin Gerson (Mercurio)

Erin Heyer (Moore)
Ryan Serra (Green)
Anna Malinkevich (Hagstrom)
Yuanyuan Chen (Kaufman)
Steve Weicksel (Sagerstrom)
Jon Belton (Dekker)
Amber Lachapelle (Gilmore)
Eric Swanson (Lawrence)
Rasim Barutcu (Walhout/Dekker)
Ly-sha Ee (Fazzio)
Timothy Chang (Zamore)
Mayuri Rege (Peterson)
Meetu Seth (Mello)
Swapnil Parhad (Theurkauf)
Melissa Greven (Rhind)
Heesun Kim (Mello)
Sungwook Choi (Ambros)
Gen Zhang (Theurkauf)
Diwash Acharya (Fazzio)
Po-Shen Chen (Fazzio)
Emma Watson (Walhout)
Ozgun Uyan (Brown)
Salih Topal (Peterson)
YongJin Lee (Zamore)
Mennatallah Albarqi (Ryder)
Mihir Mektar (Moore)
Brent Horowitz (Walhout)

Harvard Medical School:
Nate Lord (Paulsson)

Harvard University:
Nicole Follmer (Francis)
Casey Gifford (Meissner)

MIT:
Alex Tsankov (Regev)
Nicholas Burton (Horvitz)

Laboratory Personnel

Current Postdoctoral Fellows:

Ana Boskovic Oct 2014-Present
Mechanistic basis for small RNA biogenesis in the male germline

Colin Conine Oct 2014-Present

Small RNA effects on preimplantation development

Shweta Kukreja — Jan 2016-Present
Paternal effects of nicotine

Nils Krietenstein — June 2016-Present
Chromosome folding in yeast

Vera Rinaldi — February 2018-Present
Environmental regulation of epididymis function

Ebru Kaymak — March 2018-Present
Biochemical analysis of tRNA fragment function

Current Graduate Students:

Xinyang Bing — 2014-Present
Mechanisms linking tRFs to gene regulation

Io Long Chan — 2015-Present
Effects of paternal starvation on offspring in C. elegans

Carolina Galan — 2016-Present
Single-embryo analysis of chromatin structure

Marina Krykbaeva — 2017-Present
Maternal dietary effects in mammals

Hans Tobias Gustafsson — 2017-Present
Asymmetric nucleosomes in yeast

Former Lab Members:

Guocheng Yuan
Assistant Professor, Dana Farber Cancer Institute, Department of Biostatistics

June Oshiro
Consultant, Mayo Clinic

Galit Lahav
Associate Professor, Harvard Medical School Department of Systems Biology

Chih Long Liu
Lab Manager, Alizadeh Lab, Stanford University

Alex Tsankov
Postdoctoral Fellow, Meissner Lab, Harvard University

Ozlem Yildirim 2007-2012
Histone variant dynamics in embryonic stem cells
Postdoctoral fellow, Kingston Lab, Mass general Hospital

Lucas Fauquier 2008-2012
Postdoctoral Fellow, Vandel Lab, Universite Paul Sabatier, Toulousse France

Marta Radman-Livaja 2006-2012
Staff Scientist, Institute de Genetique Moleculaire de Montpelier, France

Benjamin Carone 2008-2014
Assistant Professor, Rowan University

Amanda Hughes 2008-2014
Microevolution of chromatin proteins
Postdoctoral fellow, Owen-Hughes Lab, Dundee

Jeremy Shea 2008-2015
Transgenerational reprogramming of metabolic state by paternal diet
Postdoctoral fellow, Villeda Lab, UCSF

Hsiuyi Chen 2010-2015
Network motifs and histone modification dynamics
Postdoctoral fellow, McVicker Lab, UCSD

Ryan Serra 2014-2016
Cytosine methylation dynamics in sperm
Senior Scientist, Quest Diagnostics

Markus Vallaster 2012-2017
Transgenerational effects of paternal nicotine
Senior Scientist, Intellia

Caitlin Connelly 2014-2016
Asymmetric nucleosomes in yeast
Scientist, Cancer Genomics group, Foundation Medicine

Morten Rasmussen 2015-2016
Paternal effects on metabolism
Scientist, Serum Institutet, Copenhagen

Tsung-Han Hsieh 2012-2017

Nucleosome interaction mapping in yeast
Postdoctoral fellow, Darzaq Lab, UC Berkeley

Hsin-Jung Chou 2014-2017
Effects of tRNA modifications on translation in yeast
Postdoctoral fellow, Ngai lab, UC Berkeley

Upasna Sharma 2012-2018
Soma-germline communication in murine spermatogenesis
Assistant Professor, UCSC

Service

University Committees and Service:

2007-present	Bioinformatics and Integrative Biology Search Committee
2008-2009	Embryonic Stem Cell Director Search Committee
2011-present	Systems Biology Search Committee
2012	ACE Sloan Task Force Committee
2015-present	Tenure Committee

Departmental Committees:

2008	Research/Facilities Subcommittee
2014	Teaching Subcommittee
2015	Student number recommendation task force

Grants reviewed:

2006	Wellcome Trust, mail reviewer
2008	NIH GCAT study section, ad hoc
2009	US Israel Binational Science Fund, mail reviewer
2009	RC1 Challenge Grants, mail reviewer
2012	NIH GCAT study section, ad hoc
2013	NIH MGA study section, mail reviewer
2013	John Templeton Foundation, mail reviewer
2014	NIH GCAT study section, ad hoc
2015	NIH NIDA CEBRA study section, ad hoc
2015	NIH NIDA Avenir DP1 study section, mail reviewer
2017	NIH Transformative R01 study section, mail reviewer
2017	NIH NIDA Avenir DP1 study section, second round reviewer
2017	Genome Canada 2017 LSARP, friendly review

Grants reviewed (standing member):

2010-2012	Charles A. King Postdoctoral Fellowship Program

Scientific Advisory Board:

2013-	Labex DEEP program grant (PIs Heard and Almouzni)

Journal Editorial Boards:

2008-present	Genome Research
2009-present	Epigenetics and Chromatin
2010-2014	Genome Biology
2015-present	Genetics

Academic Editor:

PLoS Biology, PLoS Genetics, PLoS Computational Biology

Manuscripts reviewed:

PLoS Biology, Nature, Nature Genetics, Nature Cell Biology, Nature Structural and Molecular Biology, Genome Research, Genome Biology, Science, Cell, Molecular Cell, PLoS Genetics, Nucleic Acids Research, Molecular Biology of the Cell, Molecular Biology and Evolution, PLoS Computational Biology, PNAS, PLoS ONE, Chromosoma, eLife

Research Publications (corresponding authorship shown in bold)

1. Kim, M., Krogan, N.J., Vasiljeva, L., Rando, O.J., Nedea, E., Greenblatt, J.F., Buratowski, S. "The yeast Rat1 exonuclease promotes transcription termination by RNA polymerase II", Nature 2004, 432: 517-22.

2. Dion, M.F., Altschuler, S.J., Wu, L.F., **Rando, O.J.** "Genomic characterization reveals a simple histone H4 acetylation code", PNAS 2005, 102, 5501-06.

3. Casolari, J.M., Brown, C.R., Drubin, D.A., Rando, O.J., Silver, P.A. "Developmentally induced changes in transcriptional program alter spatial organization across chromosomes", Genes Dev 2005, 19, 1188-98.

4. Yuan, G.C., Liu, Y.J., Dion, M.F., Slack, M.D., Wu, L.F., Altschuler, S.J., **Rando, O.J.** "Genome-scale identification of nucleosome positions in *S. cerevisiae*", Science 2005, 309, 626-30.

5. Liu, C.L., Kaplan, T., Kim, M., Buratowski, S., Schreiber, S.L., Friedman, N., **Rando, O.J.** "Single-nucleosome mapping of histone modifications in *S. cerevisiae*", PLoS Biology 2005, 3, e328.

6. Raisner, R.M., Hartley, P.D., Meneghini, M.D., Bao, M.Z., Liu, C.L., Schreiber, S.L., Rando, O.J., Madhani, H.D. "Histone variant H2A.Z marks the 5' ends of both active and inactive genes in euchromatin", Cell 2005, 123: 233-48

7. Kim, M., Vasiljeva, L., Rando, O.J., Zhelkovsky, A., Moore, C., Buratowski, S. "Distinct pathways for snoRNA and mRNA termination", Mol Cell 2006, 24, 723-34.

8. Dion, M.F., Kaplan, T., Kim, M., Buratowski, S., Friedman, N., **Rando, O.J.** "Dynamics of replication-independent histone turnover in budding yeast", Science 2007, 315, 1405-8.

9. Dennis, J.H., Fan, H.Y., Reynolds, S.M., Yuan, G., Meldrim, J.C., Richter, D.J., Peterson, D.G., Rando, O.J., Noble, W.S., Kingston, R.E. "Independent and complementary methods for large-scale structural analysis of mammalian chromatin", Genome Res 2007, 17, 928-39.

10. Whitehouse, I., Rando, O.J., Delrow, J., Tsukiyama, T. "Chromatin remodeling at promoters suppresses antisense transcription", Nature 2007, 450, 1031-5.
11. Au, W.C., Crisp, M.J., Deluca, S.Z., Rando, O.J., Basrai, M.A. "Altered Dosage and Mislocalization of Histone H3 and Cse4p Lead to Chromosome Loss in Saccharomyces cerevisiae", Genetics 2008, 179, 263-75.
12. Chechik, G., Oh, E., Rando, O., Weissman, J., Regev, A., Koller, D. "Activity motifs reveal principles of timing in transcriptional control of the yeast metabolic network", Nat Biotechnol 2008, 26, 1251-9.
13. Kaplan, T., Liu, C.L., Erkmann, J.A., Holik, J., Grunstein, M., Kaufman, P.D., Friedman, N., **Rando, O.J.** "Cell cycle- and chaperone-mediated regulation of H3K56ac incorporation in yeast", PLoS Genet 2008, 4, e1000270.
14. Rowat, A.C., Bird, J.C., Agresti, J.J., Rando, O.J., Weitz, D.A. "Tracking lineages of single cells in lines using a microfluidic device", Proc Natl Acad Sci USA 2009 Oct 13, 106, 18149-54.
15. Weiner, A., Hughes, A., Yassour, M., **Rando, O.J.****, Friedman, N.** "High-resolution nucleosome mapping reveals transcription-dependent promoter packaging", Genome Res 2010, 20, 90-100.
** Co-corresponding author
16. Radman-Livaja M., Liu C.L., Friedman, N., Schreiber, S.L., **Rando, O.J.** "Replication and active demethylation represent partially overlapping mechanisms for erasure of H3K4me3 in budding yeast", PLoS Genetics 2010, 6, e1000837.
17. Tsankov, A., Thompson, D.A., Socha, A., Regev, A., **Rando, O.J.** "The role of nucleosome positioning in the evolution of gene regulation", PLoS Biol 2010, 8, e1000414.
18. Kim, T.S., Liu, C.L., Yassour, M., Holik, J., Friedman, N., Buratowski, S., **Rando, O.J.** "RNA Polymerase mapping during stress responses reveals widespread nonproductive transcription in yeast", Genome Biol 2010, 11, R75.
19. Lopes Da Rosa, J., Holik, J., Green, E.M., **Rando, O.J.****, Kaufman, P.D.** "Overlapping Regulation of CenH3 Localization and Histone H3 Turnover by CAF-1 and HIR Proteins in Saccharomyces Cerevisiae", Genetics 2010
** Co-corresponding author
20. Ivanovska, I., Jacques, P.E., Rando, O.J., Robert, F., Winston, F. "Control of chromatin structure by Spt6: different consequences in coding and regulatory regions", Mol Cell Biol 2010
21. Carone, B.R., Fauquier, L., Habib, N., Shea, J.M., Hart, C.E., Li, R., Bock, C., Li, C., Gu, H., Zamore, P.D., Meissner, A., Weng, Z., Hofmann, H.A., Friedman, N., **Rando, O.J.** "Paternally induced transgenerational environmental reprogramming of metabolic gene expression in mammals." Cell 2010 143:1084-96.
22. Papamichos-Chronakis, M., Watanabe, S., Rando, O.J., Peterson, C.L. "Global regulation of H2A.Z Localization by the INO80 Chromatin-Remodeling Enzyme is Essential for Genome Integrity", Cell 2011 144:200-13.
23. Radman-Livaja, M., Weiner, A., Friedman, N., Kamakaka, R., **Rando, O.J.** "Dynamics of Sir complex spreading in budding yeast: secondary recruitment sites and euchromatic localization", EMBO J 2011, 30:1012-26.

24. Radman-Livaja, M., Verrzijlbergen, K., Weiner, A., Friedman, N.**, **Rando, O.J.****, van Leeuwen, F.** "Patterns and mechanisms of ancestral histone protein inheritance in budding yeast", PLoS Biol 2011, 9:e1001075.
** Co-corresponding author
25. Tsankov, A., Yanagisawa, Y., Rhind, N., Regev, A., **Rando, O.J.** "Evolutionary divergence of intrinsic and trans-regulated nucleosome positioning sequences reveals plastic rules for chromatin organization", Genome Res 2011, Sep 13 [Epub ahead of print].
26. Sikorski, T.W., Ficarro, S.B., Holik, J., Kim, T., Rando, O.J., Marto, J.A., Buratowski, S. "Sub1 and RPA associate with RNA polymerase II at different stages of transcription", Mol Cell 2011, 44:397-409.
27. Yildirim, O., Li, R., Hung, J.H., Chen, P.B., Dong, X., Ee, L., Weng, Z., **Rando, O.J.****, Fazzio, T.G.** "Mbd3/NURD complex regulates expression of 5-hydroxymethylcytosine marked genes in embryonic stem cells", Cell 2011, 147:1498-510.
** Co-corresponding author
28. Xu, J., Yanagisawa, Y., Tsankov, A.M., Hart, C., Aoki, K., Kommajosyula, N., Steinmann, K.E., Bochicchio, J., Russ, C., Regev, A., Rando, O.J., Nusbaum, C., Niki, H., Milos, P., Weng, Z., Rhind, N. "Genome-wide identification and characterization of replication origins by deep sequencing", Genome Biol 2012, 13:R27.
29. Radman-Livaja, M., Quan, T.K., Valenzuela, L., Armstrong, J.A., van Welsem, T., Kim, T., Lee, L.J., Buratowski, S. van Leeuwen, F., **Rando, O.J.****, and Hartzog, G.A.** "A key role for Chd1 in Histone H3 dynamics at the 3' ends of long genes in yeast", PLoS Genetics 2012, 8:e1002811. ** Co-corresponding author
30. Hughes, A.L., Jin, Y., **Rando, O.J.****, and Struhl, K.** "A functional evolutionary approach to identify determinants of nucleosome positioning: a unifying model for establishing the genome-wide pattern", Mol Cell 2012, 48:5-15. ** Co-corresponding author
31. Weiner, A., Chen, H.V., Liu, C.L., Rahat, A., Klein, A., Soares, L., Gudipati, M., Pfeffner, J., Regev, A., Buratowski, S., Pleiss, J.A., Friedman, N., and **Rando, O.J.** "Systematic dissection of roles for chromatin regulators in a yeast stress response", PLoS Biology 2012, 10: e1001369. PMID: 22912562. PMCID: PMC3416867.
32. Mobius, W., Osberg, B., Tsankov, A.M., Rando, O.J., and Gerland, U. "Toward a unified physical model of nucleosome patterns flanking transcription start sites", PNAS 2013, 110:5719-24. PMID: 23509245.
33. Watanabe, S., Radman-Livaja, M., Rando, O.J., and Peterson, C.L. "A histone acetylation switch regulates H2A.Z deposition by the SWR-C remodeling enzyme", Science 2013, 340:195-9. PMID: 23580526.
34. Soares, L.M., Radman-Livaja, M., Lin, S.G., Rando, O.J., and Buratowski, S. "Feedback control of Set1 protein levels is important for proper H3K4 methylation patterns", Cell Rep 2014, pii: S2211-1247. PMID: 24613354.
35. Carone, B.R., Hung, J.H., Hainer, S.J., Chou M.T., Carone, D.M., Weng, Z., Fazzio, T.G., and **Rando, O.J.** "High-resolution mapping of chromatin packaging in mouse embryonic stem cells and sperm", Dev Cell 2014, 30:11-22. PMID: 24998598. PMCID: PMC4184102.

36. Yildirim, O., Hung, J.H., Cedeno, R.J., Weng, Z., Lengner, C.J., and **Rando, O.J.** "A system for genome-wide histone variant dynamics in ES cells reveals dynamic MacroH2A2 replacement at promoters", PLoS Genet 2014, 10: e1004515. PMID: 25102063. PMCID: PMC4125097.
37. Hainer, S.J., Gu, W., Carone, B.R., Landry, B.D., Rando, O.J., Mello, C.C., and Fazzio, T.G. "Suppression of pervasive noncoding transcription in embryonic stem cells by esBAF", Genes Dev 2015, 29:362-78. PMID: 25691467
38. Weiner, A., Hsieh, T-H.S., Appleboim, A., Chen, H.V., Rahat, A., Amit, I., **Rando, O.J.** **, and Friedman, N. ** "High-resolution chromatin dynamics during a yeast stress response", Mol Cell 2015, pii: S1097-2765(15)00094-5. PMID: 25801168. ** Co-corresponding author
39. Zhao-Shea, R., DeGroot, S.R., Liu, L., Vallaster, M., Pang, X., Su, Q., Gao, G., Rando, O.J., Martin, G.E., George, O., Gardner, P.D., and Tapper, A.R., "Increased CRF signalling in a ventral tegmental area-interpeduncular nucleus-medial habenula circuit induces anxiety during nicotine withdrawal.", Nat Commun 2015, 6:6770. PMID: 25898242.
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