

CURRICULUM VITAE: Steven Henikoff

Position: Investigator, Howard Hughes Medical Institute
Professor, Basic Sciences Division

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Lab: <https://research.fredhutch.org/henikoff/en.html>

Education

1964-68 University of Chicago, Chicago, Illinois. BS in Chemistry. Research on optical properties of biopolymers, George Holzwarth, advisor.

1971-77 Harvard University, Cambridge, Massachusetts. PhD in Biochemistry and Molecular Biology. Matthew Meselson, advisor. Thesis: RNA from heat induced puff sites in *Drosophila*.

1977-80 University of Washington, Seattle, Washington. Postdoctoral fellow in Zoology. Research on position-effect variegation in *Drosophila*, Charles Laird, advisor and genetic engineering in yeast, Benjamin Hall, advisor.

Professional Experience

1981-85 Fred Hutchinson Cancer Research Center, Seattle, Washington. Assistant Member in Basic Sciences.

1981-1985-88 University of Washington, Seattle. Affiliate faculty in Genetics/Genome Sciences. Fred Hutchinson Cancer Research Center, Seattle, Washington. Associate Member in Basic Sciences.

1988- Fred Hutchinson Cancer Research Center, Seattle, Washington. Member and Professor in Basic Sciences.

1990- Investigator, Howard Hughes Medical Institute.

Current Research

Nucleosome dynamics and evolution
Transcriptional regulation
Centromere evolution
Epigenomic technologies
Histone overexpression in cancer

Ongoing Funding

Howard Hughes Medical Institute	Investigator	04/1/1990 – 1/31/2027
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Honors

2025 55th Lewis S. Rosenstiel Award for Distinguished Work in Basic Medical Research

2022 Member, American Academy of Arts and Sciences

2015 Washington State Academy of Sciences

2015 Genetics Society of America Medal

2012 Fellow, American Association for the Advancement of Science

2005 Member, US National Academy of Sciences

1978 Leukemia Society of America Postdoctoral Fellowship

1971 National Defense Service Medal, US Army

1968 National Science Foundation Graduate Student Fellowship

Activities

2025 Peer Reviewer (Remote), European Research Council
 2025 NIH NCI Grant Review Panel
 2024 Course Instructor, FHCC/UW MCB517
 2024 NIH Fellowship Grant Review Panel
 2023- Field Chief Editor, *Frontiers in Epigenetics and Epigenomics*
 2022 NIH Fellowship Grant Review Panel
 2021-2023 Scientific Advisory Board, Center for Protein Research, Copenhagen University, Denmark
 2021 NIH Blueprint for Neuroscience Research Grant Review Panel
 2021 NIH Special Emphasis Grant Review Panel
 2020 Science Advisory Board, Center for Protein Research, University of Copenhagen
 2020 Panel Member Functional Genomics Workshop, NASEM Board on Life Sciences, WA DC
 2020-2025 NIH 4D Nucleome External Program Consultant
 2020 NIH GCAT Grant Review Panel
 2018 NIH SBIR Review Panel
 2017-2018 NIH GCAT Review Panels (3)
 2017- Advisor/Visiting Professor in National Institute of Genetics, Mishima, Japan
 2016 NIH Interdisciplinary Molecular Sciences and Training Review Panel
 2016- External Scientific Advisory Board, Northwestern Physical Sciences Oncology Center
 2015-2016 NIH Transformative R01 Review Panel
 2015-2020 Scientific Advisory Board, Gregor Mendel Institute, Vienna, Austria
 2015 NIH 4D Nucleosome Project Reviewer/Consultant
 2015 NCI Site visit team member
 2014- *Genome Research*, Editorial Advisory Board
 2013 Reviewer, HHMI Investigator finalist competition
 2013 Co-organizer, Epigenetics & Chromatin: Interactions and processes, Boston, MA
 2012 Co-organizer, CoB Workshop on Epigenetic Memory, Sussex, UK
 2012 Co-organizer, Keystone Symposium on Epigenomics, Keystone, CO
 2011- External Advisory Board, Chicago Biomedical Consortium
 2011 Co-organizer, Forbeck Forum on Cancer Epigenetics, Hilton Head, SC
 2011 Reviewer, HHMI-GBMF Investigator finalists competition
 2010- *Genome Biology*, Editorial Advisory Board
 2010 External Advisory Committee, Einstein Center for Epigenomics, Bronx, NY
 2009 Co-organizer, Keystone Symposium on Epigenetics, Development and Disease, Breckenridge, CO
 2008-2014 Epizyme, Inc. Scientific Advisory Board, Boston, MA
 2008-2022 Co-Editor-in-chief, *Epigenomics & Chromatin* (BMC Press)
 2006-2010 AACR Human Epigenome Task Force
 2005-2007 NSF Maize Chromatin Project Advisory Board, Tucson, AZ
 2005-2007 The Cancer Genome Atlas (NCI-NHGRI) External Steering Committee
 2005-2008 *PLoS Computational Biology* Editorial Board
 2005- *Current Opinion in Genetics and Development*, Editorial Board
 2005 Co-organizer, EMBO Conference on Nuclear Structure and Dynamics, Avignon, France
 2004-2010 Scientific Advisory Board, Keystone Symposia, Keystone, CO
 2004 Co-organizer, Nobel Symposium on Epigenetic Reprogramming, Stockholm, Sweden
 2002-2014 Course Instructor, FHCRC/UW MCB program Conjoint 533: The Dynamic Chromosome (also 2004, 2007, 2010, 2014)
 2002 Co-organizer, NAS Sackler Symposium on self-perpetuating structural states
 2001- Contributor, *Faculty of 1000*
 2001-2002 Nebraska EPSCoR Advisory Board, Lincoln, NE
 2001-2002 Institute of Systems Biology, Scientific Advisory Board, Seattle, WA
 2000-2006 *Comparative and Functional Genomics* Section Editor for Bioinformatics
 2000-2004 Tilligen, Inc., Co-founder and Scientific Advisory Board Member, Seattle, WA
 2000 Reviewer, HHMI Computational Biology Investigator finalists competition
 1999-2002 NSF Plant Chromatin Project Advisory Board

1998- *Trends in Genetics* Editorial Board
 1997-2007 *Chromosoma* Editorial Board
 1997 Co-organizer, Epigenetics Gordon Conference, Holderness, NH
 1996-2005 *CABIOS/Bioinformatics* Editorial Board
 1996-2000 FlyBase Advisory Board
 1996-2005 *Genetics* Editorial Board
 1994-2003 *Protein Science* Editorial Advisory Board
 1993-2015 NIH *ad hoc* Study Section Reviewer/Consultant (average ~1 panel/year)
 1990-1992 Member, NIH/NHGRI Genome Research Study Section
 1990-1992 Caltech NSF Molecular Biotechnology Center External Advisory Board
 1989-1991 *Molecular and Cellular Biology* Editorial Board

Trainees

Michael Keene, postdoctoral fellow 1983-1986.
 Daniel Johnson, postdoctoral fellow 1985-1988, Assistant Professor, University of Miami.
 Tom Dreeson, postdoctoral fellow 1986-1989, Lab Manager, Pennington Biomedical Research Center.
 Deborah Wines, postdoctoral fellow 1989-1994, Assistant Professor, Montana State University
 Kate Loughney, postdoctoral fellow 1989-1991, Medical Journalist.
 Paul B. Talbert, postdoctoral 1990-1993, Staff Scientist, FHCC.
 Denise Clark, postdoctoral fellow 1990-1994. Professor, University of New Brunswick, Canada
 Linda E. Martin-Morris, postdoctoral fellow 1992-1996, Laboratory Coordinator, Dept. Genome Sciences, University of Washington
 Douglas R. Dorer, postdoctoral fellow 1992-1997, Assistant Professor of Biology, Meharry Medical College.
 Joy F. Sabl, graduate student 1992-1996, Postdoctoral fellow, Lecturer, Carnegie-Mellon University.
 Amy K. Csink, postdoctoral fellow 1994-1998, Assistant Professor of Biology, Carnegie-Mellon University.
 Shmuel Pietrokowski, postdoctoral (LSRF fellowship) 1994-1998, Senior Researcher, Weizmann Institute, Israel.
 Georgette L. Sass, HHMI Associate 1994-1998, Professor, Grand Valley State University.
 J. Suso Platero, HHMI Associate 1995-1999, Senior Research Investigator, Bristol Myers Squibb.
 Bas van Steensel, postdoctoral fellow 1998-2000. Group Leader, NKI, Amsterdam, Netherlands.
 Claire M. McCallum, graduate student 1996-2002. Research Scientist, Arcadia Biosciences, Inc., Davis, CA.
 Kami Ahmad, ACS postdoctoral fellow 1996-2002. Principal Investigator, FHCC.
 James F. Smothers, NIH postdoctoral fellow 1998-2001. Research Scientist, Amgen Corporation, Cambridge, MA.
 Amy L. Holmes, postdoctoral fellow 1998-2000.
 Danielle Vermaak, Damon Runyon postdoctoral fellow 1999-2003. Science Teacher, Lincoln High School, Seattle, WA.
 Pauline Ng, NSF and DOE graduate student 1999-2002. Group Leader, Genome Institute of Singapore.
 Harmit S. Malik, Helen Hay Whitney postdoctoral fellow 1999-2003. Professor, FHCC, HHMI Investigator.
 Trenton Colbert, postdoctoral fellow 2000-2001. Research Scientist, Arcadia Biosciences, Inc. Davis CA.
 Bradley Till, postdoctoral fellow 2000-2002, Staff scientist 2002-2007. Bioinformatics Specialist, U. California, Davis.
 Jennifer Cooper, postdoctoral fellow 2001-2009. Assistant Professor, Kennesaw State University, Georgia.
 Erin McKittrick, HHMI graduate student 2002-2005. Author.
 Robert Tran, postdoctoral fellow 2002-2006. Senior Scientist, U. California, Davis.
 Siew-Loon Ooi, postdoctoral fellow 2003-2009.

Yoshiko Mito, graduate student 2003-2007. Director, Cytogenetics and Genomics Laboratory, University of Washington.

Daniel Zilberman, Leukemia and Lymphoma Society postdoctoral fellow 2004-2007. Group Leader, Institute of Science and Technology, Austria.

Melissa Conerly, graduate student 2003-2010. Scientist, Paragon Therapeutics.

Yamini Dalal, postdoctoral fellow 2003-2008. Investigator and Group Leader, National Cancer Institute, National Institutes of Health, Bethesda, MD.

Cecilia de Bustos, Visiting graduate student (Basque Government internship) 2004-2005.

Kerry Bubb, post-doctoral fellow 2007-2008, Research Scientist, University of Washington.

Takehito Furuyama, NIH postdoctoral fellow 2003-2008. Author.

Siew-Loon Ooi, Damon Runyon postdoctoral fellow 2004-2009. Scientist, Department of Genetics, DSM, Delft, Netherlands.

Mary Gehring, Life Sciences Research Foundation postdoctoral fellow 2005-2010. Associate Professor, MIT, Member, Whitehead Institute and HHMI Investigator.

Martin Riedel, Visiting Graduate Student 2007-2008.

Roger Deal, NIH post-doctoral fellow 2007-2011. Associate Professor, Emory University.

Friedemann Loos, Fulbright Scholarship Student 2008-2009.

Florian Steiner, Swiss National Science Foundation postdoctoral fellow 2008-2014. Associate Professor, University of Geneva.

Sheila Teves, NSF graduate student, Weintraub Awardee 2009-2013. Assistant Professor, University of British Columbia.

Christopher Weber, NSF graduate student 2009-2014. Postdoctoral fellow, Stanford University

Erika Wolff, post-doctoral fellow 2009-2010. Research Scientist, University of Washington

Kristina Krassovsky, NSF graduate student 2009-2014. Postdoctoral fellow, UC Berkeley

John Latham, postdoctoral fellow 2011-2012. Senior Manager, Guardian Health, Inc.

Fan Yang, postdoctoral fellow 2011-2014

Gabriel Zentner, postdoctoral fellow 2011-2015. Assistant Professor, Indiana University.

Peter Skene, Damon Runyon Foundation postdoctoral fellow 2011-2017. Director of Molecular Biology and Biochemistry, Allen Institute for Immunology.

Anna Drinnenberg, Jane Coffin Childs Foundation postdoctoral fellow 2012-2015. (co-mentored with Harmit Malik) Group Leader, Marie Curie Institute, Paris.

Srinivas Ramachandran, postdoctoral fellow 2012-2017. Assistant Professor, University of Colorado, Denver.

Siva Kasinathan, MSTP graduate student 2012-2017. Resident, Stanford University.

Jitendra Thakur, postdoctoral fellow 2013-2020. Assistant Professor, Emory University.

Vuong Tran, postdoctoral fellow 2015-2016. Senior Scientist, Parse Biosciences, Inc.

Hatice Seda Kaya-Okur, postdoctoral fellow 2016-2019. Scholar, Altius Institute

Jay Sarthy, Damon Runyon/Sohn Pediatric Cancer Research Fellow 2017-2022. Assistant Member, Seattle Children's Research Institute

Steven Wu, graduate student 2018-2022. Computational Biologist, Freenome, Inc.

Sandipan Brahma, NIH K99/R00 postdoctoral fellow 2017-2023. Assistant Professor, University of Nebraska Medical Center

Michael Meers, NIH F32, NIH K99/R00 postdoctoral fellow 2017-2022. Assistant Professor, Washington University in St. Louis Medical School

Derek Janssens, Hartwell Foundation and NIH K22 postdoctoral fellow 2017-2024 Assistant Professor, van Andel Institute.

Ye Zheng (co-mentored with Raphael Gottardo), NIH K99/R00 postdoctoral fellow 2019-2024. Assistant Professor, MD Anderson Cancer Center

James Anderson, graduate student 2019-2023. Scientist, Epiccypher, Inc.

Matthew Wooten, NIH K99/R00 postdoctoral fellow 2020-

Nadiya Khyzha, NSERC postdoctoral fellow 2020-

Cassidy Danyko, graduate student 2021-2025.

Soyeon Showman, graduate student 2022-2024. Postdoc FHCC

Jacob Greene, graduate student 2022-
 Sarah Leichter, NIH F32 postdoctoral fellow 2022-
 Ronald Paranal, K12 postdoctoral fellow 2022-
 Weifang Wu, postdoctoral fellow 2023-

Recent Invited Presentations (2020-)

5/31-6/05/26	Chromatin Structure and Function Gordon Conference	Barcelona, Spain
4/15/26	Rosenstiel Award Lecture, Brandeis University	Waltham, MA
3/30/26	University of Toronto	Toronto, Canada
2/27/26	Northwestern University	Virtual
2/16/26	University of North Carolina	Chapel Hill, NC
1/26/26	Clemson University	Virtual
11/17/25	University of Texas Southwestern	Dallas, TX
10/21/25	Van Andel Institute	Grand Rapids, MI
9/15/25	Keynote, Regulome Summit, University of Washington	Seattle, WA
5/22/25	Keynote, Pfizer Oncology Research Unit Annual Meeting	Bellevue, WA
4/5/25	GATC Symposium, Pune, India	Virtual
3/31/25	TICCSO-3 Single-Cell & Spatial Omics, Shanghai, China	Virtual
3/25/25	Brandeis University	Waltham, MA
3/24/25	University of Massachusetts Medical School	Worcester, MA
12/19/24	Boston Children's Hospital, Harvard Medical School	Boston, MA
10/18/24	National Institutes of Health Chromatin Symposium	Bethesda, MD
10/16/24	Johns Hopkins School of Medicine	Baltimore, MD
8/14/24	Chromatin Summer School, Helmholtz University, Munich	Virtual
5/21/24	Stormo Symposium, Washington University	St. Louis, MO
5/20/24	University of Missouri	Columbia, MO
5/17/24	University of Nebraska Health Sciences Center	Omaha, NB
5/12/24	Graduate Student Symposium, University of Colorado	Boulder, CO
3/31/24	TICCSO-2 Single-Cell and Spatial Omics (Shanghai)	Virtual
3/7/24	Keynote, Epigenetics Symposium Fox-Chase CC	Philadelphia, PA
2/23/24	BMBGSA Symposium, Oklahoma State U	Stillwater, OK
8/23/23	Potter Lecture, Cincinnati Children's Hospital	Cincinnati, OH
8/14/23	Chromatin Summer School, Helmholtz University, Munich	Virtual
8/6-9/23	Penn State Summer Symposium	University Park, PA
6/11-16/23	Gordon Research Conference on Chromatin	Ventura, CA
6/7/23	Stanford University	Stanford, CA
6/5/23	Seattle Children's Hospital	Seattle, WA
5/15-18/23	EMBL meeting Chromatin and Epigenetics	Heidelberg, Germany
4/19/23	University of Illinois Urbana-Champaign	Virtual
4/12/23	Duke University	Durham, NC
4/10/21	Columbia University	New York, NY
3/24/23	University of Michigan	Ann Arbor, MI
2/24/23	All-Ireland Chromatin Consortium	Virtual
1/24-25/23	ERATO International Chromatin Symposium	Virtual
12/1/22	Oklahoma Medical Research Foundation	Oklahoma City, OK
10/19/22	University of Virginia, Charlottesville	Virtual
10/1/22	ASBMB meeting: Epigenetics and genome integrity	Seattle, WA
9/8-9/22	NIH Workshop: Chromatin control of virus infection	Bethesda, MD
8/16/22	Chromatin Summer School, Helmholtz University, Munich	Virtual
2/24/22	Johns Hopkins University, Baltimore, MD	Virtual
2/9/22	University of Illinois, Chicago, IL	Virtual
1/27/22	University of Nebraska Medical Center	Virtual
11/16/21	University of Colorado, Boulder, CO	Virtual
11/7-12/21	Epicyphe2021	Clearwater, FL

10/22/21	NIEHS, Research Triangle, NC	Virtual
10/15-16/21	Peking University, Beijing	Virtual
10/12/21	Brigham & Women's Hospital, Boston, MA	Virtual
9/23/21	Cell Signaling Technology, Inc.	Virtual
9/20/21	Broad Institute, Cambridge, MA	Virtual
9/14/21	KAUST, Saudi Arabia	Virtual
9/9/21	Science in Asia, AAAS, Beijing	Virtual
7/14/21	Cambridge Epigenetics Club	Virtual
6/15/21	NIH/NIAMS Retreat	Virtual
5/11/21	Chromatin and Epigenetics biweekly series, China	Virtual
4/23/21	University of California, Riverside	Virtual
4/6/21	University of Chicago	Virtual
3/27/21	Istanbul University Winter School	Virtual
3/12/21	Harvard Medical School	Virtual
3/1/21	Lahore University	Virtual
2/16/21	Queen Mary University (London)	Virtual
12/7-11/20	IAS Focused Meeting (Hong Kong)	Virtual
11/18/20	Cornell-Weill Medical School	Virtual
10/8/20	EpiBio 2020 (Raleigh, NC)	Virtual
10/1/20	Yale University (New Haven, CT)	Virtual
9/30/20	Fox-Chase Cancer Center (Philadelphia, PA)	Virtual
9/14/20	Mayo Clinic (Rochester, MN)	Virtual
9/2/20	Max Planck Berlin	Virtual
8/24/20	University of Pittsburgh	Virtual
8/27-9/20	EMBL Transcription (Heidelberg, Germany)	Virtual
8/20/20	Social DNAing	Virtual
8/10/20	CCMB (Hyderabad, India)	Virtual
7/16/20	Meiosis in Quarantine	Virtual
6/12/20	San Diego Chromatin Club	Virtual
6/11/20	Max Planck Göttingen	Virtual
5/27/20	Stanford University	Virtual
5/14/20	Chan-Zuckerberg Seed Network	Virtual
5/20/20	University of California, Berkeley	Virtual
2/13/20	Benaroya Institute	Seattle, WA
2/10-12/20	NAS Functional Genomics Workshop	Washington, DC
1/28/20	Baylor College of Medicine	Houston, TX
1/21/20	California Institute of Technology	Pasadena, CA

Public Websites

- CUT&Tag <https://www.protocols.io/view/bench-top-cut-amp-tag-bcuhiwt6> Monitored by Steven Henikoff.
- CUT&RUN <https://www.protocols.io/view/cut-amp-run-targeted-in-situ-genome-wide-profiling-14eqnr4ql5dy/v3> Monitored by Derek Janssens.
- CUT&Tag-direct <https://www.protocols.io/view/cut-amp-tag-direct-with-cutac-bmbfk2jn> Monitored by Steven Henikoff.
- pA-Tn5 Protein Purification and MEDS-loading <https://www.protocols.io/view/3xflag-patn5-proteinpurificationand-medsloading-8yrhvxv6> Monitored by Terri Bryson.
- CUT&Tag Data Processing and Analysis Tutorial <https://www.protocols.io/view/cut-amp-tag-data-processing-and-analysis-tutorial-bjk2kkyye> Monitored by Ye Zheng.
- RT&Tag (Reverse Transcribe & Tagment) <https://www.protocols.io/view/rt-amp-tag-reverse-transcribe-amp-tagment-x54v9jyiqg3e/v1> Monitored by Nadiya Khyzha
- CUTAC for FFPEs <https://www.protocols.io/view/cutac-for-ffpes-14eqn292zq5d/v3> Monitored by Steven Henikoff

- CUT&RUN with Drosophila tissues <https://www.protocols.io/view/cut-tag-with-drosophila-tissues-bnx5mfq6> Monitored by Kami Ahmad.
- CUT&Tag with Drosophila tissues <https://www.protocols.io/view/cut-tag-with-drosophila-tissues-3bvl4kkprvo5/v1> Monitored by Kami Ahmad
- AutoCUT&RUN <https://www.protocols.io/view/autocut-run-genome-wide-profiling-of-chromatin-pro-ufteetj/metrics> Monitored by Derek Janssens.
- AutoCUT&Tag <https://www.protocols.io/view/autocut-amp-tag-streamlined-genome-wide-profiling-bqztjx6n> Monitored by Derek Janssens.
- Peak calling by Sparse Enrichment Analysis for CUT&RUN (SEACR) <https://seacr.fredhutch.org/> Maintained by Daniel Tenenbaum.

Outreach Activities

For the past >30 years I have been committed to lowering the bar to entry for researchers around the world by being proactive in making our tools freely available and requiring little or no specialized expertise or equipment. Our Blocks Database e-mail server introduced in 1992 for detecting distant evolutionary relationships was among the first non-commercial copy-and-paste remote servers. In 1994, the BLAST server was introduced using our BLOSUM series of amino acid substitution matrices for protein alignments, and BLOSUM62 is still the default. Also in 1994 we established the Blocks Database server on the World-wide-web and later introduced other popular copy-and-paste web servers, including the SIFT server for detecting deleterious non-synonymous mutations, the CODEHOP server for designing consensus-degenerate oligonucleotide primers, and since 2019, the SEACR server for CUT&RUN and CUT&Tag peak-calling. Since 2018 my labmates and I have been a major presence on Protocols.io, with our public protocols sites accumulating >750,000 views and >4000 questions and answers, while distributing reagents directly to ~600 laboratories prior to commercial availability, with ~1500 labs ordering plasmids at low cost from Addgene for making CUT&RUN and CUT&Tag fusion proteins. Within a month of the onset of the COVID-19 pandemic in early 2020, I posted “Profiling the epigenome at home” on *bioRxiv* <https://www.biorxiv.org/content/10.1101/2020.04.15.043083v1>, which was highlighted by *The Scientist* in a feature article and chosen as one of the top technical advances of 2020: <https://www.the-scientist.com/top-technical-advances-of-2020-68297>.

Publications

ScholarGPS (Lifetime, prior 5 y): <https://scholargps.com/scholars/27628988442011/steven-henikoff>

GoogleScholar: <https://scholar.google.com/citations?user=SMwhtM8AAAAJ&hl=en>

PubMed (429 total): <https://pubmed.ncbi.nlm.nih.gov/?term=henikoff+s+%5Bau%5D&sort=date>

Peer reviewed research articles

Leichter SM, Ahmad K, **Henikoff S**. Polycomb misregulation in enterocytes drives tissue decline in the aging Drosophila intestine. *Genome Res*. 2025 Dec 10. doi: 10.1101/gr.281058.125

Ahmad K, Wooten M., Takushi BN, Vidaurre V, Chen X, **Henikoff S**. Cell-cycle-dependent repression of histone gene transcription by histone H4. Cell-cycle-dependent repression of histone gene transcription by histone H4. *Nat Struct Mol Biol* 2026 Jan. DOI: 10.1038/s41594-025-01731-1.

4D Nucleome Consortium; Dekker J, Oksuz BA, Zhang Y, Wang Y, Minsk MK, Kuang S, Yang L, Gibcus JH, Krietenstein N, Rando OJ, Xu J, Janssens DH, **Henikoff S**, Kukalev A, Willemin A, Winick-Ng W, Kempfer R, Pombo A, Yu M, Kumar P, Zhang L, Belmont AS, Sasaki T, van Schaik T, Brueckner L, Peric-Hupkes D, van Steensel B, Wang P, Chai H, Kim M, Ruan Y, Zhang R, Quinodoz SA, Bhat P, Guttman M, Zhao W, Chien S, Liu Y, Venev SV, Plewczynski D, Azcarate I, Szabó D, Thieme CJ, Szczepińska T, Chiliński M, Sengupta K, Conte M, Esposito A, Abraham A, Zhang R, Wang Y, Wen X, Wu Q, Yang Y, Liu J, Boninsegna L, Yildirim A, Zhan Y, Chiariello AM, Bianco S, Lee L, Hu M, Li Y, Barnett RJ, Cook AL, Emerson DJ, Marchal C, Zhao P, Park P, Alver BH, Schroeder A, Navelkar R, Bakker C, Ronchetti W, Ehmsen S, Veit A, Gehlenborg N, Wang T, Li D, Wang X, Nicodemi M, Ren B, Zhong S, Phillips-Cremins JE, Gilbert DM, Pollard KS, Alber F, Ma J, Noble WS, Yue F. An integrated

- view of the structure and function of the human 4D nucleome. *bioRxiv* [Preprint]. 2024 Oct 27:2024.09.17.613111. doi: 10.1101/2024.09.17.613111. PMID: 39484446; PMCID: PMC11526861.
- Eldred KC, Wooten M, Janssens DH, Hahn J, Neph SJ, Edgerton SJ, Wyatt-Draher G, Sherman SM, Ranchalis JE, Stergachis AB, Reh TA, **Henikoff S**. CUT&TIME captures the history of open chromatin in developing neurons. *bioRxiv*. 2025 Sep 6:2025.08.29.673195. doi: 10.1101/2025.08.29.673195. PMID: 40950047; PMCID: PMC12424630.
- Keogh MC, Almouzni G, Andrews AJ, Armache KJ, Arrowsmith CH, Baek SH, Bedford MT, Bernstein E, Côté J, David Y, Denu JM, Fierz B, Garcia BA, Glass KC, Gozani O, Helin K, **Henikoff S**, Jensen ON, Josefowicz SZ, Kelleher NL, Kutateladze TG, Lindner HH, Lu C, Luger K, Mallick P, Musselman CA, Muir TW, Paša-Tolić L, Schneider R, Shi X, Shi Y, Sidoli S, Smith LM, Tyler JK, Wolberger C, Workman JL, Strahl BD, Young NL. A needed nomenclature for nucleosomes. *Mol Cell*. 2025 Oct 2;85(19):3554-3561. doi: 10.1016/j.molcel.2025.08.029. PMID: 41043390.
- Khyzha N, Ahmad K, **Henikoff S**. Protocol for the spatiotemporal profiling of RNA within nuclear compartments in human cell lines using SLAM-RT&Tag. *STAR Protoc*. 2025 Sep 19;6(3):104017. doi: 10.1016/j.xpro.2025.104017. Epub 2025 Aug 9. PMID: 40788762; PMCID: PMC12357155.
- Zheng Y, Ahmad K, **Henikoff S**. (2025) **Total whole-arm chromosome losses predict malignancy in human cancer**. *Proc Natl Acad Sci U S A*. May 6;122(18):e2505385122. doi: 10.1073/pnas.2505385122.
- Wu W, Ahmad K, **Henikoff S**. (2025) **Chromatin-bound U2AF2 splicing factor ensures exon inclusion**. *Molecular Cell*. Apr 28:S1097-2765(25)00316-8. doi:10.1016/j.molcel.2025.04.013.
- Khyzha N, Ahmad K, **Henikoff S**. (2025) **Profiling transcriptome composition and dynamics within nuclear compartments using SLAM-RT&Tag**. *Molecular Cell*. Apr 3;85(7):1366-1380.e4. doi: 10.1016/j.molcel.2025.02.012.
- Henikoff S**, Zheng Y, Paranal RM, Xu Y, Greene JE, Henikoff JG, Russell ZR, Szulzewsky F, Thirimanne HN, Kugel S, Holland EC, Ahmad K. (2025) **RNA Polymerase II at histone genes predicts outcome in human cancer**. *Science*. Jan 2;387(6735):737-743. doi: 10.1126/science.ads2169.
- Fang H, Tronco AR, Bonora G, Nguyen T, Thakur J, Berletch JB, Filippova GN, **Henikoff S**, Shendure J, Noble WS, Duan Z, Disteche CM, Deng X. (2025) **CTCF-mediated insulation and chromatin environment modulate Car5b escape from X inactivation**. *BMC Biol*. Mar 3;23(1):68. doi: 10.1186/s12915-025-02137-7.
- Dekker J, Oksuz BA, Zhang Y, Wang Y, Minsk MK, Kuang S, Yang L, Gibcus JH, Krietenstein N, Rando OJ, Xu J, Janssens DH, **Henikoff S**, Kukalev A, Willemin A, Winick-Ng W, Kempfer R, Pombo A, Yu M, Kumar P, Zhang L, Belmont AS, Sasaki T, van Schaik T, Brueckner L, Peric-Hupkes D, van Steensel B, Wang P, Chai H, Kim M, Ruan Y, Zhang R, Quinodoz SA, Bhat P, Guttman M, Zhao W, Chien S, Liu Y, Venev SV, Plewczynski D, Azcarate II, Szabó D, Thieme CJ, Szczepińska T, Chyliński M, Sengupta K, Conte M, Esposito A, Abraham A, Zhang R, Wang Y, Wen X, Wu Q, Yang Y, Liu J, Boninsegna L, Yildirim A, Zhan Y, Chiariello AM, Bianco S, Lee L, Hu M, Li Y, Barnett RJ, Cook AL, Emerson DJ, Marchal C, Zhao P, Park P, Alver BH, Schroeder A, Navelkar R, Bakker C, Ronchetti W, Ehmsen S, Veit A, Gehlenborg N, Wang T, Li D, Wang X, Nicodemi M, Ren B, Zhong S, Phillips-Cremens JE, Gilbert DM, Pollard KS, Alber F, Ma J, Noble WS, Yue F. **An integrated view of the structure and function of the human 4D nucleome**. *bioRxiv* [Preprint]. 2024 Oct 27:2024.09.17.613111. doi: 10.1101/2024.09.17.613111.
- Janssens DH, Duran M, Otto DJ, Wu W, Xu Y, Kirkey D, Mullighan CG, Yi JS, Meshinchi S, Sarthy JF, Ahmad K, **Henikoff S**. (2024) **MLL oncoprotein levels influence leukemia lineage identities**. *Nat Commun*. Oct 29;15(1):9341. doi: 10.1038/s41467-024-53399-8.
- Fiorenza S, Zheng Y, Purushe J, Bock TJ, Sarthy J, Janssens DH, Sheih AS, Kimble EL, Kirchmeier D, Phi TD, Gauthier J, Hirayama AV, Riddell SR, Wu Q, Gottardo R, Maloney DG, Yang JYH, **Henikoff S**, Turtle CJ. (2024) **Histone marks identify novel transcription factors that parse CAR-T subset-of-origin, clinical potential and expansion**. *Nat Commun*. Sep

27;15(1):8309. doi: 10.1038/s41467-024-52503-2.

- Showman S, Talbert PB, Xu Y, **Henikoff S**. (2024) **Protocol to measure centromeric array size changes using droplet digital PCR-based quantification of higher- order repeats**. *STAR Protoc.* Sep 20;5(3):103218.
- Showman S, Talbert PB, Xu Y, Adeyemi RO, **Henikoff S**. (2024) **Expansion of human centromeric arrays in cells undergoing break-induced replication**. *Cell Reports* Feb 29;43(3):113851.
- Brahma S, **Henikoff S**. (2023) **The BAF chromatin remodeler synergizes with RNA polymerase II and transcription factors to evict nucleosomes**. *Nat Genet.* 2024 Jan;56(1):100-111.
- Anderson J, **Henikoff S**, Ahmad K. (2023) **Chromosome-specific maturation of the epigenome in the Drosophila male germline**. *Elife.* Nov 30;12:RP89373.
- Janssens DH, Greene JE, Wu SJ, Codomo CA, Minot SS, Furlan SN, Ahmad K, **Henikoff S**. (2023) **Scalable single-cell profiling of chromatin modifications with sciCUT&Tag**. *Nat Protoc.*
- Henikoff S**, Henikoff JG, Ahmad K, Paranal RM, Janssens DH, Russell ZR, Szulzewsky F, Kugel S, Holland EC. (2023) **Epigenomic analysis of formalin-fixed paraffin-embedded samples by CUT&Tag**. *Nat Commun.* Sep 22;14(1):5930.
- Wooten M, Takushi B, Ahmad K, **Henikoff S**. (2023) **Aclarubicin stimulates RNA polymerase II elongation at closely spaced divergent promoters**. *Sci Adv.* Jun 16;9(24):eadg3257.
- Jana S, Brahma S, Arora S, Wladyka CL, Hoang P, Blinka S, Hough R, Horn JL, Liu Y, Wang LJ, Depeille P, Smith E, Montgomery RB, Lee JK, Haffner MC, Vakar-Lopez F, Grivas P, Wright JL, Lam HM, Black PC, Roose JP, Ryazanov AG, Subramaniam AR, **Henikoff S**, **Hsieh AC**. (2023) **Transcriptional-translational conflict is a barrier to cellular transformation and cancer progression**. *Cancer Cell.* Apr 13:S1535-6108(23)00094-6.
- Hsieh E, Janssens DH, Paddison PJ, Browne EP, **Henikoff S**, OhAinle M, **Emerman M**. (2023) **A modular CRISPR screen identifies individual and combination pathways contributing to HIV-1 latency**. *PLoS Pathog.* Jan 27;19(1):e1011101.
- Islam Z, Saravanan B, Walavalkar K, Farooq U, Singh AK, Sabarinathan R, Thakur J, Pandit A, **Henikoff S**, **Notani D** (2023) **Active enhancers strengthen insulation by RNA-mediated CTCF binding at chromatin domain boundaries**. *Genome Res.* doi: 10.1101/gr.276643.122.
- De Sarkar N, Patton RD, Doebley AL, Hanratty B, Adil M, Kreitzman AJ, Sarthy JF, Ko M, Brahma S, Meers MP, Janssens DH, Ang LS, Coleman IM, Bose A, Dumpit RF, Lucas JM, Nunez TA, Nguyen HM, McClure HM, Pritchard CC, Schweizer MT, Morrissey C, Choudhury AD, Baca SC, Berchuck JE, Freedman ML, Ahmad K, Haffner MC, Montgomery RB, Corey E, **Henikoff S**, Nelson PS, **Ha G**. (2022) **Nucleosome patterns in circulating tumor DNA reveal transcriptional regulation of advanced prostate cancer phenotypes**. *Cancer Discov.* CD-22-0692. doi: 10.1158/2159-8290.CD-22-0692.
- Meers MP, Llagas G, Janssens DH, Codomo CA and **Henikoff S**. **Multifactorial chromatin regulatory landscapes at single cell resolution**. *Nat Biotechnol.* 2023 May;41(5):708-716.
- Bryson TD, De Ioannes P, Valencia-Sanchez MI, Henikoff JG, Talbert PB, La Scola B, **Armache K-J**, **Henikoff S**. **A giant virus genome is densely packaged by stable nucleosomes**. *Molecular Cell*, 82(23):4458-4470.e5.
- Khyzha N, **Henikoff S**, Ahmad K (2022) **Profiling RNA at chromatin targets in situ by antibody-targeted tagmentation**. *Nature Methods* 19(11):1383-1392.
- Janssens DH, Otto DJ, Meers MP, Setty M, Ahmad K, **Henikoff S** (2022) **CUT&Tag2for1: a modified method for simultaneous profiling of the accessible and silenced regulome in single cells**. *Genome Biol.* 23:81.
- Thirmanne HN, Wu F, Janssens DH, Swanger J, Diab A, Feldman H, Amezcua RA, Gottardo R, Paddison PJ, **Henikoff S**, **Clurman BE** (2022) **Global and context-specific transcriptional consequences of oncogenic Fbw7 mutations**. *Elife* 11:e74338.
- Bartlett DA, Dileep V, Handa T, Ohkawa Y, Kimura H, **Henikoff S**, **Gilbert DM** (2021) **High-throughput single-cell epigenomic profiling by targeted insertion of promoters (TIP-seq)**. *J Cell Biol.* 220:e202103078.
- Janssens DH, Meers MP, Wu SJ, Babaeva E, Meshinchi S, Sarthy JF, Ahmad K, **Henikoff S**. (2021) **Automated CUT&Tag profiling of chromatin heterogeneity in mixed-lineage leukemia**. *Nature Genetics*, doi:10.1038/s41588-021-00941-9.

- Ahmad K and Henikoff S (2021) **The H3.3K27M oncohistone antagonizes reprogramming in *Drosophila***. *PLoS Genetics* 17:e1009225.
- Henikoff S**, Henikoff JG, Ahmad K (2021) **Simplified Epigenome Profiling Using Antibody-tethered Tagmentation**. *bio-protocol* 11(11):e4043.
- Valencia-Sánchez MI, Abini-Agbomson S, Wang M, Lee R, Vasilyev N, Zhang J, De Ioannes P, La Scola B, Talbert P, **Henikoff S**, Nudler E, Erives A, **Armache KJ** (2021) **The structure of a virus-encoded nucleosome**. *Nat Struct Mol Biol.* 28(5):413-417.
- Wu SJ, Furlan SN, Mihalas AB, Kaya-Okur HS, Feroze AH, Emerson SN, Zheng Y, Carson K, Cimino PJ, Keene CD, Sarthy JF, Gottardo R, Ahmad K, **Henikoff S**, **Patel AP**. **Single-cell CUT&Tag analysis of chromatin modifications in differentiation and tumor progression**. *Nat Biotechnol.* 2021 Apr 12. doi: 10.1038/s41587-021-00865-z.
- Chew GL, Bleakley M, Bradley RK, Malik HS, **Henikoff S**, Molaro A, Sarthy J. **Short H2A histone variants are expressed in cancer**. *Nat Commun.* 2021 Jan 20;12(1):490.
- Molaro A, Wood AJ, Janssens D, Kindelay SM, Eickbush MT, Wu S, Singh P, Muller CH, **Henikoff S**, Malik HS. **Biparental contributions of the H2A.B histone variant control embryonic development in mice**. *PLoS Biol.* 2020 Dec 23;18(12):e3001001.
- Fang H, Bonora G, Lewandowski JP, Thakur J, Filippova GN, **Henikoff S**, Shendure J, Duan Z, Rinn JL, Deng X, Noble WS, Disteché CM. **Trans- and cis-acting effects of Firre on epigenetic features of the inactive X chromosome**. *Nat Commun.* 2020 Nov 27;11(1):6053
- Henikoff S**, Henikoff JG, Kaya-Okur HS, Ahmad K, **Efficient chromatin accessibility mapping in situ by nucleosome-tethered tagmentation**. *Elife.* 2020 Nov 16;9:e63274.
- Kaya-Okur HS, Janssens DH, Henikoff JG, Ahmad K, **Henikoff S**, **Efficient low-cost chromatin profiling with CUT&Tag**. *Nat Protoc.* 2020 Sep 10. doi: 10.1038/s41596-020-0373-x
- Sarthy JF, Meers MP, Janssens DH, Henikoff JG, Feldman H, Paddison PJ, Lockwood CM, Vitanza NA, Olson JM, Ahmad K, **Henikoff S**, **Histone deposition pathways determine the chromatin landscapes of H3.1 and H3.3 K27M oncohistones**. *Elife.* 2020 Sep 9;9:e61090. doi: 10.7554/eLife.61090.
- Zeineldin M, Federico S, Chen X, Fan Y, Xu B, Stewart E, Zhou X, Jeon J, Griffiths L, Nguyen R, Norrie J, Easton J, Mulder H, Yergeau D, Liu Y, Wu J, Van Ryn C, Naranjo A, Hogarty MD, Kamiński MM, Valentine M, Pruett-Miller SM, Pappo A, Zhang J, Clay MR, Bahrami A, Vogel P, Lee S, Shelat A, Sarthy JF, Meers MP, George RE, Mardis ER, Wilson RK, **Henikoff S**, Downing JR, Dyer MA. (2020) **MYCN amplification and ATRX mutations are incompatible in neuroblastoma**. *Nat Commun.* 2020 11:913.
- Resnick R, Wong CJ, Hamm DC, Bennett SR, Skene PJ, Hake SB, **Henikoff S**, van der Maarel SM, **Tapscott SJ**. (2019) **DUX4-Induced Histone Variants H3.X and H3.Y Mark DUX4 Target Genes for Expression**. *Cell Rep.* 29:1812-1820.
- Chereji R, Bryson TD, **Henikoff S**. (2019) **Quantitative MNase-seq accurately maps nucleosome occupancy levels**. *Genome Biology* 20:198.
- Mathsyaaraja H, Freie B, Cheng PF, Babaeva E, Catchpole JT, Janssens D, **Henikoff S**, **Eisenman RN**. (2019) **Max deletion destabilizes MYC protein and abrogates Eμ-Myc lymphomagenesis**. *Genes Dev.* 33:1252-1264.
- Meers MP, Tenenbaum D, **Henikoff S**. (2019) **Peak calling by Sparse Enrichment Analysis for CUT&RUN chromatin profiling**. *Epigenetics Chromatin.* 2019 12:42.
- Meers MP, Janssens DH, **Henikoff S**. (2019) **Pioneer Factor-Nucleosome Binding Events during Differentiation Are Motif Encoded**. *Mol Cell.* 75:562-575.
- Meers MP, Bryson TD, Henikoff JG, **Henikoff S**. (2019) **Improved CUT&RUN chromatin profiling tools**. *Elife* (2019) 8:e46314.
- Kaya-Okur HS, Wu SJ, Codomo CA, Pledger ES, Bryson TD, Henikoff JG, Ahmad K, **Henikoff S**. (2019) **CUT&Tag for efficient epigenomic profiling of small samples and single cells**. *Nat Commun.* 10:1930.
- Brahma S and **Henikoff S**. (2019) **RSC-associated Subnucleosomes Define MNase-sensitive Promoters in Yeast** *Molecular Cell*, 73:238-249.
- Janssens DH, Wu SJ, Sarthy JF, Meers MP, Myers CH, Olson JM, Ahmad K, **Henikoff S**. (2018) **Automated in situ chromatin profiling efficiently resolves cell types and gene regulatory**

- programs** *Epigenetics Chromatin*, 11(1):74.
- Skene PJ, Henikoff JG and **Henikoff S.** (2018) **Targeted in situ genome-wide profiling with high efficiency for low cell numbers.** *Nature Protocols* 13(5):1006-1019.
- Chereji RV, Ramachandran S, Bryson TD, **Henikoff S.** (2018) **Precise genome-wide mapping of single nucleosomes and linkers in vivo.** *Genome Biology* 19(1):19.
- Thakur J and **Henikoff S.** (2018) **Unexpected conformational variations of the human centromeric chromatin complex.** *Genes Dev* 32(1):20-25.
- Kasinathan S and **Henikoff S.** (2018) **Non-B-form DNA structures mark centromeres.** *Mol Biol Evol* 35(4):949-962.
- Talbert PB, Kasinathan S and **Henikoff S.** (2018) **Simple and Complex Centromeric Satellites in Drosophila Sibling Species.** *Genetics* 208(3):977-990.
- Ramachandran S, Ahmad K and **Henikoff S.** (2018) **Transcription and remodeling produce asymmetrically unwrapped nucleosomal intermediates.** *Molecular Cell* 2017 68(6):1038-1053.
- Skene PJ and **Henikoff S.** (2017) **An efficient targeted nuclease strategy for high-resolution mapping of DNA binding sites.** *eLife* e21856.
- Grünberg S., **Henikoff, S.**, Hahn, S. and **Zentner, GE** (2016) **Mediator binding to UASs is broadly uncoupled from transcription and cooperative with TFIID recruitment to promoters.** *EMBO J.* e201695020.
- Thakur, J and **Henikoff, S** (2016) **CENPT bridges adjacent CENPA nucleosomes on young human α -satellite dimers.** *Genome Res* 26:1178-87.
- Ramachandran, S. and **Henikoff, S.** (2016) **Transcriptional regulators compete with nucleosomes post-replication.** *Cell* 165:580-92.
- Zentner, G.E., Kasinathan, S., Xin, B., Rohs, R. and **Henikoff, S.** (2015) **ChEC-seq kinetics discriminate transcription factor binding sites by DNA sequence and shape in vivo.** *Nature Commun* 6:10264.
- Thakur, J., Talbert, P.B. and **Henikoff, S.** (2015) **Interactions of inner kinetochore proteins with fission yeast regional centromeres.** *Genetics* 201:543-61.
- Skene, P.J. and **Henikoff, S.** (2015) **A simple method for generating high resolution maps of genome wide protein binding.** *Elife*, e09225 2015.
- Henikoff, J.G., Thakur, J., Kasinathan, S. and **Henikoff, S.** (2015) **A unique chromatin complex occupies young alpha-satellite arrays of human centromeres.** *Science Advances* 1, e1400234.
- Yang, F., **Kemp, C.J.**, and **Henikoff, S.** (2015) **Anthracyclines induce double-strand DNA breaks at active gene promoters.** *Mutation Research-Fundamental and Molecular Mechanisms of Mutagenesis* 773, 9-15.
- Williams, B.P., Pignatta, D., **Henikoff, S.**, and **Gehring, M.** (2015) **Methylation-sensitive expression of a DNA demethylase gene serves as an epigenetic rheostat.** *PLoS genetics* 11, e1005142.
- Ramachandran, S., Zentner, G.E., and **Henikoff, S.** (2015) **Asymmetric nucleosomes flank promoters in the budding yeast genome.** *Genome Research* 25, 381-390.
- Weber, C.M., Ramachandran, S., and **Henikoff, S.** (2014) **Nucleosomes Are Context-Specific, H2A.Z-Modulated Barriers to RNA Polymerase.** *Molecular Cell* 53, 819-830.
- Teves, S.S., and **Henikoff, S.** (2014) **Transcription-generated torsional stress destabilizes nucleosomes.** *Nature Structural & Molecular Biology* 21, 88-94.
- Steiner, F.A., and **Henikoff, S.** (2014) **Holocentromeres are dispersed point centromeres localized at transcription factor hotspots.** *Elife* 3, e02025.
- Skene, P.J., Hernandez, A.E., Groudine, M., and **Henikoff, S.** (2014) **The nucleosomal barrier to promoter escape by RNA polymerase II is overcome by the chromatin remodeler Chd1.** *Elife* 3, e02042.
- Orsi, G.A., Kasinathan, S., Hughes, K.T., Saminadin-Peter, S., **Henikoff, S.**, and **Ahmad, K.** (2014) **High-resolution mapping defines the cooperative architecture of Polycomb response elements.** *Genome Research* 24, 809-820.
- Krassovsky, K., and **Henikoff, S.** (2014) **Distinct chromatin features characterize different**

- classes of repeat sequences in *Drosophila melanogaster*.** *BMC Genomics* 15, e105.
- Kasinathan, S., Orsi, G.A., Zentner, G.E., Ahmad, K., and **Henikoff, S.** (2014) **High-resolution mapping of transcription factor binding sites on native chromatin.** *Nature Methods* 11, 203-209.
- Henikoff, S.**, Ramachandran, S., Krassovsky, K., Bryson, T.D., Codomo, C.A., Brogaard, K., Widom, J., Wang, J.-P., and Henikoff, J.G. (2014) **The budding yeast Centromere DNA Element II wraps a stable Cse4 hemisome in either orientation in vivo.** *Elife* 3, e01861.
- Drinnenberg, I.A., deYoung, D., **Henikoff, S.**, and Malik, H.S. (2014) **Recurrent loss of CenH3 is associated with independent transitions to holocentricity in insects.** *eLife* 3, e03676.
- Codomo, C.A., Furuyama, T., and **Henikoff, S.** (2014) **CENP-A octamers do not confer a reduction in nucleosome height by AFM.** *Nature Structural & Molecular Biology* 21, 4-5.
- Zhang, T., Talbert, P.B., Zhang, W., Wu, Y., Yang, Z., Henikoff, J.G., **Henikoff, S.**, and Jiang, J. (2013) **The CentO satellite confers translational and rotational phasing on cenH3 nucleosomes in rice centromeres.** *Proc Natl Acad Sci USA* 110, E4875-E4883.
- Zentner, G.E., Tsukiyama, T., and **Henikoff, S.** (2013) **ISWI and CHD Chromatin Remodelers Bind Promoters but Act in Gene Bodies.** *Plos Genetics* 9, e1003317.
- Zentner, G.E., and **Henikoff, S.** (2013) **Mot1 Redistributes TBP from TATA-Containing to TATA-Less Promoters.** *Molecular and Cellular Biology* 33, 4996-5004.
- Yang, F., Kemp, C.J., and **Henikoff, S.** (2013) **Doxorubicin Enhances Nucleosome Turnover around Promoters.** *Current Biology* 23, 782-787.
- Furuyama, T., Codomo, C.A., and **Henikoff, S.** (2013) **Reconstitution of hemisomes on budding yeast centromeric DNA.** *Nucleic Acids Research* 41, 5769-5783.
- Steiner, F.A., Talbert, P.B., Kasinathan, S., Deal, R.B., and **Henikoff, S.** (2012) **Cell-type-specific nuclei purification from whole animals for genome-wide expression and chromatin profiling.** *Genome Research* 22, 766-777.
- Sim, N.-L., Kumar, P., Hu, J., **Henikoff, S.**, Schneider, G., and Ng, P.C. (2012) **SIFT web server: predicting effects of amino acid substitutions on proteins.** *Nucleic Acids Research* 40, W452-W457.
- Krassovsky, K., Henikoff, J.G., and **Henikoff, S.** (2012) **Tripartite organization of centromeric chromatin in budding yeast.** *Proc Natl Acad Sci USA* 109, 243-248.
- Henikoff, S.**, and Henikoff, J.G. (2012) **"Point" Centromeres of *Saccharomyces* Harbor Single Centromere-Specific Nucleosomes.** *Genetics* 190, 1575-1577.
- Teves, S.S., and **Henikoff, S.** (2011) **Heat shock reduces stalled RNA polymerase II and nucleosome turnover genome-wide.** *Genes & Development* 25, 2387-2397.
- Henikoff, J.G., Belsky, J.A., Krassovsky, K., MacAlpine, D.M., and **Henikoff, S.** (2011) **Epigenome characterization at single base-pair resolution.** *Proc Natl Acad Sci USA* 108, 18318-18323.
- Gehring, M., Missirian, V., and **Henikoff, S.** (2011) **Genomic Analysis of Parent-of-Origin Allelic Expression in *Arabidopsis thaliana* Seeds.** *Plos One* 6, e23687.
- Deal, R.B., and **Henikoff, S.** (2011) **The INTACT method for cell type-specific gene expression and chromatin profiling in *Arabidopsis thaliana*.** *Nature Protocols* 6, 56-68.
- Weber, C.M., Henikoff, J.G., and **Henikoff, S.** (2010) **H2A.Z nucleosomes enriched over active genes are homotypic.** *Nature Structural & Molecular Biology* 17, 1500-1507.
- Roy, S., Ernst, J., Kharchenko, P.V., Kheradpour, P., Negre, N., Eaton, M.L., Landolin, J.M., Bristow, C.A., Ma, L., Lin, M.F., Washietl, S., Arshinoff, B.I., Ay, F., Meyer, P.E., Robine, N., Washington, N.L., Di Stefano, L., Berezhikov, E., Brown, C.D., Candeias, R., Carlson, J.W., Carr, A., Jungreis, I., Marbach, D., Sealfon, R., Tolstorukov, M.Y., Will, S., Alekseyenko, A.A., Artieri, C., Booth, B.W., Brooks, A.N., Dai, Q., Davis, C.A., Duff, M.O., Feng, X., Gorchakov, A.A., Gu, T., Henikoff, J.G., Kapranov, P., Li, R., MacAlpine, H.K., Malone, J., Minoda, A., Nordman, J., Okamura, K., Perry, M., Powell, S.K., Riddle, N.C., Sakai, A., Samsonova, A., Sandler, J.E., Schwartz, Y.B., Sher, N., Spokony, R., Sturgill, D., van Baren, M., Wan, K.H., Yang, L., Yu, C., Feingold, E., Good, P., Guyer, M., Lowdon, R., Ahmad, K., Andrews, J., Berger, B., Brenner, S.E., Brent, M.R., Cherbas, L., Elgin, S.C.R., Gingeras, T.R., Grossman, R., Hoskins, R.A., Kaufman, T.C., Kent, W., Kuroda, M.I., Orr-Weaver, T., Perrimon, N., Pirrotta, V., Posakony, J.W., Ren, B., Russell, S., Cherbas, P., Graveley, B.R., Lewis, S.,

- Micklem, G., Oliver, B., Park, P.J., Celniker, S.E., **Henikoff, S.**, Karpen, G.H., Lai, E.C., MacAlpine, D.M., Stein, L.D., White, K.P., Kellis, M., and mod, E.C. (2010) **Identification of Functional Elements and Regulatory Circuits by Drosophila modENCODE**. *Science (Washington D C)* 330, 1787-1797.
- Ooi, S.L., Henikoff, J.G., and **Henikoff, S.** (2010) **A native chromatin purification system for epigenomic profiling in Caenorhabditis elegans**. *Nucleic Acids Research* 38, e26.
- Negre, N., Brown, C.D., Shah, P.K., Kheradpour, P., Morrison, C.A., Henikoff, J.G., Feng, X., Ahmad, K., Russell, S., White, R.A.H., Stein, L., **Henikoff, S.**, Kellis, M., and **White, K.P.** (2010) **A Comprehensive Map of Insulator Elements for the Drosophila Genome**. *Plos Genetics* 6, e1000814.
- Gerstein, M.B.**, Lu, Z.J., Van Nostrand, E.L., Cheng, C., Arshinoff, B.I., Liu, T., Yip, K.Y., Robilotto, R., Rechtsteiner, A., Ikegami, K., Alves, P., Chateigner, A., Perry, M., Morris, M., Auerbach, R.K., Feng, X., Leng, J., Vielle, A., Niu, W., Rhrissorakrai, K., Agarwal, A., Alexander, R.P., Barber, G., Brdlik, C.M., Brennan, J., Brouillet, J.J., Carr, A., Cheung, M.-S., Clawson, H., Contrino, S., Dannenberg, L.O., Dernburg, A.F., Desai, A., Dick, L., Dose, A.C., Du, J., Egelhofer, T., Ercan, S., Euskirchen, G., Ewing, B., Feingold, E.A., Gassmann, R., Good, P.J., Green, P., Gullier, F., Gutwein, M., Guyer, M.S., Habegger, L., Han, T., Henikoff, J.G., Henz, S.R., Hinrichs, A., Holster, H., Hyman, T., Iniguez, A.L., Janette, J., Jensen, M., Kato, M., Kent, W.J., Kephart, E., Khivansara, V., Khurana, E., Kim, J.K., Kolasinska-Zwierz, P., Lai, E.C., Latorre, I., Leahey, A., Lewis, S., Lloyd, P., Lochovsky, L., Lowdon, R.F., Lubling, Y., Lyne, R., MacCoss, M., Mackowiak, S.D., Mangone, M., McKay, S., Mecnas, D., Merrihew, G., Miller, D.M., III, Muroyama, A., Murray, J.I., Ooi, S.-L., Pham, H., Phippen, T., Preston, E.A., Rajewsky, N., Raetsch, G., Rosenbaum, H., Rozowsky, J., Rutherford, K., Ruzanov, P., Sarov, M., Sasidharan, R., Sboner, A., Scheid, P., Segal, E., Shin, H., Shou, C., Slack, F.J., Slightam, C., Smith, R., Spencer, W.C., Stinson, E.O., Taing, S., Takasaki, T., Vafeados, D., Voronina, K., Wang, G., Washington, N.L., Whittle, C.M., Wu, B., Yan, K.-K., Zeller, G., Zha, Z., Zhong, M., Zhou, X., **Ahringer, J.**, **Strome, S.**, **Gunsalus, K.C.**, **Micklem, G.**, **Liu, X.S.**, **Reinke, V.**, **Kim, S.K.**, **Hillier, L.W.**, **Henikoff, S.**, **Piano, F.**, **Snyder, M.**, **Stein, L.**, **Lieb, J.D.**, **Waterston, R.H.**, and mod, E.C. (2010) **Integrative Analysis of the Caenorhabditis elegans Genome by the modENCODE Project**. *Science* 330, 1775-1787.
- Deal, R.B., and **Henikoff, S.** (2010) **A Simple Method for Gene Expression and Chromatin Profiling of Individual Cell Types within a Tissue**. *Developmental Cell* 18, 1030-1040.
- Deal, R.B., Henikoff, J.G., and **Henikoff, S.** (2010) **Genome-Wide Kinetics of Nucleosome Turnover Determined by Metabolic Labeling of Histones**. *Science* 328, 1161-1164.
- Conerly, M.L., Teves, S.S., Diolaiti, D., Ulrich, M., Eisenman, R.N., and **Henikoff, S.** (2010) **Changes in H2A.Z occupancy and DNA methylation during B-cell lymphomagenesis**. *Genome Research* 20, 1383-1390.
- Bryson, T.D., Weber, C.M., and **Henikoff, S.** (2010) **Baculovirus-encoded protein expression for epigenomic profiling in Drosophila cells**. *Fly* 4, 258-265.
- Borinstein, S.C., Conerly, M., Dzieciatkowski, S., Biswas, S., Washington, M.K., Trobridge, P., **Henikoff, S.**, and **Grady, W.M.** (2010) **Aberrant DNA Methylation Occurs in Colon Neoplasms Arising in the Azoxymethane Colon Cancer Model**. *Molecular Carcinogenesis* 49, 94-103.
- Kumar, P., **Henikoff, S.**, and **Ng, P.C.** (2009) **Predicting the effects of coding non-synonymous variants on protein function using the SIFT algorithm**. *Nature Protocols* 4, 1073-1082.
- Henikoff, S.**, Henikoff, J.G., Sakai, A., Loeb, G.B., and Ahmad, K. (2009) **Genome-wide profiling of salt fractions maps physical properties of chromatin**. *Genome Research* 19, 460-469.
- Gehring, M., Bubb, K.L., and **Henikoff, S.** (2009) **Extensive Demethylation of Repetitive Elements During Seed Development Underlies Gene Imprinting**. *Science* 324, 1447-1451.
- Furuyama, T., and **Henikoff, S.** (2009) **Centromeric Nucleosomes Induce Positive DNA Supercoils**. *Cell* 138, 104-113.
- De Bustos, C., Ramos, E., Young, J.M., Tran, R.K., Menzel, U., Langford, C.F., Eichler, E.E., Hsu, L., **Henikoff, S.**, Dumanski, J.P., and **Trask, B.J.** (2009) **Tissue-specific variation in DNA methylation levels along human chromosome 1**. *Epigenetics & Chromatin* 2, e7.

- Zilberman, D., Coleman-Derr, D., Ballinger, T., and **Henikoff, S.** (2008) **Histone H2A.Z and DNA methylation are mutually antagonistic chromatin marks.** *Nature* 456, 125-U114.
- Yan, H., Talbert, P.B., Lee, H.-R., Jett, J., **Henikoff, S.**, Chen, F., and **Jiang, J.** (2008) **Intergenic Locations of Rice Centromeric Chromatin.** *Plos Biology* 6, 2563-2575.
- Wang, H., Dalal, Y., **Henikoff, S.**, and **Lindsay, S.** (2008) **Single-epitope recognition imaging of native chromatin.** *Epigenetics & Chromatin* 1, e10.
- Cooper, J.L., Till, B.J., Laport, R.G., Darlow, M.C., Kleffner, J.M., Jamai, A., El-Mellouki, T., Liu, S., Ritchie, R., Nielsen, N., Bilyeu, K.D., Meksem, K., Comai, L., and **Henikoff, S.** (2008) **TILLING to detect induced mutations in soybean.** *BMC Plant Biology* 8.
- Cooper, J.L., Greene, E.A., Till, B.J., Codomo, C.A., Wakimoto, B.T., and **Henikoff, S.** (2008) **Retention of induced mutations in a Drosophila reverse-genetic resource.** *Genetics* 180, 661-667.
- Zilberman, D., Gehring, M., Tran, R.K., Ballinger, T., and **Henikoff, S.** (2007) **Genome-wide analysis of Arabidopsis thaliana DNA methylation uncovers an interdependence between methylation and transcription.** *Nature Genetics* 39, 61-69.
- Till, B.J., Cooper, J., Tai, T.H., Colowit, P., Greene, E.A., **Henikoff, S.**, and **Comai, L.** (2007) **Discovery of chemically induced mutations in rice by TILLING.** *BMC Plant Biology* 7.
- Penterman, J., Zilberman, D., Huh, J.H., Ballinger, T., **Henikoff, S.**, and **Fischer, R.L.** (2007) **DNA demethylation in the Arabidopsis genome.** *Proc Natl Acad Sci USA* 104, 6752-6757.
- Mito, Y., Henikoff, J.G., and **Henikoff, S.** (2007) **Histone replacement marks the boundaries of cis-regulatory domains.** *Science* 315, 1408-1411.
- Dalal, Y., Wang, H., Lindsay, S., and **Henikoff, S.** (2007) **Tetrameric structure of centromeric nucleosomes in interphase Drosophila cells.** *Plos Biology* 5, 1798-1809.
- Till, B.J., Zerr, T., Comai, L., and **Henikoff, S.** (2006) **A protocol for TILLING and Ecotilling in plants and animals.** *Nature Protocols* 1, 2465-2477.
- Till, B.J., Zerr, T., Bowers, E., Greene, E.A., Comai, L., and **Henikoff, S.** (2006) **High-throughput discovery of rare human nucleotide polymorphisms by Ecotilling.** *Nucleic Acids Research* 34, e99.
- Ooi, S.L., Priess, J.R., and **Henikoff, S.** (2006) **Histone H3.3 variant dynamics in the germline of Caenorhabditis elegans.** *Plos Genetics* 2, 883-895.
- Furuyama, T., Dalal, Y., and **Henikoff, S.** (2006) **Chaperone-mediated assembly of centromeric chromatin in vitro.** *Proc Natl Acad Sci USA* 103, 6172-6177.
- Zerr, T., and **Henikoff, S.** (2005) **Automated band mapping in electrophoretic gel images using background information.** *Nucleic Acids Research* 33, 2806-2812.
- Yan, H.H., Jin, W.W., Nagaki, K., Tian, S.L., Ouyang, S., Buell, C.R., Talbert, P.B., **Henikoff, S.**, and **Jiang, J.M.** (2005) **Transcription and histone modifications in the recombination-free region spanning a rice centromere.** *Plant Cell* 17, 3227-3238.
- Vermaak, D., **Henikoff, S.**, and **Malik, H.S.** (2005) **Positive selection drives the evolution of rhino, a member of the heterochromatin protein 1 family in Drosophila.** *Plos Genetics* 1, 96-108.
- Tran, R.K., Zilberman, D., de Bustos, C., Ditt, R.F., Henikoff, J.G., Lindroth, A.M., Delrow, J., Boyle, T., Kwong, S., Bryson, T.D., Jacobsen, S.E., and **Henikoff, S.** (2005) **Chromatin and siRNA pathways cooperate to maintain DNA methylation of small transposable elements in Arabidopsis.** *Genome Biology* 6, R90.
- Tran, R.K., Henikoff, J.G., Zilberman, D., Ditt, R.F., Jacobsen, S.E., and **Henikoff, S.** (2005) **DNA methylation profiling identifies CG methylation clusters Arabidopsis genes.** *Current Biology* 15, 154-159.
- Mito, Y., Henikoff, J.G., and **Henikoff, S.** (2005) **Genome-scale profiling of histone H3.3 replacement patterns.** *Nature Genetics* 37, 1090-1097.
- Malik, H.S.**, and **Henikoff, S.** (2005) **Positive selection of Iris, a retroviral envelope-derived host gene in Drosophila melanogaster.** *Plos Genetics* 1, 429-443.
- Till, B.J., Reynolds, S.H., Weil, C., Springer, N., Burtner, C., Young, K., Bowers, E., Codomo, C.A., Enns, L.C., Odden, A.R., Greene, E.A., Comai, L., and **Henikoff, S.** (2004) **Discovery of induced point mutations in maize genes by TILLING.** *BMC Plant Biology* 4.
- Till, B.J., Burtner, C., Comai, L., and **Henikoff, S.** (2004) **Mismatch cleavage by single-strand**

- specific nucleases.** *Nucleic Acids Research* 32, 2632-2641.
- Talbert, P.B., Bryson, T.D., and **Henikoff, S.** (2004) **Adaptive evolution of centromere proteins in plants and animals.** *Journal of Biology* 3, 18-18.
- Nagaki, K., Cheng, Z.K., Ouyang, S., Talbert, P.B., Kim, M., Jones, K.M., **Henikoff, S.**, Buell, C.R., and **Jiang, J.M.** (2004) **Sequencing of a rice centromere uncovers active genes.** *Nature Genetics* 36, 138-145.
- McKittrick, E., Gaften, P.R., Ahmad, K., and **Henikoff, S.** (2004) **Histone H3.3 is enriched in covalent modifications associated with active chromatin.** *Proc Natl Acad Sci USA* 101, 1525-1530.
- Jin, W.W., Melo, J.R., Nagaki, K., Talbert, P.B., **Henikoff, S.**, Dawe, R.K., and **Jiang, J.M.** (2004) **Maize centromeres: Organization and functional adaptation in the genetic background of oat.** *Plant Cell* 16, 571-581.
- Cooper, J.L., and **Henikoff, S.** (2004) **Adaptive evolution of the histone fold domain in centromeric histones.** *Molecular Biology and Evolution* 21, 1712-1718.
- Comai, L.**, Young, K., Till, B.J., Reynolds, S.H., Greene, E.A., Codomo, C.A., Enns, L.C., Johnson, J.E., Burtner, C., Odden, A.R., and **Henikoff, S.** (2004) **Efficient discovery of DNA polymorphisms in natural populations by Ecotilling.** *Plant Journal* 37, 778-786.
- Till, B.J., Reynolds, S.H., Greene, E.A., Codomo, C.A., Enns, L.C., Johnson, J.E., Burtner, C., Odden, A.R., Young, K., Taylor, N.E., **Henikoff, J.G.**, **Comai, L.**, and **Henikoff, S.** (2003) **Large-scale discovery of induced point mutations with high-throughput TILLING.** *Genome Research* 13, 524-530.
- Rose, T.M.**, **Henikoff, J.G.**, and **Henikoff, S.** (2003) **CODEHOP (Consensus-DEgenerate hybrid oligonucleotide primer) PCR primer design.** *Nucleic Acids Research* 31, 3763-3766.
- Ng, P.C., and **Henikoff, S.** (2003) **SIFT: predicting amino acid changes that affect protein function.** *Nucleic Acids Research* 31, 3812-3814.
- Nagaki, K., Talbert, P.B., Zhong, C.X., Dawe, R.K., **Henikoff, S.**, and **Jiang, J.M.** (2003) **Chromatin immunoprecipitation reveals that the 180-bp satellite repeat is the key functional DNA element of Arabidopsis thaliana centromeres.** *Genetics* 163, 1221-1225.
- Greil, F., van der Kraan, I., Delrow, J., Smothers, J.F., de Wit, E., Bussemaker, H.J., van Driel, R., **Henikoff, S.**, and van **Steensel, B.** (2003) **Distinct HP1 and Su(var)3-9 complexes bind to sets of developmentally coexpressed genes depending on chromosomal location.** *Genes & Development* 17, 2825-2838.
- Greene, E.A., Codomo, C.A., Taylor, N.E., **Henikoff, J.G.**, Till, B.J., Reynolds, S.H., Enns, L.C., Burtner, C., Johnson, J.E., Odden, A.R., **Comai, L.**, and **Henikoff, S.** (2003) **Spectrum of chemically induced mutations from a large-scale reverse-genetic screen in Arabidopsis.** *Genetics* 164, 731-740.
- Vermaak, D., Hayden, H.S., and **Henikoff, S.** (2002) **Centromere targeting element within the histone fold domain of Cid.** *Molecular and Cellular Biology* 22, 7553-7561.
- Tompa, R., McCallum, C.M., Delrow, J., **Henikoff, J.G.**, van **Steensel, B.**, and **Henikoff, S.** (2002) **Genome-wide profiling of DNA methylation reveals transposon targets of CHROMOMETHYLASE3.** *Current Biology* 12, 65-68.
- Talbert, P.B., Masuelli, R., Tyagi, A.P., **Comai, L.**, and **Henikoff, S.** (2002) **Centromeric localization and adaptive evolution of an Arabidopsis histone H3 variant.** *Plant Cell* 14, 1053-1066.
- Ng, P.C., and **Henikoff, S.** (2002) **Accounting for human polymorphisms predicted to affect protein function.** *Genome Research* 12, 436-446.
- Malik, H.S., Vermaak, D., and **Henikoff, S.** (2002) **Recurrent evolution of DNA-binding motifs in the Drosophila centromeric histone.** *Proc Natl Acad Sci USA* 99, 1449-1454.
- Ahmad, K., and **Henikoff, S.** (2002) **The histone variant H3.3 marks active chromatin by replication-independent nucleosome assembly.** *Molecular Cell* 9, 1191-1200.
- Ahmad, K., and **Henikoff, S.** (2002) **Histone H3 variants specify modes of chromatin assembly.** *Proc Natl Acad Sci USA* 99, 16477-16484.
- van **Steensel, B.**, Delrow, J., and **Henikoff, S.** (2001) **Chromatin profiling using targeted DNA adenine methyltransferase.** *Nature Genetics* 27, 304-308.
- Smothers, J.F., and **Henikoff, S.** (2001) **The hinge and chrome shadow domain impart distinct**

- targeting of HP1-like proteins.** *Molecular and Cellular Biology* 21, 2555-2569.
- Ng, P.C., and **Henikoff, S.** (2001) **Predicting deleterious amino acid substitutions.** *Genome Research* 11, 863-874.
- Malik, H.S., and **Henikoff, S.** (2001) **Adaptive evolution of Cid, a centromere-specific histone in Drosophila.** *Genetics* 157, 1293-1298.
- Lindroth, A.M., Cao, X.F., Jackson, J.P., Zilberman, D., McCallum, C.M., **Henikoff, S.**, and **Jacobsen, S.E.** (2001) **Requirement of CHROMOMETHYLASE3 for maintenance of CpXpG methylation.** *Science* 292, 2077-2080.
- Colbert, T., Till, B.J., Tompa, R., Reynolds, S., Steine, M.N., Yeung, A.T., McCallum, C.M., Comai, L., and **Henikoff, S.** (2001) **High-throughput screening for induced point mutations.** *Plant Physiology* 126, 480-484.
- Ahmad, K., and **Henikoff, S.** (2001) **Modulation of a transcription factor counteracts heterochromatic gene silencing in Drosophila.** *Cell* 104, 839-847.
- Ahmad, K., and **Henikoff, S.** (2001) **Centromeres are specialized replication domains in heterochromatin.** *Journal of Cell Biology* 153, 101-109.
- van Steensel, B., and **Henikoff, S.** (2000) **Identification of in vivo DNA targets of chromatin proteins using tethered Dam methyltransferase.** *Nature Biotechnology* 18, 424-428.
- Talbert, P.B., and **Henikoff, S.** (2000) **A reexamination of spreading of position-effect variegation in the white-roughest region of Drosophila melanogaster.** *Genetics* 154, 259-272.
- Smothers, J.F., and **Henikoff, S.** (2000) **The HP1 chromo shadow domain binds a consensus peptide pentamer.** *Current Biology* 10, 27-30.
- Rubin, G.M.**, Yandell, M.D., Wortman, J.R., Miklos, G.L.G., Nelson, C.R., Hariharan, I.K., Fortini, M.E., Li, P.W., Apweiler, R., Fleischmann, W., Cherry, J.M., **Henikoff, S.**, Skupski, M.P., Misra, S., Ashburner, M., Birney, E., Boguski, M.S., Brody, T., Brokstein, P., Celniker, S.E., Chervitz, S.A., Coates, D., Cravchik, A., Gabrielian, A., Galle, R.F., Gelbart, W.M., George, R.A., Goldstein, L.S.B., Gong, F.C., Guan, P., Harris, N.L., Hay, B.A., Hoskins, R.A., Li, J.Y., Li, Z.Y., Hynes, R.O., Jones, S.J.M., Kuehl, P.M., Lemaitre, B., Littleton, J.T., Morrison, D.K., Mungall, C., O'Farrell, P.H., Pickeral, O.K., Shue, C., Vossell, L.B., Zhang, J., Zhao, Q., Zheng, X.Q.H., Zhong, F., Zhong, W.Y., Gibbs, R., Venter, J.C., Adams, M.D., and Lewis, S. (2000) **Comparative genomics of the eukaryotes.** *Science* 287, 2204-2215.
- Ng, P.C., Henikoff, J.G., and **Henikoff, S.** (2000) **PHAT: a transmembrane-specific substitution matrix.** *Bioinformatics* 16, 760-766.
- McCallum, C.M., Comai, L., Greene, E.A., and **Henikoff, S.** (2000) **Targeted screening for induced mutations.** *Nature Biotechnology* 18, 455-457.
- McCallum, C.M., Comai, L., Greene, E.A., and **Henikoff, S.** (2000) **Targeting induced local lesions in genomes (TILLING) for plant functional genomics.** *Plant Physiology* 123, 439-442.
- Malik, H.S., **Henikoff, S.**, and **Eickbush, T.H.** (2000) **Poised for contagion: Evolutionary origins of the infectious abilities of invertebrate retroviruses.** *Genome Research* 10, 1307-1318.
- Malik, H.S., and **Henikoff, S.** (2000) **Dual recognition-incision enzymes might be involved in mismatch repair and meiosis.** *Trends in Biochemical Sciences* 25, 414-418.
- Henikoff, S.**, Ahmad, K., Platero, J.S., and van Steensel, B. (2000) **Heterochromatic deposition of centromeric histone H3-like proteins.** *Proc Natl Acad Sci USA* 97, 716-721.
- Henikoff, J.G., and **Henikoff, S.** (2000) **Drosophila genomic sequence annotation using the BLOCKS plus database.** *Genome Research* 10, 543-546.
- Henikoff, J.G., Greene, E.A., Pietrokovski, S., and **Henikoff, S.** (2000) **Increased coverage of protein families with the Blocks Database servers.** *Nucleic Acids Research* 28, 228-230.
- Sass, G.L., and **Henikoff, S.** (1999) **Pairing-dependent mislocalization of a Drosophila brown gene reporter to a heterochromatic environment.** *Genetics* 152, 595-604.
- Platero, J.S., Ahmad, K., and **Henikoff, S.** (1999) **A distal heterochromatic block displays centromeric activity when detached from a natural centromere.** *Molecular Cell* 4, 995-1004.
- Henikoff, S.**, Henikoff, J.G., and **Pietrokovski, S.** (1999) **Blocks+: a non-redundant database of protein alignment blocks derived from multiple compilations.** *Bioinformatics* 15, 471-479.
- Henikoff, J.G., **Henikoff, S.**, and **Pietrokovski, S.** (1999) **New features of the blocks database**

- servers. *Nucleic Acids Research* 27, 226-228.**
- Buchwitz, B.J., Ahmad, K., Moore, L.L., Roth, M.B., and **Henikoff, S.** (1999) **Cell division - A histone-H3-like protein in C-elegans.** *Nature* 401, 547-548.
- Sass, G.L., and **Henikoff, S.** (1998) **Comparative analysis of position-effect variegation mutations in Drosophila melanogaster delineates the targets of modifiers.** *Genetics* 148, 733-741.
- Rose, T.M., Schultz, E.R., Henikoff, J.G., Pietrokovski, S., McCallum, C.M., and **Henikoff, S.** (1998) **Consensus-degenerate hybrid oligonucleotide primers for amplification of distantly related sequences.** *Nucleic Acids Research* 26, 1628-1635.
- Platero, J.S., Csink, A.K., Quintanilla, A., and **Henikoff, S.** (1998) **Changes in chromosomal localization of heterochromatin-binding proteins during the cell cycle in Drosophila.** *Journal of Cell Biology* 140, 1297-1306.
- Pietrokovski, S., Henikoff, J.G., and **Henikoff, S.** (1998) **Exploring protein homology with the Blocks server.** *Trends in Genetics* 14, 162-163.
- Henikoff, S.**, Pietrokovski, S., and Henikoff, J.G. (1998) **Superior performance in protein homology detection with the Blocks Database servers.** *Nucleic Acids Research* 26, 309-312.
- Henikoff, S.**, and Comai, L. (1998) **A DNA methyltransferase homolog with a chromodomain exists in multiple polymorphic forms in Arabidopsis.** *Genetics* 149, 307-318.
- Fanti, L., Dorer, D.R., Berloco, M., **Henikoff, S.**, and Pimpinelli, S. (1998) **Heterochromatin protein 1 binds transgene arrays.** *Chromosoma* 107, 286-292.
- Csink, A.K., and **Henikoff, S.** (1998) **Large scale chromosomal movements during interphase progression in Drosophila.** *Journal of Cell Biology* 143, 13-22.
- Clark, D.V., Sabl, J.F., and **Henikoff, S.** (1998) **Repetitive arrays containing a housekeeping gene have altered polytene chromosome morphology in Drosophila.** *Chromosoma* 107, 96-104.
- Pietrokovski, S., and **Henikoff, S.** (1997) **A helix-turn-helix DNA-binding motif predicted for transposases of DNA transposons.** *Molecular & General Genetics* 254, 689-695.
- Martin-Morris, L.E., Csink, A.K., Dorer, D.R., Talbert, P.B., and **Henikoff, S.** (1997) **Heterochromatic trans-inactivation of Drosophila white transgenes.** *Genetics* 147, 671-677.
- Henikoff, S.**, and Henikoff, J.G. (1997) **Embedding strategies for effective use of information from multiple sequence alignments.** *Protein Science* 6, 698-705.
- Henikoff, J.G., Pietrokovski, S., and **Henikoff, S.** (1997) **Recent enhancements to the Blocks Database servers.** *Nucleic Acids Research* 25, 222-225.
- Dorer, D.R., and **Henikoff, S.** (1997) **Transgene repeat arrays interact with distant heterochromatin and cause silencing in cis and trans.** *Genetics* 147, 1181-1190.
- Wines, D.R., Talbert, P.B., Clark, D.V., and **Henikoff, S.** (1996) **Introduction of a DNA methyltransferase into Drosophila to probe chromatin structure in vivo.** *Chromosoma* 104, 332-340.
- Sabl, J.F., and **Henikoff, S.** (1996) **Copy number and orientation determine the susceptibility of a gene to silencing by nearby heterochromatin in Drosophila.** *Genetics* 142, 447-458.
- Pietrokovski, S., Henikoff, J.G., and **Henikoff, S.** (1996) **The Blocks Database - A system for protein classification.** *Nucleic Acids Research* 24, 197-200.
- Henikoff, J.G., and **Henikoff, S.** (1996) **Using substitution probabilities to improve position-specific scoring matrices.** *Computer Applications in the Biosciences* 12, 135-143.
- Henikoff, S.**, Endow, S.A., and Greene, E.A. (1996) **Connecting protein family resources using the proWeb network.** *Trends in Biochemical Sciences* 21, 444-445.
- Csink, A.K., and **Henikoff, S.** (1996) **Genetic modification of heterochromatic association and nuclear organization in Drosophila.** *Nature* 381, 529-531.
- Martin-Morris, L.E., and **Henikoff, S.** (1995) **Conservation of brown gene trans-inactivation in Drosophila.** *Genetics* 140, 193-199.
- Henikoff, S.**, Jackson, J.M., and Talbert, P.B. (1995) **Distance and pairing effects on the brown(dominant) heterochromatic element in Drosophila.** *Genetics* 140, 1007-1017.
- Henikoff, S.**, Henikoff, J.G., Alford, W.J., and Pietrokovski, S. (1995) **Automated construction and**

- graphical presentation of protein blocks from unaligned sequences. *Gene* 163, GC17-GC26.
- Talbert, P.B., Leciell, C.D.S., and **Henikoff, S.** (1994) **Modification of the *Drosophila* heterochromatic mutation brown(Dominant) by linkage alterations.** *Genetics* 136, 559-571.
- Henikoff, S.**, and Henikoff, J.G. (1994) **Protein family classification based on searching a database of blocks.** *Genomics* 19, 97-107.
- Henikoff, S.**, and Henikoff, J.G. (1994) **Position-based sequence weights.** *Journal of Molecular Biology* 243, 574-578.
- Dorer, D.R., and **Henikoff, S.** (1994) **Expansions of transgene repeats cause heterochromatin formation and gene silencing in *Drosophila*.** *Cell* 77, 993-1002.
- Henikoff, S.**, and Henikoff, J.G. (1993) **Performance evaluation of amino-acid substitution matrices.** *Proteins* 17, 49-61.
- Henikoff, S.** (1993) **Sequence-analysis by electronic mail server.** *Trends in Biochemical Sciences* 18, 267-268.
- Henikoff, S.** (1993) **Transcriptional activator components and poxvirus DNA-dependent ATPases comprise a single-family.** *Trends in Biochemical Sciences* 18, 291-292.
- Coco, W.M., Rothmel, R.K., **Henikoff, S.**, and **Chakrabarty, A.M.** (1993) **Nucleotide-sequence and initial functional-characterization of the *ClcR* gene encoding a LysR family activator of the *Clcabd* chlorocatechol operon in *Pseudomonas-putida*.** *Journal of Bacteriology* 175, 417-427.
- Wines, D.R., and **Henikoff, S.** (1992) **Somatic instability of a *Drosophila* chromosome.** *Genetics* 131, 683-691.
- Wallace, J.C., and **Henikoff, S.** (1992) **Patmat - a searching and extraction program for sequence, pattern and block queries and databases.** *Computer Applications in the Biosciences* 8, 249-254.
- Hinchman, S.K., **Henikoff, S.**, and **Schuster, S.M.** (1992) **A relationship between Asparagine Synthetase-a and Aspartyl Transfer-RNA Synthetase.** *Journal of Biological Chemistry* 267, 144-149.
- Henikoff, S.**, and Henikoff, J.G. (1992) **Amino-acid substitution matrices from protein blocks.** *Proc Natl Acad Sci USA* 89, 10915-10919.
- Henikoff, S.** (1992) **Detection of *Caenorhabditis* transposon homologs in diverse organisms.** *New Biologist* 4, 382-388.
- Clark, D.V., and **Henikoff, S.** (1992) **Unusual organizational features of the *Drosophila*-GART locus are not conserved within diptera.** *Journal of Molecular Evolution* 35, 51-59.
- Viale, A.M., Kobayashi, H., Akazawa, T., and **Henikoff, S.** (1991) **RcbR, a gene coding for a member of the LysR family of transcriptional regulators, is located upstream of the expressed set of Ribulose 1,5-bisphosphate carboxylase oxygenase genes in the photosynthetic bacterium *Chromatium-vinosum*.** *Journal of Bacteriology* 173, 5224-5229.
- Henikoff, S.**, and Henikoff, J.G. (1991) **Automated assembly of protein blocks for database searching.** *Nucleic Acids Research* 19, 6565-6572.
- Dreesen, T.D., **Henikoff, S.**, and Loughney, K. (1991) **A pairing-sensitive element that mediates trans-inactivation is associated with the *Drosophila* brown gene.** *Genes & Development* 5, 331-340.
- Henikoff, S.** (1990) **Ordered deletions for DNA sequencing and invitro mutagenesis by polymerase extension and exonuclease-III gapping of circular templates.** *Nucleic Acids Research* 18, 2961-2966.
- Endow, S.A.**, **Henikoff, S.**, and Solerniedziela, L. (1990) **Mediation of meiotic and early mitotic chromosome segregation in *Drosophila* by a protein related to kinesin.** *Nature* 345, 81-83.
- Johnson, D., and **Henikoff, S.** (1989) **A moveable 5' splice site in adenine phosphoribosyltransferase genes of *Drosophila* species.** *Molecular and Cellular Biology* 9, 2220-2223.
- Henikoff, S.**, and Smith, J.M. (1989) **The human messenger RNA that provides the N-terminus of**

- chimeric G6PD encodes GMP reductase. *Cell* 58, 1021-1022.
- Henikoff, S.**, and Dreesen, T.D. (1989) **Trans-inactivation of the *Drosophila* brown gene - evidence for transcriptional repression and somatic pairing dependence.** *Proc Natl Acad Sci USA* 86, 6704-6708.
- Henikoff, S.**, and Wallace, J.C. (1988) **Detection of protein similarities using nucleotide-sequence databases.** *Nucleic Acids Research* 16, 6191-6204.
- Henikoff, S.**, and Plasterk, R.H.A. (1988) **Related transposons in *C. elegans* and *Drosophila melanogaster*.** *Nucleic Acids Research* 16, 6234-6234.
- Henikoff, S.**, Haughn, G.W., Calvo, J.M., and Wallace, J.C. (1988) **A large family of bacterial activator proteins.** *Proc Natl Acad Sci USA* 85, 6602-6606.
- Dreesen, T.D., Johnson, D.H., and **Henikoff, S.** (1988) **The brown protein of *Drosophila melanogaster* is similar to the white protein and to components of active-transport complexes.** *Molecular and Cellular Biology* 8, 5206-5215.
- Henikoff, S.**, and Eghtedarzadeh, M.K. (1987) **Conserved arrangement of nested genes at the *Drosophila* GART locus.** *Genetics* 117, 711-725.
- Henikoff, S.**, Nash, D., Hards, R., Bleskan, J., Woolford, J.F., Naguib, F., and Patterson, D. (1986) **Two *Drosophila melanogaster* mutations block successive steps of de novo purine synthesis.** *Proc Natl Acad Sci USA* 83, 3919-3923.
- Henikoff, S.**, Keene, M.A., Sloan, J.S., Bleskan, J., Hards, R., and Patterson, D. (1986) **Multiple purine pathway enzyme-activities are encoded at a single genetic-locus in *Drosophila*.** *Proc Natl Acad Sci USA* 83, 720-724.
- Henikoff, S.**, Keene, M.A., Fachtel, K., and Fristrom, J.W. (1986) **Gene within a gene - nested *Drosophila* genes encode unrelated proteins on opposite DNA strands.** *Cell* 44, 33-42.
- Henikoff, S.** (1986) **The *Saccharomyces-cerevisiae* ade5,7 protein is homologous to overlapping *Drosophila-melanogaster*-gart polypeptides.** *Journal of Molecular Biology* 190, 519-528.
- Eghtedarzadeh, M.K., and **Henikoff, S.** (1986) **Use of oligonucleotides to generate large deletions.** *Nucleic Acids Research* 14, 5115-5115.
- Daubner, S.C., Schrimsher, J.L., Schendel, F.J., Young, M., **Henikoff, S.**, Patterson, D., Stubbe, J., and Benkovic, S.J. (1985) **A multifunctional protein possessing Glycinamide Ribonucleotide Synthetase, Glycinamide Ribonucleotide Transformylase, and Aminoimidazole Ribonucleotide Synthetase activities in de novo purine biosynthesis.** *Biochemistry* 24, 7059-7062.
- Henikoff, S.**, and Cohen, E.H. (1984) **Sequences responsible for transcription termination on a gene segment in *Saccharomyces cerevisiae*.** *Molecular and Cellular Biology* 4, 1515-1520.
- Henikoff, S.** (1984) **Unidirectional digestion with Exonuclease III creates targeted breakpoints for DNA sequencing.** *Gene* 28, 351-359.
- Henikoff, S.**, Sloan, J.S., and Kelly, J.D. (1983) **A *Drosophila* metabolic gene transcript is alternatively processed.** *Cell* 34, 405-414.
- Henikoff, S.**, Kelly, J.D., and Cohen, E.H. (1983) **Transcription terminates in yeast distal to a control sequence.** *Cell* 33, 607-614.
- Henikoff, S.**, and Furlong, C.E. (1983) **Sequence of a *Drosophila* DNA segment that functions in *Saccharomyces cerevisiae* and its regulation by a yeast promoter.** *Nucleic Acids Research* 11, 789-800.
- Henikoff, S.** (1983) **Cloning exons for mapping of transcription - characterization of the *Drosophila melanogaster* alcohol dehydrogenase gene.** *Nucleic Acids Research* 11, 4735-4752.
- Henikoff, S.**, Tatchell, K., Hall, B.D., and Nasmyth, K.A. (1981) **Isolation of a gene from *Drosophila* by complementation in yeast.** *Nature* 289, 33-37.
- Henikoff, S.** (1981) **Position-effect variegation and chromosome structure of a heat-shock puff in *Drosophila*.** *Chromosoma* 83, 381-393.
- Henikoff, S.** (1979) **Position effects and variegation enhancers in an autosomal region of *Drosophila-melanogaster*.** *Genetics* 93, 105-115.
- Henikoff, S.**, and Meselson, M. (1977) **Transcription at two heat shock loci in *Drosophila*.** *Cell* 12,

441-451.

McKenzie, S.L., **Henikoff, S.**, and Meselson, M. (1975) **Localization of rna from heat induced polysomes at puff sites in *Drosophila melanogaster*.** *Proc Natl Acad Sci USA* 72, 1117-1121.

Henikoff, S., Heywood, J., and Meselson, M. (1974) **Orientation of repeating units in *Xenopus* chromosomal ribosomal DNA - test of a stochastic-model for maintaining intraspecies homogeneity.** *Journal of Molecular Biology* 85, 445-450.

Peer reviewed review articles

Ahmad K **Henikoff S** (2025) Profiling regulatory elements in vivo by genome-wide methods. *Current Opinion in Structural Biology*. 92:103064. doi: 10.1016/j.sbi.2025.103064.

Henikoff S, Ahmad K (2025) **Hansemann's anaplastic theory of cancer after 135 years.** *Frontiers in Epigenetics & Epigenomics*. May 1;3. doi: 10.3389/freae.2025.1607433

Henikoff S, Levens DL. (2025) **The plusses and minuses of DNA torsion.** *Elife*. Mar 3;14:e106351. doi: 10.7554/eLife.106351.

Neefjes J, Gurova K, Sarthy J, Szabó G, **Henikoff S** (2024). **Chromatin as an old and new anticancer target.** *Trends Cancer*. Aug;10(8):696-707. doi: 10.1016/j.trecan.2024.05.005.

Ahmad K, Brahma S, **Henikoff S**. (2023) **Epigenetic pioneering by SWI/SNF family remodelers.** *Mol Cell*. Nov 16:S1097-2765(23)00916-4.

Talbert PB, **Henikoff S**, Armache KJ. (2023) **Giant variations in giant virus genome packaging.** *Trends Biochem Sci*. Dec;48(12):1071-1082.

Henikoff S. (2023) **The epigenetic landscape: An evolving concept.** *Frontiers in Epigenetics and Epigenomics* 1, 1.

Talbert P, **Henikoff S** (2022) **Centromere drive: chromatin conflict in meiosis.** *Curr Opin Genet Dev*. Dec;77:102005.

Ahmad K, **Henikoff S** (2022) **The *Drosophila* embryo as a tabula rasa for the epigenome.** *Fac Rev*. Dec 23;11:40. doi: 10.12703/r/11-40.

Henikoff S, Ahmad K (2022) **In situ tools for chromatin structural epigenomics.** *Protein Sci*. Nov;31(11):e4458. doi: 10.1002/pro.4458.

Brahma S, **Henikoff S** (2022) **CUT&RUN Profiling of the Budding Yeast Epigenome.** *Methods Mol Biol*. 2477:129-147. doi: 10.1007/978-1-0716-2257-5_9.

Talbert PB, Armache KJ, **Henikoff S** (2022) **Viral histones: pickpocket's prize or primordial progenitor?** *Epigenetics Chromatin* 15(1):21.

Talbert PB, **Henikoff S** (2022) **The genetics and epigenetics of satellite centromeres.** *Genome Research* 32:608-615.

Ahmad K, **Henikoff S**, Ramachandran S (2022) **Managing the Steady State Chromatin Landscape by Nucleosome Dynamics.** *Annu Rev Biochem*. 91:183-195.

Talbert PB, **Henikoff S**. **The yin and yang of histone marks in transcription.** *Ann Rev Genomics Hum Genet*. 2021 Mar 29. doi: 10.1146/annurev-genom-120220-085159.

Talbert PB, **Henikoff S**. **Histone variants at a glance.** *J Cell Sci*. 2021 Mar 26;134(6):jcs244749. doi: 10.1242/jcs.244749.

Talbert PB, **Henikoff S**. (2020) What makes a centromere? *Exp Cell Res*. 389:111895.

Brahma S and **Henikoff S**. (2020) **Epigenome Regulation by Dynamic Nucleosome Unwrapping.** *Trends in Biochemical Sciences*, 45:13-26.

Sarthy JF and **Henikoff S**. (2019) **Bringing oncohistones into the fold.** *Cancer Discovery* 9(10):1346- 1348.

Talbert PB, Meers MP, **Henikoff S**. (2019) **Old cogs, new tricks: the evolution of gene expression in a chromatin context.** *Nat Rev Genet*. 20:283-297

Sarthy JF, **Henikoff S**, Ahmad K. (2019) **Chromatin Bottlenecks in Cancer.** *Trends Cancer*. 5:183-194.

Talbert and **Henikoff S**. **Transcribing centromeres: Noncoding RNAs and kinetochore assembly.** *Trends Genet*. 2018 doi: 10.1016/j.tig.2018.05.001.

Henikoff, S. and Church, GM (2018) **Simultaneous Discovery of Cell-Free DNA and the Nucleosome Ladder.** *Genetics* 209(1):27-29.

Ramachandran S, Ahmad K, **Henikoff S**. (2017) **Capitalizing on disaster: Establishing chromatin**

- specificity behind the replication fork.** *Bioessays* DOI: 10.1002/bies.201600150.
- Talbert P.B. and **Henikoff S.** (2016) **Histone variants on the move: substrates for chromatin dynamics.** *Nature Reviews Mol Cell Biol.* 18:115-126.
- Henikoff S.** (2016) **Mechanisms of Nucleosome Dynamics In Vivo.** *Cold Spring Harb Perspect Med.* 6, a026666.
- Ramachandran S. and **Henikoff S.** (2016) **Nucleosome dynamics during chromatin remodeling in vivo.** *Nucleus* 2016 7, 20-6
- Drinnenberg, I.A., **Henikoff, S** and **Malik, H.S.** (2016) **Evolutionary Turnover of Kinetochore Proteins: A Ship of Theseus?** *Trends Cell Biol.* 26:498-510.
- Ramachandran, S., and **Henikoff, S** (2015) **Replicating nucleosomes.** *Science Advances,* 1:e1500187.
- Steiner, F.A., and **Henikoff, S** (2015) **Diversity in the organization of centromeric chromatin.** *Current Opinion in Genetics and Development* 31:28-35.
- Henikoff, S.**, and Smith, M.M. (2015) **Histone Variants and Epigenetics.** *Cold Spring Harbor Perspectives in Biology* 7:a019364.
- Zentner, G.E., and **Henikoff, S.** (2014) **High-resolution digital profiling of the epigenome.** *Nature Reviews Genetics* 15, 814-827.
- Yang, F., Teves, S.S., Kemp, C.J., and **Henikoff, S.** (2014) **Doxorubicin, DNA torsion, and chromatin dynamics.** *Biochim Biophys Acta-Reviews on Cancer* 1845, 84-89.
- Weber, C.M., and **Henikoff, S.** (2014) **Histone variants: dynamic punctuation in transcription.** *Genes & Development* 28, 672-682.
- Teves, S.S., Weber, C.M., and **Henikoff, S.** (2014) **Transcribing through the nucleosome.** *Trends in Biochemical Sciences* 39, 577-586.
- Talbert, P.B., and **Henikoff, S.** (2014) **Environmental responses mediated by histone variants.** *Trends in Cell Biology* 24, 642-650.
- Zentner, G.E., and **Henikoff, S.** (2013) **Regulation of nucleosome dynamics by histone modifications.** *Nature Structural & Molecular Biology* 20, 259-266.
- Talbert, P.B., and **Henikoff, S.** (2013) **Phylogeny as the basis for naming histones.** *Trends in Genetics* 29, 499-500.
- Skene, P.J., and **Henikoff, S.** (2013) **Histone variants in pluripotency and disease.** *Development* 140, 2513-2524.
- Zentner, G.E., and **Henikoff, S.** (2012) **Surveying the epigenomic landscape, one base at a time.** *Genome Biology* 13, e250.
- Talbert, P.B., Ahmad, K., Almouzni, G., Ausio, J., Berger, F., Bhalla, P.L., Bonner, W.M., Cande, W.Z., Chadwick, B.P., Chan, S.W.L., Cross, G.A.M., Cui, L., Dimitrov, S.I., Doenecke, D., Eirin-Lopez, J.M., Gorovsky, M.A., Hake, S.B., Hamkalo, B.A., Holec, S., Jacobsen, S.E., Kamieniarz, K., Khochbin, S., Ladurner, A.G., Landsman, D., Latham, J.A., Loppin, B., Malik, H.S., Marzluff, W.F., Pehrson, J.R., Postberg, J., Schneider, R., Singh, M.B., Smith, M.M., Thompson, E., Torres-Padilla, M.-E., Tremethick, D.J., Turner, B.M., Waterborg, J.H., Wollmann, H., Yelagandula, R., Zhu, B., and **Henikoff, S.** (2012) **A unified phylogeny-based nomenclature for histone variants.** *Epigenetics & Chromatin* 5, e7.
- Henikoff, S.**, and Furuyama, T. (2012) **The unconventional structure of centromeric nucleosomes.** *Chromosoma* 121, 341-352.
- Henikoff, S.**, and Shilatifard, A. (2011) **Histone modification: cause or cog?** *Trends in Genetics* 27, 389-396.
- Talbert, P.B., and **Henikoff, S.** (2010) **Histone variants - ancient wrap artists of the epigenome.** *Nature Reviews Mol Cell Biol* 11, 264-275.
- Deal, R.B., and **Henikoff, S.** (2010) **Capturing the dynamic epigenome.** *Genome Biology* 11, e218.
- Talbert, P.B., and **Henikoff, S.** (2009) **Chromatin-based transcriptional punctuation.** *Genes & Development* 23, 1037-1041.
- Malik, H.S.**, and **Henikoff, S.** (2009) **Major Evolutionary Transitions in Centromere Complexity.** *Cell* 138, 1067-1082.
- Gehring, M., Reik, W., and **Henikoff, S.** (2009) **DNA demethylation by DNA repair.** *Trends in Genetics* 25, 82-90.

- Henikoff, S.** (2008) **Nucleosome destabilization in the epigenetic regulation of gene expression.** *Nature Reviews Genet* 9, 15-26.
- Zilberman, D., and Henikoff, S.** (2007) **Genome-wide analysis of DNA methylation patterns.** *Development* 134, 3959-3965.
- Gehring, M., and Henikoff, S.** (2007) **DNA methylation dynamics in plant genomes.** *Biochim Biophys Acta-Gene Structure and Expression* 1769, 276-286.
- Talbert, P.B., and Henikoff, S.** (2006) **Spreading of silent chromatin: inaction at a distance.** *Nature Reviews Genet* 7, 793-803.
- Ng, P.C., and Henikoff, S.** (2006) **Predicting the effects of amino acid substitutions on protein function.** *Ann Rev Genomics and Human Genetics*, pp. 61-80.
- Feinberg, A.P., Ohlsson, R., and Henikoff, S.** (2006) **The epigenetic progenitor origin of human cancer.** *Nature Reviews Genet* 7, 21-33.
- Dawe, R.K., and Henikoff, S.** (2006) **Centromeres put epigenetics in the driver's seat.** *Trends in Biochemical Sciences* 31, 662-669.
- Comai, L., and Henikoff, S.** (2006) **TILLING: practical single-nucleotide mutation discovery.** *Plant Journal* 45, 684-694.
- Henikoff, S., and Ahmad, K.** (2005) **Assembly of variant histones into chromatin.** *In Ann Rev Cell and Developmental Biology*, pp. 133-153.
- Henikoff, S.** (2005) **Rapid changes in plant genomes.** *Plant Cell* 17, 2852-2855.
- Zilberman, D., and Henikoff, S.** (2004) **Silencing of transposons in plant genomes: kick them when they're down.** *Genome Biology* 5, e249.
- Henikoff, S., Till, B.J., and Comai, L.** (2004) **TILLING. Traditional mutagenesis meets functional genomics.** *Plant Physiology* 135, 630-636.
- Henikoff, S., Furuyama, T., and Ahmad, K.** (2004) **Histone variants, nucleosome assembly and epigenetic inheritance.** *Trends in Genetics* 20, 320-326.
- Malik, H.S., and Henikoff, S.** (2003) **Phylogenomics of the nucleosome.** *Nature Structural Biology* 10, 882-891.
- Henikoff, S., and Comai, L.** (2003) **Single-nucleotide mutations for plant functional genomics.** *Ann Rev Plant Biol* 54, 375-401.
- Henikoff, S.** (2002) **Near the edge of a chromosome's 'black hole'.** *Trends in Genetics* 18, 165-167.
- Henikoff, S., Ahmad, K., and Malik, H.S.** (2001) **The centromere paradox: Stable inheritance with rapidly evolving DNA.** *Science* 293, 1098-1102.
- Rubin, G.M., Yandell, M.D., Wortman, J.R., Miklos, G.L.G., Nelson, C.R., Hariharan, I.K., Fortini, M.E., Li, P.W., Apweiler, R., Fleischmann, W., Cherry, J.M., Henikoff, S., Skupski, M.P., Misra, S., Ashburner, M., Birney, E., Boguski, M.S., Brody, T., Brokstein, P., Celniker, S.E., Chervitz, S.A., Coates, D., Cravchik, A., Gabrielian, A., Galle, R.F., Gelbart, W.M., George, R.A., Goldstein, L.S.B., Gong, F.C., Guan, P., Harris, N.L., Hay, B.A., Hoskins, R.A., Li, J.Y., Li, Z.Y., Hynes, R.O., Jones, S.J.M., Kuehl, P.M., Lemaitre, B., Littleton, J.T., Morrison, D.K., Mungall, C., O'Farrell, P.H., Pickeral, O.K., Shue, C., Voshall, L.B., Zhang, J., Zhao, Q., Zheng, X.Q.H., Zhong, F., Zhong, W.Y., Gibbs, R., Venter, J.C., Adams, M.D., and Lewis, S.** (2000) **Comparative genomics of the eukaryotes.** *Science* 287, 2204-2215.
- Henikoff, S.** (2000) **Heterochromatin function in complex genomes.** *Biochim Biophys Acta-Reviews on Cancer* 1470, O1-O8.
- Henikoff, S., and Henikoff, J.G.** (2000) **Amino acid substitution matrices.** *Advances in Protein Chemistry, Vol 54* 54, 73-97.
- Henikoff, S., and Comai, L.** (1998) **Trans-sensing effects: The ups and downs of being together.** *Cell* 93, 329-332.
- Henikoff, S.** (1998) **Conspiracy of silence among repeated transgenes.** *Bioessays* 20, 532-535.
- Csink, A.K., and Henikoff, S.** (1998) **Something from nothing: The evolution and utility of satellite repeats.** *Trends in Genetics* 14, 200-204.
- Henikoff, S., and Henikoff, J.G.** (2000) **Amino acid substitution matrices.** *Advances in Protein Chemistry, Vol 54* 54, 73-97.
- Henikoff, S., Greene, E.A., Pietrokovski, S., Bork, P., Attwood, T.K., and Hood, L.** (1997) **Gene**

- families: **The taxonomy of protein paralogs and chimeras.** *Science* 278, 609-614.
- Henikoff, S.** (1996) **Dosage-dependent modification of position-effect variegation in *Drosophila*.** *Bioessays* 18, 401-409.
- Tartof, K.D., and **Henikoff, S.** (1991) **Trans-sensing effects from *Drosophila* to humans.** *Cell* 65, 201-203.
- Henikoff, S.** (1995) **Comparative methods for identifying functional domains in protein sequences.** *Biotechnology Annual Reviews* 1, 129-147.
- Henikoff, S.** (1990) **Position-effect variegation after 60 years.** *Trends in Genetics* 6, 422-426.
- Henikoff, S.** (1987) **Multifunctional polypeptides for purine denovo synthesis.** *Bioessays* 6, 8-13.

Other publications (selected)

- Talbert PB, **Henikoff S.** (2025) **Centromeres drive and take a break.** *Chromosome Research*. Aug 4;33(1):17. doi: 10.1007/s10577-025-09777-z.
- Khyzha N, **Ahmad K, Henikoff S.** (2025) **Protocol for the spatiotemporal profiling of RNA within nuclear compartments in human cell lines using SLAM-RT&Tag.** *STAR Protocols*. Aug 9;6(3):104017. doi: 10.1016/j.xpro.2025.104017.
- Ahmad K, Henikoff S.** (2025) **Profiling regulatory elements in vivo by genome-wide methods.** *Current Opinion Structural Biology*. Jun;92:103064. doi: 10.1016/j.sbi.2025.103064.
- Ahmad K, Wooten M, Takushi NB, Vidaurre V, Chen X, Henikoff S.** (2025) **Cell-cycle-dependent repression of histone gene transcription by histone H4.** *bioRxiv*. DOI: <https://www.biorxiv.org/content/10.1101/2024.12.23.630206v2>.
- Ahmad K, Brahma S, Henikoff S.** (2024) **Response to "Learning from chromatin reconstitution: Pioneering factors enabling nucleosome remodelers".** *Mol Cell*. Apr 3:S1097-2765(24)00230-2. DOI: <https://doi.org/10.1016/j.molcel.2024.03.020>.
- Kaonis S, Smith JL, Katiyar N, Merrill M, Hyelkma T, Namciu S, Le Q, Babaeva E, Ishida T, Morris SM, Girard E, Furuyama S, Ries R, Bernstein I, Meshinchi S, Henikoff S, Meers M, Hadland B, Sarthy JF.** (2023) **Chromatin Profiling of CBFA2T3-GLIS2 AMLs Identifies Key Transcription Factor Dependencies and BRG1 Inhibition as a Novel Therapeutic Strategy.** *bioRxiv* DOI: <https://doi.org/10.1101/2023.08.30.555598>.
- Leichter SM, Henikoff S.** (2023) **β -catenin repositions over time.** *Cell Syst*. Jul 19;14(7):549-550.
- Talbert P and Henikoff S.** **Centromeres organize (epi)genome architecture.** *Cell*. 2022 Aug 18;185(17):3083-3085. doi: 10.1016/j.cell.2022.07.022.
- Brahma, S. Henikoff S.** (2022) **CUT&RUN Profiling of the Budding Yeast Epigenome.** In: Devaux F. (eds) *Yeast Functional Genomics. Methods in Molecular Biology*, vol 2477. Humana, New York, NY.
- Talbert PB, Henikoff S.** **Remodeler-variant tag team slams transposons.** *Nat Cell Biol*. 2021 Apr;23(4):297-298.
- Henikoff S, Ahmad K, Evolution: Heterochromatin diversity in early-branching land plants.** *Curr Biol*. 2020 Feb 24; 30(4); R161-R163
- Thakur J, Henikoff S, Architectural RNA in chromatin organization.** *Biochem Soc Trans*. 2020 Sep 8;BST20191226. doi: 10.1042/BST20191226.
- Henikoff S, Ahmad K.** (2020) **Evolution: Heterochromatin Diversity in Early-Branching Land Plants.** *Curr Biol* 30:R161-R163.
- Henikoff S and Ahmad K.** (2019) **Nucleosomes know where they were.** *Proc Natl Acad Sci USA* doi: 10.1073/pnas.1914581116.
- Sarthy, JF and Henikoff S.** (2019) **Bringing oncohistones into the fold.** *Cancer Discovery* Oct;9(10):1346-1348.
- Ahmad K. and Henikoff S.** (2018) **No strand left behind.** *Science* 361:1311-1312.
- Henikoff S. and Ramachandran S.** (2018) **Pioneers invade the nucleosome landscape.** *Mol Cell* 71:193-94.
- Henikoff S. and Church G.M.** (2018) **Simultaneous discovery of cell-free DNA and the nucleosome ladder.** *Genetics* 209:27-29.
- Ramachandran S. and Henikoff S.** (2018) *Methods in molecular biology* (Clifton, N.J.) 1832:159-168,
- Henikoff S.** (2018) **Darwin meets Waddington.** *Current Biology* 28:R682-4.

- Henikoff S.**, Thakur J, Kasinathan S and Talbert PB. (2017) **Remarkable evolutionary plasticity of centromeric chromatin.** *Cold Spring Harb Symp Quant Biol.* Dec 1 doi: 10.1101/sqb.2017.82.033605.
- Henikoff S.** (2017) **Structural biology: Probing the origin of chromatin.** *Current Biology* 27:R1118-1120.
- Armstrong, S., **Henikoff S.** and Vakoc, C. (editors) **Chromatin Dereglulation in Cancer.** Cold Spring Harbor Press, 382 pages, 2017.
- Kasinathan S., Zentner G.E., Xin B., Rohs R. and **Henikoff S.** (2017) **Correspondence: Reply to 'DNA shape is insufficient to explain binding'** *Nat Commun.* Jun 5;8:15644.
- Henikoff, S.** and Grealley, J.M. (2016) **Epigenetics, cellular memory and gene regulation.** *Current Biology*, 26, R644-8.
- Henikoff, S.** (2015) **The genetic map enters its second century.** *Genetics* 200:671-674.
- Henikoff, S.** (2015) **Cell-type-specific neuronal epigenomics.** *Neuron* 86:1319-1321.
- Zentner, G.E., and **Henikoff, S.** (2015) **Epigenome editing made easy.** *Nature Biotechnology* 33:606-607.
- Steiner, F.A., and **Henikoff, S.** (2015) **Cell Type-Specific Affinity Purification of Nuclei for Chromatin Profiling in Whole Animals.** In *Nucleus, 2nd Edition*, R. Hancock, ed., pp. 3-14.
- Orsi, G.A., Kasinathan, S., Zentner, G.E., **Henikoff, S.**, and Ahmad, K. (2015) **Mapping regulatory factors by immunoprecipitation from native chromatin.** *Current protocols in molecular biology.* 110, 21.31.21.
- Teves, S.S., and **Henikoff, S.** (2014) **DNA torsion as a feedback mediator of transcription and chromatin dynamics.** *Nucleus-Austin* 5, 211-218.
- Skene, P.J., and **Henikoff, S.** (2014) **Histones push the envelope.** *Nature Structural & Molecular Biology* 21, 651-652.
- Kasinathan, S., and **Henikoff, S.** (2014) **5-Aza-CdR Delivers a Gene Body Blow.** *Cancer Cell* 26, 449-451.
- Teves, S.S., and **Henikoff, S.** (2013) **The heat shock response: A case study of chromatin dynamics in gene regulation.** *Biochemistry and Cell Biology-Biochimie Et Biologie Cellulaire* 91, 42-48.
- Henikoff, S.**, and Grosveld, F. (2013) **Epigenetics & chromatin: interactions and processes.** *Epigenetics & Chromatin* 6, e2.
- Doolittle, W.F., Fraser, P., Gerstein, M.B., Graveley, B.R., **Henikoff, S.**, Huttenhower, C., Oshlack, A., Ponting, C.P., Rinn, J.L., Schatz, M.C., Ule, J., Weigel, D., and Weinstock, G.M. (2013) **Sixty years of genome biology.** *Genome Biology* 14.
- Cooper, J.L., **Henikoff, S.**, Comai, L., and Till, B.J. (2013) **TILLING and ecotilling for rice.** *Methods in molecular biology (Clifton, N.J.)* 956, 39-56.
- Till, B.J., Zerr, T., Comai, L., and **Henikoff, S.** (2012) **A Protocol for TILLING and Eco-TILLING.**
- Teves, S.S., and **Henikoff, S.** (2012) **Salt Fractionation of Nucleosomes for Genome-Wide Profiling.** In *Chromatin Remodeling: Methods and Protocols*, R.H. Morse, ed., pp. 421-432.
- Teves, S.S., Deal, R.B., and **Henikoff, S.** (2012) **Measuring Genome-Wide Nucleosome Turnover Using CATCH-IT.** In *Nucleosomes, Histones & Chromatin, Pt B*, C. Wu, and C.D. Allis, eds., pp. 169-184.
- Talbert, P.B., and **Henikoff, S.** (2012) **Chromatin: Packaging without Nucleosomes.** *Current Biology* 22, R1040-R1043.
- Skene, P.J., and **Henikoff, S.** (2012) **Chromatin roadblocks to reprogramming 50 years on.** *BMC Biology* 10, e83.
- Henikoff, S.** (2012) **Q & A Steven Henikoff.** *Current Biology* 22, R106-R107.
- Deal, R.B., and **Henikoff, S.** (2011) **Histone variants and modifications in plant gene regulation.** *Current Opinion in Plant Biology* 14, 116-122.
- Talbert, P.B., and **Henikoff, S.** (2010) **Centromeres Convert but Don't Cross.** *Plos Biology* 8, e1000326.
- Henikoff, S.**, and Furuyama, T. (2010) **Epigenetic inheritance of centromeres.** *CSHSQB* 75, 51-60.
- Henikoff, S.** (2010) **Summary: The nucleus--a close-knit community of dynamic structures.** *CSHSQB* 75, 607-615.

- Deal, R.B., and **Henikoff, S.** (2010) **Catching a glimpse of nucleosome dynamics.** *Cell Cycle* 9, 3389-3390.
- Talbert, P.B., Bayes, J.J., and **Henikoff, S.** (2009) **Evolution of Centromeres and Kinetochores: A Two-Part Fugue.**
- Henikoff, S.**, and **Grosveld, F.** (2009) **Epigenetics & Chromatin celebrates its first anniversary.** *Epigenetics & Chromatin* 2, e13.
- Henikoff, S.** (2009) **Labile H3.3+H2A.Z nucleosomes mark 'nucleosome-free regions'.** *Nature Genetics* 41, 865-866.
- Henikoff, S.** (2009) **Epigenetic profiling of histone variants.** *Epigenomics*, Ferguson-Smith, Greally & Martienssen, Editors, 101-118.
- Till, B.J., Comai, L., and **Henikoff, S.** (2008) **Tilling and ecotilling for crop improvement.** *In Springer Series on Biofilms*, N. Balaban, ed., pp. 333-349.
- Cooper, J.L., Till, B.J., and **Henikoff, S.** (2008) **Fly-TILL Reverse genetics using a living point mutation resource.** *Fly* 2, 300-302.
- Henikoff, S.**, Strahl, B.D., and Warburton, P.E. (2008) **Epigenomics: A Roadmap to Chromatin.** *Science* 322, 853-853.
- Henikoff, S.**, and **Grosveld, F.** (2008) **Welcome to Epigenetics & Chromatin.** *Epigenetics & Chromatin* 1, e1.
- Gehring, M., and **Henikoff, S.** (2008) **DNA methylation and demethylation in Arabidopsis.** *The Arabidopsis Book* 6:e0102.
- American Association for Cancer Research Human Epigenome Task, F., and European Union, N.o.E.S.A.B. (2008) **Moving AHEAD with an international human epigenome project.** *Nature* 454, 711-715.
- Greene, E.A., Pietrokovski, S., **Henikoff, S.**, Bork, P., Attwood, T.K., Hood, L., and Bairoch, A. (1997) **Building gene families.** *Science* 278, 615-626.
- Ooi, S.L., and **Henikoff, S.** (2007) **Germline histone dynamics and epigenetics.** *Current Opinion in Cell Biology* 19, 257-265.
- Henikoff, S.** (2007) **Nucleosomes at active promoters: Unforgettable loss.** *Cancer Cell* 12, 407-409.
- Dalai, Y., Furuyama, T., Vermaak, D., and **Henikoff, S.** (2007) **Structure, dynamics, and evolution of centromeric nucleosomes.** *Proc Natl Acad Sci USA* 104, 15974-15981.
- Till, B.J., Colbert, T., Codomo, C., Enns, L., Johnson, J., Reynolds, S.H., Henikoff, J.G., Greene, E.A., Steine, M.N., Comai, L., and **Henikoff, S.** (2006) **High-throughput TILLING for Arabidopsis.** *In Methods in Molecular Biology*, pp. 127-135.
- Furuyama, T., and **Henikoff, S.** (2006) **Biotin-tag affinity purification of a centromeric nucleosome assembly complex.** *Cell Cycle* 5, 1269-1274.
- Zilberman, D., and **Henikoff, S.** (2005) **Epigenetic inheritance in Arabidopsis: selective silence.** *Current Opinion in Genetics & Development* 15, 557-562.
- Weil, C.F., Monde, R.A., Till, B.J., Comai, L., and **Henikoff, S.** (2005) **Mutagenesis and functional genomics in Maize.** *Maydica* 50, 415-424.
- Henikoff, S.**, and Dalai, Y. (2005) **Centromeric chromatin: what makes it unique?** *Current Opinion in Genetics & Development* 15, 177-184.
- Henikoff, S.** (2005) **Histone modifications: Combinatorial complexity or cumulative simplicity?** *Proc Natl Acad Sci USA* 102, 5308-5309.
- Henikoff, S.**, McKittrick, E., and Ahmad, K. (2004) **Epigenetics, histone H3 variants, and the inheritance of chromatin states.** *CSHSQB* 69, 235-243.
- Henikoff, S.** (2004) **Visualizing gene expression: an unfolding story.** *Cell* 116, 633-634.
- Vermaak, D., Ahmad, K., and **Henikoff, S.** (2003) **Maintenance of chromatin states: an open-and-shut case.** *Current Opinion in Cell Biology* 15, 266-274.
- van Steensel, B., and **Henikoff, S.** (2003) **Epigenomic profiling using microarrays.** *Biotechniques* 35, 346-357.
- Till, B.J., Colbert, T., Tompa, R., Enns, L.C., Codomo, C.A., Johnson, J.E., Reynolds, S.H., Henikoff, J.G., Greene, E.A., Steine, M.N., Comai, L., and **Henikoff, S.** (2003) **High-throughput TILLING for functional genomics.** *Methods in molecular biology* 236, 205-220.

- Rutherford, S.L., and **Henikoff, S.** (2003) **Quantitative epigenetics.** *Nature Genetics* 33, 6-8.
- Smothers, J.F., **Henikoff, S.**, and **Carter, P.** (2002) **Affinity selection from biological libraries.** *Science* 298, 621-622.
- Malik, H.S., and **Henikoff, S.** (2002) **Conflict begets complexity: the evolution of centromeres.** *Current Opinion in Genetics & Development* 12, 711-718.
- Lindquist, S.L.**, and **Henikoff, S.** (2002) **Self-perpetuating structural states in biology, disease, and genetics.** *Proc Natl Acad Sci USA* 99, 16377-16377.
- Henikoff, S.**, and Malik, H.S. (2002) **Selfish drivers.** *Nature* 417, 227-227.
- Henikoff, S.** (2002) **Beyond the central dogma.** *Bioinformatics* 18, 223-225.
- Henikoff, J.G.**, **Greene, E.A.**, **Taylor, N.**, **Henikoff, S.**, and **Petrokovski, S.** (2002) **Using the blocks database to recognize functional domains.** *Current protocols in bioinformatics.* Chapter 2, Unit 2.2-Unit 2.2.
- Ahmad, K., and **Henikoff, S.** (2002) **Epigenetic consequences of nucleosome dynamics.** *Cell* 111, 281-284.
- Smothers, J.F.**, **Henikoff, S.** (2001) **Predicting in vivo protein-peptide interactions with random phage display.** *Combinatorial Chemistry & High Throughput Screening* 4, 585-591.
- Henikoff, J.G.**, **Petrokovski, S.**, **McCallum, C.M.**, and **Henikoff, S.** (2000) **Blocks-based methods for detecting protein homology.** *Electrophoresis* 21, 1700-1706.
- Henikoff, S.**, and **Vermaak, D.** (2000) **Bugs on drugs go GAGAA.** *Cell* 103, 695-698.
- Henikoff, S.**, **Eissenberg, J.C.**, **Hilliker, A.J.**, **Schmidt, E.R.**, and **Wallrath, L.L.** (2000) **Reaching for new heitz.** *Genetica* 109, 7-8.
- Martienssen, R.**, and **Henikoff, S.** (1999) **The House & Garden guide to chromatin remodelling.** *Nature Genetics* 22, 6-7.
- Henikoff, S.**, and **Matzke, M.A.** (1997) **Exploring and explaining epigenetic effects.** *Trends in Genetics* 13, 293-295.
- Levis, R.W.**, and **Henikoff, S.** (1997) **You read it here first.** *Nature* 387, 843-843.
- Henikoff, S.** (1997) **Nuclear organization and gene expression: Homologous pairing and long-range interactions.** *Current Opinion in Cell Biology* 9, 388-395.
- Henikoff, S.** (1996) **Position-effect variegation in Drosophila: Recent progress.** In *Cold Spring Harbor Monograph Series; Epigenetic mechanisms of gene regulation*, V.E.A. Russo, R.A. Martienssen, and A.D. Riggs, eds., pp. 319-334.
- Henikoff, S.** (1996) **Scores for sequence searches and alignments.** *Current Opinion in Structural Biology* 6, 353-360.
- Henikoff, J.G.**, and **Henikoff, S.** (1996) **Blocks database and its applications.** *Computer Methods for Macromolecular Sequence Analysis* 266, 88-105.
- Henikoff, S.** (1995) **Gene silencing in Drosophila.** *Gene Silencing in Higher Plants and Related Phenomena in Other Eukaryotes* 197, 193-208.
- Henikoff, S.** (1995) **Detecting dinosaur DNA.** *Science* 268, 1192-1192.
- Mount, S.**, and **Henikoff, S.** (1993) **Gene organization - nested genes take flight.** *Current Biology* 3, 372-374.
- Martin-Morris, L.E.**, **Loughney, K.**, **Kershisnik, E.O.**, **Poortinga, G.**, and **Henikoff, S.** (1993) **Characterization of sequences responsible for trans-inactivation of the drosophila brown gene.** In *CSHSQB; DNA and chromosomes*, pp. 577-584.
- Henikoff, S.**, and **Meneely, P.M.** (1993) **Unwinding dosage compensation.** *Cell* 72, 1-2.
- Henikoff, S.**, **Loughney, K.**, and **Dreesen, T.D.** (1993) **The enigma of dominant position-effect variegation in Drosophila.** In *"The Chromosome"* (J.D. Heslop-Harrison & R.B. Flavell, eds.) pp. 183-196, BIOS, Oxford, UK.
- Henikoff, S.** (1992) **Position effect and related phenomena.** *Current opinion in genetics & development* 2, 907-912.
- Christensen, A.C.**, and **Henikoff, S.** (1992) **Fact and fiction in alignment.** *Nature* 358, 271-271.
- Henikoff, S.** (1991) **Playing with blocks - some pitfalls of forcing multiple alignments.** *New Biologist* 3, 1148-1154.
- Henikoff, S.**, **Wallace, J.C.**, and **Brown, J.P.** (1990) **Finding protein similarities with nucleotide-sequence databases.** *Methods in Enzymology* 183, 111-132.

Henikoff, S. (1987) **Unidirectional digestion with exonuclease III in DNA-sequence analysis.**
Methods in Enzymology 155, 156-165.