

CURRICULUM VITAE: Steven Henikoff

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

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Education

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

1971-77 Harvard University, Cambridge, Massachusetts. PhD in Biochemistry and Molecular Biology. Dr. M. 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*, Dr. C. Laird, advisor, Leukemia Society of America fellow.

Professional Experience

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

1981- University of Washington, Seattle. Affiliate faculty in Genetics/Genome Sciences.

1985-88 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
Transcriptional regulation
Centromere evolution
Epigenomic technologies

Ongoing Funding

Howard Hughes Medical Institute	Investigator	04/1/1990 – 10/31/2021
National Institutes of Health	PI (R01 1R01HG010492)	04/19/2019 – 01/31/2024
Chan-Zuckerberg Initiative	PI (HCA Seed Network)	08/1/2019 – 07/31/2022

Honors and awards

2021 Keynote speaker, Epicypther2021, Cancun, Mexico

2021 Keynote speaker, NIEHS Retreat, Research Triangle Park, NC

2021 Keynote speaker, Cambridge Epigenetics Club Summer Symposium, Cambridge, UK

2020 Keynote speaker, 4th Int. Conf. on Epigenetics & Bioengineering, Raleigh, NC

2020 Keynote speaker, Cold Spring Harbor Systems Biology Symposium Asia, Suzhou, China

2019 Keynote speaker, NIH/NHGRI ENCODE User's Meeting, Seattle, WA

2018 Keynote speaker, Yeast Transcription Meeting, Costa Brava, Spain

2018 Konrad Bloch Lecture, Harvard University, Cambridge, MA

2018 Keynote speaker, Cold Spring Harbor Systems Biology Symposium, NY

2017 Gast Lecture, Baylor College of Medicine, Houston, TX
 2016 Widom Lecture, Northwestern University, Evanston, IL
 2016 Keynote speaker, Abcam Chromatin Conference, Copenhagen, Denmark
 2015 Genetics Society of America 2015 Medal
 2015 Glaser Seminars, Florida International University, Miami
 2015 Elected Chair, Biological Sciences Section, American Association for the Advancement of Science
 2014 Keynote speaker, Mizzou Epigenetics Day, Columbia, MO
 2014 Keynote speaker, Centromere Gordon Conference, Waltham, MA
 2014 Keynote speaker, ASBMB Transcription Symposium, Snowbird, UT
 2014 Keynote speaker, Plant Genomic Stability and Change Conference, Asilomar, CA
 2014 Keynote speaker, Oslo Epigenetics Symposium, Oslo, Norway
 2012- Elected Fellow, American Association for the Advancement of Science
 2012 Keynote, FASEB Biological Methylation Meeting, Snowmass, CO
 2012 Keynote speaker, Genetics Society of Israel, Rehovot, Israel
 2012 Keynote speaker, 23rd Annual Arabidopsis Conference, Vienna, Austria
 2012 Keynote speaker, Cold Spring Harbor Epigenetics Symposium, Suzhou, China
 2012 Penn State Marker Lectures, University Park, PA
 2011 Mendel Lecture, Masaryk University, Brno, Czech Republic
 2011 Max Birnstiel Lecture, IMP, Vienna, Austria
 2011 Keynote speaker, IEEE Bioinformatics & Bioengineering Symposium, Atlanta, GA
 2011 Dayhoff Lecture, Georgia Tech Genomics Symposium, Atlanta, GA
 2011 Keynote speaker, UCSD Genetics Retreat, San Diego, CA
 2010 Keynote speaker, Molecular Biology Retreat, University of Iowa, Ames, IA
 2010 Meeting Summary, 75th Cold Spring Harbor Symposium: Dynamic Organization of Nuclear Function
 2010 Keynote speaker, Cold Spring Harbor Systems Biology Symposium, NY
 2009 Novum Lecture, Karolinska Institute, Stockholm, Sweden
 2009 Keynote speaker, Plant Molecular Biology Symposium, Ohio State University
 2006 Keynote speaker, Abcam Symposium on Chromatin Structure and Function, Punta Cana, Dominican Republic
 2005- Elected Member, US National Academy of Sciences
 2005 Keynote speaker, Chicago Chromatin Club
 2004 Keynote speaker, EMBL Transcription Meeting, Heidelberg, Germany
 2003 Keynote speaker, FEBS Chromatin Workshop, Wageningen, Netherlands
 2003 Keynote speaker, Chromatin Assembly Symposium, Munich, Germany
 2003 Keynote speaker, University of Missouri Symposium, Columbia, MO
 2001 Keynote speaker, 12th International Arabidopsis Conference, Madison, WI

Selected editorial and advisory activities

2021- 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- 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 finalists 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- 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- 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 (since 2000)

Bas van Steensel, postdoctoral fellow 1998-2000. Currently, Group Leader, NKI, Amsterdam, Netherlands.

Claire M. McCallum, graduate student 1996-2002. Currently, Research Scientist, Arcadia Biosciences, Inc., Davis, CA.

Kami Ahmad, ACS postdoctoral fellow 1996-2002. Currently, Principal Investigator, FHCRC.

James F. Smothers, NIH postdoctoral fellow 1998-2001. Currently, Research Scientist, Amgen Corporation, Cambridge, MA.

Amy L. Holmes, postdoctoral fellow 1998-2000.
Danielle Vermaak, Damon Runyon postdoctoral fellow 1999-2003.
Pauline Ng, NSF and DOE graduate student 1999-2002. Currently, Group Leader, Genome Institute of Singapore.
Harmit S. Malik, Helen Hay Whitney postdoctoral fellow 1999-2003. Currently, Member, FHRC, HHMI Investigator.
Trenton Colbert, postdoctoral fellow 2000-2001. Currently, Research Scientist, Arcadia Biosciences, Inc. Davis CA.
Bradley Till, postdoctoral fellow 2000-2002, Staff scientist 2002-2007. Currently, Bioinformatics Specialist, U. California, Davis.
Jennifer Cooper, postdoctoral fellow 2001-2009. Currently, Assistant Professor, University of Akron, Akron OH.
Erin McKittrick, HHMI graduate student 2002-2005.
Robert Tran, postdoctoral fellow 2002-2006. Currently, Senior Scientist, U. California, Davis.
Yoshiko Mito, graduate student 2003-2007. Currently: Assistant Professor, Icahn School of Medicine at Mount Sinai
Daniel Zilberman, Leukemia and Lymphoma Society postdoctoral fellow 2004-2007. Currently, Professor, John Innes Centre, UK.
Melissa Conerly, graduate student 2003-2010. Currently Scientist, Seattle Genetics.
Yamini Dalal, postdoctoral fellow 2003-2008. Currently 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, Currently Research Scientist, University of Washington.
Takehito Furuyama, NIH postdoctoral fellow 2003-2008.
Siew-Loon Ooi, Damon Runyon postdoctoral fellow 2004-2009. Currently: Scientist, Department of Genetics, DSM, Delft, Netherlands.
Mary Gehring, Life Sciences Research Foundation postdoctoral fellow 2005-2010. Currently, Associate Professor, MIT and Member, Whitehead Institute.
Martin Riedel, Visiting Graduate Student 2007-2008.
Roger Deal, NIH post-doctoral fellow 2007-2011. Currently: Associate Professor, Emory University.
Friedemann Loos, Fulbright Scholarship Student 2008-2009.
Florian Steiner, Swiss National Science Foundation postdoctoral fellow 2008-2014. Currently: Assistant Professor, University of Geneva.
Sheila Teves, NSF graduate student, Weintraub Awardee 2009-2013. Currently: Assistant Professor, University of British Columbia.
Christopher Weber, NSF graduate student 2009-2014. Currently: Postdoctoral fellow, Stanford University
Erika Wolff, post-doctoral fellow 2009-2010. Currently, Research Scientist, University of Washington
Kristina Krassovsky, NSF graduate student 2009-2014. Currently: Postdoctoral fellow, UC Berkeley
John Latham, postdoctoral fellow 2011-2012. Currently, Senior Manager, Guardian Health, Inc.
Fan Yang, postdoctoral fellow 2011-2014
Gabriel Zentner, postdoctoral fellow 2011-2015. Currently, Assistant Professor, Indiana University.
Peter Skene, Damon Runyon Foundation postdoctoral fellow 2011-2017. Currently: Director of Molecular Biology and Biochemistry, Allen Institute for Immunology.
Anna Drinnenberg, Jane Coffin Childs Foundation postdoctoral fellow 2012-2015. Currently: Group Leader, Marie Curie Institute, Paris.
Srinivas Ramachandran, postdoctoral fellow 2012-2017. Currently: Assistant Professor, University of Colorado, Denver.
Siva Kasinathan, MSTP graduate student 2012-2017, Currently Resident, Stanford University.
Jitendra Thakur, postdoctoral fellow 2013-2020. Currently: Assistant Professor, Emory University.
Vuong Tran, postdoctoral fellow 2015-2016. Currently: Senior Scientist, Parse Biosciences, Inc.
Hatice Seda Kaya, postdoctoral fellow 2016-2019. Currently: Scholar, Altius Institute
Jay Sarthy, Damon Runyon/Sohn Pediatric Cancer Research Fellow 2017-

Sandipan Brahma, NIH K99/R00 postdoctoral fellow 2017-
 Michael Meers, NIH K99/R00 postdoctoral fellow 2017-
 Derek Janssens, postdoctoral fellow 2017-
 Steven Wu, graduate student 2018-
 James Anderson, graduate student 2019-
 Matthew Wooten, postdoctoral fellow 2020-
 Nadiya Khyzha, postdoctoral fellow 2020-
 Cassidy Danyko, graduate student 2021-

Invited Presentations (since 2015)

1/26-30/15	Florida International University (Glaser lectures)	Miami, FL
3/12/15	University of Colorado Health Sciences	Denver, CO
3/30-4/3/15	Keystone Epigenomics meeting	Keystone, CO
4/14/15	University of Kentucky	Lexington, KY
4/15/15	University of Michigan	Ann Arbor, MI
4/17/15	Michigan State University	East Lansing, MI
9/8/15	University of Geneva	Geneva, Switzerland
9/10/15	Max Planck Institute	Dresden, Germany
9/24-27/15	AACR Chromatin and Epigenetics in Cancer	Atlanta, GA
9/30/15	Oregon State University	Corvallis, OR
10/15/15	University of Southern California	Los Angeles, CA
11/9/15	University of Cambridge	Cambridge, UK
12/5-6/15	American Society of Hematology Genomics Symposium	Orlando, FL
3/17-18/16	Universidad Nacional Autonoma de Mexico Symposium	Mexico City, MX
3/29/16	Stanley Center, Broad Institute	Cambridge, MA
3/31/16	National Institutes of Health	Bethesda, MD
4/13/16	University of Wisconsin	Madison, WI
4/29/16	Memorial Sloan-Kettering Cancer Research Center	New York, NY
5/9-13/16	Cold Spring Harbor Asia Epigenetics Meeting	Suzhou, China
5/19/16	Northwestern University	Evanston, IL
6/9/16	Johns Hopkins University	Baltimore, MD
7/24-29/16	Centromere Biology Gordon Research Conference	West Dover, VT
9/13-17/16	Cold Spring Harbor Epigenetics and Chromatin Meeting	Cold Spring, NY
9/27/16	MD Anderson Cancer Research Center	Houston, TX
10/3/16	IRCM Montreal	Montreal, QC
10/19-21/16	Abcam Chromatin Conference (keynote)	Copenhagen, Denmark
11/16/16	Northwestern University Medical School	Chicago, IL
11/17/16	University of Chicago	Chicago, IL
2/21/17	University of Massachusetts Medical School	Worcester, MA
3/8/17	University of California, San Francisco	San Francisco, CA
3/27/17	University of Florida	Gainesville, FL
3/28/17	Emory University	Atlanta, GA
4/1/17	AACR Meeting Educational Session	Washington, DC
4/6/17	University of California, Los Angeles	Los Angeles, CA
5/8/2017	Northwestern University PS-OC Symposium	Evanston, IL
5/31-6/4/17	CSHL Symposium on Chromosome Segregation	Cold Spring H., NY
6/19-20/17	MPI Epigenetics Symposium	Berlin, Germany
7/13-17.17	Society for Developmental Biology Meeting	Minneapolis, MN
8/30-9/1/17	EMBO Nucleosome Symposium	Heidelberg, Germany
9/7-8/17	EMBO Histone variants workshop	Munich, Germany
10/10/17	Ohio State University	Columbus, OH
10/27/17	Cornell University	Ithaca, NY
10/31/17	Pasteur Institute	Paris, France
11/21-22/17	National Institute of Genetics	Mishima, Japan

11/24/17	Chinese Academy of Sciences	Beijing, China
1/18/17	Baylor College of Medicine	Houston, TX
3/20-23/17	Cold Spring Harbor Systems Biology Meeting	Cold Spring H., NY
4/14/18	AACR Meeting Educational Session	Chicago, IL
4/19/18	Harvard University	Cambridge, MA
6/9-14/18	Yeast Transcription Meeting	Costa Brava, Spain
7/22-27/18	Gordon Research Conference – Chromatin	Sunday River, ME
9/11-15/18	Cold Spring Harbor Chromatin & Epigenetics Meeting	Cold Spring H., NY
10/4-6/18	Klenk Symposium	Cologne, Germany
10/8/18	University of Copenhagen	Copenhagen, Denmark
10/9/18	Erasmus University	Rotterdam, Netherlands
10/10/18	National Cancer Institute (NKI)	Amsterdam, Netherlands
10/11-12/18	Grosveld Symposium	Rotterdam, Netherlands
11/4-7/18	ChromEvo Workshop	Sussex, England
11/30/18	Simpson Querrey Epigenetics Symposium	Chicago, IL
12/9-11/18	Weizmann Institute Graduate Student Symposium	Rehovot, Israel
1/9/19	University of Arizona	Tucson, AZ
1/31/19	University of California, San Diego	La Jolla, CA
3/7/19	Washington University	St. Louis, MO
5/1-4/19	EMBL Chromatin & Epigenetics Meeting	Heidelberg, Germany
5/23/19	National Institutes of Aging	Baltimore, MD
11/21/19	Vanderbilt University	Nashville, TN
10/18/19	University of Zurich	Zurich, Switzerland
11/10-12/19	National Institute of Genetics	Mishima, Japan
1/21/20	California Institute of Technology	Pasadena, CA
1/28/20	Baylor College of Medicine	Houston, TX
2/10-12/20	NAS Functional Genomics Workshop	Washington, DC
2/13/20	Benaroya Institute	Seattle, WA
5/20/20	University of California, Berkeley	Virtual
5/14/20	Chan-Zuckerberg Seed Network	Virtual
5/27/20	Stanford University	Virtual
6/11/20	Max Planck Göttingen	Virtual
6/12/20	San Diego Chromatin Club	Virtual
7/16/20	Meiosis in Quarantine	Virtual
8/10/20	CCMB (Hyderabad, India)	Virtual
8/20/20	Social DNAing	Virtual
8/27-9/20	EMBL Transcription (Heidelberg, Germany)	Virtual
8/24/20	University of Pittsburgh	Virtual
9/2/20	Max Planck Berlin	Virtual
9/14/20	Mayo Clinic (Rochester, MN)	Virtual
9/30/20	Fox-Chase Cancer Center (Philadelphia, PA)	Virtual
10/1/20	Yale University (New Haven, CT)	Virtual
10/8/20	EpiBio 2020 (Raleigh, NC)	Virtual
11/18/20	Cornell-Weill Medical School	Virtual
12/7-11/20	IAS Focused Meeting (Hong Kong)	Virtual
2/16/21	Queen Mary University (London)	Virtual
3/1/21	Lahore University	Virtual
3/12/21	Harvard Medical School	Virtual
3/27/21	Istanbul University	Virtual
4/6/21	University of Chicago	Virtual
4/23/21	University of California, Riverside	Virtual
5/11/21	Chromatin and Epigenetics biweekly series, China	Virtual
6/15/21	NIH/NIAMS Retreat	Virtual
7/14/21	Cambridge Epigenetics Club	Virtual

9/9/21	Science in Asia, AAAS, Beijing	Virtual
9/14/21	KAUST, Saudi Arabia	Virtual
9/20/21	Broad Institute, Cambridge, MA	Virtual
10/12/21	Brigham & Women's Hospital, Boston, MA	Virtual
10/15-16/21	Peking University, Beijing	Virtual
10/22/21	NIEHS, Research Triangle, NC	Virtual
11/7-12/21	Epicypther2021	Clearwater, FL

Publications (384 total. Reprints at <http://research.fredhutch.org/henikoff/en/publications.html>)
<https://pubmed.ncbi.nlm.nih.gov/?term=henikoff+s&sort=date>

Peer reviewed research articles

- Janssens DH, Meers MP, Wu SJ, Babaeva E, Meshinchi S, Sarthy JF, Ahmad K, Henikoff S. (2020) **Automated CUT&Tag profiling of chromatin heterogeneity in mixed-lineage leukemia.** Nature Genetics, In press.
- 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., Berezikov, 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-rough 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.
- Petrokovski, 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 Petrokovski, 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., Fechtel, 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

- 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., 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.

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.

Csank, 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., Pietrovski, 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 de novo synthesis.** *Bioessays* 6, 8-13.

Other publications (selected)

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* (in press).
- 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. Remarkable evolutionary plasticity of centromeric chromatin. *Cold Spring Harb Symp Quant Biol*. 2017 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 Deregulation 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, Grealley & 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.