

**1. PERSONAL DATA**

Steven Henikoff  
Place of Birth: Chicago, IL

**2. EDUCATION**

1964-1968 BS, University of Chicago, Chicago, IL  
1971-1977 PhD, Harvard University, Cambridge, MA

**3. POSTGRADUATE TRAINING**

1977-1980 Postdoctoral Fellow, University of Washington, Seattle, WA

**4. FACULTY POSITIONS HELD**

1981-1985 Assistant Member, Fred Hutchinson Cancer Research Center, Seattle WA  
1981- Affiliate Faculty, University of Washington, Seattle WA  
1985-1988 Associate Member, Fred Hutchinson Cancer Research Center, Seattle WA  
1988- Member, Fred Hutchinson Cancer Research Center, Seattle WA  
1990- Investigator, Howard Hughes Medical Institute, Chevy Chase, MD

**5. HONORS**

1968 National Science Foundation Graduate Student Fellowship  
1969-1971 National Defense Service Medal, US Army  
1978-1981 Leukemia Society of America Postdoctoral Fellowship  
2005- Member, US National Academy of Sciences  
2012 Fellow, American Association for the Advancement of Science  
2015 Genetics Society of America Medal  
2015 Washington State Academy of Sciences  
2022 Member, American Academy of Arts and Sciences

**6. RESEARCH FUNDING**

**A. Active**

2021-2027 Sponsor: Howard Hughes Medical Institute (HHMI)  
Title: *Henikoff Lab Support*  
Total Costs: \$6,464,253  
Role: Investigator

2024-2026 Sponsor: Stuart and Molly Sloan Precision Oncology Institute  
Title: *Affordable precision oncology based on FFPE-CUTAC*  
Total Costs: \$440,000  
Role: Principal Investigator

**B. Pending**

2025-2027 Sponsor: Andy Hill CARE Fund  
Title: *Affordable precision oncology based on FFPE-CUTAC*  
Total Costs: \$592,886  
Role: Principal Investigator

2025-2030 Sponsor: National Cancer Institute (NCI)  
Title: *Epigenetic monoallelic expression in human brain and breast cancers*  
Total Costs: \$439,630  
Role: Subaward Investigator

2025-2030 Sponsor: National Human Genome Research Institute (NHGRI)

Title: *Epigenomic analysis of formalin-fixed paraffin-embedded samples by CUT&Tag*

Total Costs: \$4,391,580

Role: Principal Investigator

### C. Past (last 5 years)

- 2017-2019      Sponsor: UC San Diego (NCI)  
Title: The Organizational Hub and Web Portal for the 4D Nucleosome Network  
Total Costs: \$920,710  
Role: Subaward Investigator
- 2016-2021      Sponsor: Howard Hughes Medical Institute (HHMI)  
Title: *Henikoff Lab Support*  
Total Costs: \$5,217,805  
Role: Investigator
- 2019-2023      Sponsor: Chan Zuckerberg Initiative  
Title: Single-cell chromatin profiling by high efficiency tethered integrase  
Total Costs: \$999,900  
Role: Principal Investigator
- 2022-2023      Sponsor: Chan Zuckerberg Initiative  
Title: Single-cell chromatin profiling by high efficiency tethered integrase (Supplement)  
Total Costs: \$293,341  
Role: Principal Investigator
- 2022-2023      Sponsor: Various  
Title: Koss Shared Resources Funding Henikoff Lab  
Total Costs: \$8,800  
Role: Principal Investigator
- 2019-2024      Sponsor: National Human Genome Research Institute (NHGRI)  
Title: Epigenomic profiling of complex tissues with single-cell CUT&RUN  
Total Costs: \$5,217,805  
Role: Principal Investigator

## 7. BIBLIOGRAPHY

### A. Manuscripts

- 1: **Henikoff S**, Heywood J, Meselson M. Orientation of repeating units in *Xenopus* chromosomal ribosomal DNA: A test of a stochastic model for maintaining intraspecies homogeneity. *J Mol Biol.* 1974 May 25;85(3):445-50. doi: 10.1016/0022-2836(74)90443-4. PMID: 22003577.
- 2: McKenzie SL, **Henikoff S**, Meselson M. Localization of RNA from heat-induced polysomes at puff sites in *Drosophila melanogaster*. *Proc Natl Acad Sci U S A.* 1975 Mar;72(3):1117-21. doi: 10.1073/pnas.72.3.1117. PMID: 805422; PMCID: PMC432477.
- 3: **Henikoff S**, Meselson M. Transcription at two heat shock loci in *Drosophila*. *Cell.* 1977 Oct;12(2):441-51. doi: 10.1016/0092-8674(77)90120-9. PMID: 410501.

- 4: **Henikoff S**. Position Effects and Variegation Enhancers in an Autosomal Region of *DROSOPHILA MELANOGASTER*. *Genetics*. 1979 Sep;93(1):105-15. doi: 10.1093/genetics/93.1.105. PMID: 17248959; PMCID: PMC1217818.
- 5: **Henikoff S**. Position-effect variegation and chromosome structure of a heat shock puff in *Drosophila*. *Chromosoma*. 1981;83(3):381-93. doi: 10.1007/BF00327360. PMID: 6168446.
- 6: **Henikoff S**, Tatchell K, Hall BD, Nasmyth KA. Isolation of a gene from *Drosophila* by complementation in yeast. *Nature*. 1981 Jan 1;289(5793):33-7. doi: 10.1038/289033a0. PMID: 6256646.
- 7: **Henikoff S**, Furlong CE. Sequence of a *Drosophila* DNA segment that functions in *Saccharomyces cerevisiae* and its regulation by a yeast promoter. *Nucleic Acids Res*. 1983 Feb 11;11(3):789-800. doi: 10.1093/nar/11.3.789. PMID: 6300768; PMCID: PMC325753.
- 8: **Henikoff S**, Kelly JD, Cohen EH. Transcription terminates in yeast distal to a control sequence. *Cell*. 1983 Jun;33(2):607-14. doi: 10.1016/0092-8674(83)90441-5. PMID: 6305514.
- 9: **Henikoff S**. Cloning exons of mapping of transcription: characterization of the *Drosophila melanogaster* alcohol dehydrogenase gene. *Nucleic Acids Res*. 1983 Jul 25;11(14):4735-52. doi: 10.1093/nar/11.14.4735. PMID: 6410356; PMCID: PMC326083.
- 10: **Henikoff S**, Sloan JS, Kelly JD. A *Drosophila* metabolic gene transcript is alternatively processed. *Cell*. 1983 Sep;34(2):405-14. doi: 10.1016/0092-8674(83)90374-4. PMID: 6413075.
- 11: **Henikoff S**. Unidirectional digestion with exonuclease III creates targeted breakpoints for DNA sequencing. *Gene*. 1984 Jun;28(3):351-9. doi: 10.1016/0378-1119(84)90153-7. PMID: 6235151.
- 12: **Henikoff S**, Cohen EH. Sequences responsible for transcription termination on a gene segment in *Saccharomyces cerevisiae*. *Mol Cell Biol*. 1984 Aug;4(8):1515-20. doi: 10.1128/mcb.4.8.1515-1520.1984. PMID: 6436686; PMCID: PMC368942.
- 13: Daubner SC, Schrimsher JL, Schendel FJ, Young M, **Henikoff S**, Patterson D, Stubbe J, Benkovic SJ. A multifunctional protein possessing glycinamide ribonucleotide synthetase, glycinamide ribonucleotide transformylase, and aminoimidazole ribonucleotide synthetase activities in de novo purine biosynthesis. *Biochemistry*. 1985 Dec 3;24(25):7059-62. doi: 10.1021/bi00346a006. PMID: 4084560.
- \*14: **Henikoff S**, Keene MA, Fechtel K, Fristrom JW. Gene within a gene: nested *Drosophila* genes encode unrelated proteins on opposite DNA strands. *Cell*. 1986 Jan 17;44(1):33-42. doi: 10.1016/0092-8674(86)90482-4. PMID: 3079672.
- 15: **Henikoff S**, Keene MA, Sloan JS, Bleskan J, Hards R, Patterson D. Multiple purine pathway enzyme activities are encoded at a single genetic locus in *Drosophila*. *Proc Natl Acad Sci U S A*. 1986 Feb;83(3):720-4. doi: 10.1073/pnas.83.3.720. PMID: 3080748; PMCID: PMC322936.
- 16: **Henikoff S**, Nash D, Hards R, Bleskan J, Woolford JF, Naguib F, Patterson D. Two *Drosophila melanogaster* mutations block successive steps of de novo purine synthesis. *Proc Natl Acad Sci U S A*. 1986 Jun;83(11):3919-23. doi: 10.1073/pnas.83.11.3919. PMID: 3086869; PMCID: PMC323636.
- 17: Eghtedarzadeh MK, **Henikoff S**. Use of oligonucleotides to generate large deletions. *Nucleic Acids Res*. 1986 Jun 25;14(12):5115. doi: 10.1093/nar/14.12.5115. PMID: 3460029; PMCID: PMC311518.

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- 26: Johnson D, **Henikoff S**. A moveable 5' splice site in adenine phosphoribosyltransferase genes of *Drosophila* species. *Mol Cell Biol.* 1989 May;9(5):2220-3. doi: 10.1128/mcb.9.5.2220-2223.1989. PMID: 2501662; PMCID: PMC363017.
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- 46: **Henikoff S**. Position effect and related phenomena. *Curr Opin Genet Dev.* 1992 Dec;2(6):907-12. doi: 10.1016/s0959-437x(05)80114-5. PMID: 1477535.
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- 61: **Henikoff S**. Comparative methods for identifying functional domains in protein sequences. *Biotechnol Annu Rev.* 1995;1:129-47. doi: 10.1016/s1387-2656(08)70050-4. PMID: 9704087.
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## B. Book chapters

Listed in Publications (Manuscripts)

## C. Published Books, Video, Software, etc.

### Books:

1. Armstrong, S, **Henikoff, S**, Vakoc, C. Chromatin Deregulation in Cancer. Cold Spring Harbor Laboratory Press (2017), [https://www.cshlpress.com/default.tpl?cart=173567417848607067&fromlink=T&linkaction=full&linksortby=oop\\_title&--eqSKUdatarq=1095](https://www.cshlpress.com/default.tpl?cart=173567417848607067&fromlink=T&linkaction=full&linksortby=oop_title&--eqSKUdatarq=1095), ISBN: 978-1-621821-40-3.

### Public Websites:

1. CUT&Tag <https://www.protocols.io/view/bench-top-cut-amp-tag-bcuihw6> Monitored by Steven Henikoff.
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5. CUT&Tag Data Processing and Analysis Tutorial <https://www.protocols.io/view/cut-amp-tag-data-processing-and-analysistutorial-bjk2kkye> Monitored by Ye Zheng.
6. RT&Tag (Reverse Transcribe & Tagment) <https://www.protocols.io/view/rt-amp-tag-reverse-transcribe-amp-tagment-x54v9jyjqg3e/v1> Monitored by Nadiya Khyzha
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10. AutoCUT&RUN <https://www.protocols.io/view/autocut-run-genome-wide-profiling-of-chromatin-pro-ufetjje/metrics> Monitored by Derek Janssens.
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12. Peak calling by Sparse Enrichment Analysis for CUT&RUN (SEACR) <https://seacr.fredhutch.org/> Maintained by Daniel Tenenbaum.

## D. Other Publications

N/A

## E. Manuscripts Under Review

1. Steven Henikoff, Ye Zheng and Kami Ahmad "Mitotic errors do not explain most aneuploidies in cancer" Submitted to Trends in Genetics 8/25/2024.
2. Kami Ahmad, Matthew Wooten, Brittany N Takushi, Velinda Vidaurre, Xin Chen & Steven Henikoff "Histone H4 limits transcription of the histone locus in Drosophila" Submitted to Plos Biology: 11/26/24.
3. Nadiya Khyzha, Kami Ahmad and Steven Henikoff "Profiling transcriptome composition and dynamics within nuclear compartments using SLAM-RT&Tag" Submitted to Cell: 7/15/2024, transferred to Molecular Cell: 12/9/2024.
4. Weifang Wu, Kami Ahmad and Steven Henikoff "Chromatin-bound U2AF2 splicing factor ensures exon inclusion" Submitted to Cell: 9/24/2024, transferred to Molecular Cell: 1/8/2025.
5. Steven Henikoff, Ye Zheng, Ronald M. Parana, Yiling Xu, Jacob E. Greene, Jorja G. Henikoff, Zachary R. Russell, Frank Szulzewsky, H. Nayanga Thirimanne, Sita Kugel, Eric C. Holland & Kami Ahmad "RNA Polymerase II at histone genes predicts outcome in human cancer" Submitted to Science: 8/2/2024, Provisionally accepted: 1/10/2025.

## 8. OUTREACH

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 >700,000 views and ~4500 questions and answers through 2024, 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://doi.org/10.1101/2020.04.15.043083>, 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>.

## 9. PROFESSIONAL ORGANIZATIONS (last 5 years)

1981-	Genetics Society of America
1981-	American Association for the Advancement of Science
2001-	American Society of Plant Biologists
2011-	American Society for Microbiology

## 10. EDUCATION AND TRAINING RESPONSIBILITIES

### A. Didactic Teaching (last 5 years)

2024- MCB 517 Epigenetics and Epigenomics, University of Washington 100%

### B. Thesis Committee Membership (last 5 years)

All UW except as noted and PhD or PhD part of MSTP program

Chair:  
2018-2022 Steven Wu (Bioengineering)

2019-2023	James Anderson (MCB)
2022-2024	Soyeon Showman (MCB)
2021-	Cassidy Danyko, Predoctoral
2022-	Jacob Greene, Predoctoral
Member:	
2017-2021	Sanjay Srivatsan (Genome Sciences)
2017-2021	Hannah Arbach (MCB)
2018-2021	Nick Pease (MCB)
2018-2023	Emma Hoppe (MCB)
2023	Yihao Yang (Rockefeller University – served on PhD thesis reading committee)
2020-2024	Jihoon Lee (MCB)
2020-	Jon Chu (MCB)
2021-	Scott Best (MCB)
2021-	Chase Suiter (MCB)
2021-	Morgan Hamm (Genome Sciences)
2022-	Lucy Kwiatkowski (Microbiology)
2022-	Jobelle Peralta (MCB)
2023-	Elliot Swanson (Genome Sciences)
2024-	Aiden Keith (Genome Sciences)

### C. Advising/Mentorship (last 5 years)

2016-2019	Hatice Kaya Okur, Postdoctoral, 2x per week
2017-2019	Jay Sarthy, Postdoctoral & Research Associate, 2x per week
2013-2020	Jitendra Thakur, Postdoctoral, 2x per week
2018-2022	Steven Wu, Predoctoral, 2x per week
2017-2022	Michael Meers, Postdoctoral, 2x per week
2017-2023	Sandipan Brahma, Postdoctoral, 2x per week
2019-2023	James Anderson, Predoctoral, 2x per week
2017-2024	Derek Janssens, Postdoctoral, 2x per week
2022-2024	Soyeon Showman, Predoctoral, 2x per week
2023-2024	Ye Zheng, Postdoctoral, 2x per week
2024	Kevin Nguyen, Summer Intern, 2x per week
2020-	Matthew Wooten, Postdoctoral, 2x per week
2020-	Nadiya Kyhzhza, Postdoctoral, 2x per week
2021-	Cassidy Danyko, Predoctoral, 2x per week
2022-	Jacob Greene, Predoctoral, 2x per week
2022-	Jobelle Peralta, Advisee, monthly

### D. Curriculum and Training Program Development (last 5 years)

2024-	MCB 517 Epigenetics and Epigenomics, University of Washington 100%
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### E. Other N/A

## 11. EDITORIAL RESPONSIBILITIES

### A. Editorial Boards (last 5 years)

1998-	<i>Trends in Genetics</i> Editorial Board
2005-	<i>Current Opinion in Genetics and Development</i> Editorial Board
2010-	<i>Genome Biology</i> , Editorial Advisory Board
2014-	<i>Genome Research</i> , Editorial Board
2021-	Frontiers in Epigenetics and Epigenomics, Field Chief Editor

### B. Ad hoc Reviewing Responsibilities

2020- On average ~1 paper per week for numerous top- and middle-tier journals from major publishers.

## 12. SPECIAL RESPONSIBILITIES AND SERVICE (last 5 years)

### A. International

2021-23 Scientific Advisory Board, Center for Protein Research, U. of Copenhagen, Denmark

### B. National

2020 NIH GCAT Grant Review Panel

2020 Panel Member Functional Genomics Workshop, NASEM Board on Life Sciences

2021 NIH Blueprint for Neuroscience Research Grant Review Panel

2022 NIH Fellowship Grant Review Panel

2024 External Advisory Committee, Michael Smith Laboratory, University of British Columbia

2024- NIH Fellowship Grant Review Panel

## 13. OTHER

### A. Invited External Lectures (last 5 years)

- 2025 Histone overexpression in cancer, University of Massachusetts Medical School, Worcester, MA
- 2025 Histone overexpression in cancer, Biology and Neuroscience, Brandeis University
- 2024 Histone overexpression in cancer, Boston Children's Hospital, Harvard Medical School, Boston, MA
- 2024 Epigenomic profiling for personalized medicine, University of Michigan, Ann Arbor, MI (virtual)
- 2024 CUT&RUN and CUT&Tag, Helmholtz Summer School on Chromatin Biology, Munich, Germany (virtual)
- 2024 Genome-wide mapping of chromatin dynamics in situ, Gary Stormo Symposium, Washington University School of Medicine
- 2024 Genome-wide mapping of chromatin dynamics in situ, Johns Hopkins Institute for Cell Engineering Lecture Series, Johns Hopkins Medical Institute
- 2024 Genome-wide mapping of chromatin dynamics in situ, Center for Excellence in Chromosome Biology Symposium, National Cancer Institute
- 2024 Genome-wide mapping of chromatin dynamics in situ, University of Missouri
- 2024 Cancer from a chromatin perspective, Seminar, University of Nebraska Medical Center
- 2024 Genome-wide mapping of chromatin dynamics in situ, BMBGSA Symposium, Oklahoma State University
- 2024 Genome-wide mapping of chromatin dynamics in situ, Epigenetics Symposium, Fox-Chase Cancer Center
- 2024 Epigenomics for personalized medicine, Signaling and Cellular Regulation Symposium, University of Colorado
- 2023 Genome-wide mapping of protein-DNA interaction dynamics, Duke Distinguished Lecturer Series in Genetics and Genomics, Duke University
- 2023 CUT&RUN and CUT&Tag, Helmholtz Summer School on Chromatin Biology, Munich, Germany (virtual)
- 2023 Genome-wide mapping of chromatin dynamics in situ, Potter Lecture, Cincinnati Children's Hospital
- 2023 Genome-wide mapping of protein-DNA interaction dynamics, Summer Symposium in Molecular Biology and Epigenetic Regulation of Transcription, Penn State University

- 2023 Genome-wide mapping of protein-DNA interaction dynamics, Department of Biochemistry and Molecular Genetics, University of Illinois (virtual)
- 2023 Genome-wide mapping of protein-DNA interaction dynamics, Gordon Research Conference - Genome Architecture in Cell Fate and Disease, Ventura, CA
- 2023 Genome-wide mapping of protein-DNA interaction dynamics, Frontiers in Biology Seminar Series, Stanford University
- 2023 Genome-wide mapping of chromatin dynamics, EMBL Conference: Chromatin and Epigenetics, Heidelberg, Germany
- 2023 Genome-wide mapping of chromatin dynamics, C4 Symposium, Seattle Children's Research Institute
- 2023 Genome-wide mapping of protein-DNA interaction dynamics, Genetics and Genomics, Duke University
- 2023 Genome-wide mapping of protein-DNA interaction dynamics, Genetics and Development, Columbia University
- 2023 Genome-wide mapping of protein-DNA interaction dynamics, University of Michigan RNA Biomedicine Symposium
- 2023 Revisiting "open" chromatin, HHMI Investigators meeting, Chevy Chase, MD
- 2023 Genome-wide mapping of protein-DNA interaction dynamics, All-Ireland Chromatin Club (virtual)
- 2023 Genome-wide mapping of protein-DNA interaction dynamics, ERATO Symposium, University of Tokyo (virtual)
- 2022 Genome-wide mapping of protein-DNA interaction dynamics, Oklahoma Medical Research Foundation, Oklahoma City, OK
- 2022 New strategies for antibody-directed in situ chromatin profiling, Single Cell Omics Beijing 2022, Peking University (virtual)
- 2022 Genome-wide mapping of protein-DNA interactions, Genome Sciences, University of Virginia (virtual)
- 2022 Genome-wide mapping of protein-DNA interaction dynamics, Chemical Biology and Therapeutics, St. Jude Children's Research Hospital (virtual)
- 2022 Genome-wide mapping of protein-DNA interaction dynamics. Interplay between Epigenetic Regulation and Genome Stability Symposium, ASBMB Seattle
- 2022 Virus-encoded histones, Chromatin Control of Viral Infection Symposium, National Institutes of Health (virtual)
- 2022 CUT&RUN and CUT&Tag, Helmholtz Summer School on Chromatin Biology, Munich, Germany (virtual)
- 2022 Genome-wide mapping of chromatin dynamics, Pharmacology, University of Washington (virtual)
- 2022 Genome-wide mapping of chromatin dynamics, Institute for Cell Engineering, Johns Hopkins University (virtual)
- 2022 Genome-wide mapping of protein-DNA interactions, Biochemistry and Molecular Genetics, University of Illinois, Chicago (virtual)
- 2022 Genome-wide mapping of chromatin dynamics, Eppley Institute, University of Nebraska, Omaha
- 2021 Keynote: Genome-wide mapping of protein-DNA interaction dynamics, Biological and Clinical Frontiers in Epigenetics, Epiccypher 2021, Clearwater, FL
- 2021 Genome-wide mapping of protein-DNA dynamics, Genentech (virtual)
- 2021 Single-cell Profiling of Chromatin Landscapes, Single Cell Omics Beijing 2021, Peking University (virtual)

- 2021 Genome-wide mapping of protein-DNA dynamics, Molecular and Genomic Medicine, Brigham and Women's Hospital (virtual)
- 2021 Genome-wide mapping of protein-DNA interaction dynamics, Cell Signaling Technologies (virtual)
- 2021 Chromatin Dynamics, Cell Circuits and Epigenomics Symposium, Broad Institute (virtual)
- 2021 Genome-wide mapping of protein-DNA interaction dynamics, King Abdullah University of Science and Technology, Saudi Arabia (virtual)
- 2021 Genome-wide mapping of protein-DNA interaction dynamics, University of Colorado Cancer Center Symposium (virtual)
- 2021 Genome-wide mapping of protein-DNA interaction dynamics, Science in Asia 2021: Genome Biology and Disease, Zhongguancun, China (virtual)
- 2021 Keynote: Genome-wide mapping of protein-DNA interaction dynamics, Cambridge Epigenetics Club Summer Symposium (virtual)
- 2021 Genome-wide mapping of protein-DNA interaction dynamics, National Institute of Arthritis and Musculoskeletal and Skin Diseases Retreat (virtual)
- 2021 Genome-wide mapping of protein-DNA interaction dynamics, Chromatin & Epigenetics, China (virtual)
- 2021 Genome-wide mapping of protein-DNA interaction dynamics Institute for Integrative Genome Biology Symposium, UC Riverside (virtual)
- 2021 Genome-wide mapping of protein-DNA Interaction Dynamics, Genetics, Genomics & Systems Biology, University of Chicago (virtual)
- 2021 Genome-wide mapping of protein-DNA dynamics, Istanbul University 18<sup>th</sup> Winter School (virtual)
- 2021 Genome-wide mapping of protein-DNA interaction dynamics, Molecular and Cellular Biology, Lahore University (virtual)
- 2021 Genome-wide mapping of protein-DNA interaction dynamics, Queen Mary University of London (virtual)
- 2021 Genome-wide mapping of protein-DNA interaction dynamics, Medical Genetics, University of Washington (virtual)
- 2020 Genome-wide mapping of protein-DNA interaction dynamics, Mechanisms of Transcription and its Regulation, HongKong (virtual)
- 2020 Genome-wide mapping of protein-DNA interaction dynamics, Weill-Cornell Medical School (virtual)
- 2020 Genome-wide mapping of protein-DNA interaction dynamics, Cell and Developmental Biology meeting, HHMI (virtual)
- 2020 Genome-wide mapping of protein-DNA interaction dynamics, Fox Chase Cancer Center (virtual)
- 2020 Genome-wide mapping of protein-DNA interaction dynamics, Molecular, Cellular and Developmental Biology, Yale University (virtual)
- 2020 Profiling the epigenome at home, Epigenomics Journal Club, Mayo Clinic (virtual)
- 2020 Genome-wide mapping of protein-DNA interaction dynamics, Department of Biological Sciences at the University of Pittsburgh (virtual)
- 2020 Genome-wide mapping of protein-DNA interaction dynamics, Transcription and Chromatin Conference, EMBL, Heidelberg, Germany (virtual)
- 2020 Genome-wide mapping of protein-DNA interaction dynamics, Social DNAing (virtual)

- 2020 Genome-wide mapping of protein-DNA interaction dynamics, CCMB Biologue (virtual)
- 2020 Profiling the epigenome at home, Meiosis in Quarantine Journal Club (virtual)
- 2020 Genome-wide mapping of protein-DNA interaction dynamics, San Diego Chromatin Club (virtual)
- 2020 Genome-wide mapping of protein-DNA interaction dynamics, Frontiers in Biology, Stanford University (virtual)
- 2020 CUT&Tag: Efficient chromatin profiling for diverse applications, Chan-Zuckerberg Institute (virtual)
- 2020 Genome-wide mapping of protein-DNA interaction dynamics, Benaroya Institute
- 2020 Low-cost high-resolution chromatin profiling, Functional Genomics Workshop, National Academy of Sciences
- 2020 Genome-wide Mapping of Protein-DNA Interaction Dynamics, Seminar, Baylor College of Medicine
- 2020 Genome-wide mapping of protein-DNA interaction dynamics, California Institute of Technology