

DAVID C. KLEIN

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I am currently a fifth-year PhD Candidate in Sarah Hainer's lab at the University of Pittsburgh. I specialize in genomic and bioinformatic dissection of chromatin- and transcription-related disease regulatory mechanisms.

EDUCATION

PhD	Molecular, Cellular, and Developmental Biology <i>University of Pittsburgh, Pittsburgh, PA</i> Advisor: Sarah J. Hainer	May 2023 (expected)
BS	Biology and Religion <i>Furman University, Greenville, SC</i>	May 2017

RESEARCH EXPERIENCE

PhD Candidate	2018 – Present
University of Pittsburgh, Hainer Lab	
<i>Thesis title: Cell fate decisions are altered through regulation and misregulation of gene-distal elements in embryonic stem cells and acute myeloid leukemia</i>	
• Safety Officer	
Graduate Rotation	2018
University of Pittsburgh, Hainer Lab	
<i>Project Title: The essential histone chaperone Spt16 is necessary for maintenance of pluripotency in murine embryonic stem cells</i>	
Graduate Rotation	2017 – 2018
University of Pittsburgh, Arndt Lab	
<i>Project Title: Differential expression of Cdc73 in S. cerevisiae with implications for human cancer</i>	
Graduate Rotation	2017
University of Pittsburgh, Schwacha Lab	
<i>Project Title: A novel system for production and purification of the Mcm2-7 replicative helicase</i>	
Research Assistant, Furman University	2015 – 2017
Furman University, Chosed Lab	
<i>Project Title: Modeling the MLL1 multiprotein complex in S. cerevisiae</i>	

SCHOLARSHIPS, GRANTS, AND FUNDING SOURCES

University of Pittsburgh Arts and Sciences Graduate Fellowship (\$42,561)	2017
National Institutes of Health – SC-INBRE (\$4500)	2016
Furman Advantage Fellow (\$3000)	2015

Research Assistant
Furman University, Greenville, SC

2015 – 2018

- Mentored eight undergraduate researchers, teaching techniques, practices, and theory of working in a biochemistry laboratory.

PUBLICATIONS

Klein, D.C., Troy, K., Tripplehorn, S. A., and Hainer, S. J., “Nucleosome remodelers stimulate overlapping dinucleosome formation *in vivo*.” In preparation.

Klein, D.C., Lardo, S. M., McCannell, K. N., and Hainer, S. J., “FACT regulates pluripotency through distal regulation of gene expression in murine embryonic stem cells.” *BioRxiv*. DOI: 10.1101/2021.07.30.454509 [in review]

Klein, D.C., and Hainer, S. J., “Chromatin Regulation and Dynamics in Stem Cells.” 2020. *Current Topics in Developmental Biology* **138**, 1-71. DOI: 10.1016/bs.ctdb.2019.11.002

Klein, D.C., Hainer, S.J. Genomic methods in profiling DNA accessibility and factor localization. 2020. *Chromosome Res* **28**, 69–85. DOI:10.1007/s10577-019-09619-9

Klein, D., Lal, A. Longan, E., Baker M., Gogoli S., Wang J., Alkoutami S., Zibas E., and Chosed, R.J., “Construction of hybrid yeast-human histone methyltransferase complexes in *Saccharomyces cerevisiae* clarifies the roles of Bre2 and Ash2L for mixed lineage leukemia.” 2019. *Biomedical Genetics and Genomics*. DOI:10.15761/BGG.1000142

WORK PRESENTED

Selected Talk, “Differential roles of copper-binding transcription factors and the subfamilies of the SWI/SNF complex in the transcriptional regulation of the skeletal muscle lineage” FASEB Trace Elements in Biology and Medicine Conference, June 12th – 16th, 2022. Presenter: Teresita Padilla-Benevides.

Seminar, “The ncBAF complex regulates gene expression through altered gene-distal chromatin accessibility in acute myeloid leukemia,” University of Pittsburgh Department of Biological Sciences Departmental Seminar. April 1st, 2022. Presenter: **Dave Klein**.

Poster Presentation, “Identification of BRD9-dependent gene regulation by the non-canonical BAF complex” Fox Chase Cancer Center Epigenetics Symposium, March 2nd, 2022. Presenter: **Dave Klein**.

Invited Talk, “Nucleosome dynamics and non-coding RNAs coordinate to regulate cell state,” Senior Vice Chancellor’s Research Seminar. November 12th, 2021. Presenter: Sarah Hainer.

Selected Talk, “FACT maintains pluripotency factor expression through gene-distal regulation in embryonic stem cells,” Cold Spring Harbor Mechanisms of Eukaryotic Transcription Meeting. August 31st – September 2nd, 2021. Presenter: Sarah Hainer.

Seminar, “The essential histone chaperone FACT is necessary for maintenance of pluripotency in murine embryonic stem cells,” University of Pittsburgh Grad Expo. March 19th, 2021. Presenter: **Dave Klein**.

Seminar, “Identifying a BAF-driven mechanism of enhancer regulation in acute myeloid leukemia,” University of Pittsburgh Department of Biological Sciences Departmental Seminar. February 5th, 2021. Presenter: **Dave Klein**.

Seminar, “Determining whether the GBAF complex regulates enhancers to promote leukemogenesis,” University of Pittsburgh Department of Biological Sciences Departmental Seminar. December 6th, 2019. Presenter: **Dave Klein**.

Poster Presentation, “The essential histone chaperone FACT is necessary for maintenance of pluripotency in murine embryonic stem cells” Penn State 38th Summer Symposium in Molecular Biology: Chromatin and Epigenetic Regulation of Transcription, July 30th – August 2nd, 2019. Presenter: **Dave Klein**.

Paper Presentation, “The Theravada Kathina Rite at a Carolina Wat: a Reinterpretation” Furman Engaged Symposium, April 4th, 2017. Presenter: **Dave Klein**.
<https://scholarexchange.furman.edu/furmanengaged/2017/all/275/>

Poster Presentation, “Modeling the MLL1 multiprotein complex in *Saccharomyces cerevisiae*” NIH-SC-INBRE Conference, August 27th, 2016. Presenter: **Dave Klein**.

Poster Presentation, “Modeling the MLL1 multiprotein complex in *Saccharomyces cerevisiae*” Furman Engaged Symposium, April 12th, 2016. Presenter: **Dave Klein**.
<https://scholarexchange.furman.edu/furmanengaged/2016/all/364/>

Poster Presentation, “Modeling the MLL1 multiprotein complex in *Saccharomyces cerevisiae*” Association of Southeastern Biologists Conference, March 31st – April 2nd, 2016. Presenter: **Dave Klein**.
http://www.sebiologists.org/uploads/1/0/3/0/103013314/seb_63_2_apr_2016.pdf (p. 178, #P51)

Poster Presentation, “Modeling the MLL1 multiprotein complex in *Saccharomyces cerevisiae*” South Carolina EPSCoR IDEA Conference, January 25th, 2016. Presenter: **Dave Klein**.

PROFESSIONAL SERVICE AND AFFILIATIONS

Manuscripts co-reviewed:

BMC Genomics	2020
Cell Reports	2020
eLife	2021
Genetics	2020
Nature Communications (2)	2019, 2020
Nature Protocols	2021
Nature Reviews Methods Primer	2020
WIRE	2019

Association of Southeastern Biologists 2016 – 2017

HONORS AND AWARDS

Rex Eugene Kerstetter Award for Excellence in Biology	2017
Beta Beta Beta Biological Honor Society	2016 – 2017
Phi Eta Sigma Honor Society	2014 – 2017
Theta Alpha Kappa Religion Honor Society	2016 – 2017

TECHNICAL SKILLS

Benchtop/Experimental

- CUT&RUN and CUT&Tag
- ChIP-seq
- Nascent and traditional RNA-seq
- ATAC-seq
- MNase-seq
- Chromatin Conformation Capture (3C)
- Mammalian cell culture (adherent and suspension)
- Embryonic stem cell culture and characterization
- Fungal and bacterial culture
- CRISPR/Cas9-mediated genome editing
- siRNA design, generation, and purification
- Mammalian RNAi and transient transfection
- Inducible protein degradation
- Protein overexpression and purification
- Plasmid prep and purification
- SDS-PAGE, co-immunoprecipitation, and Western blotting
- PCR genotyping and Sanger sequencing
- Agarose gel electrophoresis

Bioinformatics

- Scripting competence in Unix, python, and R
- NGS technique data analysis
 - Genome alignment using bowtie, bowtie2, STAR, Hisat2, BWA, Salmon
 - Quality control and data cleaning using Picard, SAMtools, bedtools, bedops, deeptools
 - Data summarization and visualization using HOMER, deeptools
 - Peak calling using HOMER, macs2, Genrich, nucleoATAC, Danpos2/3, SEACR
 - Motif- and GO-term enrichment using HOMER, Metascape, macs2
 - Coding and non-coding transcript assignment using Subread, HTseq
 - Differential gene expression using DESeq2, edgeR
- Familiarity with standardized data analysis pipelines (PEP, NextFlow, Snakemake, ENCODE) and containerized software environments (Docker, Bulker, Singularity)
- High-throughput computing and job parallelization (SLURM)