**CURRICULUM VITAE**

**CHRISTOPHER A. MILLER, PH.D.**

**DATE:** Aug 24, 2022

**CITIZENSHIP:** United States of America

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**PRESENT POSITION:** Associate Professor**,** Division of Oncology**,** Washington University School of

Medicine

**EDUCATION:**

May 2005 B.S. Biology and Computer Science

Truman State University, Kirksville, MO

May 2011 Ph.D. Structural and Computational Biology and Molecular Biophysics Program

Baylor College of Medicine, Houston, TX

Thesis topic: Computational Cancer Genomics

**ACADEMIC POSITIONS:**  
2011-2013 Staff Scientist - Medical Genomics**,** The Genome Institute

Washington University in St Louis

2013-2017 Cancer Analysis Group Leader, The Genome Institute

Washington University in St Louis

2015-2016 Instructor in Medicine, Division of Genomics and Bioinformatics

Washington University School of Medicine

2016-2022 Assistant Professor in Medicine, Division of Oncology

Washington University School of Medicine

2022-Present Associate Professor in Medicine, Division of Oncology

Washington University School of Medicine

**MEDICAL LICENSURE AND BOARD CERTIFICATION:**

**HONORS AND AWARDS:**

**EDITORIAL/REVIEW RESPONSIBILITIES:**

Reviewer for *Bioinformatics*, *Cancer Cell*, *Genome Biology*, *PLoS Computational Biology*, *Nucleic Acids Research, Nature Communications, Genome Research, Blood Cancer Discovery, Scientific Data, BMC Evolutionary Biology*  
Grant reviewer for Dutch Cancer Society (KWF Kankerbestrijding)

Grant reviewer for Siteman Cancer Center Investment Fund

**PROFESSIONAL SOCITIES:** American Association for Cancer Research  
 International Society for Computational Biology

**Oral Presentations (conference - title):**

2012 TCGA Symposium - Assessing Tumor Heterogeneity and Tracking Clonal Evolution Using Whole Genome or Exome Sequencing

2013 TCGA Steering Committee Meeting - Automatic inference of theraputically relevant subclones in heterogeneous tumors

2013 Precision Medicine: Personal Genomes and Pharmacogenomics – SciClone: Inferring clonal architecture and tracking the spatial and temporal patterns of tumor evolution and therapy resistance

2014 TCGA Symposium - Ultra-deep whole-genome sequencing reveals clinically relevant low-frequency subclones in an acute myeloid leukemia

2015 Genome Informatics - Assessing tumor heterogeneity and tracking clonal clearance in response to therapy

2016 Festival of Genomics - Genomic insights into tumor evolution and therapy response

2016 Genome Informatics - Characterizing genomic responses to cancer

immunotherapy

2019 Genomics in Medicine - Tumor Heterogeneity and Evolution

2020 Genomics Education Partnership (GEP) Workshop - Sequencing, Variant Calling, and Cancer Genomics

2021 Institute of Medical Informatics in Münster, Germany - Genomic and Transcriptional evolution of AML at single-cell resolution

**RESEARCH SUPPORT:**

1 R50 CA211782 (PI)

NIH-NCI 09/01/2017-08/31/2027

Title: Comprehensive informatic analyses of AML genomes and epigenomes

1 PO1 CA101937 (Core C Director - Sequencing and Bioinformatic Analysis - 2016-present)

NIH-NCI 09/19/03-03/31/2023

Title: Genomics of Acute Myeloid Leukemia (PPG)

**TEACHING TITLE AND RESPONSIBILITES:**

2005 Teaching Assistant - Advanced Topics: Quantitative Biology (BCM)

2007-2008 Teaching Assistant - Computer Aided Discovery Methods (BCM)

2008 Teaching Assistant - Computational Mathematics for Biomedical Scientists (BCM)

2015-2017 Lecturer - Investigating Eukaryotic Genomes (WUSTL)

2015-2019 Lecturer - Molecular Basis of Heredity (WUSTL)  
2017-2021 Lecturer - Computational Statistical Genetics (WUSTL)

2018 Lecturer - Research Explorations in Genomics (WUSTL)  
2019-2021 Lecturer - Human Genetics (WUSTL)

2019 Lecturer - High-Throughput Biology: From Sequence to Networks   
(CSHL/CBW Course)

2017- Co-organizer - WUSTL Bioinformatics Workshop

- full academic year course, developed curriculum, recruited faculty

- delivered lectures on sequencing, informatics, somatic variant calling,

bisulfite sequencing and analysis, bash, HPC/LSF/Docker, Tumor

Heterogeneity, etc

2021- Instructor - Advanced Sequencing Technologies & Bioinformatics Analysis

(CSHL course)

**TRAINEE RECORD:**

Mentor to undergraduate research students

Yang Li 2013 Software Engineer at Emory University

Callie Federer 2014 PhD, now scientist at RadiaSoft

Jonas Neichen 2017 Medical Student at Rush Medical College  
Megan Neveau 2017 Graduate Student at Iowa State University  
Zhaohe Zhao 2020 Student at WUSTL

Andrew Li 2021 Student at Missouri S&T

Payton Redeemer 2022 Student at Missouri S&T

Training and Supervision of WUSTL computational staff, including

Dr. Gue Su Chang 2013- Cancer Analysis Group, TGI

Dr. Tiandao Li 2013- Cancer Analysis Group, TGI

Dr. Allegra Petti 2013-16 Cancer Analysis Group, TGI

Dr. Yevgeniy Gindin 2014-15 Cancer Analysis Group, TGI

Dr. Charles Lu 2013-15 Cancer Analysis Group, TGI

Sai Mukund Ramakrishnan 2019- AML PPG Core C Staff

Additional formal and informal bioinformatics training of dozens of internal and

external collaborators

**BIBLIOGRAPHY:**

(\* indicates co-first authorship)

1. Cancer Genome Atlas Network. Comprehensive genomic characterization defines human glioblastoma genes and core pathways. Nature. 2008 Oct 23;455(7216):1061-8. doi: 10.1038/nature07385. Epub 2008 Sep 4. PMID: 18772890 PMCID: PMC2671642

2. Hampton OA, Den Hollander P, **Miller CA**, Delgado DA, Li J, Coarfa C, Harris RA, Richards S, Scherer SE, Muzny DM, Gibbs RA, Lee AV, Milosavljevic A. A sequence-level map of chromosomal breakpoints in the MCF-7 breast cancer cell line yields insights into the evolution of a cancer genome. Genome Research. 2009 Feb;19(2):167-77. doi: 10.1101/gr.080259.108. Epub 2008 Dec 3. PMID: 19056696 PMCID: PMC2652200

3. Coarfa C, Yu F, **Miller CA**, Chen Z, Harris RA, Milosavljevic A. Pash 3.0: A versatile software package for read mapping and integrative analysis of genomic and epigenomic variation using massively parallel DNA sequencing. BMC Bioinformatics. 2010 Nov 23;11:572. doi: 10.1186/1471-2105-11-572. PMID: 21092284 PMCID: PMC3001746

4.  **Miller CA**, Hampton O, Coarfa C, Milosavljevic A. ReadDepth: a parallel R package for detecting copy number alterations from short sequencing reads. PLoS One. 2011 Jan 31;6(1):e16327. doi: 10.1371/journal.pone.0016327. PMID: 21305028 PMCID: PMC3031566

5. **Miller CA**, Settle SH, Sulman EP, Aldape KD, Milosavljevic A. Discovering functional modules by identifying recurrent and mutually exclusive mutational patterns in tumors. BMC Med Genomics. 2011 Apr 14;4:34. doi: 10.1186/1755-8794-4-34. PMID: 21489305 PMCID: PMC3102606

6. Hampton OA, Koriabine M, **Miller CA**, Coarfa C, Li J, Den Hollander P, Schoenherr C, Carbone L, Nefedov M, Ten Hallers BF, Lee AV, De Jong PJ, Milosavljevic A. Long-range massively parallel mate pair sequencing detects distinct mutations and similar patterns of structural mutability in two breast cancer cell lines. Cancer Genet. 2011 Aug;204(8):447-57. doi: 10.1016/j.cancergen.2011.07.009. PMID: 21962895 PMCID: PMC3185296

7. Parnell LD, Lindenbaum P, Shameer K, Dall'Olio GM, Swan DC, Jensen LJ, Cockell SJ, Pedersen BS, Mangan ME, **Miller CA**, Albert I. BioStar: an online question & answer resource for the bioinformatics community. PLoS Computational Biology. 2011 Oct;7(10):e1002216. doi: 10.1371/journal.pcbi.1002216. Epub 2011 Oct 27. PMID: 22046109 PMCID: PMC3203049

8. Ding L, Ley TJ, Larson DE, **Miller CA,** Koboldt DC, Welch JS, Ritchey JK, Young MA, Lamprecht T, McLellan MD, McMichael JF, Wallis JW, Lu C, Shen D, Harris CC, Dooling DJ, Fulton RS, Fulton LL, Chen K, Schmidt H, Kalicki-Veizer J, Magrini VJ, Cook L, McGrath SD, Vickery TL, Wendl MC, Heath S, Watson MA, Link DC, Tomasson MH, Shannon WD, Payton JE, Kulkarni S, Westervelt P, Walter MJ, Graubert TA, Mardis ER, Wilson RK, DiPersio JF. Clonal evolution in relapsed acute myeloid leukaemia revealed by whole-genome sequencing. Nature. 2012 Jan 11;481(7382):506-10. doi: 10.1038/nature10738. PMID: 22237025 PMCID: PMC3267864

9. Ellis MJ, Ding L, Shen D, Luo J, Suman VJ, Wallis JW, Van Tine BA, Hoog J, Goiffon RJ, Goldstein TC, Ng S, Lin L, Crowder R, Snider J, Ballman K, Weber J, Chen K, Koboldt DC, Kandoth C, Schierding WS, McMichael JF, **Miller CA**, Lu C, Harris CC, McLellan MD, Wendl MC, DeSchryver K, Allred DC, Esserman L, Unzeitig G, Margenthaler J, Babiera GV, Marcom PK, Guenther JM, Leitch M, Hunt K, Olson J, Tao Y, Maher CA, Fulton LL, Fulton RS, Harrison M, Oberkfell B, Du F, Demeter R, Vickery TL, Elhammali A, Piwnica-Worms H, McDonald S, Watson M, Dooling DJ, Ota D, Chang LW, Bose R, Ley TJ, Piwnica-Worms D, Stuart JM, Wilson RK, Mardis ER. Whole-genome analysis informs breast cancer response to aromatase inhibition. Nature. 2012 Jan 11;481(7382):506-10. doi: 10.1038/nature10738. PMID: 22237025 PMCID: PMC3267864

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11. Young MA, Larson DE, Sun CW, George DR, Ding L, **Miller CA**, Lin L, Pawlik KM, Chen K, Fan X, Schmidt H, Kalicki-Veizer J, Cook LL, Swift GW, Demeter RT, Wendl MC, Sands MS, Mardis ER, Wilson RK, Townes TM, Ley TJ. Background mutations in parental cells account for most of the genetic heterogeneity of induced pluripotent stem cells. 2012 May 4;10(5):570-82. doi: 10.1016/j.stem.2012.03.002. Epub 2012 Apr 26. PMID: 22542160 PMCID: PMC3348423

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25. **Miller CA\***, White BS\*, Dees ND, Griffith M, Welch JS, Griffith OL, Vij R, Tomasson MH, Graubert TA, Walter MJ, Ellis MJ, Schierding W, DiPersio JF, Ley TJ, Mardis ER, Wilson RK, Ding L. Sciclone: Inferring clonal architecture and tracking the spatial and temporal patterns of tumor evolution. PLoS Computational Biology. 2014 Aug 7;10(8):e1003665. doi: 10.1371/journal.pcbi.1003665. eCollection 2014 Aug. PMID: 25102416 PMCID: PMC4125065

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32. Wong TN\*, Ramsingh G\*, Young AL\*, **Miller CA**, Touma W, Welch JS, Lamprecht TL, Shen D, Hundal J, Fulton RS, Heath S, Baty JD, Klco JM, Ding L, Mardis ER, Westervelt P, DiPersio JF, Walter MJ, Graubert TA, Ley TJ, Druley TE, Link DC, Wilson RK. Role of TP53 mutations in the origin and evolution of therapy-related acute myeloid leukaemia. Nature. 2015 Feb 26;518(7540):552-555. doi: 10.1038/nature13968. Epub 2014 Dec 8. PMID: 25487151 PMCID: PMC4403236

33. Li C, Klco JM, Helton NM, George DR, Mudd JL, **Miller CA**, Lu C, Fulton R, O'Laughlin M, Fronick C, Wilson RK, Ley TJ. Genetic heterogeneity of induced pluripotent stem cells: results from 24 clones derived from a single C57BL/6 mouse. PloS one. 2015 Mar 23;10(3):e0120585. doi: 10.1371/journal.pone.0120585. eCollection 2015. PMID: 25799070 PMCID: PMC4370741

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