

BIOGRAPHICAL SKETCH

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NAME: Nathan C. Sheffield

eRA COMMONS USER NAME (credential, e.g., agency login): NSHEFF

POSITION TITLE: Assistant Professor

EDUCATION/TRAINING (*Begin with baccalaureate or other initial professional education, such as nursing, include postdoctoral training and residency training if applicable. Add/delete rows as necessary.*)

INSTITUTION AND LOCATION	DEGREE	Completion Date	FIELD OF STUDY
Brigham Young University, Provo, UT	B.S	04/2008	Bioinformatics
Duke University, Durham, NC	Ph.D.	05/2013	Bioinformatics and Computational Biology
Center for Molecular Medicine, Vienna, Austria	Postdoctoral	12/2015	Computational Epigenomics
Stanford University, Stanford, CA	Postdoctoral	08/2016	Computational Epigenomics

A. Personal Statement

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B. Positions and Honors*Positions and Employment*

2016-pres. Assistant Professor, Center for Public Health Genomics, University of Virginia

2016-pres. Assistant Professor, Department of Biomedical Engineering, University of Virginia

Honors and Awards

2014 EMBO Long-term Postdoctoral Fellowship, European Molecular Biology Organization

2014 HFSP Long-term Postdoctoral Fellowship, Human Frontier Science Program

C. Contributions to Science

H-index: 18. ORCID: [0000-0001-5643-4068](https://orcid.org/0000-0001-5643-4068). Links and citation info: [My NCBI](#) or www.databio.org.

Sheffield NC, Pierron G, Klughammer J, Datlinger P, Schönegger A, Schuster M, Hadler J, Surdez D, Guillemot D, Lapouble E, Freneaux P, Champigneulle J, Bouvier R, Walder D, Ambros IM, Hutter C, Sorz E, Amaral AT, de Álava E, Schallmoser K, Strunk D, Rinner B, Liegl-Atzwanger B, Huppertz B, Leithner A, de Pinieux G, Terrier P, Laurence V, Michon J, Ladenstein R, Holter W, Windhager R, Dirksen U, Ambros PF, Delattre O, Kovar H, Bock C, and Tomazou EM. DNA methylation heterogeneity defines a disease spectrum in Ewing sarcoma. **2017**. *Nat. Med* 23: 386–395. DOI:[10.1038/nm.4273](https://doi.org/10.1038/nm.4273)

Sheffield NC, and Bock C. LOLA: enrichment analysis for genomic region sets and regulatory elements in R and Bioconductor. **2016**. *Bioinformatics* 32: 587–589. PMID:PMC4743627 DOI:[10.1093/bioinformatics/btv612](https://doi.org/10.1093/bioinformatics/btv612)

Kovar H, Amatruda J, Brunet E, Burdach S, Cidre-Aranaz F, de Alva E, Dirksen U, van der Ent W, Grohar P, Grunewald TG, Helman L, Houghton P, Iljin K, Korsching E, Ladanyi M, Lawlor E, Lessnick S, Ludwig J, Meltzer P, Metzler M, Mora J, Moriggl R, Nakamura T, Papamarkou T, Sarikas BR, Redini F, Richter GH, Rossig C, Schadler K, Schafer BW, Scotlandi K, **Sheffield NC**, Shelat A, Snaar-Jagalska E, Sorensen P, Stegmaier K, Stewart E, Sweet-Cordero A, Szuhai K, Tirado OM, Tirode F, Toretsky J, Tsafou K, Uren A, Zinovyev A, and Delattre O. The second European interdisciplinary Ewing sarcoma research summit - A joint effort to deconstructing the multiple layers of a complex disease. **2016**. *Oncotarget*. PMID:PMC4890991 DOI:[10.18632/oncotarget.6937](https://doi.org/10.18632/oncotarget.6937)

Tomazou EM, **Sheffield NC**, Schmidl C, Schuster M, Schönegger A, Datlinger P, Kubicek S, Bock C, and Kovar H. Epigenome mapping reveals distinct modes of gene regulation and widespread enhancer reprogramming by the oncogenic fusion protein EWS-FLI1. **2015**. *Cell Reports* 10: 1082–1095. PMID:PMC4542316 DOI:[10.1016/j.celrep.2015.01.042](https://doi.org/10.1016/j.celrep.2015.01.042)

D. Research Support

Active

UVA start-up funds (PI:Sheffield) 8/23/2016-no end date

University of Virginia

Title: New faculty start-up funds from the University of Virginia

Role: PI

4-VA at UVA Collaborative (PI:Sheffield) 06/01/2018-05/31/2019

4-VA program

Title: A standardized database format for genomic locus enrichment analysis

Role: PI