

Jeff Vierstra, Ph.D.

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Current Appointment

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| Investigator Altius Institute for Biomedical Sciences, Seattle, WA | 2016-present |
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Training

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| Senior research fellow University of Washington, Seattle, WA Mentor: John A. Stamatoyannopoulos, MD | 2014-2015 |
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| Graduate research assistant University of Washington, Seattle, WA Advisor: John A. Stamatoyannopoulos, MD | 2009-2014 |
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| Research fellow University of Wisconsin, Madison, WI Advisor: Timothy Donohue, Ph.D. | 2005-2009 |
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Education

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| Ph.D. Genome Sciences University of Washington, Seattle, WA Thesis title: <i>Organization and evolution of transcription factor occupancy within the human genome</i> | 2014 |
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| Bachelor of Sciences University of Wisconsin, Madison, WI Major in Genetics, Certificate in Computer Sciences | 2009 |
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Awards and Honors

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| Hilldale Undergraduate Research Fellowship | 2008 |
| BACTER Undergraduate Research Fellow | 2009 |
| American Society of Human Genetics Charles Epstein Award Finalist | 2013 |
| National Science Foundation Graduate Research Fellowship (NSF GRFP) | 2011-2014 |

Teaching experience

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| Genome 361: Introduction to Genetics Teaching assistant, University of Washington, Seattle, WA | Summer 2012 |
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Professional organizations and affiliations

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| Member American Society for Human Genetics | 2013-present |
| Member American Association for the Advancement of Science (AAAS) | 2016-present |

Editorial and review experience

Ad-hoc peer review referee for Nature Genetics, Science, Cell Reports, PNAS, PLoS ONE, Nucleic Acids Research, Epigenetics & Chromatin, Genome Research, Nature Methods, Bioinformatics

Other responsibilities

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| Planning committee, Dept. of Genome Sciences 10th Anniversary Symposium | 2010 |
| Mentor, Undergraduate Research Program, University of Washington, Seattle, WA | 2011-2012 |

Invited seminars

Memorial Sloan-Kettering Cancer Center, New York, NY (3/2014)
National Cancer Institute, NIH, Bethesda, MD (3/2015)
Department of Genome Sciences Combi Seminar, Seattle, WA (4/2106)
CSHL: Chromatin, epigenetics, and gene expression course, Cold Spring Harbor, NY (8/2018)

Presentations: meetings and symposia

ENCODE Consortium Meeting, Stanford, CA (5/2013)
ASHG 63rd Annual Meeting, Boston, MA (10/2013)
ISCB/RECOMB Meeting, Toronto, Canada (11/2013)
ENCODE Consortium Meeting, Palo Alto, CA (7/2014)
ASHG 64th Annual Meeting, San Diego, CA (10/2014)
Banff International Research Station/Casa Matemática, Oaxaca, México (6/2015)
EMBO Next-generation Immunology, Weizmann Institute, Israel (2/2016)
20th Hemoglobin Switching Meeting, Asilomar, CA (9/2016)
CSHL: Global regulation of gene expression, Cold Spring Harbor, NY (3/2018)
Banff International Research Station/Casa Matemática, Oaxaca, Mexco (6/2018)
21st Hemoglobin Switching Meeting, Oxford, UK (9/2018)
Meeting on single-cell & massively parallel reporter assays, Bellairs Research Station, Barbados (2/2019)
ENCODE Users & Applications Meeting, Seattle, WA (7/2019)

Presented posters

CSHL: Mechanisms of Eukaryotic Transcription, Cold Spring Harbor, NY (9/2011)
NCI Symposium: Epigenetics and Development, Bethesda, MD (5/2013)
CSHL: Global regulation of gene expression, Cold Spring Harbor, NY (3/2014)
ASHG 65th Annual Meeting, Baltimore, MD (10/2015)

Patents

Riek A, Stamatoyannopoulos JA, **Vierstra J**. Nuclease-mediated regulation of gene-expression. US Patent 9,957,501.

Trainees (graduate students)

Grigorios Georgolopoulos (joint with M. Yiangou)

2016-present

Peer reviewed publications

(reverse chronological order; * equal contribution, † corresponding author)

Manuscripts submitted or in preparation:

1. Wang H*, Iwata M*, Shafer T*, Georgolopoulos G, Som T, Sandstrom R, Stamatoyannopoulos JA†, **Vierstra J**†. A rapid, scalable and sensitive method for reference quality mapping of accessible chromatin. *In preparation*.
2. **Vierstra J**†, Lazar J, Hughes T, Stamatoyannopoulos JA. A comprehensive statistical framework for the sensitive detection of nuclease footprints. *In preparation*.

Manuscripts published or in press:

3. Georgolopoulos G†, Iwata M, Psatha N, Yiangou M, **Vierstra J**† (2019). Unbiased phenotypic identification of functionally distinct hematopoietic progenitors. *J Biol Res (Thessalon)*, (26)4.
4. Breeze CE, Reynolds AP, van Dongen J, Dunham I, Lazar J, Neph S, **Vierstra J**, Bourque G, Teschendorff AE, Stamatoyannopoulos JA, Beck S (2019). eFORGE v2.0: updated analysis of cell type-specific signal in epigenomic data. *Bioinformatics*, *in press*.
5. Sieber KB, Batorsky A, Siebenthall KT, Hudkins KL, **Vierstra J**, Sullivan S, Sur A, McNulty M, Sandstrom R, Reynolds A, Bates D, Diegel M, Dunn D, Nelson J, Buckley M, Kaul R, Sampson MG, Himmelfarb J, Alpers CE, Waterworth D, Akilesh S (2019). Integrated Functional Genomic Analysis Enables Annotation of Kidney Genome-Wide Association Study Loci. *J Am Soc Nephrol*, 30(3):421-41.
6. Siebenthall KT, Miller CP, **Vierstra J**, Mathieu J, Tretiakova M, Reynolds A, Sandstrom R, Rynes E, Haugen E, Johnson A, Nelson J, Bates D, Diegel M, Dunn D, Frerker M, Buckley M, Kaul R, Zheng Y, Himmelfarb J, Ruohola-Baker H, Akilesh S (2019). Integrated epigenomic profiling reveals endogenous retrovirus reactivation in renal cell carcinoma. *EBioMedicine*, 41:427-442.
7. He X, Tillo D, **Vierstra J**, Syed KS, Deng C, Ray JG, Stamatoyannopoulos JA, Fitzgerald PC, Vinson C (2015). Methylated cytosines mutate to transcription factor binding sites that drive tetrapod evolution. *Genome Biol Evol*, 7(11):3155-69.
8. Maurano MT, Haugen E, Sandstrom R, **Vierstra J**, Shafer T and Stamatoyannopoulos JA (2015). Large-scale identification of functional variants impacting human transcription factor occupancy in vivo. *Nat Genetics*, 47(12):1393-401.
9. ***Vierstra J**, *Reik A, Chang KH, Stehling-Sun S, Zhou YY, Hinkley SJ, Paschon DE, Zhang L, Psatha N, Bendana YR, O'Neill CM, Song AH, Mich A, Liu P-Q, Lee G, Bauer DE, Holmes MC, Orkin SH,

- Papayannopoulou T, Stamatoyannopoulos G, Rebar EJ, Gregory PD, Urnov FD, Stamatoyannopoulos JA (2015). Functional footprinting of regulatory DNA. *Nat Methods*, 12(10):927-930.
10. Mayer A, di Lulio J, Maleri S, Eser U, **Vierstra J**, Reynolds A, Sandstrom R, Stamatoyannopoulos JA, Churchman LS (2015). Native elongating transcript sequencing reveals human transcriptional activity at nucleotide resolution. *Cell*, 161(3):541-554.
 11. Wilken MS, Brzezinski JA, La Torre A, Siebenthall K, Thurman R, Sabo P, Sandstrom RS, **Vierstra J**, Canfield TK, Hansen RS, Bender MA, Stamatoyannopoulos J, Reh TA (2015). DNase I hypersensitivity analysis of the mouse brain and retina identifies region-specific regulatory elements. *Epigenetics Chromatin*, 8(1):8.
 12. Stergachis AB, Neph S, Sandstrom R, Haugen E, Reynolds AP, Zhang M, Byron R, Canfield T, Stelting-Sun S, Lee K, Thurman RE, Vong S, Bates D, Neri F, Diegel M, Giste E, Dunn D, **Vierstra J**, Hansen RS, Johnson AK, Sabo PJ, Wilken MS, Reh TA, Treuting PM, Kaul R, Groudine M, Bender MA, Borenstein E, Stamatoyannopoulos JA. (2014). Conservation of trans-acting circuitry during mammalian regulatory evolution. *Nature*, 515(7527):355-364.
 13. Mouse ENCODE Project Consortium, *Yue F, *Cheng Y, *Breschi A, ***Vierstra J**, *Wu W, *Ryba T, *Ma Z, *Davis C, *Pope BD, *Shen Y et al. (2014). An integrated and comparative encyclopedia of DNA elements in the mouse genome. *Nature*, 515(7527):365-370.
 14. **Vierstra J**, Rynes E, Sandstrom R, Thurman RE et al. (2014). Mouse regulatory DNA landscapes reveal global principles of cis-regulatory evolution. *Science*, 346(6212):1007-1012.
 15. **Vierstra J**, Wang H, John S, Sandstrom R, Stamatoyannopoulos JA. (2014). Coupling transcription factor occupancy to nucleosome architecture with DNase-FLASH. *Nat Methods*, 11(1):66–72.
Commentary: Raj and McVicker (2014). The genome shows its sensitive side. Nat Methods, 11(1):39-40.
 16. Kamran SC, Lessard S, Xu J, Fujiwara Y, Lin C, Shao Z, Canver MC, Smith EC, Pinello L, Sabo PJ, **Vierstra J**, Voit RA, Yuan GC, Porteus MH, Stamatoyannopoulos JA, Lettre G, Orkin SH. (2013). Fine-Mapping and Genome Editing Reveal An Essential Erythroid Enhancer At The HbF-Associated BCL11A Locus. *Blood*, 122 (21):437-437.
 17. Bauer DE, Kamran SC, Lessard S, Xu J, Fujiwara Y, Lin C, Shao Z, Canver MC, Smith EC, Pinello L, Sabo PJ, **Vierstra J**, Voit RA, Yuan GC, Porteus MH, Stamatoyannopoulos JA, Lettre G, Orkin SH. (2013). An Erythroid Enhancer of BCL11A Subject to Genetic Variation Determines Fetal Hemoglobin Level. *Science*, 342(6155):253-257.
 18. John S, Sabo PJ, Canfield TK, Lee K, Vong S, Weaver M, Wang H, **Vierstra J**, Reynolds AP, Thurman RE, Stamatoyannopoulos JA. (2013). Genome-scale mapping of DNase I hypersensitivity. *Curr Protoc Mol Biol.*, Chapter 27: Unit 21.27.
 19. Vernot B, Stergachis AB, Maurano MT, **Vierstra J**, Neph S, Thurman RE, Stamatoyannopoulos JA, Akey JM. (2012). Personal and population genomics of human regulatory variation. *Genome Res.*, 22(9):1689-97.
 20. *Neph S, ***Vierstra J**, *Stergachis AB, *Reynolds AP, Haugen E, Vernot B, Thurman RE, John S, Sandstrom R, Johnson AK, Maurano MT, Humbert R, Rynes E, Wang H, Vong S, Lee K, Bates D, Diegel M, Roach V, Dunn D, Neri J, Schafer A, Hansen RS, Kuttyavin T, Giste E, Weaver M, Canfield T, Sabo P, Zhang M, Balasundaram G, Byron R, MacCoss MJ, Akey JM, Bender MA, Groudine M, Kaul R, Stamatoyannopoulos JA. (2012). An expansive human regulatory lexicon encoded in transcription factor footprints. *Nature*, 489(7414):83-90.
 21. Thurman RE, Rynes E, Humbert R, **Vierstra J**, Maurano MT, Haugen E, Sheffield NC, Stergachis AB, Wang H, Vernot B, Garg K, John S, Sandstrom R, Bates D, Boatman L, Canfield TK, Diegel M, Dunn D, Ebersol AK, Frum T, Giste E, Johnson AK, Johnson EM, Kuttyavin T, Lajoie B, Lee BK, Lee K, London D, Lotakis D, Neph S, Neri F, Nguyen ED, Qu H, Reynolds AP, Roach V, Safi A, Sanchez ME, Sanyal A, Shafer A, Simon JM, Song L, Vong S, Weaver M, Yan Y, Zhang Z, Zhang Z, Lenhard B, Tewari M, Dorschner MO,

Hansen RS, Navas PA, Stamatoyannopoulos G, Iyer VR, Lieb JD, Sunyaev SR, Akey JM, Sabo PJ, Kaul R, Furey TS, Dekker J, Crawford GE, Stamatoyannopoulos JA. (2012). The accessible chromatin landscape of the human genome. *Nature*, 489(7414):75-82.

22. ENCODE Project Consortium, Dunham I, Kundaje A, et al. [410 authors]. (2012). An integrated encyclopedia of DNA elements in the human genome. *Nature*, 489(7414):57-74.
23. Neph S, Kuehn MS, Reynolds AP, Haugen E, Thurman RE, Johnson AK, Rynes E, Maurano MT, **Vierstra J**, Thomas S, Sandstrom R, Humbert R, Stamatoyannopoulos JA. (2012). BEDOPS: high-performance genomic feature operations. *Bioinformatics*, 28(14):1919-20.

Review articles

1. **Vierstra J**[†] and Stamatoyannopoulos JA (2016). Genomic footprinting. *Nat Methods*, 13(3):213–221. Featured cover with editorial commentary: The power of disagreement (2016). *Nat Methods*, 13(3):185.