

JEFF VIERSTRA, PHD

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EDUCATION AND TRAINING

2003-2009 BSc – Genetics and Computer Science, University of Wisconsin, Madison, WI
2009-2014 PhD – Department of Genome Sciences, University of Washington, Seattle, WA
2014-2016 Post-doctoral research, University of Washington, Seattle, WA

RESEARCH EXPERIENCE

2016- Investigator
Altius Institute for Biomedical Sciences, Seattle, WA
2014-2015 Senior research fellow
Genome Sciences, University of Washington, Seattle, WA
2009-2014 Research fellow
University of Wisconsin, Madison, WI

ACADEMIC AWARDS AND HONORS

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

TEACHING

2012 (Sum.) Teaching assistant, University of Washington, Seattle, WA
Genome 361: Introduction to Genetics
2012 (Aut.) Teaching assistant, University of Washington, Seattle, WA
Genome 372: Genomics and Proteomics

PROFESSIONAL ORGANIZATION AFFILIATIONS

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

SERVICE TO PROFESSION

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

SELECTED INVITED SEMINARS

- 2019** Lecture at ENCODE Users & Applications Meeting (Invited lecture), Seattle, WA
2018 21st Hemoglobin Switching Meeting (Invited lecture), Oxford, UK
2018 Lecture at Chromatin, epigenetics, and gene expression course, Cold Spring Harbor, NY
2016 Seminar in Department of Genome Sciences Combi Seminar, Seattle, WA
2015 Lecture at National Cancer Institute, NIH, Bethesda, MD
2014 Lecture at Memorial Sloan-Kettering Cancer Center, New York, NY

SELECTED ORAL PRESENTATIONS IN SCIENTIFIC MEETINGS

- 2019** Molecular Biosystems Conference, Puerto Varas, Chile
2019 Meeting on single-cell & massively parallel reporter assays, Bellairs Research Station, Barbados
2018 Banff International Research Station/Casa Matemática, Oaxaca, México
2018 CSHL: Global regulation of gene expression, Cold Spring Harbor, NY
2016 20th Hemoglobin Switching Meeting, Asilomar, CA
2016 EMBO Next-generation Immunology, Weizmann Institute, Israel
2015 Banff International Research Station/Casa Matemática, Oaxaca, México
2014 ASHG 64th Annual Meeting, San Diego, CA
2014 ENCODE Consortium Meeting, Palo Alto, CA
2013 ISCB/RECOMB Meeting, Toronto, Canada
2013 ASHG 63rd Annual Meeting, Boston, MA
2013 ENCODE Consortium Meeting, Stanford, CA

MENTORSHIP

- 2016-2019** Dr. Grigorios Georgolopoulos (PhD mentored jointly with M. Yiangou, Aristotle University of Thassaloniki, Greece)

BIBLIOGRAPHY

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

Pre-prints:

- Georgolopoulos G, Iwata M, Psatha N, Nishida A, Som T, Yiangou M, Stamatoyannopoulos JA, **Vierstra J*** (2020). Chromatin dynamics during hematopoiesis reveal discrete regulatory modules instructing differentiation. *bioRxiv*, <https://doi.org/10.1101/2020.04.02.022566>.
- Vierstra J***, Lazar J, Sandstrom R et al. (2020). Global reference mapping and dynamics of human transcription factor footprints. *bioRxiv*, <https://doi.org/10.1101/2020.01.31.927798>.
- Meuleman W, Muratov A, Rynes E, Halow J, Lee K, Bates D, Diegel M, Dunn D, Neri F, Teodosiadis A, Reynolds A, Haugen E, Nelson J, Johnson AK, Frerker M, Buckley M, Sandstrom R, **Vierstra J**, Kaul, Stamatoyannopoulos JA (2020). Index and biological spectrum of accessible DNA elements in the human genome. *bioRxiv*, <https://doi.org/10.1101/822510>.

Published or in press:

4. 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.
5. 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*.
6. 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.
7. 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.
8. **Vierstra J*** and Stamatoyannopoulos JA (2016). Genomic footprinting. *Nat Methods*, 13(3):213–221. *Review*.
Featured cover with editorial commentary: The power of disagreement (2016). Nat Methods, 13(3):185.
9. 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.
10. 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.
11. **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.
12. 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.
13. 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.
14. Stergachis AB, Neph S, Sandstrom R, Haugen E, Reynolds AP, Zhang M, Byron R, Canfield T, Stehling-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.

15. Mouse ENCODE Project Consortium, Yue F¹, Cheng Y¹, Breschi A¹, **Vierstra J**¹, Wu W¹, Ryba T¹, Ma Z¹, Davis C¹, Pope BD¹, Shen Y¹ et al. (2014). An integrated and comparative encyclopedia of DNA elements in the mouse genome. **Nature**, 515(7527):365-370.
16. **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.
17. **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.
Featured commentary: Raj and McVicker (2014). The genome shows its sensitive side. *Nat Methods*, 11(1):39-40.
18. 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.
19. 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.
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21. 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.
22. Neph S¹, **Vierstra J**¹, Stergachis AB¹, Reynolds AP¹, 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, Kutayavin 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.
23. 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, Kutayavin 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.
24. 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.
25. 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.

PATENTS

US Patent 9,957,50. "Nuclease-mediated regulation of gene-expression" Riek A, Stamatoyannopoulos JA, Vierstra J.