# Elisabeth F. Heuston, Ph.D.

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*Interdisciplinary genomics bench scientist and bioinformatician at the National Institutes of Health*

**Center for Research on Genomics and Global Health**

As a Staff Scientist, I am responsible for both leading independent research projects and contributing insights related to my unique background. Given my expertise in single cell technologies, my primary focus is to functionally characterize genomic architecture of complex traits related to cardiometabolic disorders in individuals of African descent. Towards this objective, in one project I am developing a novel method to assay archived human skeletal muscle from sub-Saharan Africans using single cell RNA, chromatin, and spatial transcriptomic technologies. In a second project, I am integrating publicly available single cell data sets with our own epidemiological studies to describe systemic mechanisms in individuals with obesity that lead to type 2 diabetes.

My secondary focus is to develop animal models that test the impact of genetic variants on cardiometabolic traits. I initiated our Center's first animal study protocol and designed the CRISPR knock-out scheme for genes identified in our population studies. We have currently established mouse models for Aldh7a1, Nlrp9b, Sema4d, and Zranb3, and are testing them for changes in glucose metabolism, insulin signaling, and other altered cardiometabolic traits.

**Degrees**

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| 2012 | Ph.D. \| Johns Hopkins School of Medicine, Baltimore, MD<br>Cellular and Molecular Medicine Graduate Program |
| 2006 | B.A. *cum laude* \| Dartmouth College, Hanover, NH<br>Dual major in Genetics and Biophysical Chemistry with honors thesis |

**Employment and Research Experience**

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| 5/22/2022 – present | Staff Scientist \| Center for Research on Genomics and Global Health, NIH, Bethesda, MD<br>*Generate functional and bioinformatic analyses to define genomic elements influencing cardiometabolic disease in minority populations. Design in vivo and in vitro models to test genetic variants identified in human populations and protocols to produce genomic sequence on archived tissues.* |
| 1/1/2017 – 5/21/2022 | Research Fellow \| National Genome Research Institute, NIH, Bethesda, MD<br>*Data processing and integrated bioinformatics analysis of single cell transcriptional and epigenetic maps of blood cell lineages. Leveraged genomic data to direct isolation, in vitro expansion, and fluorescence imaging of newly identified populations that contribute to cell proliferation disorders.* |
| 7/1/2012 – 12/31/2016 | Postdoctoral Fellow \| National Genome Research Institute, NIH, Bethesda, MD<br>*Applied RNA and DNA sequencing to establish developmental relationships between blood cell populations. Generated model of myeloid lineage differentiation from hematopoietic stem cells.* |
| 6/30/2006 – 6/1/2012 | Graduate Research Program \| Johns Hopkins School of Medicine, Baltimore, MD<br>*Identified impact of chemotherapy and DNA methylation on genome stability in acute myeloid leukemia. Developed cell line models to identify common mechanisms of cellular response across different types of acute myeloid leukemias.* |
| 6/30/2003 – 6/4/2006 | Undergraduate Research Program \| Dartmouth College, Hanover, NH<br>*Expressed, crystalized, and analyzed the structure of a human kinesin motor protein. Developed a force-producing mechanism to explain inverted movement by the family of kinesin molecular motors.* |

**Select Honors and Distinctions**

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| 2019 | ASH Abstract Achievement Award |
| 2018 | Intramural Research Award |
| 2018 | NHGRI Symposium Research Award |
| 2017 | ASH Abstract Achievement Award |
| 2017 | NHGRI Symposium Speaker |
| 2016 | ASH Abstract Achievement Award |
| 2015 | NHGRI Symposium Research Award |
| 2015 | ASH Abstract Achievement Award |
| 2013 | ASH Abstract Achievement Award |
| 2008 | Pollard Scholars Tutor |
| 2006 | Chandler t. White 1916 Research Prize |
| 2006 | Sigma XI Scientific Research Society |
| 2005 – 2006 | Distinguished Achievement Citations in Undergraduate Coursework |
| 2004 – 2005 | Dartmouth College Presidential Scholars Program |

**Select Training and Certificates**

2022 Computational Genomics Course | Cold Spring Harbor Laboratory, Cold Spring Harbor, NY

2022 Google Project Management Certificate | Coursera

2019 Bioinformatics and molecular biology sabbatical, including training and instructing | MRC Weatherall Institute of Molecular Medicine, Oxford, UK

2017 Data Integration, Analysis, and Visualization | National Institutes of Health, Bethesda, MD

2016 College Teaching in the 21st Century | National Institutes of Health, Bethesda, MD

2016 Research Mentorship Training | National Institutes of Health, Bethesda, MD

**Select Teaching Experience**

2019 Molecular and Quantitative Animal Genetics Instructor | University of Maryland, College Park, MD

2019 Biomedical Data Science Seminar Speaker | MRC Weatherall Institute of Molecular Medicine, Oxford, UK

2016 Recombinant DNA Laboratory Course Designer and Lecturer | University of Maryland, College Park, MD

2016 Science Skills Boot Camp Instructor | National Institutes of Health, Bethesda, MD

2015 FAES BioTech 8 Instructor | National Institutes of Health, Bethesda, MD

**Technical skills**

*Bioinformatics*: Single cell and bulk sequencing alignment and quality control, read enrichment and clustering analyses, trajectory and comparative analyses

*Scripting languages*: R, Python, Perl

*Experimental techniques*: Single cell and bulk next generation sequencing, ATAC, fluorescence microscopy, flow *cytometry*, clonogenic assays, chromatin immunoprecipitation, murine models, metabolic assays, tumor models, and survival studies

*Academic instruction and mentorship*: Academic instructor, workshop instructor, official and unofficial student mentoring (high school through graduate-age students).

**Select Publications** (*ORCiD 0000-0002-1603-4083*)

Xiang G, Giardine B, et al., Snapshot: a package for clustering and visualizing epigenetic history during cell differentiation. BMC Bioinformatics. 2023 Mar 20;24(1):102.

Roy A, Wang G, Iskander E, et al. (2021). Transitions in lineage specification and gene regulatory networks in hematopoietic stem/progenitor cells over human development. Cell Rep, 36(11):109698.

Iskander D, Wang G, Heuston EF, et al. (2021). Single-cell profiling of human bone marrow progenitors reveals mechanisms of failing erythropoiesis in Diamond-Blackfan anemia. SciTranMed, 13;610.

Keller CA, Wixom AQ, Heuston EF, et al., (2021) Effects of sheared chromatin length on ChIP-seq quality and sensitivity. G3 Genes. Advance online publication.

The ENCODE Consortium, Moore J, et al., (2020). Expanded encyclopedias of DNA elements in the human and mouse genomes. Nature. 583, 699-710.

Psaila B, Wang G, Rodriguez M, Heuston EF, et al. (2020). Single-cell analyses reveal megakaryocyte-biased hematopoiesis in myelofibrosis and identify mutant clone-specific targets. Molecular Cell. 78(3); 477-492.

Xiang G, Keller CA, Heuston EF, et al., (2020). An integrative view of the regulatory and transcriptional landscapes in mouse hematopoiesis. Genome Res. 30; 472-484.

Hardison, RC, Zhang, Y, Keller, CA, et al. (2020). Systematic integration of GATA transcription factors and epigenomes via IDEAS paints the regulatory landscape of hematopoietic cells. IUBMB Life. 72; 27– 38.

Heuston EF et al. (2018) Hematopoietic stem cells preferentially establish megakaryocytic transcriptional and epigenetic signatures during erythro-megakaryopoiesis. Epigenetics & Chromatin, 28;11(1):22.

Heuston EF (2016). The Potential of a Single Enhancer. Blood, 127; 2943-2944.

Abd Elmoneim A, Heuston EF, et al. (2016). Synergistic and Antagonistic AML Cell Type-specific Responses to 5-Aza-2-deoxycitidine and 1-h-D-Arabinofuranoside. Anticancer Res., 32(2); 691-696.

Lichtenberg J, Heuston EF, Mishra T, Keller C, Hardison R, Bodine D (2015). SBR-Blood: systems biology repository for hematopoietic cells. Nuc. Acids Res, 44(D1); D925-D931.

Glait-Santar C, Desmond R, Feng X, Bat T, Chen J, Heuston EF, et al. (2015). Functional niche competition between normal hematopoietic stem and progenitor cells and myeloid leukemia cells. Stem Cells, 33(12); 3635-3642.

Heuston EF, Lemon K, Arceci RJ (2011). The beginning of the road for non-coding RNAs in normal hematopoiesis and hematologic malignancies. Front. Gene, 2:94.

Heuston EF, Bronner CE, Kull FJ, Endow SE (2010). A kinesin motor in a force-producing conformation. BMC Structural Biology, Jul 5; 10-19.

**Selected Presentations**

Single cell analysis of pancreatic islet cells in type 2 diabetes reveals pathogenic mechanisms enriched in populations of African ancestry. American Society of Human Genetics Conference (Speaker), D.C., 2023

Metabolites and proteins differentially expressed between obese and lean individuals are regulated by STAT3 and detected in adipocytes and pancreas. International Conference of Human Genetics (Poster), Cape Town, South Africa., 2023

Mouse erythroid cells originate from a megakaryocyte precursor in common myeloid progenitors, American Society of Hematology Conference (Speaker), Orlando, FA, 2019

Mouse erythroid commitment occurs in common myeloid progenitors, Gordon Research Conference: Red Cells (Poster), Newport, RI, 2019

A biologist's approach to bioinformatics, (Speaker), MRC Weatherall Institute of Molecular Medicine, Oxford University, Oxford, UK, 2019

Single cell RNASeq demonstrates that mouse erythroid cells emerges last, American Society of Hematology Conference (Poster), San Diego, CA, 2018

Erythroid is the last lineage to emerge in mouse hematopoiesis, Red Cell Conference (Speaker), New Haven, CT, 2018

Single cell RNASeq demonstrates that mouse erythroid cells are the last to emerge, Hemoglobin Switching Conference (Poster), Oxford, England, 2018

Megakaryocyte differentiation precedes erythroid specification during normal hematopoiesis, Molecular Biology Single Cell Research Symposium (Poster), Bethesda, MD, 2018

Diverting hematopoietic stem and progenitor cells from megakaryocytes toward erythrocytes, NHGRI Research Symposium (Speaker), Bethesda, MD, 20892, 2017

Epigenetic and Single Cell Analyses Reveal Dual Fate Decision Points in Pre-Primed Hematopoietic Stem Cells during Erythro-Megakaryopoiesis, American Society of Hematology Conference (Poster), Atlanta, GA, 2017

Diverting hematopoietic stem and progenitor cells from megakaryocytes toward erythrocytes, Red Cell Conference (Speaker), Cincinnati, OH, 2017

Establishment of enhancer elements during erythro-megakaryopoiesis, American Society of Hematology Conference (Poster), San Diego, CA, 2016

Establishment of enhancers during erythro-megakaryopoiesis, Hemoglobin Switching Conference (Poster), Pacific Grove, CA, 2016

Enhancer Accessibility during Erythropoiesis and Megakaryopoiesis Correlates with Lineage-Specific Gene expression, American Society of Hematology Conference (Poster), New Orleans, LA, 2015

Enhancer element activity during erythropoiesis and megakaryopoiesis correlates with lineage-specific gene expression, Research Symposium (Poster), National Human Genome Research Institute, Bethesda, MD, 2015

Differences in epigenetic signatures of coding and non-coding RNA genes in mouse erythroblasts and megakaryocytes, Hemoglobin Switching Conference (Poster), Oxford, England, 2014

Differences in the genome-wide epigenetic signatures of mRNA and long non-coding RNA genes in mouse erythroblasts and megakaryocytes, American Society of Hematology Conference (Poster), New Orleans, LA, 2013

5-Aza-2’-deoxycytidine and cytarabine have distinct effects on clonogenic growth, genome wide methylation, and RNA expression in AML cell lines, American Association for Cancer Research (Poster), Orlando, FL, 2011

Selective and titratable effects on AML genome wide methylation patterning, transcription and clonogenicity using low concentrations of 5-Aza-2’ Deoxycytidine, American Society of Hematology Conference (Poster), New Orleans, LA, 2009