

RUSSELL ELDON DURRETT

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EDUCATION AND TRAINING

2015-Present	Ph.D., Cell and Molecular Biology, University of Texas
2011-2014	M.S., Biotechnology and Entrepreneurship, New York University
2006-2010	B.A., Anthropology, New York University
2006-2010	B.S., Biochemistry, New York University

RESEARCH AND PROFESSIONAL EXPERIENCE

Recombine, Chief Scientific Officer, 2014

Coordinated clinical implementation of microarray, sanger validation, and targeted exome sequencing and interpretation service.

Recombine, Director of Bioinformatics, 2013

Developed and validated semicustom microarray platform including novel diagnostic and quality control methodologies, augmented interpretation with several types of publicly available data.

Weill Cornell Medical College, SMRT Lab, Research Specialist, 2012-2013

Formed a Pacific Biosciences-based Sequencing Service. Coded and executed bioinformatics pipelines for dozens of NGS projects focused on *de novo* genome assembly, human resequencing and metagenomics.

Weill Cornell Medical College, Mason Lab, Research Tech , 2010-2012

Supported several exome and whole-genome sequencing projects through Illumina library prep, HiSeq and MiSeq operations.

NYC iGEM Team Lead – “Radiation-resistant E.coli” – Summer 2011

NYU iGEM Team Lead – “immunoYeast” – Summer 2010

Genspace NYC, Co-Founder and Secretary – 2009-2012

Executed on the construction and operations of a Brooklyn molecular biology lab and teaching area operated through member and class fees.

Washington National Primate Research Center, Animal Technician, Spring 2007

Cleaned up monkey poop.

PUBLICATIONS - JOURNAL ARTICLES

Two methods for full-length RNA sequencing for low quantities of cells and single cells.

Pan X, Durrett RE, Zhu H, Tanaka Y, Zi X, Marjani SL, Euskirchen G, Ma C, Lamotte RH, Park IH, Snyder MP, Mason CE, Weissman SM. *PNAS*. 2013 Jan 8.

Genome Sequence of the Bacillus subtilis Biofilm-Forming Transformable Strain PS216.

Durrett R *et. al. Genome Ann.* 2013 Jun 20.

Assembly and Diploid Architecture of an Individual Human Genome via Single

Molecule Technologies. M Pendleton *et. al. Nature Methods*, 2015 Jun 29