

CURRICULUM VITAE

JOHN R EDWARDS

Date Prepared: June 8th, 2018

Personal Information

Gender: Male
Date of Birth: August 8, 1976
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Present Position: Associate Professor of Medicine, Washington University School of Medicine, St. Louis, MO

Education:

1994 - 1998 B.S. (Chemical Engineering), Completed requirements for B.A. in Mathematics, Johns Hopkins University, Baltimore, MD
1999 - 2001 M.S. (Chemical Engineering and Applied Chemistry), Columbia University, New York, NY
1999 - 2003 M.Phil. (Chemical Engineering), Columbia University, New York, NY
1999 - 2003 Ph.D. (Chemical Engineering, Genomics), Columbia University, New York, NY

Academic Positions/Employment:

2003 – 2006 Post-Doctoral Researcher, Columbia Genome Center, Columbia University, New York, NY

- 2006 – 2009 Associate Research Scientist, Columbia Genome Center and Department of Genetics and Development, Columbia University, New York, NY
- 2009 - 2017 Assistant Professor, Department of Medicine and Center for Pharmacogenomics, Washington University School of Medicine, St. Louis, MO
- 2018 - Associate Professor, Department of Medicine and Center for Pharmacogenomics, Washington University School of Medicine, St. Louis, MO

University and Hospital Appointments and Committees:

- 2010 - 2017 Member, DBBS Admissions Committee B, Washington University School of Medicine
- 2010 - Member, Institute of Clinical and Translational Sciences, Washington University School of Medicine
- 2011 - Member, Siteman Cancer Center, Washington University
- 2014 - 2016 Member, Application Review Committee for Amgen Scholars and BiomedRap Summer Research Programs, Washington University School of Medicine
- 2015 - Member, DBBS Molecular Genetics and Genomics Steering Committee, Washington University School of Medicine
- 2016 - Member, Department of Medicine Cultural Awareness and Inclusion (CAI) Faculty Task Force, Washington School of Medicine
- 2018 - Director Molecular Genetics and Genomics Graduate Program, DBBS
- 2018 Member, DBBS Admissions Review Committee

Honors and Awards:

- 1998 Member of Tau Beta Pi Engineering Honor Society
- 2000 International Genomic Sequencing and Analysis Conference, Miami, FL, Student Travel Award
- 2003 Awarded distinction for PhD dissertation, Columbia University
- 2007 International Conference on Genomics, Shenzhen, China, Mentee Award
- 2008 NIH Pathway to Independence award (K99/R00)
- 2009 AACR Susan G. Komen Scholar-in-Training Award, AACR 100th Annual Meeting
- 2011 Siteman Cancer Center Breast Cancer Program Career Development Award

Editorial/Reviewer Responsibilities:

Ad hoc Journal Reviewer:

Genome Research; Proceedings of the National Academy of Science (PNAS); Genome Biology; Nucleic Acids Research; Nature Communications; Breast Cancer Research; Epigenetics & Chromatin; BMC Genetics; BMC Bioinformatics; PLOS One; Journal of Theoretical Biology, 2009 - present

NIH Study Sections Ad hoc Reviewer:

NCI K99/R00 Special Emphasis Panel/Scientific Review Group, Mail reviewer, October 2013
NIGMS SCORE Program Special Emphasis Panel/Scientific Review Group, October 2014
NCI K22 and K99/R00 Special Emphasis Panel/Scientific Review Group, October 2015
NIGMS PRAT Fellowship (F12) Scientific Review Group, March 2016
NIDDK Special Emphasis Program Project Panel ZDK1 GRB 1 (2016), April 2016
Emerging Technologies in Neuroscience, Special Emphasis Panel, October 2016
NIGMS PRAT Fellowship (F12) Scientific Review Group, March 2017
NIGMS COBRE Scientific Review Group, July 2017
NIGMS MSFB Study Section, June 2018

Institutional Grant Reviews Ad hoc Reviewer:

Siteman Investment Program Review Committee; Cycle 2, 2015
Siteman Investment Program Review Committee; Cycle 1, 2016
Siteman Investment Program Review Committee; Cycle 1, 2018

Other Granting Agencies Ad hoc Mail Reviewer:

Austrian Science Foundation, 2011

Major Invited Professorships and Lectureships

- April, 2015 “A genomic perspective on the establishment and maintenance of DNA methylation patterns” Institute of Biotechnology, National Taiwan University, Taipei, Taiwan.
- April, 2015 “Finding meaning in ‘-omics’ data: Lessons from studying DNA methylation changes in cancer” Academia Sinica, Taipei, Taiwan

Research Support:

Current/Completed

Governmental

Principal Investigator \$225,000 (Annual Direct Costs)
R01 GM108811
NIH/NIGMS
“Modeling DNA methylation’s role in gene regulation”
August 2014 – April 2019

Principal Investigator \$275,000 (Total Direct Costs)
R21 LM012395
NIH/NLM
“Deconvolution of Epigenomic Data to Characterize Cellular Subpopulations”
July 2017 – June 2019

Principal Investigator \$189,240 (Total Direct Costs)
R21 LM011199
NIH/NLM
“A Machine Learning Approach For Fine-Scale Genome Wide DNA Methylation Analysis”
September 2012 – August 2014

Principal Investigator \$159,638 (Total Direct Costs)
W81XWH-11-1-0401
DOD/CDMRP (Collaborative Idea Award with Dr. Anne Peaston)
“Mammary Cancer and Activation of Transposable Elements”
September 2011 – September 2013

Principal Investigator \$491,448 (Total Direct Costs)
R00 CA127360
NIH/NCI
“Novel Approach to Whole Genome Methylation Profiling of Breast Cancer”
April 2010 – March 2013

Principal Investigator \$105,603 (Total Direct Costs)
K99 CA127360
NIH/NCI
“Novel Approach to Whole Genome Methylation Profiling of Breast Cancer”
June 2008 – March 2010

Non-governmental
Co-investigator \$23,737 (Total Direct Costs for Edwards’
subcontract)
2014-010
Sloan Kettering Institute for Cancer Research, Tri-Institutional Stem Cell Initiative Grant
“Epigenetic regulation of hematopoietic stem cells by 5-hydroxymethylcytosine”
PI: Mary Goll
October 2014 – September 2016

Principal Investigator \$50,000 (Total Direct Costs)
Career Development Award, Siteman Cancer Center Breast Cancer Program
“Uncovering the interplay between genetic and epigenetic signals in breast cancer”
May 2011 – April 2012

Patents and Intellectual Property:

1. Ju J, **Edwards JR**, Li Z. (2001) “High-fidelity DNA Sequencing Using Solid Phase Capturable Dideoxynucleotides and Mass Spectrometry.” US Patent application filed March, 2001 (US patent application 20030027140).
2. Ju J, Li Z, **Edwards JR**, Itagaki Y. (2003) “Massive parallel method for decoding DNA and RNA.” United States Patent 6,664,079.
3. Bestor TH, **Edwards JR**, Ju J, Li X. (2008) “Universal Methylation Profiling Methods” (US Patent Application Filed July 22, 2008).
4. **Edwards JR**, VanderKraats ND. (2013) “WIMSi – Washington University Interpolated Methylation Signatures”, Copyrighted Software Package.
5. **Edwards JR**, Schlosberg C. (2016) “ME-Class – Methylation-based Gene Expression Classification”, Copyrighted Software Package.
6. **Edwards JR**, Schlosberg C. (2018) “ME-Class2 – Methylation-based Gene Expression Classification v2”, Copyrighted Software Package.

Teaching Title and Responsibilities:

2003-2004	Lecturer, Transcriptome Assembly, Genomic Sequencing Laboratory, Columbia University, one-hour lecture per Spring semester.
2005-2006	Center of Excellence in Genomic Science Summer Scholars Program Project Director; Trained four undergraduate students in current state-of-the-art genomic technologies in the context of encouraging students to pursue careers in genomic science during an 8-week summer program. Columbia University
2007-2008	Lecturer, Bioinformatics, Genetics, Columbia University, one-hour lecture per Spring semester.
2009-	Member of 16 PhD and MSTP (MD/PhD) thesis committees (3 as chair), Washington University School of Medicine
2009-	Member of 19 qualifier committees (6 as chair) for Computational and Systems Biology, Molecular Genetics and Genomics, Human Statistical Genetics, and Biomedical Engineering, Washington University School of Medicine
2011-2012	Lecturer, Pharmacogenomics, Summer institute for training in biostatistics, Washington University School of Medicine, one-hour lecture per Summer
2012-2013, 2017	Discussion Group Facilitator, Ethics and Research Science (Biology 5011), Washington University School of Medicine, 6 discussions per year.
2012-	Lecturer, DNA Methylation, Research Explorations in Genomics (Biology 4342), Washington University, one-hour course per Spring semester

2013-	Lecturer, Epigenetics I & II, Fundamentals of Mammalian Genetics (BIO5285), Washington University School of Medicine, three hours instruction per Fall semester
2014-	Faculty Mentor, DBBS Connections Student-led initiative, Washington University School of Medicine
2015, 2016	Lecturer, DNA Methylation, Investigating Eukaryotic Genomes (Biology 193), Washington University, one-hour course per Fall semester
2017-2018	Member of 1 MA Research Advisory Committee

Trainees (Previous/Current):

<u>Name</u>	<u>Position (Previous/Current)</u>	<u>Yrs Trained</u>
Alexandra Payne	Homer G. Phillips Research FOCUS program, Undergraduate Research, Washington University / Health Assistant at Johns Hopkins University, Center for Talented Youth	2010
David Xiong	Undergraduate Research, Washington University / Medical Student, Case Western Reserve University	2010-2011
Keith Decker, PhD	Post-doc, Washington University School of Medicine / Data Scientist, Monsanto	2010-2013
Nathan VanderKraats, PhD	Post-doc, Washington University School of Medicine / Data Scientist, Monsanto	2010-2014
Kyle Jung	Undergraduate Research, Washington University / Staff Research Associate, Univ. of California, San Francisco	2010-2014
Margaret Akinhanmi	Post-Baccalaureate, Opportunities in Genomics Research Program, Washington University School of Medicine / PhD Student, Mayo Clinic	2013-2014
Alexis Fennoy	Post-Baccalaureate, Opportunities in Genomics Research Program, Washington University School of Medicine / PhD Student, Washington University in Saint Louis	2014-2015
Pooja Tripathy	Undergraduate Research, Washington University / Operations Associate, Collective Health	2014-2015

Geoffrey Cheng	Undergraduate Research, Washington University / Project Manager, Epic Systems Corporation	2014-2015
Tolison Fowler	Undergraduate Research Washington University / Medical Student Creighton University School of Medicine	2014-2016
Jared Litcharge	Undergraduate Research Washington University	2015
Justine Garin	Undergraduate Research Washington University	2016
Christopher Schlosberg	PhD Student, Washington University School of Medicine / Data Scientist, Monsanto	2011-2017
James McDonald	PhD Student, Washington University School of Medicine / Postdoc, George Washington University	2012-2017
Jerry Fong	MSTP Student Washington University School of Medicine	2015-
Rachel Dreher	Undergraduate Research Washington University	2017-
Jacob Blum	Undergraduate Research Washington University	2018-
Dakota Warren	SEPA Research Scholar, Washington University School of Medicine	2018-

Bibliography:

a. Peer reviewed manuscripts

1. **Edwards JR**, Itagaki Y, Ju J. DNA Sequencing Using Solid Phase Capturable Dideoxynucleotides and Mass Spectrometry. *Nucleic Acids Res.*, 2001; 29:e104 (p. 1-6).
2. Kim S, **Edwards JR**, Deng L, Chung W, Ju, J. Solid Phase Capturable Dideoxynucleotides for Multiplex Genotyping Using Mass Spectrometry. *Nucleic Acids Res.* 2002; 30:e78 (p. 1-6).
3. Kim S, Shi S, Bonome T, **Edwards JR**, Fodstad H, Beggs AH, Russo JJ, Ju J. Multiplex Genotyping of the Human β 2-Adrenergic Receptor Gene Using Solid Phase Capturable Dideoxynucleotides and Mass Spectrometry. *Anal Biochem.* 2003; 316:251-8.

4. Chien M, Morozova I, Shi S, *et al.*, **Edwards JR**, Pampou S, *et al.*, Russo JJ. The Genomic Sequence of the Accidental Pathogen *Legionella pneumophila*. *Science*. 2004; 305:1966-1968.
5. **Edwards JR**, Ruparel H, Ju J. Mass-spectrometry DNA sequencing. *Mutation Research*. 2005; 573:3-12.
6. Bai X., **Edwards JR**, Ju J. Molecular engineering approaches for DNA sequencing and analysis. *Expert Rev Mol Diagn*. 2005; 5: 797-808.
7. Moroz LL*, **Edwards JR***, Puthanveetil SV*, Kohn A*, Ha T, Heyland A, Knudsen B, Sahni A, Yu F, Liu L, Jezzini S, Sadreyev R, Lovell P, Iannuccilli W, Chen M, Nguyen T, Sheng H, Shaw R, Kalachikov S, Panchin Y, Farmerie W, Russo JJ, Ju J, Kandel ER. Neuronal Transcriptome of *Aplysia*: Neuronal Compartments and Circuitry. *Cell*. 2006; 127:1453-1467. *These authors contributed equally to this work.
8. Ju J, Kim DH, Bi L, Meng Q, Bai X, Li Z, Li X, Marma MS, Shi S, Wu J, **Edwards JR**, Romu A and Turro NJ. Four-color DNA sequencing by synthesis using cleavable fluorescent nucleotide reversible terminators. *PNAS*. 2006; 103:19635-19640.
9. Rollins RA, Haghighi F, **Edwards JR**, Das R, Zhang MQ, Ju J, Bestor TH. Large-Scale Structure of Genomic Methylation Patterns. *Genome Research*. 2006; 16:157-163.
10. Das R, Dimitrova N, Xuan ZY, Rollins RA, Haghighi FG, **Edwards JR**, Ju J, Bestor TH, Zhang MQ. Computational prediction of DNA methylation landscape in the human genome. *PNAS*. 2006; 103:10713-10716.
11. **Edwards JR**, Bestor TH. Stochastic and deterministic effects in gene regulation. *Heredity*. 2007; 99:243-244.
12. Xi Y, **Edwards JR**, Ju J. Investigation of miRNA Biology by Bioinformatic Tools and Impact of miRNAs in Colorectal Cancer—Regulatory Relationship of c-Myc and p53 with miRNAs. *Cancer Informatics*. 2007; 3:245-253.
13. **Edwards JR**, Kim D, Ju J. “An Integrated System for DNA Sequencing by Synthesis” in New High Throughput Technologies for DNA Sequencing and Genomics, Volume 2, ed. Keith Mitchelson (Elsevier), 2007.
14. Starke RM, Kim GH, Komotar RJ, Hickman ZL, Black EM, Rosales M, Kellner CP, Hahn DK, Otten ML, **Edwards J**, Wang T, Russo JJ, Connolly ES. Endothelial Nitric Oxide Synthase Gene Single Nucleotide Polymorphism Predicts Cerebral Vasospasm following Aneurysmal Subarachnoid Hemorrhage. *J Cereb Blood Flow Metab*. 2008; 28:1204-11.
15. **Edwards JR***, O’Donnell AH*, Rollins R, Peckham H, Lee C, Milekic MH, Chanrion B, Su T, Hibshoosh H, Gringrich JA, Haghighi F, Nutter R, Bestor TH. The Fine Structure of Genomic Methylation Patterns. *Genome Research*. 2010; 20:972-80. *These authors contributed equally to this work.
16. Hu Y, Matkovich SJ, Hecker PA, Zhang Y, **Edwards JR**, Dorn GW 2nd. Epigenetic orchestration of genetic reprogramming is an emergent property of stress-regulated cardiac microRNAs. *PNAS*. 2012; 109:19864-9.

17. Decker KF, Zheng D, He Y, Bowman T, **Edwards JR***, Jia L*. Androgen receptor-mediated transcription reprogrammed after hormone depletion. *Nucleic Acids Res.* 2012; 40:10765-79. *Co-corresponding authors.
18. Cruickshanks HA, McBryan T, Shah PP, Nelson DM, Donahue G, VanderKraats ND, **Edwards JR**, Berger SL, Adams PD. Features of the cancer epigenome are acquired as primary human cells approach senescence. *Nature Cell Biology.* 2013; 15:1495-1506.
19. Li S, Shen D, Shao J, Crowder R, Luo J, Liu W, Prat A, Hoog J, Goncalves R, Lu C, Ding L, McMichael JF, Miller C, Larson D, Fulton RS, Harrison M, *et al.* Mills G, **Edwards JR**, Gonzalez-Angulo A, Maher C, Perou C, Mardis E, Ellis MJ. Xenografting of advanced stage breast cancer preserves the genomic and clonal architecture of advanced breast cancer and generates luminal tumors harboring mutations and gene rearrangements in ESR1. *Cell Reports.* 2013; 4:1116-30.
20. VanderKraats ND, Decker KF, Hiken JF, **Edwards JR**. Method to discover high-resolution patterns of differential DNA methylation that associate with transcription changes. *Nucleic Acids Res.* 2013; 41:6816-27.
21. Tian F, Zhan F, VanderKraats ND, Hiken JF, **Edwards JR***, Zhang H, Zhao K, Song J*. DNMT gene expression and methylome in Marek's disease resistant and susceptible chickens prior to and following infection by MDV. *Epigenetics.* 2013; 8:431-444. *Co-corresponding authors.
22. Milekic MH, Xin Y, O'Donnell A, Kumar KK, Bradley-Moore M, Malaspina D, Moore H, Brunner D, Ge Y, **Edwards J**, Paul S, Haghghi FG, Gingrich JA. Age-related sperm DNA methylation changes are transmitted to offspring and associated with abnormal behavior and dysregulated gene expression. *Mol Psychiatry.* 2014; 20:995-1001.
23. Lund K, Cole JJ, VanderKraats ND, McBryan T, Pchelintsev NA, Clark W, Copland M, **Edwards JR**, Adams PD. DNMT inhibitors reverse a specific signature of aberrant promoter DNA methylation and associated gene silencing in AML. *Genome Biol.* 2014; 15:406.
24. Matkovich SJ, **Edwards JR**, Grossenheider TC, de Guzman Strong C, Dorn GW 2nd. Epigenetic coordination of embryonic heart transcription by dynamically regulated long noncoding RNAs. *PNAS.* 2014; 111:12264-9.
25. Boulard M, **Edwards JR**, Bestor TH. FBXL10 protects Polycomb-bound genes from hypermethylation. *Nat Genet.* 2015; 47:479-85.
26. Bestor TH, **Edwards JR**, Boulard M. Notes on the role of dynamic DNA methylation in mammalian development. *PNAS.* 2015; 112:6796-9.
27. Boulard M, **Edwards JR**, Bestor TH. "Abnormal X chromosome inactivation and sex-specific gene dysregulation after ablation of FBXL10." *Epigenetics & Chromatin.* 2016; 9:22.
28. Ruhland MK, Loza AJ, Capietto AH, Luo X, Knolhoff BL, Flanagan KC, Belt BA, Alspach E, Leahy K, Luo J, Schaffer A, **Edwards JR**, Longmore G, Faccio R, DeNardo DG, Stewart SA. "Stromal senescence establishes an immunosuppressive microenvironment that drives tumorigenesis." *Nature Commun.* 2016; 7:11762.

29. Powell E, Shao J, Yuan Y, Chen HC, Cai S, Echeverria GV, Mistry N, Decker KF, Schlosberg C, Do KA, **Edwards JR**, Liang H, Piwnica-Worms D, Piwnica-Worms H. “p53 deficiency linked to B cell translocation gene 2 (BTG2) loss enhances metastatic potential by promoting tumor growth in primary and metastatic sites in patient-derived xenograft (PDX) models of triple-negative breast cancer.” *Breast Cancer Res.* 2016; 18:13.
30. McDonald JI, Celik H, Rois LE, Fishberger G, Fowler T, Rees R, Kramer A, Martens A, **Edwards JR***, Challen GA*. Reprogrammable CRISPR/Cas9-based system for inducing site-specific DNA methylation. *Bio Open.* 2016; 5:866-74. *Co-corresponding authors.
31. Hiken JF, McDonald JI, Decker KD, Sanchez C, Hoog J, VanderKraats ND, Jung KL, Akinhanmi M, Rois LE, Ellis MJ, **Edwards JR**. An epigenetic switch controls prostaglandin receptor EP4 in endocrine therapy resistant breast cancer. *Oncogene.* 2017; 36:2319-2327.
32. Schlosberg CS, VanderKraats ND, **Edwards JR**. Modeling complex patterns of differential DNA methylation that associate with gene expression changes. *Nucleic Acids Res.* 2017; 45:5100-5111
33. **Edwards JR**, Yarychivska O, Boulard M, Bestor TH. DNA Methylation and DNA Methyltransferases. *Epigenetics & Chromatin.* 2017; 10:23.
34. Powell E, Shao J, Picon HM, Bristow C, Ge Z, Peoples M, Robinson F, Jeter-Jones SL, Schlosberg C, Grzeskowiak CL, Yang F, Wu Y, Wistuba I, Moulder SL, Symmans WF, Scott KL, **Edwards JR**, Liang H, Heffernan TP, Piwnica-Worms H. A functional genomic screen in vivo identifies CEACAM5 as a clinically relevant driver of breast cancer metastasis. *NPJ Breast Cancer.* 2018; 4:9.
35. He Y, Zuo Q, **Edwards J**, Zhao K, Lei J, Cai W, Nie Q, Li B, Song J. DNA Methylation and Regulatory Elements during Chicken Germline Stem Cell Differentiation. *Stem Cell Reports.* 2018; 10:1793-1806.

b. Published preprints

1. Schlosberg CS, **Edwards JR**. Integrative analysis of 5-methyl- and 5-hydroxymethylcytosine indicates a role for 5-hydroxymethylcytosine as a repressive epigenetic mark. *bioRxiv.* 2018; <https://doi.org/10.1101/318808>.