October 2022

CURRICULUM VITAE

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EDUCATION

Undergraduate	B.A., Biology , Saint Olaf College, Northfield, Minnesota (*Summa Cum Laude*)	1989
Medical School	M.D., School of Medicine, Case Western Reserve University, Cleveland, Ohio	2005
Graduate	Ph.D., Genetics, Case Western Reserve University, Cleveland, Ohio Thesis: *Genome-wide detection and analysis of segmental duplications* Advisor: E. E. Eichler	2002

POSTGRADUATE TRAINING

Postdoctoral Fellowship	Research Associate, NIH Postdoctoral Fellowship for the Computational Genomic Epidemiology of Cancer, Department of Genetics and Comprehensive Cancer Center, Case Western Reserve University and University Hospitals, Cleveland, Ohio	2002-2003
Residency	Clinical Pathology Resident (Year 3), Pathology Department, Case Western Reserve University and University Hospitals, Cleveland, Ohio	2008-2009
	Clinical Pathology Resident (Years 1 and 2), Pathology Department, Case Western Reserve University and University Hospitals, Cleveland, Ohio	2005-2007
Fellowship	Transfusion Medicine Fellow, American Red Cross, Cleveland Clinic, and University Hospitals, Cleveland, Ohio	2007-2008

HONORS AND AWARDS

Masters of Arts, *ad eundem*, Brown University, Providence, Rhode Island	2019
CDC Charles C. Shepard Science Award Nominee	2017

CDC James H. Nakano Citation for Outstanding Scientific Publication	2017
UMass Medical School Commencement Humanitarian Honor for ACCEL	2015
Red Cross' Britney Gengel International Humanitarian Award (UMassMed Ebola Relief, including ACCEL)	2015
Paul G Allen Ebola Fighters Breakfast, Washington DC	2015
College of American Pathology Foundation Travel Award for Anatomic Pathology Informatics and Imaging Support for Translational Medicine Meeting	2007
Frederick C. Robbins Fellowship in International Health	2004
American Society of Human Genetics Award for Basic Postdoctoral Research	2002
NIH Medical Scientist Training Program, Case Western Reserve University	1995-2005
Departmental Distinction in Biology, Saint Olaf College	1989
Phi Beta Kappa, Saint Olaf College	1989
Dean's List, Saint Olaf College	1985-1989

PROFESSIONAL LICENSES AND BOARD CERTIFICATION

State of Rhode Island Medical License	2018-present
Commonwealth of Massachusetts Medical License	2009-present
State of Ohio Medical License	Inactive
Diplomate, American Board of Pathology	
Clinical Pathology	2009-2029
Transfusion Medicine Board Certification	2011-2031

ACADEMIC APPOINTMENTS

Associate Professor Department of Pathology and Laboratory Medicine, Brown University, Alpert School of Medicine, Providence, Rhode Island	2018-present
Adjunct Professor, West African Centre for Cell Biology and Infectious Pathogens (WACCBIP), University of Ghana, Legion, Accra	2019-present
Assistant Professor Department of Medicine (Division of Transfusion Medicine) and Program in Bioinformatics and Integrative Biology, University of Massachusetts Medical School, Worcester, Massachusetts	2009-2018

HOSPITAL APPOINTMENTS

Associate Director of Coagulation and Transfusion Medicine Lifespan Academic Medical Center (Rhode Island & Miriam Hospitals) Providence, RI	2018-present
Associate Director of the Blood Bank UMASS Memorial Medical Center, Worcester, Massachusetts	2009-2018

OTHER APPOINTMENTS AND EMPLOYMENT

Advisory Board Member, International Cancer Institute, Eldoret Kenya	2020-2022

Member, AABB Global Transfusion Forum Research Committee	2019-present
Graduate Program Director of Bioinformatics and Computational Biology University of Massachusetts Medical School, Worcester, Massachusetts	2017-2018
Chair, Statistical Analysis Cluster, Center for Microbiome Research, University of Massachusetts	2013-2018
Member, Medical Advisory Committee, American Red Cross Northeast Region	2013-2018
Laboratory Director Academic Consortium Combating Ebola in Liberia University of Massachusetts Medical School, Worcester, Massachusetts	2014-2016
Member, AMPATH Hematology Committee	2011-2013
Research Assistant, School of Pharmacology, University of Michigan, Ann Arbor, Michigan	1994-1995
Research Assistant, Department of Rheumatology, University of Michigan, Ann Arbor, Michigan	1993-1994
Research Assistant, Department of Pediatric Infectious Diseases, University of Minnesota, Minneapolis, Minnesota	1993
Junior and Senior High School Mathematics and Science Teacher, United States Peace, Liberia and Botswana, Africa	1990-1992
Undergraduate Teaching Assistant, Microbiology and Genetics, Saint Olaf College, Northfield, MN	1987-1989

Other Editorial Responsibilities

Reviewer: American Journal of Human Genetics	Reviewer: Genome Research
Reviewer: Annals of Human Genetics	Reviewer: Human Molecular Genomics
Reviewer: BMC Bioinformatics	Reviewer: Mammalian Genome
Reviewer: BMC Genomics	Reviewer: Nucleic Acids Research
Reviewer: BMC Evolutionary Biology	Reviewer: PLoS One
Reviewer: Journal of Intensive Care	Reviewer: PLoS NTD
Reviewer: Genome Biology	Reviewer: Science
Reviewer: Genome Biology and Evolution	Reviewer: Transfusion Medicine

UNIVERSITY COMMITTEES

Member, Global Health Initiative Framework Executive Committee	2022-present
Member, MD PhD Admissions Committee	2020-present
Member, Computational Biology Admissions Committee	2021-present
Member, Research Continuity Committee, Brown University	2020-2021
Chair, COVID-19 Research Task Force, Brown University	2020-2021
Member, Cancer Biology Faculty Search Committee, Brown University	2019-present
Global Health Pathways Advisory Committee, UMass Medical School	2014-2018
Voting Member, Information Technology Committee, UMass Medical School	2014-2018
Chair, Bioinformatics & Statistical Analysis Cluster, Center for Microbiome Research	2014-2018
Voting Member, Global Health Advisory Committee, UMass Medical School	2014-2017
Voting Member, Massachusetts Green High Performance Computing Center User Group Steering Committee	2011-2014

Voting Member, Biomedical Computing Committee, UMass Medical School	2012-2103
Molecular Medicine Training Grant Steering Committee, BMP, UMass Med School	2011-2012

HOSPITAL COMMITTEES

Member, COVID-19 Multi-institutional Biobank Steering Committee	2020-2022
Member, Transfusion Committee, Rhode Island Hospital	2020-
Member, Transfusion Committee, Miriam Hospital	2019-
Member, Transfusion Committee, UMass Memorial Medical Center	2009-2018

MEMBERSHIP IN SOCIETIES

dAABB	2007-
American Society for Hematology	2019-
American Society for Clinical Pathology	2008 -
American Society of Human Genetics	2004-
American Society of Tropical Medicine and Hygiene	2005-

PUBLICATIONS

Original Publications Peer-Reviewed Journals

1. Halushka MK, Mathews DJ, **Bailey JA**, Chakravarti A. GIST: a web tool for collecting gene information. Physiol Genomics. 1999 Aug 31;1(2):75-81. PMID: 11015564
2. Lynn A, Kashuk C, Petersen MB, **Bailey JA**, Cox DR, Antonarakis SE, Chakravarti A. Patterns of meiotic recombination on the long arm of human chromosome 21. Genome Res. 2000 Sep;10(9):1319-32. PMID: 10984450
3. **Bailey JA**, Carrel L, Chakravarti A, Eichler EE. Molecular evidence for a relationship between LINE-1 elements and X chromosome inactivation: the Lyon repeat hypothesis. Proc Natl Acad Sci U S A. 2000 Jun 6;97(12):6634-9. PMID: 10841562.
4. Kariuki HC, Mbugua G, Magak P, **Bailey JA**, Muchiri EM, Thiongo FW, King CH, Butterworth AE, Ouma JH, Blanton RE. Prevalence and familial aggregation of schistosomal liver morbidity in Kenya: evaluation by new ultrasound criteria. J Infect Dis. 2001 Mar 15;183(6):960-6. Epub 2001 Feb 13. PMID: 11237814.
5. **Bailey JA**, Yavor AM, Massa HF, Trask BJ, Eichler EE. Segmental duplications: organization and impact within the current human genome project assembly. Genome Res. 2001 Jun;11(6):1005-17. PMID: 11381028.
6. Lander ES, Linton LM, Birren B, Nusbaum C, Zody MC, Baldwin J, Devon K, Dewar K, Doyle M, FitzHugh W, Funke R, Gage D, Harris K, Heaford A, Howland J, Kann L, Lehoczky J, LeVine R, McEwan P, McKernan K, Meldrim J, Mesirov JP, Miranda C, Morris W, Naylor J, Raymond C, Rosetti M, Santos R, Sheridan A, Sougnez C, Stange-Thomann Y, Stojanovic N, Subramanian A, Wyman D, Rogers J, Sulston J, Ainscough R, Beck S, Bentley D, Burton J, Clee C, Carter N, Coulson A, Deadman R, Deloukas P, Dunham A, Dunham I, Durbin R, French L, Grafham D, Gregory S, Hubbard T, Humphray S, Hunt A, Jones M, Lloyd C, McMurray A, Matthews L, Mercer S, Milne S, Mullikin JC, Mungall A, Plumb R, Ross M, Shownkeen R, Sims S, Waterston RH, Wilson RK, Hillier LW, McPherson JD, Marra MA, Mardis ER, Fulton LA, Chinwalla AT, Pepin KH, Gish WR, Chissoe SL, Wendl MC, Delehaunty KD, Miner TL, Delehaunty A, Kramer JB, Cook LL, Fulton RS, Johnson DL, Minx PJ, Clifton SW, Hawkins T, Branscomb E, Predki P, Richardson P, Wenning S, Slezak T, Doggett N, Cheng JF, Olsen A, Lucas S, Elkin C,

Uberbacher E, Frazier M, Gibbs RA, Muzny DM, Scherer SE, Bouck JB, Sodergren EJ, Worley KC, Rives CM, Gorrell JH, Metzker ML, Naylor SL, Kucherlapati RS, Nelson DL, Weinstock GM, Sakaki Y, Fujiyama A, Hattori M, Yada T, Toyoda A, Itoh T, Kawagoe C, Watanabe H, Totoki Y, Taylor T, Weissenbach J, Heilig R, Saurin W, Artiguenave F, Brottier P, Bruls T, Pelletier E, Robert C, Wincker P, Smith DR, Doucette-Stamm L, Rubenfield M, Weinstock K, Lee HM, Dubois J, Rosenthal A, Platzer M, Nyakatura G, Taudien S, Rump A, Yang H, Yu J, Wang J, Huang G, Gu J, Hood L, Rowen L, Madan A, Qin S, Davis RW, Federspiel NA, Abola AP, Proctor MJ, Myers RM, Schmutz J, Dickson M, Grimwood J, Cox DR, Olson MV, Kaul R, Raymond C, Shimizu N, Kawasaki K, Minoshima S, Evans GA, Athanasiou M, Schultz R, Roe BA, Chen F, Pan H, Ramser J, Lehrach H, Reinhardt R, McCombie WR, de la Bastide M, Dedhia N, Blöcker H, Hornischer K, Nordsiek G, Agarwala R, Aravind L, **Bailey JA**, Bateman A, Batzoglou S, Birney E, Bork P, Brown DG, Burge CB, Cerutti L, Chen HC, Church D, Clamp M, Copley RR, Doerks T, Eddy SR, Eichler EE, Furey TS, Galagan J, Gilbert JG, Harmon C, Hayashizaki Y, Haussler D, Hermjakob H, Hokamp K, Jang W, Johnson LS, Jones TA, Kasif S, Kaspryzk A, Kennedy S, Kent WJ, Kitts P, Koonin EV, Korf I, Kulp D, Lancet D, Lowe TM, McLysaght A, Mikkelsen T, Moran JV, Mulder N, Pollara VJ, Ponting CP, Schuler G, Schultz J, Slater G, Smit AF, Stupka E, Szustakowki J, Thierry-Mieg D, Thierry-Mieg J, Wagner L, Wallis J, Wheeler R, Williams A, Wolf YI, Wolfe KH, Yang SP, Yeh RF, Collins F, Guyer MS, Peterson J, Felsenfeld A, Wetterstrand KA, Patrinos A, Morgan MJ, de Jong P, Catanese JJ, Osoegawa K, Shizuya H, Choi S, Chen YJ, Szustakowki J, International Human Genome Sequencing Consortium. Initial sequencing and analysis of the human genome. Nature. 2001 Feb 15;409(6822):860-921. Erratum in: Nature 2001 Aug 2;412(6846):565. Nature 2001 Jun 7;411(6838):720. Szustakowski J. PMID: 11237011. **[Bailey JA** and Eichler EE contributed the segmental duplication section.]

7. Cheung VG, Nowak N, Jang W, Kirsch IR, Zhao S, Chen XN, Furey TS, Kim UJ, Kuo WL, Olivier M, Conroy J, Kasprzyk A, Massa H, Yonescu R, Sait S, Thoreen C, Snijders A, Lemyre E, **Bailey JA,** Bruzel A, Burrill WD, Clegg SM, Collins S, Dhami P, Friedman C, Han CS, Herrick S, Lee J, Ligon AH, Lowry S, Morley M, Narasimhan S, Osoegawa K, Peng Z, Plajzer-Frick I, Quade BJ, Scott D, Sirotkin K, Thorpe AA, Gray JW, Hudson J, Pinkel D, Ried T, Rowen L, Shen-Ong GL, Strausberg RL, Birney E, Callen DF, Cheng JF, Cox DR, Doggett NA, Carter NP, Eichler EE, Haussler D, Korenberg JR, Morton CC, Albertson D, Schuler G, de Jong PJ, Trask BJ; BAC Resource Consortium. Integration of cytogenetic landmarks into the draft sequence of the human genome. Nature. 2001 Feb 15;409(6822):953-8. PMID: 11237021

8. Johnson ME, Viggiano L, **Bailey JA**, Abdul-Rauf M, Goodwin G, Rocchi M, Eichler EE. Positive selection of a gene family during the emergence of humans and African apes. Nature. 2001 Oct 4;413(6855):514-9. PMID: 11586358.

9. **Bailey JA**, Yavor AM, Viggiano L, Misceo D, Horvath JE, Archidiacono N, Schwartz S, Rocchi M, Eichler EE. Human-specific duplication and mosaic transcripts: the recent paralogous structure of chromosome 22. Am J Hum Genet. 2002 Jan;70(1):83-100. Epub 2001 Nov 30. PMID: 11731936.

10. **Bailey JA**, Gu Z, Clark RA, Reinert K, Samonte RV, Schwartz S, Adams MD, Myers EW, Li PW, Eichler EE. Recent segmental duplications in the human genome. Science. 2002 Aug 9;297(5583):1003-7. PMID: 12169732.

11. Guy J, Hearn T, Crosier M, Mudge J, Viggiano L, Koczan D, Thiesen HJ, **Bailey JA**, Horvath JE, Eichler EE, Earthrowl ME, Deloukas P, French L, Rogers J, Bentley D, Jackson MS. Genomic sequence and transcriptional profile of the boundary between pericentromeric satellites and genes on human chromosome arm 10p. Genome Res. 2003 Feb;13(2):159-72. PMID: 12566394.

12. Liu G; NISC Comparative Sequencing Program, Zhao S, **Bailey JA**, Sahinalp SC, Alkan C, Tuzun E, Green ED, Eichler EE. Analysis of primate genomic variation reveals a repeat-driven expansion of the human genome. Genome Res. 2003 Mar;13(3):358-68. PMID: 12618366.

13. Hillier LW, Fulton RS, Fulton LA, Graves TA, Pepin KH, Wagner-McPherson C, Layman D, Maas J, Jaeger S, Walker R, Wylie K, Sekhon M, Becker MC, O'Laughlin MD, Schaller ME, Fewell GA, Delehaunty KD, Miner TL, Nash WE, Cordes M, Du H, Sun H, Edwards J, Bradshaw-Cordum H, Ali J, Andrews S, Isak A, Vanbrunt A, Nguyen C, Du F, Lamar B, Courtney L, Kalicki J, Ozersky P, Bielicki L, Scott K, Holmes A, Harkins R, Harris A, Strong CM, Hou S, Tomlinson C, Dauphin-Kohlberg S, Kozlowicz-Reilly A, Leonard S, Rohlfing T, Rock SM, Tin-Wollam AM, Abbott A, Minx P, Maupin R, Strowmatt C, Latreille P, Miller N, Johnson D, Murray J, Woessner JP, Wendl MC, Yang SP, Schultz BR, Wallis JW, Spieth J, Bieri TA, Nelson JO, Berkowicz N, Wohldmann PE, Cook LL, Hickenbotham MT, Eldred J, Williams D, Bedell JA, Mardis ER, Clifton SW, Chissoe SL, Marra MA, Raymond C, Haugen E, Gillett W, Zhou Y, James R, Phelps K, Iadanoto S, Bubb K, Simms E, Levy R, Clendenning J, Kaul R, Kent WJ, Furey TS, Baertsch RA, Brent MR, Keibler E, Flicek P, Bork P, Suyama M, **Bailey JA**, Portnoy ME, Torrents D, Chinwalla AT, Gish WR, Eddy SR, McPherson JD, Olson MV, Eichler EE, Green ED, Waterston RH, Wilson RK. Chromosome 7 Sequencing Consortium. The DNA sequence of human chromosome 7. Nature. 2003 Jul 10;424(6945):157-64. PMID: 12853948. [**Bailey JA** and Eichler EE contributed the repeat and segmental duplication section.]

14. Horvath JE, Gulden CL, **Bailey JA**, Yohn C, Mcpherson JD, Prescott A, Roe BA, de Jong PJ, Ventura M, Misceo D, Archidiacono N, Zhao S, Schwartz S, Rocchi M, Eichler EE. Using a pericentromeric interspersed repeat to recapitulate the phylogeny and expansion of human centromeric segmental duplications. Mol Biol Evol. 2003 Sep;20(9):1463-79. Epub 2003 May 30. PMID: 12777517.

15. **Bailey JA**, Liu G, Eichler EE. An Alu transposition model for the origin and expansion of human segmental duplications. Am J Hum Genet. 2003 Oct;73(4):823-34. Epub 2003 Sep 22. PMID: 14505274.

16. Alkan C, **Bailey JA**, Eichler EE, Sahinalp SC, Tuzun E. An algorithmic analysis of the role of unequal crossover in alpha-satellite DNA evolution. Genome Inform. 2002;13:93-102. PMID: 14571378.

17. Gibbs RA, Weinstock GM, Metzker ML, Muzny DM, Sodergren EJ, Scherer S, Scott G, Steffen D, Worley KC, Burch PE, Okwuonu G, Hines S, Lewis L, DeRamo C, Delgado O, Dugan-Rocha S, Miner G, Morgan M, Hawes A, Gill R, Celera, Holt RA, Adams MD, Amanatides PG, Baden-Tillson H, Barnstead M, Chin S, Evans CA, Ferriera S, Fosler C, Glodek A, Gu Z, Jennings D, Kraft CL, Nguyen T, Pfannkoch CM, Sitter C, Sutton GG, Venter JC, Woodage T, Smith D, Lee HM, Gustafson E, Cahill P, Kana A, Doucette-Stamm L, Weinstock K, Fechtel K, Weiss RB, Dunn DM, Green ED, Blakesley RW, Bouffard GG, De Jong PJ, Osoegawa K, Zhu B, Marra M, Schein J, Bosdet I, Fjell C, Jones S, Krzywinski M, Mathewson C, Siddiqui A, Wye N, McPherson J, Zhao S, Fraser CM, Shetty J, Shatsman S, Geer K, Chen Y, Abramzon S, Nierman WC, Havlak PH, Chen R, Durbin KJ, Egan A, Ren Y, Song XZ, Li B, Liu Y, Qin X, Cawley S, Worley KC, Cooney AJ, D'Souza LM, Martin K, Wu JQ, Gonzalez-Garay ML, Jackson AR, Kalafus KJ, McLeod MP, Milosavljevic A, Virk D, Volkov A, Wheeler DA, Zhang Z, **Bailey JA**, Eichler EE, Tuzun E, Birney E, Mongin E, Ureta-Vidal A, Woodwark C, Zdobnov E, Bork P, Suyama M, Torrents D, Alexandersson M, Trask BJ, Young JM, Huang H, Wang H, Xing H, Daniels S, Gietzen D, Schmidt J, Stevens K, Vitt U, Wingrove J, Camara F, Mar Albà M, Abril JF, Guigo R, Smit A, Dubchak I, Rubin EM, Couronne O, Poliakov A, Hübner N, Ganten D, Goesele C, Hummel O, Kreitler T, Lee YA, Monti J, Schulz H, Zimdahl H, Himmelbauer H, Lehrach H, Jacob HJ, Bromberg S, Gullings-Handley J, Jensen-Seaman MI, Kwitek AE, Lazar J, Pasko D, Tonellato PJ, Twigger S, Ponting CP, Duarte JM, Rice S, Goodstadt L, Beatson SA, Emes RD, Winter EE, Webber C, Brandt P, Nyakatura G, Adetobi M, Chiaromonte F, Elnitski L, Eswara P, Hardison RC, Hou M, Kolbe D, Makova K, Miller W, Nekrutenko A, Riemer C, Schwartz S, Taylor J, Yang S, Zhang Y, Lindpaintner K, Andrews TD, Caccamo M, Clamp M, Clarke L, Curwen V, Durbin R, Eyras E, Searle SM, Cooper GM, Batzoglou S, Brudno M, Sidow A, Stone EA, Venter JC, Payseur BA, Bourque G, López-Otín C, Puente XS, Chakrabarti K, Chatterji S, Dewey C, Pachter L, Bray N, Yap VB, Caspi A, Tesler G, Pevzner PA, Haussler D, Roskin KM, Baertsch R, Clawson H, Furey TS, Hinrichs AS, Karolchik D, Kent WJ, Rosenbloom KR, Trumbower H,

Weirauch M, Cooper DN, Stenson PD, Ma B, Brent M, Arumugam M, Shteynberg D, Copley RR, Taylor MS, Riethman H, Mudunuri U, Peterson J, Guyer M, Felsenfeld A, Old S, Mockrin S, Collins F; Rat Genome Sequencing Project Consortium. Genome sequence of the Brown Norway rat yields insights into mammalian evolution. Nature. 2004 Apr 1;428(6982):493-521. PMID: 15057822. [Tuzun E, **Bailey JA** and Eichler EE contributed the segmental duplication section.]

18. **Bailey JA**, Baertsch R, Kent WJ, Haussler D, Eichler EE. Hotspots of mammalian chromosomal evolution. Genome Biol. 2004;5(4):R23. Epub 2004 Mar 8. PMID: 15059256.
19. Tuzun E, **Bailey JA**, Eichler EE. Recent segmental duplications in the working draft assembly of the brown Norway rat. Genome Res. 2004 Apr;14(4):493-506. PMID: 15059990.
20. **Bailey JA,** Church DM, Ventura, M, Rocchi M, Eichler EE. Analysis of segmental duplications and genome assembly in the mouse. Genome Res. 2004 May;14(5):789-801. PMID: 15123579.
21. She X, Horvath JE, Jiang Z, Liu G, Furey TS, Christ L, Clark R, Graves T, Gulden CL, Alkan C, **Bailey JA**, Sahinalp C, Rocchi M, Haussler D, Wilson RK, Miller W, Schwartz S, Eichler EE. The structure and evolution of centromeric transition regions within the human genome. Nature. 2004 Aug 19;430(7002):857-64. PMID: 15318213.
22. Alkan C, Eichler EE, **Bailey JA**, Sahinalp SC, Tüzün E. The role of unequal crossover in alpha-satellite DNA evolution: a computational analysis. J Comput Biol. 2004;11(5):933-44. PMID: 15700410.
23. Tuzun E*, Sharp AJ*, **Bailey JA***, Kaul R, Morrison VA, Pertz LM, Haugen E, Hayden H, Albertson D, Pinkel D, Olson MV, Eichler EE. Fine-scale structural variation of the human genome. Nat Genet. 2005 Jul;37(7):727-32. Epub 2005 May 15. PMID: 15895083.
24. Sharp AJ, Locke DP, McGrath SD, Cheng Z, **Bailey JA**, Valente RU, Pertz LM, Clark RA, Schwartz S, Segraves R, Oseroff VV, Albertson DG, Pinkel D, Eichler EE. Segmental duplications and copy-number variation in the human genome. Am J Hum Genet. 2005 Jul;77(1):78-88. Epub 2005 May 25. PMID: 15918152.
25. Alkan C, Tüzün E, Buard J, Lethiec F, Eichler EE, **Bailey JA**, Sahinalp SC. Manipulating multiple sequence alignments via MaM and WebMaM. Nucleic Acids Res. 2005 Jul 1;33(Web Server issue):W295-8. PMID: 15980474.
26. **Bailey JA**, Kidd JM, Eichler EE. Copy number variation in human genes. Cytogenet Genome Res. 2008;123(1-4):234-43. doi: 10.1159/000184713. Epub 2009 Mar 11. PMID: 19287160.
27. Klapper E, Zhang Y, Figueroa P, Ness P, Stubbs J, Abumuhor I, **Bailey J**, Epperson L, Tauscher C, Enriquez E, Hashmi G, Seul M. Toward extended phenotype matching: a new operational paradigm for the transfusion service. Transfusion. 2010 Mar;50(3):536-46. doi: 10.1111/j.1537-2995.2009.02462.x. Epub 2009 Nov 19. PMID: 19929860.
28. Xia A, Sharakhova MV, Leman SC, Tu Z, **Bailey JA**, Smith CD, Sharakhov IV. Genome landscape and evolutionary plasticity of chromosomes in malaria mosquitoes. PLoS One. 2010 May 12;5(5):e10592. doi: 10.1371/journal.pone.0010592. PMID: 20485676.
29. Sharakhova MV, George P, Brusentsova IV, Leman SC, **Bailey JA**, Smith CD, Sharakhov IV. Genome mapping and characterization of the Anopheles gambiae heterochromatin. BMC Genomics. 2010 Aug 4;11:459. doi: 10.1186/1471-2164-11-459. PMID: 20684766.
30. Meyerson HJ, **Bailey J**, Miedler J, Olobatuyi F. Marginal zone B cell lymphomas with extensive plasmocytic differentiation are neoplasms of precursor plasma cells. Cytometry B Clin Cytom. 2011 Mar;80(2):71-82. doi: 10.1002/cyto.b.20571. Epub 2010 Nov 20. PMID: 21337490.
31. **Bailey JA**, Mvalo T, Aragam N, Weiser M, Congdon S, Kamwendo D, Martinson F, Hoffman I, Meshnick SR, Juliano JJ. Use of massively parallel pyrosequencing to evaluation the diversity of and selection on Plasmodium falciparum csp T-cell epitopes in Lilongwe, Malawi. J Infect Dis. 2012 Aug 15;206(4):580-7. doi: 10.1093/infdis/jis329. Epub 2012 May 2. PMID: 22551816.

32. Johnson ME, Rowsey RA, Shirley S, Vandevoort C, **Bailey J**, Hassold T. A specific family of interspersed repeats (SINEs) facilitates meiotic synapsis in mammals. Mol Cytogenet. 2013 Jan 1;6(1):1. doi: 10.1186/1755-8166-6-1. PMID: 23276256.

33. Aragam NR, Thayer KM, Nge N, Hoffman I, Martinson F, Kamwendo D, Lin FC, Sutherland C, **Bailey JA**+, Juliano JJ. Diversity of T cell epitopes in Plasmodium falciparum circumsporozoite protein likely due to protein-protein interactions. PLoS One. 2013 May 7;8(5):e62427. doi: 10.1371/journal.pone.0062427. Print 2013.PMID: 23667476. [+Corresponding author]

34. Mulama DH, **Bailey JA**, Foley J, Chelimo K, Ouma C, Jura WG, Otieno J, Vulule J, Moormann AM. Sickle cell trait is not associated with endemic Burkitt lymphoma: an ethnicity and malaria endemicity-matched case-control study suggests factors controlling EBV may serve as a predictive biomarker for this pediatric cancer. Int J Cancer. 2014 Feb 1;134(3):645-53. doi: 10.1002/ijc.28378. Epub 2013 Aug 16. PMID: 23832374.

35. Weinstein R, Kershaw G, **Bailey J**, Greene M, Chhibber V, Vauthrin M, Nath R, Galvin Karr E. Safety and efficacy of autologous hematopoietic progenitor cell collection in tandem with hemodialysis in multiple myeloma with myeloma cast nephropathy. J Clin Apher. 2014 Apr;29(2):83-9. doi: 10.1002/jca.21295. Epub 2013 Aug 19. PMID: 23959911.

36. Chhibber V, Green M, Vauthrin M, **Bailey J**, Weinstein R. Is group A thawed plasma suitable as the first option for emergency release transfusion? Transfusion. 2014 Jul;54(7):1751-5; quiz 1750. doi: 10.1111/trf.12537. Epub 2014 Jan 8. PMID: 24400951.

37. Simkin AT, **Bailey JA**, Gao FB, Jensen JD. Inferring the evolutionary history of primate microRNA binding sites: overcoming motif counting biases. Mol Biol Evol. 2014 Jul;31(7):1894-901. doi: 10.1093/molbev/msu129. Epub 2014 Apr 9. PMID: 24723422.

38. Parobek CP, **Bailey JA**, Hathaway NJ, Socheat D, Rogers WO, Juliano JJ. Differing patterns of selection and geospatial genetic diversity within two leading Plasmodium vivax candidate vaccine antigens. PLoS Negl Trop Dis. 2014 Apr 17;8(4):e2796. doi: 10.1371/journal.pntd.0002796. eCollection 2014 Apr. PMID: 24743266.

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Gwanzura L, Mutambu S, Stevenson JC, Thuma PE, Norris DE, **Bailey JA**, Juliano JJ, Chongwe G, Mulenga M, Simulundu E, Mharakurwa S, Agre P, Moss WJ; Southern and Central Africa International Center of Excellence for Malaria Research. Policy Implications of the Southern and Central Africa International Center of Excellence for Malaria Research: Ten Years of Malaria Control Impact Assessments in Hypo-, Meso-, and Holoendemic Transmission Zones in Zambia and Zimbabwe Am J Trop Med Hyg. 2022 Oct 11;107(4_Suppl):68-74. PMID: 36228913

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Other Peer Reviewed Publications

1. Horvath JE, **Bailey JA**, Locke DP, EE. Lessons from the human genome: transitions between euchromatin and heterochromatin. Hum Mol Genet 10:2215-23 (2001)
2. **Bailey JA** and Eichler EE. Origins and consequences of primate segmental duplications: crucibles of evolution, diversity and disease. Nat Rev Genet 7:552-64 (2006)
3. Wojewoda CM, **Bailey J**, Sandhaus LM. Rings in red blood cells: intracellular red cell parasites. DC Fuller, JP Orsulak: Checksample Hematology (2009)
4. Mideo N, Kennedy DA, Carlton JM, **Bailey JA**, Juliano JJ, Read AF. Ahead of the curve: next generation estimators of drug resistance in malaria infections. Trends Parasitol 29:321-328 (2013)
5. Moormann AM and **Bailey JA**. Malaria - how this parasitic infection aids and abets EBV-associated Burkitt lymphomagenesis. Curr Opin Virol. 20:78-84 (2016).
6. Wesolowski A, Taylor A, Chang H, Verity R, Tessema S, **Bailey JA**, Perkins TA, Neafsey D Greenhouse B, Buckee CO, Mapping malaria by combining parasite genomic and epidemiologic data. BMC Med 16:190 (2018)
7. Ghansah A, Kamau E, Amambua-Ngwa A, Ishengoma DS, Maiga-Ascofare O, Amenga-Etego L, Deme A, Yavo W, Randrianarivelojosia M. Plasmodium Diversity Network Africa, Ochola-Oyier LI, Helegbe GK, **Bailey J,** Alifrangis M, Djimde A. Targeted Next Generation Sequencing for malaria research in Africa: current status and outlook. Malar J. 2019 Sep 23;18(1):324. doi: 10.1186/s12936-019-2944-2. PMID: 31547818; PMCID: PMC6757370
8. Bloch EM, Shoham S, Casadevall A, Sachais BS, Shaz B, Winters JL, van Buskirk C, Grossman BJ, Joyner M, Henderson JP, Pekosz A, Lau B, Wesolowski A, Katz L, Shan H, Auwaerter PG, Thomas D, Sullivan DJ, Paneth N, Gehrie E, Spitalnik S, Hod EA, Pollack L, Nicholson WT, Pirofski LA, **Bailey JA**, Tobian AA. Deployment of convalescent plasma for the prevention and treatment of COVID-19. J Clin Invest. 2020 Jun 1;130(6):2757-2765. doi: 10.1172/JCI138745. PMID: 32254064; PMCID: PMC7259988
9. Bell GJ, Agnandji ST, Asante KP, Ghansah A, Kamthunzi P, Emch M, **Bailey JA**. Impacts of Ecology, Parasite Antigenic Variation, and Human Genetics on RTS,S/AS01e Malaria Vaccine Efficacy. Curr Epidemiol Rep. 2021 Jul 30:1-10. doi: 10.1007/s40471-021-00271-8. Epub ahead of print. PMID: 34367877; PMCID: PMC8324449
10. Lyimo BM, Popkin-Hall ZR, Giesbrecht DJ, Mandara CI, Madebe RA, Bakari C, Pereus D, Seth MD, Ngamba RM, Mbwambo RB, MacInnis B, Mbwambo D, Garimo I, Chacky F, Aaron S, Lusasi A, Molteni F, Njau R, Cunningham JA, Lazaro S, Mohamed A, Juliano JJ, **Bailey JA**, Ishengoma DS. Potential Opportunities and Challenges of Deploying Next Generation Sequencing and

CRISPR-Cas Systems to Support Diagnostics and Surveillance Towards Malaria Control and Elimination in Africa. Front Cell Infect Microbiol. 2022 Jul 13;12:757844. doi: 10.3389/fcimb.2022.757844. eCollection 2022. PMID: 35909968

Books and Book Chapters

1. **Bailey JA** and Eichler EE. Genome-wide detection and analysis of recent segmental duplications within mammalian organisms. In: The Genome of Homo Sapiens: Cold Spring Harbor Symposia on Quantitative Biology LXVIII (B. Stillman and D. Stewart, eds.) Cold Spring Harbor Laboratory Press (2003)
2. **Bailey JA**, Weinstein R. Therapeutic phlebotomy and specialized hemapheresis. In: Simon TL, McCullough J, Snyder EL, Solheim BG, Strauss RG eds. Rossi's Principles of Transfusion Medicine 5th Ed. West Sussex, UK; John Wiley & Sons, Ltd. pp 407-417 (2016)
3. Brunker PA and **Bailey JA**. Therapeutic phlebotomy and specialized hemapheresis. In: Simon TL, McCullough J, Snyder EL, Solheim BG, Strauss RG eds. Rossi's Principles of Transfusion Medicine 6th Ed. West Sussex, UK; John Wiley & Sons, Ltd. *in press*.

Talks International

Invited Speaker. Kenya Medical Research Institute Institute (KEMRI)I Annual Scientific and Health (KASH) Conference Large-scale genomics towards understanding and tracking Plasmodium falciparum drug and diagnostic resistance in Africa	6/1/2022
Invited Speaker. National Institute of Medical Research Annual Meeting Plenary Session, Dar es Salaam. Tracking the emergence of drug and diagnostic resistance in Africa	5/18/2022
Invited Speaker. Vaccines: State of the art and challenges (Curso Vacinas: o estado da arte e desafios). Symposium Brazil Society of Immunology, Via Zoom. Title. Malaria Vaccines: learning from the circumsporozoite-based vaccines	9/21/2020
Invited Speaker. Noguchi Memorial Medical Research Institute. Campus Research Seminar Series. Accra, Ghana. Title: High-throughput targeted sequencing for malaria drug resistance and population genetics	5/28/2019
Speaker. Imperial College. School of Public Health. London, UK. Infectious Disease Seminar Series. Title: High-throughput targeted sequencing of malaria for large-scale surveillance	6/7/2018
Speaker. University of Ghana. Accra, Ghana. West African Center for Cell Biology of Infectious Parasites (WACCBIP) Annual Conference. Title: Expanding the horizons of malaria molecular epidemiology with high-throughput sequencing in Plasmodium falciparum	7/6/2017
Speaker. Kenya Medical Research Institute, Kisumu, Kenya. Title: Methods for human and parasite sequencing: moving to multiplexing with molecular inversion probes (MIPs)	3/6/2017
Speaker. Ethiopian Public Health Institute. Addis Ababa, Ethiopia. Title: Deeper, Wider and Swifter: improving high-throughput sequencing and analysis for malaria and other infectious diseases	2/16/2017
Speaker. Research Seminar Series. Kenya Medical Research Institute, Kisumu,	7/20/2016

Kenya.
Title: Deep sequencing in Plasmodium: probing inter and intra host dynamics.

Speaker. Fundação Oswaldo Cruz Minas Seminar Series, Belo Horizonte, Brazil. Title: Next-generation sequencing approaches to dissect intrahost variation and drug resistance in malaria — 3/13/2015

Speaker. ID Seminar Series. London School of Hygiene and Tropical Medicine, London, UK. Title: Leveraging genetic variation in malaria: inroads into tracking parasite strains within infections, delineating drug resistance, and understanding Burkitt lymphoma — 6/12/2014

Speaker. Cold Spring Harbor Laboratory Asia. Bioinformatics of Human and Animal Genomics. China. Title: Lessons from a parasite: more accurate correction of sequence GC-bias to improve read-depth-based detection of copy number variation — 4/9/2012

Speaker. Topics in Transfusion Medicine. Eldoret Hematology Symposium, AMPATH and Moi Medical School, Eldoret, Kenya — 7/24/2011

Speaker. Research Seminar Series. Kenya Medical Research Institute, Kisumu, Kenya. Title: Copy number variation in malaria — 7/29/2010

Talks National

Speaker. Setting the Medium to Long-Term Agenda for IR Molecular Surveillance for Malaria. Invited Workshop (Virtual). Bill and Melinda Gates Foundation. Title: Highly Multiplexed Molecular Inversion Probe Sequencing for Targeted Molecular Surveillance — 3/23/2022

Speaker. Pathology Grand Rounds. Department of Pathology. Johns Hopkins University. Title: Integrative Genomics of Endemic Burkitt Lymphoma and Epstein Barr Virus — 3/14/2022

Speaker. Department of Immunology and Infectious Disease Seminar. Harvard T.H. Chan School of Public Health — 2/24/2021

Speaker. Maliyale Interest Group. School of Public Health, Yale University, New Haven Connecticut, Title: High-throughput genetic epidemiology of malaria — 5/29/2019

Speaker. Genomic investigations of Epstein Barr virus in endemic Burkitt lymphoma and other cancers, University of Florida. — 3/12/2019

Speaker. High-throughput targeted sequencing in malaria. March Malaria Madness. University of Florida — 3/8/2019

Speaker. Seminar. Rhode Island Hospital. Providence, RI. Title: Epstein Barr Virus in malaria-driven endemic Burkitt lymphoma and other cancers — 5/3/2018

Speaker. Seminar. Department of Pathology and Laboratory Medicine Seminar. Brown University. Providence, RI. Title: High-throughput targeted sequencing for malaria drug resistance and population genetics — 3/28/2018

Speaker. Joint Malaria Group Meeting. Harvard School of Public Health and Broad Institute. Cambridge, MA. Title: Drug resistance and population structure of Plasmodium falciparum across the Democratic Republic of Congo using high-throughput molecular inversion probes — 2/8/2018

Speaker. Department of Biology Seminar Series. Worcester Polytechnic Institute. Worcester, MA. Title: leveraging genetic variation to understand and control malaria — 12/5/2017

Speaker. Infectious Disease and Global Health Seminar. Ryan White Center for Pediatrics. Indiana University School of Medicine. Indianapolis, IN. Title: Leveraging genetic variation to understand malaria — 10/30/2017

Speaker. Cancer Center Grand rounds. Indiana University School of Medicine. Indianapolis, IN. Title: Endemic Burkitt lymphoma immunology and genomics — 10/27/2017

Speaker. Pathology Grand Rounds. Case Western Reserve University School of Medicine. Cleveland, OH. Title: Endemic Burkitt lymphoma -- genomic investigations at the infectious disease and cancer nexus — 3/22/2017

Speaker. Swarthmore College Integrative Biology Seminars, Philadelphia, PA. Title: Leveraging genetic variation to understand infection disease and cancer--within the nexus of malaria, EBV and Burkitt lymphoma — 9/23/2016

Speaker. American Society for Apheresis Annual Meeting 2015. San Antonio,TX. Title: Collection and use of convalescent plasma and the rebuilding of healthcare systems in Liberia — 4/15/2015

Speaker. Genetics and Genomics Series. University of North Carolina, Chapel Hill, NC. Title: Driving deep sequencing to answer questions in parasite biology — 12/16/2015

Speaker. Cancer Institute's Genetics and Genomics Seminar Series. Duke University. Durham, NC. Title: International Epidemiology and Integrative Genomics: continuing Lessons from East Africa and endemic Burkitt Lymphoma — 12/15/2015

Speaker. Symposium on the Advancement of Field-Robots for Ebola Response (SAFER) Worcester Polytechnic Institute. Worcester, MA. Title: Perspective on the Ebola Outbreak — 11/7/2014

Speaker. Center for International Health Research Seminar Series. Brown University. Providence, RI. Title: Copy number variation in malaria — 1/30/2012

Speaker. Walter Reed Army Institute of Research and Uniformed Services University of the Health Sciences. Title: Copy number variation in malaria: from drug resistance to disease susceptibility--assessing host and parasite genomes — 4/13/2011

Speaker. Malaria Group Meeting, Harvard and Broad Institute, Malaria Group Meeting, Harvard and Broad Institute, Boston, MA. Title: Detection of Copy number variation in Plasmodium falciparum — 2/12/2011

Talks Regional

Speaker. Hematological Malignancies Translational Research Disease Group (TRDG. Brown University, Providence, RI Title: Genomics of endemic Burkitt lymphoma and EBV. — 2/11/2021

Speaker. Pediatric Research Colloquium. Lifespan, Providence RI. Title: High-throughput genetic epidemiology of malaria and infectious disease — 12/6/2019

Speaker. Global Health Initiative Lecture Series. Brown, Providence RI. Title: — 12/4/2019

Speaker. Center for International Health Research, Lifespan and Brown, Providence RI. Title: Endemic Burkitt lymphoma in Africa: understanding the role of Epstein-Barr Virus and falciparum malaria using integrative approaches. — 5/28/2019

Speaker. Center for Computational Molecular Biology, Brown University. Title: Leveraging genetic variation to understand malaria and associated Burkitt lymphoma — 5/1/2019

Speaker. Advisory Council on Biology and Medicine, Alpert Medical School. Providence RI. Title: Global Health: fighting infectious disease and cancer in Africa — 3/28/2019

Speaker. Research Seminar. Department of Medicine, UMass Medical School — 10/18/2017

Speaker. Tap Talk Series. Program in Systems Biology. UMass Medical School, Worcester MA. Title: Malaria to microbiomes: dissecting the genetics of malaria and other infectious diseases — 12/18/2015

Speaker. Worcester Drug Resistance Interest Group. UMass Medical School, Worcester MA. Title: Next gen seq--methods and applications for dissecting drug — 5/22/2015

resistance in models and in the field

Speaker. Hematology and Oncology Grand Rounds. UMass Medical School, Worcester MA. Title: Endemic Burkitt lymphoma: a multidisciplinary approach towards understanding pathogenesis and outcomes — 12/18/2014

Speaker. UMass Center for Clinical and Translational Science Seminar Series. UMass Medical School, Worcester MA Title: molecular studies of malaria: from drug resistance to Burkitt lymphoma — 3/15/2014

Speaker. Clinical Pathology Conference, UMass Medical School. Worcester MA Title:High-throughput sequencing methods in malaria and infectious disease — 3/27/2014

Speaker. Bioinformatics Core Seminar Series, UMASS Medical School. Title: Targeted resequencing applications in clinical malaria for strain diversity and beyond — 1/10/2014

Speaker. Immunohematology conference. Division of Transfusion Medicine. UMass Medical School. Worcester MA. Title: Natural selection and copy number variation in malaria — 5/16/2012

Speaker. Quantitative Methods Seminar Series, Department of Quantitative Health. UMass Medical School. Title: Computational approaches to analyzing copy number variation and standing segmental duplication — 4/16/2012

GRANTS

Current

NIH - NIAID R01 AI15667 Bailey/Juliano/Mazarati 2021-2025
Artemisinin Resistance in Africa: its emergence and evolution in Rwanda
The major goals of this project are to use large-scale genomics, experimental systems, and mathematical modeling to map and study the emergence and spread of Pf K13 561H resistance in an effort to improve understanding of the biology and evolution, and help predict its spread and allow development of interventions.
Role: Contact Principal Investigator
Award: $2,816,019

NIH - NIAID R01 AI137410 Bailey/Emch 2018-2023
Impacts of Environment, Host Genetics and Antigen Diversity on Malaria Vaccine Efficacy.
This multi-site study in Africa is the first major attempt at understanding the impact of spatial ecology of malaria vaccine efficacy and the first integration of human and parasite genetics into an ecological vaccine trial analysis.
Role: Contact Principal Investigator
Award: $3,126,881

NIH - NIAID R01 AI139520 Bailey 2018-2023
Tracking the flow of malaria parasites and drug resistance within the DRC and across its borders
High-throughput genomic approach to define the genetics of parasite flow and drug resistance across the entire Democratic Republic of Congo and neighboring countries in order to model the spread of drug resistance to inform public health control interventions.
Role: Principal Investigator
Award: $3,356,144

NIH - NIAID R01 AI 139520 – 04S1 Bailey 2021-2023
Tracking the flow of malaria parasites and drug resistance within the DRC and across its borders

This diversity supplement provide Ruthly François, a MD/PhD student at UNC-CH, the opportunity to gain new skills in statistical data analysis and genetic and spatial epidemiology, and apply them to real-life datasets, with the potential to inform evidence-based interventions that curb the burden of malaria in the DRC.
Role: Principal Investigator
Award: $166,472 (subproject)

NIH - NIAID U19 AI089680 Moss 2017-2024
Malaria Transmission and the Impact of Control Efforts in Southern and Central Africa
Malaria genomics epidemiology as part of the malaria genomics core for Southern and Central Africa International Center Excellence in Malaria Research at Johns Hopkins University.
Role: Investigator
Award: $360,191 (subproject)

NIH - NCI R01 CA189806 Moormann 2014-2025
Impact of malaria on shaping immunity to EBV in the etiology of Burkitt lymphoma
This study focuses on Plasmodium falciparum malaria's impact on the development and maintenance of functional EBV-specific T cell immunity in Kenyan children who experience these co-infections early in life and are therefore at increased risk for developing endemic Burkitt lymphoma, the most prevalent pediatric cancer in Equatorial Africa.
Role: Investigator
Award: $530,568 (current) $70,323 (previous)

NIH - NIAID R01 AI132547 Juliano 2018-2023

RDT-undetectable Malaria in the DR Congo: Epidemiology and Development of Alternatives
This grant will model the evolution and spread of HRP2/3 deletions. The Bailey lab provides support for genomic sequencing and bioinformatics within this collaboration.
Role: Investigator
Award: $707,629 (subproject)

NIH - NIAID R01 AI137395 Lin 2018-2023
Determinants of malaria by submicroscopic gametocytemia
A field study in Tanzania that will determine which asymptomatic persons contribute to transmission and pilot a field test to target these infectious carriers for treatment, as an alternative to mass drug administration.
Role: Investigator
Award: $406,770 (subproject)

NIH -NIAID R01 AI139179 Rosenthal 2018-2023
Mechanisms of varied sensitivity of P. falciparum field isolates to the antimalarial drug pipeline
This project collaborating with investigators at UCSF and Uganda involves testing both laboratory and field isolates against leading antimalarial candidates in current discovery pipelines to determine the role of known drug resistant mutations and standing variation in African parasite populations.
Role: Investigator
Award: $181,991 (subproject)

NIH - NCI 2 R01 CA234348 Luftig 2019-2024

Dissecting the roles of EBV and *P.falciparum* malaria in endemic Burkitt lymphoma pathogenesis

This grant aims to understand how *Plasmodium falciparum* and EBV interact to promote and maintain Burkitt lymphoma. The Bailey lab will support bioinformatic analysis and the sequencing of B-cell receptors and EBV genome variation using targeted sequencing.
Role: Investigator
Award: $204,750 (subproject)

Bill & Melinda Gates Foundation Ishengoma 2020-2023
Molecular surveillance of malaria in Tanzania

The major goals of this project are to establish and implement a temporal and spatial surveillance system to monitor parasite populations in response to current and future interventions, in addition to tracking hrp2/hrp3 gene deletion and antimalarial resistance markers.
Role: Investigator
Award: $483,122 (subproject)

NIH - NIAID R01 AI137037 Greenhouse 2020-2025
Drivers of strain-specific and strain-transcendent antimalarial immunity in childhood
To comprehensively detect the most important loci where strain specific immunity engenders strong protection in order to identify optimal candidates for next generation of malaria vaccines.
Role: Investigator
Award: $591,894 (subproject)

NIH - NCI U54 CA254518 Loehrer 2020-2025
The East Africa Consortium for HPV and Cervical Cancer in Women Living with HIV/AIDS
This grant supports research on HIV-associated cancers in low-and-middle-income countries (LMICs) through the formation of collaborative partnerships between investigators in the U.S. and LMICs that would foster the development of junior investigators from both the U.S. and LMICs.
Role: Investigator
Award: $250,810 (subproject)

2021-2025
NIH - NIAID 2 R01 AI075045 Rosenthal
Resistance of Malaria Parasites to Artemisinin-Based Combination Therapies in Uganda
To support high-throughput sequencing assays and analysis to characterize and define genetic variation in P. Falciparum parasites in association with artemisinin combination therapy resistance.
Role: Investigator
Award: $218,815 (subproject)

NIH - NIAID R01 AI155730 Juliano 2021-2025
Importation and transmission of malaria in Zanzibar: a case study for elimination
The main goal of this project is to conduct a combined genomics and epidemiologic assessment of the factors preventing malaria elimination in Zanzibar, including importation and local transmission.
Role: Investigator
Award: $321,763 (subproject)

NIH - NIAID R01 AI165524 Moormann 2022-2027
A systems immunology approach to evaluate malaria vaccine performance in endemic regions of Kenya. The focus of this proposal is to determine which combination of vaccine-elicited immune responses protect these children against malaria, in contrast to factors that result in malaria vaccine failures. This knowledge will help improve the next generation of malaria vaccines intended for children who bear the burden of this disease.

Role: Investigator
Award: $903,880 (subproject)

Completed

US Dept of Defense W911QY2090012 Shoham & Sullivan 2020-2021
Convalescent Plasma Randomized Clinical Trials for Early COVID-19 Treatment are Foundational for Subsequent Hyperimmune Globulin and Vaccines Expanded randomized double-blinded phase 2 multicenter trials of COVID-19 convalescent plasma towards prophylaxis from infection and from severe disease.
Role: Local Site (Lifespan RIH and Miriam) Investigator

NIH - NIAID R01 AI121558 Juliano 2015-2020
Variation in resistance and fitness to Artemisinin in African malaria
Dissecting intrahost parasite diversity in order to find resistant parasite subgroups that may be resistant within the context of a sensitive majority of parasites
Role: Investigator

Johns Hopkins University CSSC-01 Shoham 2020

Convalescent Plasma to Stem Coronavirus
A Randomized Controlled Double Blinded Phase 2 Study Comparing the Efficacy and Safety of Human Coronavirus Immune Plasma versus control among Adults Exposed to COVID-19
Role: Local Site (Lifespan RIH and Miriam) sub-Investigator coordinating blood bank
2020

Johns Hopkins University CSSC-04 Sullivan
Convalescent Plasma to Limit Coronavirus Associated Complication
A Randomized, Double-Blind, Controlled, Phase 2 Study Comparing the Efficacy and Safety of Human Coronavirus Immune Plasma versus Control Plasma Among Outpatients with Symptomatic COVID-19
Role: Local Site (Lifespan RIH and Miriam) sub-Investigator coordinating blood bank

ADA 1-16-ICTS-086 Mordes 2016-2018
Identification of T cell receptor genes responsible for susceptibility to type 1 diabetes
Testing the hypothesis that cognate variation in the TCR variable genes interacts with known HLA susceptibility alleles in imparting unaccounted for genetic risk in type 1 diabetes.
Role: Investigator

NIH - NIAID R01AI099473 Bailey 2012-2017
Human copy number polymorphisms in severe malaria
Large scale case control study using array comparative genomic hybridization and high-throughput genomics to determine the impact of copy number polymorphisms on severe malaria risk.
Role: Principal Investigator

NIH -NIGMS R01GM107604 Lawrence 2011-2017
The repeat genome in interphase chromosome structure and regulation
This proposal focuses on an innovative aspect with high significance for biology of all chromosomes: interspersed repeat RNAs as chromosomal structural RNAs.
Role: Co-Investigator

NIH – NIAID R21 AI111108 Juliano/Bailey 2014-2016
Dissecting chloroquine resistance in the Plasmodium vivax cross
Whole genome sequencing of Plasmodium vivax progeny from a cross between a chloroquine

resistant and sensitive strains performed using chimpanzee intermediate host with the goal of determining the loci underlying chloroquine resistance in P. vivax.
Role: Co-Principal Investigator

CDC U2GGH001659 Bailey 2015-2016
Sustained strengthening of public health laboratory, transfusion services, and health care worker infection control practices for ebola virus disease in Liberia
This cooperative agreement with CDC ensured continued vigilance against Ebola and other highly infectious diseases in Liberia by providing long-term support and systems strengthening focused on infection prevention control within hospitals and technologist training and testing methods within public health laboratories.
Role: Principal Investigator

CDC Foundation FDN/MOA# 287-LIB-SC Bailey 2015-2016
Further strengthening for EVD Testing in Liberia during secondary outbreak
Provide additional laboratory testing support during subsequent Ebola outbreak for rapid containment.
Role: Principal Investigator

Paul G Allen Foundation MIE Services/ACCEL McQuilkin/Bailey 2014-2015
Academic Consortium to Combat Ebola in Liberia
Provide acute Ebola relief and health care rebuilding in Liberia. Supporting 3 main aims: (1) staffing Ebola treatment units, (2) reopening hospitals and providing infection control and prevention training, and (3) supporting laboratory and transfusion services.
Role: Co-Principal Investigator

UMCCTS Pilot Project 5UL1TR000161-05 Bailey/Moormann 2013-2015
Endemic Burkitt lymphoma transcriptome and genome profiles associated with clinical presentation, treatment response, relapse and survival
Pilot analyses of endemic Burkitt lymphoma RNA-seq analysis along with viral genomics to determine molecular biomarkers associated with clinical phenotypes and survival, and to compare and contrast endemic BL with the sporadic form.
Role: Co-Principal Investigator (contact PI)

Massachusetts Life Science Center Young Investigator Bailey 2009-2011
Dissecting the role of human copy number variation in severe malaria
Pilot development of comprehensive array comparative genomic hybridization for human CNVs and preliminary case-control studies of severe malaria.
Role: Principal Investigator

NIH - NIAID KL2RR031981 Sullivan 2009-2012
Determining the role of human copy number variation in severe malaria
Elucidate the role of candidate copy number variants genes in severe malaria through the comparison of severe malaria anemia cases and controls.
Role: Trainee

TEACHING, ADVISING AND MENTORING ROLES

Teaching Activities

Lecture and Facilitator. East Africa Malaria Genomics Training Workshop 2022
Kampala, Uganda. (8 hours, September 13-17)

Lecturer. "High-throughput sequencing and targeted approaches" 3 day 2022
workshop Addis Ababa and facilitator (3 hours)

Lecturer: “Primer on high-throughput sequencing and targeted approaches.” Ghana Genomics Workshop, Noguchi Memorial Institute of Medical Research, University of Ghana, Acara (Mar 15, 1.5 hours contact)	2022
Guest Lecturer: Global Health: Inequality, Culture, and Human Well-being Around the World, Pre-College Program (July 22, 0.5 contact hours)	2021
Lecturer: “Immunogenetics” for Malaria Epidemiology and Control (PMO569), Uniformed Services University of the Health Sciences, Bethesda, MD (1.5 contact hours / year)	2018-2021
Instructor, Brown Resident and Fellow Course in Transfusion Medicine and Coagulation, Residency and Fellows, (Feb 2021 - 18 contact hours; March 2020 - 10 contact hours; April 2019- 4 contact hours)	2019-2021
Lecturer, “West Africa Ebola Outbreak: lessons we are still learning”. Global Health Systems Master of Applied Science (MMASc) Uganda Field School, Western University, London, Ontario (May - 2 contact hours)	2020-2021
Instructor: Global Health Systems Master of Applied Science (MMASc) Uganda Field School, Western University, London, Ontario (10 hours class contact, 50 contact hours overall, 2 weeks in Uganda)	2019
Small Group Lead, MDP 740 (3 contact hours), University of Massachusetts Medical School, Worcester, MA	2018
Lecturer: GSBS Core Course, Bioinformatics Boot camp Deep Sequencing (2 contact hours) ,University of Massachusetts Medical School, Worcester, MA	2017
GSBS Core Course, Foundations in Bioinformatics Science -- section Host Pathogen Population Genetics (co-lead Elinor Karlsson 10 contact hours per year),University of Massachusetts Medical School, Worcester, MA	2016, 2017
Lecturer: “Clinical Genome Sequencing”, Medical School Year 1: Principles of Human Genetics, University of Massachusetts Medical School, Worcester, MA (2 contact hour/year)	2013, 2014
Lecturer: “Genome Sequencing Potential and Pitfalls” for Designing Solutions to Research Problems (MD740) (1.5 contact hours), University of Massachusetts Medical School, Worcester, MA	2013, 2014
Small Group Leader: BBS612R: RAPS Block 2 (3 contact hrs), University of Massachusetts Medical School, Worcester, MA	2013, 2015
Small Group Leader: BBS612R: RAPS Block 2 (3 contact hrs), University of Massachusetts Medical School, Worcester, MA	2013
Lecturer: “Computational Approaches for analyzing copy number variation and standing segmental duplication.” (2 contact hr/yr) QHS Methods Core Lecture Series, University of Massachusetts Medical School, Worcester, MA	2013, 2014
Lecturer: “Identification of Single Gene Disease”, Medical School Year 1: Principles of Human Genetics, (1 contact hour/year) University of Massachusetts Medical School, Worcester, MA	2012
BBS 785: Quantitative Informatics in Translational Medicine. Co-director, teaching genome structure, population genetics and (6 contact hrs/year), University of Massachusetts Medical School, Worcester, MA	2011,-2012
BBS 705: Molecular Evolution: Lectures on Genome evolution, whole-genome duplication, segmental duplication, copy number variation (6 contact hours/year), advance graduate student course, University of Massachusetts Medical School, Worcester, MA	2010-2012, 2014, 2016
BBS 741: Advance Topics in Bioinformatics Lecturer: Introduction to Perl programming, Introduction to Linux, segmental duplications, copy number variation, transposons (8 contact hours/year), advance graduate student	2009-2013

course, University of Massachusetts Medical School, Worcester, MA

Current Undergraduates

Kaleb Zuckerman, Brown University, Providence (Computational Biology)	2022-
Enrique Puig, Brown University, Providence (Neuroscience)	2022-
Jillian Belluck, Brown University, Providence (Computational Biology)	2022-
Afnan Nuruzzaman, Brown University, Providence (Computational Biology) UTRA 2022 Spring	2021-
Cecile Schreidah, Brown University, Providence RI (Biology)	2021-

Current Graduate Student Trainees

Titus Manea, PhD student, Pathobiology, Brown University, Providence RI	2020-
Sawyer Smith, PhD student, Pathobiology, Brown University, Providence RI	2021-
Issac Kim, MD/PhD student, Computational biology, Brown University, Providence Biology	2021-
Eddie Agwati, PhD student, Maseno University, Maseno, Kenya (scientific mentor with Maseno mentor Cyrus Ayiego)	2022-
Neeva Wernsman Young, MS Biotechnology, Brown University, Providence RI	2021-
Weiting Lyo, MS Biotechnology student , Brown University, Providence RI	2022-
Hongyu Ma, MS Biotechnology student, Brown University, Providence RI	2022-

Current Postdoctoral Trainees

Cliff Oduor, PhD, Pathology and Laboratory Medicine, Brown University, Providence, RI	2018-
David Giesbrecht, PhD, Pathology and Laboratory Medicine, Brown University, Providence RI	2020-
Karamoko Niare, PhD, Pathology and Laboratory Medicine, Brown University, Providence RI	2020-
Abebe Fola, PhD, Pathology and Laboratory Medicine, Brown University	2021-

Former High-School Students

Kazen Gallman, North Kingstown High School, North Kingstown, RI	2019-2020
Ramviknesh Ramanathan, Massachusetts Academy of Math & Science, Worcester MA	2016-2018
Jagath Jai Kumar, Massachusetts Academy of Math & Science, Worcester MA	2014-2016
Xiayue Wang, Massachusetts Academy of Math & Science, Worcester MA	2013-2014

Former Undergraduate Students

Rebecca Kirby, Brown University, Providence RI (Biology, Global Health) BIO1950 (Fall 2021) BIO1960 (Spring 2022), Honors, Global Health Award	2019-2022
Ijeoma Meremikwu Brown University, Providence RI (Computational Biology)	2021-2022
Karyna Atha, Brown University, Providence, RI (BIO1960, BIO1950, Honors)	2019-2021
Savannah Lewis, Brown University, Providence, RI (Biology, BIO1950,	2020-2021

BIO1960, Honors)

Daniella Longhi, Brown University, Providence, RI (Biology BIO1950, BIO1960, Honors)	2019-2021
Abbie Hui, Brown University, Providence, RI (Biology BIO1950, BIO1960, Honors)	2019-2021
Priya Chohan, Biology Brown University, Providence, RI (BIO1960, BIO1950)	2019-2020
Aiden Meyer, Brown University, Providence, RI (Summer SPRINT)	2020
Jordan Wise, Xavier University of Louisiana, New Orleans (Leadership Alliance Summer Intern Program Brown University)	2019
Amanda Sargent, Major Qualifying Project, Worcester Polytechnic Institute, Worcester MA	2011-2012
Laura Miggins, Major Qualifying Project, Worcester Polytechnic Institute, Worcester, MA	2010-2011

Former Graduate Students

Abbie Hui, MS Pathobiology, Brown University, Providence RI	2021-2022
Eddie Agwati, MS student, Maseno University, Maseno, Kenya (scientific mentor with Maseno mentor Cyrus Ayiego)	2019-2021
Jonathan Kpaka, MS Cell and Molecular Biology, WACCBIP, University of Ghana, Accra, Ghana (scientific mentor with UG faculty Anita Ghansah)	2018-2021
Joonhwa Jung, MS student in Biotechnology Brown University, Providence, RI	2020-2021
Mercedeh Javanbakht Movassagh, PhD, UMMS Bioinformatics and Computational Biology, UMass Medical School, April 2019	2015-2019
Jennifer Moon, PhD student, GSBS, UMMS (co-mentor with Jeanne Lawrence)	2015-2018
Benedicta Mensah, PhD, Department of Biology, University of Ghana, Legion Campus, Accra Ghana, August (co-mentor research with Anita Ghansah)	2015-2019
Cliff Oduor, PhD student, Department of Biomedical Science and Technology, Maseno University, Kenya, August 2018 (scientific mentor withMaseno faculty Kiprotich Chelimo)	2014-2018
Peter Owuor, MS, Department of Biomedical Science and Technology, Maseno University, Kenya, August 2018	2015-2018
Nicholas Hathaway, PhD, Medical Scientist Training Program , \ Bioinformatics and Computational Biology, UMass Medical School, April 2018	2013-2018
Yasin Kaymaz PhD, UMMS Bioinformatics and Computational Biology (co-mentor with Ann Moormann), UMass Medical School, July 2017	2012-2017
Derrick DeConti PhD, Interdisciplinary Graduate Program, UMass Medical School, May 2015	2010-2015
Guang Xu MS, Interdisciplinary Graduate Program, (co-mentor with Robert Brown), UMass Medical School,, August 2017	2011-2017
Zachary Olgary, MS, Maseno University, Kenya, July 2014	2011-2014

Former Postdoctoral Trainees

Oliver Watson, PhD, Pathology and Laboratory Medicine, Brown University, Providence RI	2019-2020

Srinivas Niranj Chandrasekaran, Ph.D., Program in Bioinformatics and Integrative Biology, UMMS, Worcester MA 2016-2018

Özkan Aydemir, PhD, Program in Bioinformatics and Integrative Biology, UMMS, Worcester MA 2013-2017

Former Faculty

Özkan Aydemir, PhD, Assistant Professor Research, Pathology and Laboratory, Brown University, Providence, RI 2018-2021

Rachel Gerstein PhD, Professor, UMMS, UMass Vitality Grant Mentee 2015-2016

Richard Lambrecht PhD, Instructor, Program in Bioinformatics and Integrative Biology, UMMS, Worcester MA 2009-2012

Thesis Committees (*chair)

Peyton De La Cruz, Pathobiology, Brown, RI (Advisor: Christian Nixon) 2020

Jenna Zuromski, Pathobiology, Brown, RI (Advisor Jonathan Kurtis) 2019-

Karen Ferreira, PhD Candidate, Biomedical Engineering University of Massachusetts Dartmouth, North Dartmouth, MA (Advisor: Frank Scarano) 2019-2020

Brian Grussner, PhD candidate, Worcester Polytechnic Institute, Worcester, MA 2017-2019

John Haran*, Microbiology, UMMS (Advisor Beth McCormick) 2015-2018

Michael Purcaro*, BCB PhD, UMMS, (Advisor: Zhiping Weng) 2014-2018

Jill Moore*, BCB PhD, UMMS (Advisor: Zhiping Weng) 2014-2017

Jaymin Patel, Genetics, PhD, UNC, (Advisor Steven Meshnick) 2014-2016

Patricia McQuilken*, MS, (Advisors: Ann Moormann/Rob Goldberg) 2013-2016

Christian Parobek, Genetics, UNC, (Advisor: Jon Juliano) 2013-2016

Jiali Zhuang*, Bioinformatics, UMMS, (Advisor: Zhiping Weng) 2013-2016

Jessica Crisci, Bioinformatics, UMMS, (Advisor: Jeff Jensen) 2013

Sarah Sheppard, MSTP, UMMS, Advisor: Nathan Lawson 2013

Brian Lajoie, Interdisciplinary Graduate Program, (Advisor: Job Dekker) 2012-2016

Wei Wang, Bioinformatics, UMMS, (Advisor: Phil Zamore and Zhiping Wang) 2012-2015

Heather Kolpa, Cell Biology, UMMS, (Advisor: Jeanne Lawrence) 2012-2016

Sourav Roy Choudhury, IGP, UMMS , (Advisor: Miguel Esteves) 2011-2015

Alfred Simkin, BCB, UMMS, (Advisor: Jeff Jensen) 2010-2014

Qualifying Examiner (*chair)

Jenna Zuromski (Brown Pathobiology 8/20), Heather Kolpa (UMMS Cell Biology 4/11), Wei Wang (UMMS BCB 4/12), Brian Lajoie (UMMS BCB 4/12), Jiali Zhuang (UMMS IGP 4/12), Lindsay Romano (MSTP 5/14), Jill Moore* (GSBS 5/14), Lindsay Romo (MSTP 4/14) Michael Purcaro* (UMMS MSTP 6/14), Christian Parobek (UNC Program in Genetics, 8/14), Jaymin Patel (UNC 1/15), John Haran (UMMS 3/15), Xue Li (UMMS BCB 4/16), Gaurav Chauhan* (UMMS BCB 5/17), Betul Akgol Oksuz (UMMS 4/18 BCB), Serkan Sayin (UMMS BCB 5/18), Henry Pratt* (UMMS MSTP 6/18)

External Examiner

Hui Yee Greenaway, University of New South Wales (Advisor: Vanessa Venturi) 2012

Anwar Firoz, University of New South Wales (Advisor: Miles Davenport)	2013
Linda Boettger, Harvard University (Advisor: Steve McCarroll)	2014
Christian Parobek, University of North Carolina (Advisor: Jon Juliano)	2015
Jaymin Patel, University of North Carolina (Advisor:Steven Meshnick)	2016
Wesley Wong, Harvard University (Advisor: Dyann Wirth)	2017
Bernice Anane Mawului (Advisor: Yaw Afrane)	2022

HOSPITAL TEACHING

Residency and Fellow Teaching

Pathology Resident Boot Camp (31 contact hours -2 weeks daily) March 9-20, 2020, Providence, RI	2022
Pathology Resident Boot Camp (15 contact hours -2 weeks daily) March 9-20, 2020, Providence, RI	2021
Pathology Resident and Hematology Fellow Boot Camp (15 contact hours -2 weeks daily) March 9-20, 2020, Providence, RI	2020
"Transfusion Reactions" and "Overview of Pretransfusion Testing", Pathology Resident and Hematology Oncology Fellows (4 contact hours)	2019
Blood Donor criteria and testing and pretransfusion testing (4 contact hours/year), Pathology resident lectures. University of Massachusetts Medical School, Worcester, MA	2010-2016
Lecturer: Hematology/Oncology Fellow Review Lecture, Transfusion, University of Massachusetts Medical School, Worcester, MA	2014
Blood Donor criteria and testing and pretransfusion testing (4 contact hours/year), Pathology resident lectures. University of Massachusetts Medical School, Worcester, MA	2010-2016
Lecturer: Hematology/Oncology Fellow Review Lecture, Transfusion, University of Massachusetts Medical School, Worcester, MA	2014
Transfusion Medicine Clinical Supervision and Teaching: Supervising and didactic teaching clinical pathology residents, anesthesiology residents, and hematology fellows daily during my 2 months a year attending in Transfusion Medicine.	2009-2018

Former Medical Students

Omar Hadzipasic, MD, Capstone Project, UMass Medical School	2015-2017